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14. ABSTRACT Purpose: Participate as an active and productive member of the Prostate Cancer Clinical Trial Consortium (PCCTC)							
throughout the funding period.							
Scope: This report	t summarizes total	site activities for the	University of Wash	ington (UWasl	h) for the funding period		
30Sep2017-29Sep	2022.						
Major Progress: U	JWash was the lea	d/co-lead site on 19	trials in which we pa	articipated dur	ing this funding period.		
Results: UWash a	Iccrued 5 patient	s to PCCTC trials, p	roposed 11 LOIs, ai	nd accrued 52	patients (1 .5%) from a DAP.		
Significance: The	PCCIC provides a	a mechanism for pai	rticipation in early cl	Inical develop	ment of novel agents and rapid		
bionsy of metastat	ic tissue or complic	ated pharmacokinet	tics/pharmacodynan	nics and colle	ction of correlative biomarkers. The		
PCCTC is well pos	itioned to conduct	such trials that migh	it not be possible ou	itside of sites t	hat specialize in prostate cancer		
translational resea	rch. Shortening dru	g development time	with better trial des	sign, patient se	election, and validation of		
biomarkers will brii	ng new agents to p	rostate cancer patie	nts faster, optimize	treatment for t	he individual patient, and avoid		
treating others with	n ineffective therapi	es.					
15. SUBJECT TERMS			• ·				
Prostate cancer, ca	astration resistant,	phase I/II, immunotł	nerapy, novel agent,	, androgen rec	eptor, biopsy, circulating tumor		
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1. INTRODUCTION:

The University of Washington (UWash) has been a member of the Department of Defense Prostate Cancer Clinical Trials Consortium (PCCTC) since 2006. The purpose of the PCCTC is to provide a mechanism for collaboration among institutions with specialized expertise in prostate cancer in order to develop new agents and combinations of drugs in phase 1 and 2 trials. The mission of the PCCTC is aligned with that of the CDMRP: to eliminate deaths from prostate cancer and to enhance the well-being of men experiencing the impact of prostate cancer.

2. KEYWORDS:

Prostate cancer, castration resistant, phase I/II, immunotherapy, novel agent, androgen receptor, biopsy, circulating tumor cells, germline genetics

3. ACCOMPLISHMENTS:

a. What were the major goals of the project?

- i. Accrue at least 25 patients per year to PCCTC trials
- ii. Accrue at least 5% patients from disproportionately affected populations per year
- iii. Propose a minimum of two trials per year or eight trials over 4 years, which may include biomarker studies
- iv. Participate in a minimum of eight trials initiated by other sites over 4 years
- v. Ensure timely submission of quality data
- vi. Participate in ≥1 PCCTC committee
- vii. Attend all face-to-face meetings of the PCCTC
- viii. Participate in scheduled consortium conference calls
- ix. Participate in review meetings/evaluation by the External Advisory Board (EAB)
- x. Compliance with the operations manual of the Consortium regarding tasks such as (but not limited to): publication of major findings, intellectual and material property issues, quality assurance and control procedures, data submission and management plans

b. What was accomplished under these goals?

- i. Site accrued 359 patients to PCCTC trials, 93 patients to therapeutic and 266 patients to non-therapeutic trials. See Appendix 1 for details.
- ii. 52 of 359 patients (14.5%) accrued during this reporting period were members of disproportionately affected populations, including 18 (5%) Vietnam era veterans.
- iii. Site submitted the following LOIs (11) in this award period: c18-211, c19-244 (jointly submitted with OHSU), c19-248, c20-258, c20-259, c21-271, c21-274, c21-275, c21-295 (jointly submitted with Columbia), c22-297 (jointly submitted with Columbia), and c22-303.
- iv. Site participated in 26 PCCTC trials: 7 trials initiated by other PCCTC sites, 8 initiated by UWash with another site, and 11 initiated by UWash. In addition, 2 trials initiated by UWash with another site were in start-up at the end of the award period.
- v. Site met requirements of timely submission of quality data.
- vi. Dr. Cheng [PI] is the Chairperson and Dr. Yu [co-PI] is a member of the Germline Genetics Working Group. Drs. Cheng and Yu are also members of the Recognizing/Tackling Disparities Working Group.

- vii. PCCTC meetings at GU ASCO, ASCO, and PCF were attended by Drs. Cheng, Yu and Schweizer. (Former PI, Dr. Higano, also attended meetings until her retirement in June 2020.)
- viii. Coordinator participates in site conference calls. PI and/or co-I and subinvestigators participate in all monthly PI conference calls.
- ix. All EAB meetings were attended by PI [Cheng &/or Higano]. Co-PIs [Yu &/or Schweizer] also attended the EAB meeting beginning year 2 of award period.
- x. Procedures are in place and the UWash site is in compliance with the operations manual of the PCCTC.

c. What opportunities for training and professional development has the project provided?

Junior faculty members have had the opportunity to meet senior leaders of the PCCTC and to benefit academically from these contacts. The PI, Dr. Cheng, was nominated to chair the PCCTC Germline Genetics Working Group. She led the development, and is the senior or co-senior author, of three PCCTC-led papers on this topic, which have also featured junior investigators and thus opportunities for other faculty to become more involved in prostate cancer genetics. Dr. Cheng's participation in the PCCTC helped accelerate her reputation as a recognized international expert in germline genetics in prostate cancer. Dr. Cheng is also partnering with Dr. Channing Paller at Johns Hopkins, together with PCCTC, to lead the PROMISE prostate cancer genetics registry.

Dr. Schweizer is leading "A Phase II Trial of Durvalumab and Olaparib for treatment of biochemically-recurrent prostate cancer in men predicted to have a high neoantigen load" (LOI in process). The study was presented by Dr. Alexandra Sokolova (UWash former mentee, now faculty at OHSU) on 8/20/2020 at Monthly PI Call). The trial will also be conducted by Dr. Jacob Berman (DFCI). In addition, Drs. Schweizer and Sokolova have discussed with Dr. Karen Autio of MSKCC and PI of PCCTC trial c17-192 about opportunities for collaborating on biomarker studies from respective studies.

UWash has recruited several new faculty members whose training and careers will benefit from participation in the PCCTC: Dr. Emily Weg is a radiation oncologist who was recruited to UWash from MSKCC. She is interested in germline genetics and somatic biomarkers as related to radiation treatment selection, response and resistance. She has become involved with the Germline Genetics Working Group and she will be site PI for the c20-252 DASL-HICAP study.

Dr. Jessica Hawley is a medical oncologist recently recruited to UWash (started 9/2021) from Columbia, where she was mentored by Drs. Charles Drake and Mark Stein. She has expertise in prostate cancer clinical research and is particularly interested in the immunomodulatory effects of androgen signaling and inhibition. Drs. Yu, Schweizer and Cheng are helping her find and develop research interests and career opportunities.

Moreover, recent UWash fellows have gone on to accept prestigious academic faculty positions at other institutions, including PCCTC site OHSU (Dr. Sokolova), University of Colorado (Dr. Laura Graham), University of Pittsburg (Dr. Risa Wong), and Stanford (Dr. Ali Khaki). Thus, PCCTC participation has fostered both

collaboration and academic growth for trainees and junior faculty at our institution, the larger PCCTC and prostate cancer research community.

d. How were the results disseminated to communities of interest?

We believe that informed patients make the best decisions, are more satisfied, and have the best outcomes. To that end, we have a long history of educating patients about prostate cancer, the role of clinical research, and new treatments available, not only at our institution, but around the country. We have typically two annual meetings directed at men with prostate cancer:

The Institute for Prostate Cancer Research (IPCR) at UWash was founded to develop interdisciplinary institutional programs for prostate cancer research. In addition to fund-raising, the meeting reports on the status of research endeavors in prostate cancer to the lay public.

Dr. Yu is the Director of the Clinical Core of the PC SPORE grant and continues the SPORE Advocates Committee. This committee is engaged in numerous outreach activities in the Pacific Northwest and includes consumer advocates from Vancouver, BC, Seattle, WA and Portland, OR. Members of this committee participate in the SPORE lecture series as well as the SPORE external advisory board meetings where they hear results from SPORE related clinical trials and basic research.

Drs. Cheng, Schweizer and Yu, as well as their colleagues Drs. Montgomery, Nyame, Gore, Lin, Wright, and others are also actively engaged in educational and CME activities, particularly around their research topics of interest and clinical trials. Faculty at UWash are regularly invited to speak at monthly prostate cancer support groups in Washington (Seattle, Tacoma, Olympia, Shelton, Centralia), Oregon (Portland), and British Columbia (Vancouver).

e. What do you plan to do during the next reporting period to accomplish the goals?

Nothing to Report.

4. IMPACT:

a. What was the impact on the development of the principal discipline(s) of the project?

Investigators at UWash and other PCCTC institutions continue to focus on the evolving role of genetics and genomics in prostate cancer. Our group has driven changes in NCCN guidelines since 2019 and published extensively with the PCCTC Germline Genetic Working Group and through efforts such as the PROMISE registry. In addition, our efforts also include developing better diagnostic strategies for precision oncology, including recent publication led by Dr. Schweizer on concordance between primary prostate tumor and metastases that will inform testing for PARPi candidacy.

To provide needed genetics expertise in the clinic, Dr. Cheng organized a unique prostate cancer genetics clinic at UWash, and leads both UWash and PCCTC efforts in this area. She chairs the PCCTC Prostate Cancer Genetics Working Group and is PI of the GENTIeMEN study that enables men with prostate cancer to enroll on the trial to receive free germline testing.

b. What was the impact on other disciplines?

- Provide guidance to primary care physicians and urologists on the importance of complete family history and education about germline genetic testing.
- Educate oncologists, urologists and radiation oncologists about germline genetic testing for understanding cancer risk versus tumor biomarker testing for treatment decisions.
- Developing more education in radiation oncology (with help of Dr. Weg).
- Address the critical role for genetic counseling of prostate cancer patients with pathogenic germline mutations.
- Provide a model of care to meet the need for genetics expertise in prostate cancer in the clinic.
- Develop infrastructure to help identify more rare germline variants with prostate cancer.
- c. What was the impact on technology transfer? Nothing to Report.
- d. What was the impact on society beyond science and technology?

NCCN guidelines for prostate cancer therapy were amended based on work that came out of PCCTC involvement in early development of enzalutamide, abiraterone, radium-223, rucaparib and Olaparib, and input from members of the PCCTC, including the PI, who are on the Prostate Panel of the NCCN. In addition, guidelines around germline genetic testing and tumor sequencing and liquid biopsies have also arisen from work from our group. We are also focused on therapeutic strategies to address treatment emergent disease, further developing immunotherapeutic approaches, and incorporating novel imaging and theranostics, each of which has potential to reduce the impact of suffering from prostate cancer.

5. CHANGES/PROBLEMS:

- a. Changes in approach and reasons for change Nothing to Report.
- b. Actual or anticipated problems or delays and actions or plans to resolve them Nothing to Report.
- c. Changes that had a significant impact on expenditures Nothing to Report.
- d. Significant changes in use or care of human subjects, vertebrate animals, biohazards, and/or select agents Nothing to Report.

6. **PRODUCTS:**

a. Publications, conference papers, abstracts, and presentations (UWash author)

Abstracts:

Armstrong AJ, Lin P, <u>Higano CS</u>, Iversen P, Sternberg CN, Tombal B, Phung D, Parli T, Krivoshik A, Beer TM. Prognostic Associates of Prostate-Specific Antigen (PSA) Decline With Survival, Radiographic Response and Progression in Chemotherapy-Naïve Men With Metastatic Castration-Resistant Prostate Cancer (mCRPC) Treated With Enzalutamide. Abstract #2105. Submitted for presentation, ESMO Congress 2017, Madrid, Spain, September 2017.

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Mateo J, <u>Cheng HH</u>, Beltran H, Dolling D, Xu W, Pritchard C, Mossop H, Rescigno P, Perez-Lopez R, Sailer V, Kolinsky MP, Balasopoulou A, Bertran C, Carreira S, Thorne H, <u>Montgomery RB</u>, Sandhu SK, Rubin MA, Nelson P, De Bone JS. Clinical outcome of patients with germline DNA repair mutations: Results from a retrospective international study. *J Clin Oncol* 36, 2018 (suppl 6S; abstr 218). Poster presentation, ASCO 2018 Genitourinary Cancers Symposium, San Francisco, CA, February 2018.

McKay RR, Xie W, Lis R, Ye H, Zhang Z, Trinh QD, Chang SL, Harshman LC, Ross A, Pienta KJ, Lin DW, Ellis WJ, <u>Montgomery RB</u>, Chang P, Wagner A, Bubley G, Kibel AS, Taplin ME. Results of a phase II trial of neoadjuvant abiraterone + prednisone + enzalutamide + leuprolide (APEL) versus enzalutamide + leuprolide (EL) for patients with high-risk localized prostate cancer (PC) undergoing radical prostatectomy (RP). J *Clin Oncol* 36, 2018 (suppl 6S; abstr 79). Poster presentation, ASCO 2018 Genitourinary Cancers Symposium, San Francisco, CA, February 2018.

Lim DM, Gulati R, Aleshin-Guendel S, <u>Cheng HH</u>, Gawne AM, Wingate JT, Etzioni RD, <u>Yu EY</u>. Proportion of biochemically-recurrent prostate cancer patients with durable undetectable PSA after short-course androgen deprivation therapy. *J Clin Oncol* 36, 2018 (suppl 6S; abstr 207). Poster presentation, ASCO 2018 Genitourinary Cancers Symposium, San Francisco, CA, February 2018.

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<u>Cheng HH</u>, Bowen D, Klemfuss N, Sievers CM, Kang SH, Zhou A, Pritchard C, Nelson P, <u>Montgomery RB</u>. The GENTIeMEN study: Genetic testing for men with metastatic prostate cancer in Washington state and beyond. *J Clin Oncol* 36, 2018 (suppl; abstr TPS5098). Poster presentation, ASCO Annual Meeting, Chicago, IL, June 2018.

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Rathkopf DE, Autio KA, Antonarakis ES, <u>Cheng HH</u>, Arauz G, Slack A, Hullings M, Scher HI, Feng FY, Knudsen KE. c15-160: Enzalutamide (ENZA) plus CC-115 in men with metastatic castration-resistant prostate cancer (mCRPC): A phase 1b Prostate Cancer Clinical Trials Consortium study. *J Clin Oncol* 36, 2018 (suppl; abstr 5045). Poster presentation, ASCO Annual Meeting, Chicago, IL, June 2018.

De Bono JS, <u>Higano C</u>, Saad F, Miller K, Casey M, Czibere A, Healy C, Fizazi K. TALAPRO-1: An open-label, response rate phase II study of talazoparib (TALA) in men with DNA damage repair defects (DDR) and metastatic castrationresistant prostate cancer (mCRPC) who previously received taxane-based chemotherapy (CT) and progressed on > 1 novel hormonal therapy (NHT). *Ann of Oncol* (2018) 29 (suppl 8). Poster presentation. ESMO Congress 2018, Munich Germany. October 2018.

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b. Journal publications (UWash author)

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- c. Books or other non-periodical, one-time publications Nothing to report.
- d. **Other publications, conference papers, and presentations** Nothing to report.
- e. Website(s) or other Internet site(s) The following site is publicly accessible and includes presentations of the IPCR educational conferences for patients described above in section 3.d. Institute for Prostate Cancer Research <u>https://www.fredhutch.org/en/research/institutes-networks-ircs/institute-for-prostatecancer-research.html</u>
- f. **Technologies or techniques** Nothing to Report.
- g. **Inventions, patent applications, and/or licenses** Nothing to Report.
- h. Other Products Nothing to Report

7. PARTICIPANTS & OTHER COLLABORATING ORGANIZATIONS a. What individuals have worked on the project?

Name:	Heather Cheng, MD, PhD
Person months worked:	5
Project Role:	Principal Investigator (01Jul2020-29Sep2022)
Contribution to project:	Responsible for site's overall performance, assure site's goals are met as outlined in the SOW, participate as a
	senior PCCTC member and mentor.

Name: Person months worked: Project Role: Contribution to project:	Celestia Higano, MD 11 Principal Investigator (30Sep2017-30Jun2020) Responsible for site's overall performance, assure site's goals are met as outlined in the SOW, participate as a senior PCCTC member and mentor.
Name: Person months worked: Project Role: Contribution to project:	Evan Yu, MD 5 Co-Principal Investigator Conduct and recruit to PCCTC clinical trials, participate in weekly research and monthly PCCTC protocol meetings, attend face-to-face PCCTC meetings.
Name: Person months worked: Project Role: Contribution to project:	Michael Schweizer, MD 2 Co-Principal Investigator Conduct and recruit to PCCTC clinical trials, participate in weekly research and monthly PCCTC protocol meetings, attend face-to-face PCCTC meetings.
Name: Person months worked: Project Role: Contribution to project:	Zoya Bauer 6 Assistant CRC (01Dec2019-30Jun2020) Participate in PCCTC conference calls. Oversee research team in management of protocol adherence and timeliness/quality of data collection. Support data and regulatory coordinators, ensuring data collection is accurate and timely, and that all regulatory procedures meet local IRB requirements.
Project Role: Contribution to project:	PCCTC CRC (01Feb2021-03Dec2021) Track trial accruals, LOI submissions, and provide updates to PCCTC. Serve as point person for PCCTC activities. Participate in PCCTC coordinator conference calls. Manage consortium budget and contract process, provide monthly reports, oversee start-up process for PCCTC clinical trials, and post award accounting of DOD contract. Assist PI and co-PIs with preparation and submission of required semi-annual and annual reports.
Name: Person months worked: Project Role: Contribution to project:	M Jackie Campbell 3 PCCTC CRC (30Sep2017-15Jun2018) Track trial accruals, LOI submissions, and provide updates to PCCTC. Ensure research team adherence to protocols, timeliness and quality of data collection. Serve as point person for PCCTC activities and participate in bi-weekly PCCTC conference calls.

Name: Person months worked: Project Role: Contribution to project:	Nathan Conrad 3 Data Coordinator Track and enter data, including enrollment demographics, for PCCTC studies. Set up research charts and work-flow plans, and ensure timely submission of quality data for all UWash PCCTC trials.
Name: Person months worked: Project Role: Contribution to project:	Kelly Crowder 4 Asst PCCTC CRC (30Sep2017-30Jun2019) Participate in bi-weekly PCCTC conference calls. Work with PCCTC CRC to ensure research team adherence to protocols. Support data and regulatory coordinators, ensuring data collection is accurate and timely, and that all regulatory procedures meet local IRB requirements.
Project Role: Contribution to project:	PCCTC CRC (04Dec2021-29Sep2022) Disseminate LOIs, review PCCTC protocols, and manage patient accruals on PCCTC trials. Ensure implementation of all consortium trials in accordance with timelines set by consortium, and that accrual goals are met, with special focus on disproportionately affected populations. Assist faculty in protocol logistics and CRF design for PCCTC trials.
Name: Person months worked: Project Role: Contribution to project:	Randall Davis 6 Budget Startup Specialist (01Dec2019-29Sep2022) Develop site budgets for PCCTC studies, and negotiate amendments based on protocol modifications as needed.
Name: Person months worked: Project Role: Contribution to project:	Tina Dinh 2 Budget Startup Specialist (01May2018-15Aug2019) Develop site budgets for PCCTC studies, and negotiate amendments based on protocol modifications as needed.
Name: Person months worked: Project Role: Contribution to project:	Sara Fernandez 1 Correlative Science Coordinator (01Jan2020-30Jun2020) Manage acquisition, delivery and storage of biological samples, and oversee collection, processing and mailing of samples per protocol specifications.
Name: Person months worked: Project Role: Contribution to project:	Anne Lee 2 Regulatory Coordinator (01Jan2018-30Jan2019) Manage IRB submissions and renewals for PCCTC studies.

Name: Person months worked: Project Role: Contribution to project:	Sarah Finkelstein 10 Budget/Contract Manager (30Sep2017-31Jan2021) Manage consortium budgets and contracts, provide monthly reports to PI and PCCTC CRC, oversee start-up process for PCCTC clinical trials, and post-award accounting of DOD contract. Assist PI and co-PI with preparation and submission of required semi-annual and annual reports
Project Role: Contribution to project:	PCCTC CRC (01Jul2020-31Jan2021) Track trial accruals, LOI submissions, and provide updates to PCCTC. Serve as point person for PCCTC activities. Participate in PCCTC coordinator conference calls.
Project Role: Contribution to project:	Operations Support (01Feb2021-29Sep2022) Support PCCTC CRC in tracking accruals and LOI submissions. Serve as resource to UWash team with respect to DOD award requirements. Assist PI, co-PI and PCCTC CRC with preparation and submission of semi- annual and annual reports.
Name: Project Role: Person months worked: Contribution to project:	Michelle Haug Interim PCCTC CRC (16Jun2018-30Jun2020) 4 Track trial accruals, LOI submissions, and provide updates to PCCTC. Ensure research team adherence to protocols, and timeliness and quality of data collection. Serve as point person for PCCTC activities and articipate in PCCTC coordinator conference calls.
Name: Person months worked: Project Role: Contribution to project:	Sarah Kang 3 Research Assistant (01Jan-30Jun2018) Assist with filing and managing of regulatory documentation, subject demographic data, and report preparation.
Name: Person months worked: Project Role: Contribution to project:	Martha Lee 3 Administrative Support (thru 15Mar2020) Provide administrative support for consortium related activities for the PI and research team.
Name: Person months worked: Project Role: Contribution to project:	Hannah Loesch 1 Research Coordinator (01Sep2021-29Sep2022) Serve as a resource for the conduct of protocol specified laboratory correlative projects and overall protocol coordination for PCCTC studies.

Name:Colin SieversPerson months worked:2Project Role:Research Coordinator (01Jan2021-31Jul2021)Contribution to project:Serve as a resource for the conduct of protocol specified
laboratory correlative projects and overall protocol
coordination for PCCTC studies.

- b. Has there been a change in the active other support of the PD/PI(s) or senior/key personnel since the last reporting period? Nothing to Report
- c. What other organizations were involved as partners? Nothing to Report
- 8. **SPECIAL REPORTING REQUIREMENTS** Not applicable.

9. APPENDICES:

Appendix 1 – PCCTC trials, status and accruals at UWash clinical research site during funding period

Appendix 2 – Copies of original publications

Appendix 3 – Curricula vitae for Cheng (PI), Yu (co-PI) and Schweizer (sub-I)

APPENDIX 1

PCCTC trials, status, and accruals at UWash clinical research site 30Sep2017-29Sep2022

Table A UWash PCCTC Trials, Open and in Start-Up9/30/2017-9/29/2022

PCCTC# (UW#)	Trial Title	UWash Accrual	Status	Lead Site
c13-131 (UW13024)	A Phase I Multicenter Study to Assess AZD8186 in Patients with Advanced CRPC	6	Closed 11/2018	UWash
c14-146 (UW15029)	Phase 2 Study of VT-464 in Patients with Castration-Resistant Prostate Cancer	0	Closed 2/2018	MSKCC
c15-148 (CC9279)	A Phase I/II Trial of Concurrent Chemohormonal Therapy Using Enzalutamide and Cabazitaxel in Patients with mCRPC	11	Closed 6/2019	UWash OHSU
c15-156 (CC9342)	A Randomized Phase II Study Comparing Bipolar Androgen Therapy vs Enzalutamide in Asymptomatic Men with mCRPC Transformer	3	Closed 9/2018	JHU
c15-157 (UW14052)	A Phase I Study of ES414 in Patients with Metastatic Castration-Resistant Prostate Cancer	1	Closed 11/2018	UCSF UWash
c15-160 (CC9767)	A Phase 1b Study of Enzalutamide plus CC- 115 in Men with CRPC	4	Closed 2/2020	MSKCC
c15-161 (CC9389)	A Phase I Study of a DNA Vaccine Encoding Androgen Receptor Ligand-Binding Domain (AR LBD) in Patients with Metastatic Prostate Cancer	2	Closed 12/2017	UWisc
c15-166 (UW18003)	A Phase 1 Safety and Tolerability Study of ZEN003694 in Combination with Enzalutamide in Patients with mCRPC	6	Closed 2/2019	UCSF
c16-169 (UW15030)	A Phase 1 Study of Escalating Doses of a Vaccine Based Immunotherapy Regimen (VBIR) for Prostate Cancer	5	Closed 02/2021	UWash Duke MSKCC
c16-174 (CC10054)	Phase III Trial of Docetaxel vs Docetaxel and Radium-223 for mCRPC (DORA)	1	Closed 7/2020	MSKCC UWash
c16-181 (UW16081)	Phase Ib/II Trial of Pembrolizumab (MK- 3475) Combination Therapies in… (mCRPC) (KEYNOTE-365)	13	Open	UWash
c17-187 (CC9297)	A Pilot Study of Mobilization and Treatment of Disseminated Tumor Cells in Men with Metastatic Prostate Cancer	0	Closed 6/2018	UWash
c17-188 (UW16010)	A Phase IB, Open-Label Study… of Atezolizumab in combination with Radium- 223 Dichloride in Patients with CRPC…	0	Closed 7/2018	КСС

(abbreviation mCRPC = metastatic castration resistant prostate cancer)

PCCTC# (UW#)	Trial Title	UWash Accrual	Status	Lead Site
c17-189 (UW16062)	A Phase 2 Efficacy and Safety Study of Niraparib in Men with mCRPC and DNA- Repair Anomalies	1	Closed 5/2020	UWash OHSU
c17-198 (UW17076)	A Multi-Center Trial of Major Adverse Cardiovascular Events in Patients with Prostate Cancer and Cardiovascular DiseasePRONOUNCE	0	Closed 3/2020	MSKCC UWash
c18-211 (UW17031)	A Phase 2 Study of Talazoparib in Men with DNA Repair Defects and mCRPC who Previously Received Taxane-Based Chemotherapy	0	Closed 3/2020	UWash
c19-231 (UW18051)	eFT508: A Phase 2… Study Examining the Effect of eFT508 in Patients with Advanced Castrate-resistant Prostate Cancer (CRPC)	3	Closed 3/2019	DFCI UWash
c19-248 (UW18002)	A Phase I Study of PF-06821497 in the Treatment of Adult Patients with Castration Resistant Prostate Cancer (CRPC)	13	Open	UWash
c20-259 (RG1004978)	A Phase 1, First-in-Human, Dose Escalation Study of JNJ-63898081 in Subjects with Advanced Stage Solid Tumors	10	Closed 1/2022	UWash
c21-274 (RG1005474)	Aphase 2 study of I-131-1095 Radiotherapy in combination with enzalutamide in mCRPC patients Who are 18F-DCFPyL prostate-specific membrane antigen (PSMA)-avid (ARROW)	11	Closed 6/2022	UWash
c21-275 (RG1007001)	Durvalumab (MEDI4736) and Olaparib (AZD2281) for treatment of biochemically recurrent prostate cancer in men predicted to have a high neoantigen load: a pilot study	2	Open	UWash
c21-295 (RG1007001)	A Phase 1/Phase 2 Trial of VTP-850 Prostate Cancer Immunotherapeutic in Men with Biochemical Recurrence after Definitive Local Therapy for Prostate Cancer	0	Start-up	UWash Columbia
c22-297 (RG1122235)	A Phase 1 Study of JNJ-78278343, a T-Cell- Redirecting Agent Targeting Human Kallikrein 2 (KLK2), for Advanced Prostate Cancer	0	Start-up	UWash Columbia
c22-303 (RG1122292)	A Phase 2 Trial of SRF617 in Combination With AB928 (Etrumadenant) and AB122 (Zimberelimab) in Patients With Metastatic Castration-Resistant Prostate Cancer	1	Open	UWash
	Total Therapeutic accruals:	93		

PCCTC# (UW#)	Trial Title	UWash Accrual	Status	Lead Site
c16-170 (CC9853)	Prostate Cancer Outcomes: An International Registry to Improve Outcomes in Men with Advanced Prostate Cancer (IRONMAN)	58	Open	Duke MSKCC DFCI
c19-235 (RG1006494)	PROMISE: A Prostate Cancer Registry of Outcomes and Germline Mutations for Improved Survival and Treatment Effectiveness		Open	UWash JHU
c20-258 (RG1006011)	The impact of DNA repair pathway alterations identified by circulating tumor DNA on sensitivity to Radium-223 in bone metastatic castration-resistant prostate cancer	15	Open	UWash
c21-271 (RG1006494)	Darolutamide Observational Study in non- metastatic castration-resistant prostate cancer patients	5	Open	UWash
	Total non-therapeutic accruals			

Appendix 2

Copies of original journal articles

abstracts

787PD

Prognostic associations of prostate-specific antigen (PSA) decline with survival, radiographic response and progression in chemotherapy-naïve men with metastatic castration-resistant prostate cancer (mCRPC) treated with enzalutamide

<u>A.J. Armstrong</u>¹, P. Lin², C.S. Higano³, P. Iversen⁴, C.N. Sternberg⁵, B. Tombal⁶, D. Phung⁷, T. Parli⁸, A. Krivoshik⁹, T.M. Beer¹⁰

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Background: In the PREVAIL clinical trial, enzalutamide provided significant improvements vs placebo in radiographic progression-free survival (rPFS) and overall survival (OS) in chemotherapy-naïve men with mCRPC. This post hoc analysis aimed to evaluate the prognostic association between the magnitude of PSA decline from baseline and clinical outcomes in PREVAIL.

Methods: Men from the enzalutamide and placebo arms of PREVAIL were grouped into categories of confirmed maximal PSA decline from baseline at month 3 of

abstracts

Table: 787PD

Outcome Maximal PSA Decline From Baseline at Month 3 in the Enzalutamide Arm (N = 872) No Decline/ Decline < 30% > 30% Decline > 50% Decline > 90% Decline (n = 94/872) (n = 701/872)(n = 639/872) (n = 307/872)Best objective soft-tissue response (CR or PR), % (95% Cl) 12.0 (4.5-24.3) 70.6 (65.1-75.6) 74.8 (69.2-79.9) 89.7 (82.8-95.0) Median (95% CI) time to PSA progression, mo 3.7 (3.7-4.6) 13.8 (11.3-14.0) 13.9 (13.8-16.6) 22.5 (16.8-NYR) Median (95% CI) rPFS, mo 7.9 (3.7-NYR) NYR (13.8-NYR) NYR (13.8-NYR) NYR (13.8-NYR) HR (95% CI) for rPFS 0.20 (0.13-0.31) 0.17 (0.11-0.27) 0.10 (0.05-0.19) 10 (ref) Median (95% CI) OS, mo 23.1 (17.8-28.0) 32.4 (31.5-NYR) NYR (31.5-NYR) NYR (NYR-NYR) HR (95% CI) for OS 1.0 (ref) 0.31 (0.22-0.42) 0.28 (0.20-0.39) 0.19 (0.12-0.28)

Abbreviations: CI, confidence interval; CR, complete response; HR, hazard ratio; mo, months; NYR, not yet reached; OS, overall survival; PR, partial response; PSA, prostate-specific antigen; ref, reference, rPFS, radiographic progression-free survival.

treatment: no decline/decline < 30% and \geq 30%, \geq 50% or \geq 90% decline. Confirmation required PSA decline on \geq 1 consecutive visit after month 3. Best overall soft-tissue response (per RECIST v1.1) was determined for patients with measurable disease at baseline (data cutoff: 16 Sep 2013). Time to PSA progression (data cutoff: 16 Sep 2013), rPFS (per PCWG2; data cutoff: 6 May 2012) and OS (data cutoff: 16 Sep 2013) were estimated using the Kaplan-Meier method.

Results: In PREVAIL, men were randomized to enzalutamide (n = 872) or placebo (n = 845). Most men in the placebo arm (66%, 558/845) had no PSA decline/decline < 30%, in contrast to 11% (94/872) in the enzalutamide arm. In the enzalutamide arm, 81% (701/872) of men had a PSA decline of $\geq 30\%$ from baseline at week 13, 73% (639/872) had a PSA decline of $\geq 50\%$ and 35% (307/872) had a PSA decline of $\geq 90\%$. Key outcomes for the enzalutamide arm are provided by PSA decline category in the Table. PSA flare (rise followed by a fall) after 3 months was rare with enzalutamide (< 1%).

Conclusions: PSA declines after 3 months of enzalutamide therapy are strongly associated with soft-tissue response and improvements in rPFS and OS. Providing updated prognostic information to chemotherapy-naïve men with mCRPC can be of clinical value given the heterogeneity of long-term outcomes.

Clinical trial identification: NCT01212991

Legal entity responsible for the study: This study was sponsored by Medivation, Inc. (which was was acquired by Pfizer, Inc. in September 2016) and Astellas Pharma, Inc., the co-developers of enzalutamide.

Funding: This study was sponsored by Medivation, Inc., (which was acquired by Pfizer, Inc. in September 2016) and Astellas Pharma, Inc., the co-developers of enzalutamide.

Disclosure: A.J. Armstrong: Consultant: Bayer, Sanofi, Novartis, Dendreon, Medivation, Janssen Biotech, Eisai Bureau: Dendreon, Sanofi, Medivation, Janssen Biotech Grant/Patent (inst) Dendron, Sanofi, Bayer, Pfizer, Novartis, BMS, Janssen Oncology, Medivation, Astellas, Gilead. P. Lin, T. Parli: Employment: Pfizer, Inc. C.S. Higano: Consulting/Travel: Dendreon, Bayer, Medivation, Ferring, J&J, AbbVie, Genentech, Pfizer, BHR, Orion, Sanofi, Amgen, Ockham, Teva, Astellas. P. Iversen: Consultant/Advisor, Meeting Participant/Lecturer, Scientific Study/Trial and Clinical Research Collaboration: Astellas Pharma, Medivation. C.N. Sternberg: Honoraria: Pfizer, Bristol-Myers Squibb, Novartis, Janssen, Bayer, Astellas Pharma, Sanofi, Eisai, Ipsen, GlaxoSmithKline, MSD. B. Tombal: Consulting: Astella, Bayer, Ferring, Janssen, Takeda, Steba Biotech, Sanofi Speakers Bureau: Amgen, Janssen Travel/Honoraria: Amgen, Astellas, Bayer, Ferring, Janssen, Sanofi. D. Phung: Employment: Astellas Pharma. A. Krivoshik: Employment and Travel/Expenses: Astellas Pharma Stock/ Ownership Interests: Abbott Laboratories, AbbVie. T.M. Beer: Consulting: Astellas, Bayer, Dendreon, Janssen Japan, Novartis, AstraZeneca, Churchill, Proacta Stock/ Ownership: Salarius.

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Hepatic effects assessed by review of safety data in enzalutamide castration-resistant prostate cancer (CRPC) trials. Presented Thursday, February 8, 2018

Authors:

Tomasz M. Beer, Simon Chowdhury, Fred Saad, Neal D. Shore, Celestia S. Higano, Peter Iversen, Karim Fizazi, Kurt Miller, Axel Heidenreich, Choung Soo Kim, De Phung, Jeffrey Kent Barrus, Natalia Nikolayeva, Andrew Krivoshik, Javier Waksman, Bertrand F. Tombal; Knight Cancer Institute, Oregon Health & Science University, Portland, OR; Guy's and St Thomas' Hospital NHS Foundation Trust, London, United Kingdom; Centre Hospitalier de l'Université de Montréal/CRCHUM, Montreal, QC, Canada; Carolina Urologic Research Center, Myrtle Beach, SC; University of Washington and Fred Hutchinson Cancer Research Center, Seattle, WA; University of Copenhagen, Rigshospitalet, Copenhagen, Denmark; Institut Gustave Roussy, University of Paris Sud, Paris, France; Charité Campus Benjamin Franklin, Berlin, Germany; Cologne University, Cologne, Germany; University of Ulsan College of Medicine/ Asan Medical Center, Seoul, Korea, Republic of (South); Astellas Pharma Inc., Leiden, Netherlands; Astellas Pharma Inc., Northbrook, IL; Pfizer Inc., San Francisco, CA; Cliniques Universitaires Saint-Luc, Brussels, Belgium

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Abstract Disclosures

Background:

Androgen receptor inhibitor enzalutamide (ENZA) improves survival in patients with metastatic CRPC. As the liver is the main route of ENZA elimination, this post hoc analysis evaluated the hepatic effects of ENZA versus comparators in controlled CRPC trials.

Methods:

Safety data from two large Phase 3, placebo (PBO)- (PREVAIL, NCT0121299; AFFIRM, NCT00974311) and two smaller Phase 2, bicalutamide (BIC)-controlled (STRIVE, NCT01664923; TERRAIN, NCT01288911) ENZA trials in men with CRPC were assessed for hepatic impairment-related adverse events (AEs) using the following standardized narrow MedDRA queries V19.1: hepatic failure, fibrosis and cirrhosis, and other liver damage-related conditions; hepatitis, non-infectious; and liver-related investigation, signs, and symptoms. Liver-related laboratory test results were also evaluated. Data were summarized as follows: patients receiving ENZA in Phase 3 trials (n = 1671); patients receiving PBO (n = 1243); patients receiving BIC (n = 387); and combined ENZA-treated patients (n = 2051).

Results:

Percentages of hepatic impairment-related AEs ranged between 2.9% and 4.5% with ENZA, and were 2.7% with PBO and 5.4% with BIC (Table). The most common hepatic impairment-related AEs were increased aspartate (AST) and alanine aminotransferase (ALT; Table). Within each trial, the incidences of grade \geq 3 AEs were similar, and dose reductions or discontinuations due to hepatic impairment-related AEs were low (Table). When adjusted for treatment exposure, AEs per 100 patient-years were lower with ENZA versus either PBO or BIC (Table).

Conclusions:

This combined analysis of CRPC trials demonstrates no hepatic safety signal with ENZA and thus routine liver tests are not required. Clinical trial information: NCT0121299; NCT00974311; NCT01664923; NCT01288911.

Potential hepatic impairment-related AE*	Phase 3 ENZA (n = 1671)	Phase 2 ENZA (n = 380)	Combined ENZA (n = 2051)	PBO (n = 1243)	BIC (n = 387)
Any AE	2.9	4.5	3.2	2.7	5.4
AST increased	0.9	0.8	0.9	1.0	1.8
ALT increased	0.7	1.3	0.8	0.6	1.3
Any grade ≥3	0.9	1.1	0.9	0.8	0.5
Leading to treatment discontinuation	0.2	0.3	0.2	0.2	0.3
Leading to dose reduction	< 0.1	0	< 0.1	0.2	0
AE rates per 100 patient-years	3.7	5.4	4.0	6.4	8.6

*Results all in %

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Clinical outcome of patients with germline DNA repair mutations: Results from a retrospective international study.

Presented Thursday, February 8, 2018

Authors:

Joaquin Mateo, Heather H. Cheng, Himisha Beltran, David Dolling, Wen Xu, Colin Pritchard, Helen Mossop, Pasquale Rescigno, Raquel Perez-Lopez, Verena Sailer, Michael Paul Kolinsky, Ada Balasopoulou, Claudia Bertan, Suzanne Carreira, Heather Thorne, Robert B. Montgomery, Shahneen Kaur Sandhu, Mark A. Rubin, Peter Nelson, Johann S. De Bono; Institute of Cancer Research and The Royal Marsden Hospital, London, United Kingdom; University of Washington, Seattle, WA; Weill Cornell Medical College, New York, NY; Institute of Cancer Research, London, United Kingdom; Princess Alexandra Hospital, Moorooka, Queensland, Australia; Institute of Cancer Research and The Royal Marsden NHS Trust Foundation, Sutton, United Kingdom; Institute of Cancer Research and The Royal Marsden NHS Foundation Trust, Sutton, United Kingdom; Weill Cornell Medicine, New York, NY; Peter MacCallum Cancer Centre, Melbourne, Australia; University of Washington Oncology, Seattle, WA; Peter MacCallum Cancer Research Center, Seattle, WA

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Abstract Disclosures

Background:

CRPC is enriched for germline mutations in DNA damage repair genes (gDDRm). BRCA2 mutations (g*BRCA2*m) associate with poor prognosis from localized PC, but prognostic and predictive value for standard therapy in CRPC is unclear. We reviewed clinical outcome of 390 patients previously tested for gDDRm.

Methods:

Patient records were reviewed for 372 patients from 3 institutions (Royal Marsden UK, Weill-Cornell NY, University of Washington, WA) with gDDRm status previously published (Pritchard et al, NEJM 2016) and 18 *gBRCA1/2*m carriers from KConFab consortium (Australia). Baseline characteristics and survival were annotated. Response (PSA50%/RECIST) and PFS (RECIST/PSA progression or start of a new therapy due to clinical progression) were collected for Abiraterone, Enzalutamide and Docetaxel. To account for potential differences between cohorts, a mixed effect model (Weibull distribution) with random intercept per cohort was pursued.

Results:

dDDRm status was available for n = 390 (60 gDDRm+, including 37 gBRCA2m, and 330 gDDRm-). Overall, 74% and 69% received Docetaxel and Abiraterone/Enzalutamide respectively; 47% gDDRm+ and 34% gDDRm- received PARPi and/or platinum. Median overall survival from CRPC was 3.0 vs 3.2 years in gDDRm+ vs gDDRm- (p = 0.73; gBRCA2m = 3.0 years, p = 0.72). Age and Gleason score at diagnosis were associated with survival from castration-resistance in multivariate analysis. Median PFS on Docetaxel for gDDRm+ (6.8 months; 6.3 for gBRCA2m) and gDDRm- (5.1 months) were not significantly different (p = 0.2). Similarly, RR to Docetaxel was similar for the two groups (61% vs 54% in gDDRm+ vs gDDRm-; 63% gBRCA2m). Median PFS and RR on first Abiraterone/Enzalutamide were similar across groups (PFS: 8.3 months gDDRm+, 8.3 months for gDDRm-; p = 0.9; RR 46% vs 56% respectively) The Interaction of PARPi/platinum therapy among gDDRm+ patients resulted in an aHR for OS from CRPC of 0.59 (95%CI 0.28-1.25; p = 0.17).

Conclusions:

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In this retrospective analysis, CRPC patients with gDDRm still benefited from standard therapies similarly to non-mutation carriers; interpretation of survival data should consider the high proportion treated with PARPi/platinum.

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Results of a phase II trial of neoadjuvant abiraterone + prednisone+ enzalutamide + leuprolide (APEL) versus enzalutamide + leuprolide (EL) for patients with high-risk localized prostate cancer (PC) undergoing radical prostatectomy (RP).

Presented Thursday, February 8, 2018

Authors:

Rana R. McKay, Wanling Xie, Rosina Lis, Huihui Ye, Zhenwei Zhang, Quoc-Dien Trinh, Steven Lee Chang, Lauren Christine Harshman, Ashley Ross, Kenneth J. Pienta, Daniel W. Lin, William J Ellis, Robert B. Montgomery, Peter Chang, Andrew Wagner, Glenn Bubley, Adam S. Kibel, Mary-Ellen Taplin; Dana-Farber Cancer Institute, Boston, MA; Beth Israel Deaconess Medical Center, Boston, MA; Brigham and Women's Hospital/ Harvard Medical School, Boston, MA; Brigham and Women's Hospital, Boston, MA; Stanford University School of Medicine, Stanford, CA; Johns Hopkins Medicine, Baltimore, MD; James Buchanan Brady Urological Institute, Johns Hopkins University School of Medicine, Baltimore, MD; University Print Washington, Seattle, WA; University of Washington Oncology, Seattle, WA; Brigham and Women's Hospital/ Dana-Farber Cancer Center, Boston, MA

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Abstract Disclosures

Background:

Patients with high-risk PC have an increased risk of recurrence and mortality despite therapy. Abiraterone, a CYP17 inhibitor, and enzalutamide, a next generation anti-androgen, have demonstrated improved overall survival in metastatic PC. In this multicenter randomized phase II trial, we evaluate the impact of second generation hormone therapy on RP pathologic outcomes.

Methods:

Eligible patients had biopsy Gleason score \geq 4+3=7, PSA >20 ng/mL or cT3 disease (by prostate MRI). Lymph node were require to be <20 mm. Patients were randomized 2:1 to APE:EL for 6 cycles (24 weeks) followed by RP. All RPs underwent central pathology review. The primary endpoint was the rate of pathologic complete response (pCR) or minimum residual disease (MRD, tumor \leq 5 mm). Secondary endpoints include PSA response, surgical staging at RP, positive margin rate, and safety.

Results:

75 patients were enrolled at four sites: DFCI/BWH (n=55), BIDMC (n=11), UW (n=5), JHU (n=4). Median age was 62 years. Most patients had NCCN high-risk disease [n=66, 88%; cT3 n=21 (28%), Gleason 8-10 n=59 (79%), PSA >20 ng/mL n=17 (23%)]. All patients completed 6 cycles followed by RP. Median PSA nadir was 0.03 and 0.02 ng/mL and time to nadir was 3.7 and 4.6 months in the APEL and EL arms, respectively. The combined pCR or MRD rate was 30% (n=15/50) in the APEL arm and 16% (n=4/25) in the EL arm. The response difference was 14% (80% CI -3%-30%, p=0.263). 15 patients (14 in APEL; 1 in EL) had grade 3 adverse events (AEs). The most common grade 3 AEs were hypertension (n=7) and ALT increase (n=5). No grade 4-5 AEs occurred.

Conclusions:

Neoadjuvant hormone therapy plus RP in men with high-risk PC resulted in favorable pathologic responses (<5 mm residual tumor) in 16-30% with a trend towards improved pathologic outcomes with APEL and acceptable safety profile. Follow-up is necessary to evaluate the impact of therapy on recurrence rates. Clinical trial information: NCT02268175

Pathologic outcomes at RP.

pT2 38% 36% 37%	
pT3 50% 56% 52%	t
+ Margins 18% 12% 16%	
+ Seminal Vesicles 18% 28% 21%	
+ Lymph Nodes 10% 12% 11%	
pCR 12% 8% 11%	
MRD 18% 8% 15%	

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Proportion of biochemically-recurrent prostate cancer patients with durable undetectable PSA after short-course androgen deprivation therapy.

Presented Thursday, February 8, 2018

Authors:

Daniel M. Lim, Roman Gulati, Serge Aleshin-Guendel, Heather H. Cheng, Agnes M. Gawne, Jonathan T. Wingate, Ruth Douglas Etzioni, Evan Y. Yu; University of Washington, Seattle, WA; Fred Hutchinson Cancer Research Center, Seattle, WA; U.S. Army, Tacoma, WA, US

Abstract Disclosures

Background:

Print

Optimal utilization of novel therapies for advanced prostate cancer is challenging without a validated surrogate efficacy endpoint. Ongoing trials are using durable undetectable prostate specific antigen (PSA) levels as a marker of efficacy. The proportion of patients and clinical relevance of those with a prolonged undetectable PSA after a short course of androgen deprivation therapy (ADT) is uncertain.

Methods:

The University of Washington Caisis database was queried for radical prostatectomy patients who received 6–12 months of ADT after biochemical recurrence (BCR), defined as PSA \geq 0.2 ng/mL and no radiographically detectable metastasis. Proportions of patients with undetectable PSA 12 and 24 months after ending ADT were compared to a hypothesized 5% rate using exact binomial tests. Associations with patient and tumor characteristics were examined using logistic regression, and associations with risk of subsequent metastasis and death from any cause were evaluated by log-rank tests.

Results:

After ineligibility exclusions, data were abstracted from 93 patients. Proportions of patients with undetectable PSA 12 and 24 months after ending ADT were n=23/93 (24.7%; 95% CI 16.4–34.8%; P<0.001) and n=14/93 (15.1%; 95% CI 8.5–24.0%; P<0.001), respectively. Proportions of patients with undetectable

PSA 12 and 24 months after testosterone recovery \geq 50 ng/dL were n=16/65 (24.6%; 95% CI 14.8-36.9%) and n=10/65 (15.4%; 95% CI 7.6-26.5%), respectively. Being 1 year older at diagnosis was associated with an 11.5% (95% CI 3.1–21.9%; P=0.01) increase in the odds of having a detectable PSA after controlling for PSA at diagnosis, Gleason sum and time from initial therapy to BCR. Detectable PSA was associated with increased risk of metastasis (P=0.006) with marginal evidence of association with death from any cause (P=0.07).

Conclusions:

This single-institution retrospective analysis shows that it is not uncommon to have undetectable PSA 12 or 24 months after a short course of ADT. Additional analysis is needed to demonstrate the clinical value of this measure as a surrogate for prostate cancer outcomes and for consideration as a trial endpoint.

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Association of undetectable PSA with time to metastasis and survival after shortcourse androgen deprivation therapy for biochemically-recurrent prostate cancer patients.

Authors:

Evan Y. Yu, Roman Gulati, Serge Aleshin-Guendel, Heather H. Cheng, Agnes M. Gawne, Jonathan T. Wingate, Ruth Douglas Etzioni, Daniel M. Lim; Seattle Cancer Care Alliance, Seattle, WA; Fred Hutchinson Cancer Research Center, Seattle, WA; University of Washington, Seattle, WA; U.S. Army, Tacoma, WA, US

Abstract Disclosures

Background:

Optimal utilization of novel therapies for advanced prostate cancer is challenging without a validated surrogate efficacy endpoint. Durable undetectable prostate-specific antigen (PSA) levels are being used in ongoing trials as a marker of efficacy. The clinical relevance of patients with a prolonged undetectable PSA after short course androgen deprivation therapy (ADT) is uncertain.

Methods:

The University of Washington Caisis database was queried for radical prostatectomy patients who received 6–12 months of ADT after biochemical recurrence (BCR), defined as PSA \geq 0.2 ng/mL and no radiographically detectable metastasis. Proportions of patients with undetectable PSA 12 and 24 months after ending ADT were compared to a hypothesized 5% rate using exact binomial tests. Associations with patient and tumor characteristics were examined using logistic regression, and associations with risk of subsequent metastasis and death were evaluated by log-rank tests.

Results:

After ineligibility exclusions, 23/93 (24.7%; 95% CI 16.4–34.8%; P < 0.001) and 14/93 (15.1%; 95% CI 8.5–24.0%; P < 0.001) of patients had undetectable PSA 12 and 24 months after ending ADT, respectively. Being 1 year older at diagnosis was associated with a 14% (95% CI 5.1–23.7%; P = 0.006) decrease in the odds of detectable PSA after controlling for PSA at diagnosis, PSA doubling time, Gleason sum and time from initial therapy to BCR. Detectable PSA at 12 months was associated with increased risk of metastasis (P = 0.006), prostate cancer-specific death (P = 0.028) and death from any cause (P = 0.065).

Conclusions:

This single-institution retrospective analysis shows that it is not uncommon to have undetectable PSA 12 or 24 months after a short course of ADT, and this finding correlates with lower risk of metastasis and prostate cancer-specific death. No baseline prognostic characteristic other than age was associated with a durable undetectable PSA. Because of association with lower risks of metastasis and prostate cancer-specific death, it may be reasonable to consider undetectable PSA as a clinical trial endpoint.

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Evaluation of an immunotherapeutic DNA-vaccine in biochemically relapsed prostate cancer.

Presented Saturday, June 2, 2018

Authors:

Neal D. Shore, Elisabeth I. Heath, Luke T. Nordquist, Heather H. Cheng, Kamalnayan Bhatt, Matthew Morrow, Trevor McMullan, Kimberly Kraynyak, Jessica Lee, Brian Sacchetta, Li Liu, Samantha Rosencranz, Scott T. Tagawa, Rahul Atul Parikh, Ronald F Tutrone, Jorge A. Garcia, Young E. Whang, William Kevin Kelly, Ildiko Csiki, Mark L. Bagarazzi; Carolina Urologic Research Center, Myrtle Beach, SC; Barbara Ann Karmanos Cancer Institute, Wayne State University, Detroit, MI; Urology Cancer Center and GU Research Network, Omaha, NE; University of Washington, Seattle, WA; Inovio Pharmaceuticals, Inc., Plymouth, PA; Inovio Pharmaceuticals, Plymouth Meeting, PA; Inovio Pharmaceuticals, Inc., Collegeville, PA; Inovio Pharmaceuticals, Inc., Blue Bell, PA; Sandra and Edward Meyer Cancer Center, New York, NY; University of Kansas, Kansas City, KS; Chesapeake Urology, Towson, MD; Cleveland Clinic Taussig Cancer Institute, Cleveland, OH; University of North Carolina at Chapel Hill, Chapel Hill, NC; Sidney Kimmel Cancer Center at Thomas Jefferson University, Philadelphia, PA; Inovio Pharmaceuticals, Plymouth Meeting, PA, US

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Abstract Disclosures

Background:

The DNA immunotherapy, INO-5150 (PSA and PSMA) +/- INO-9012 (IL-12) was assessed for safety, immunogenicity and the effect on PSA kinetics in biochemically recurrent prostate cancer patients (pts).

Methods:

Phase I, open-label, multi-center study included pts with rising PSA after surgery and/or RT, PSA doubling time (PSADT) > 3 months (mos), testosterone > 150 ng/dL, no concurrent ADT and no evidence of metastases by conventional imaging. Safety, immunogenicity and efficacy were evaluated in 4 treatment arms in 60 planned pts (A: 16, 2mg INO-5150; B: 15, 8.5 mg INO-5150; C: 15, 2mg INO-5150+1mg INO-9012; D: 16, 8.5mg INO-5150+1mg INO-9012). Pts received 4 IM doses of vaccine followed by electroporation on day 0, wks 3, 12 and 24 and followed for 72 wks.

Results:

The study has concluded and 50/62 (80%) pts completed all visits. 90% of pts had Grade (Gr) 1-3 AEs, primarily injection site reactions which were Gr 1. Across 4 cohorts, 47/61 (77%) of all evaluable pts demonstrated immunogenicity, [35/58 (60%) had IFN- γ reactivity by ELISPOT, 6/61 (10%) and 5/61 (8%) had antibody titers against PSA and PSMA, respectively, and 19/50 (38%) had CD38, Perforin+CD8 T cell responses]. Pts (38%) with CD38 and Perforin + CD8 T cell immune reactivity had attenuated % PSA rise compared to non-reactive pts (p = 0.05, n = 50). Pts with no known progression during the study showed significant differences in log₂PSA change and PSADT pre-treatment baseline (D0) vs wk 27 (post-immunotherapy time point, n = 34, p < 0.0001) or wk 72 (end of follow-up, n = 27, p < 0.0001). Furthermore, pts with D0 PSADT≤ 6 mos and no known progression during the study showed significant differences in log₂PSA change and PSADT in D0 vs wk 27 (n = 15, p < 0.0001) or wk 72 (n = 10, p = 0.002).

Conclusions:

INO-5150 +/- INO-9012 was safe, well tolerated and immunogenic. A clinical effect was demonstrated by evidence of dampening % rise in PSA and increased PSADT in the majority of patients. In patients with no known disease progression during the study, a significant PSA stabilizing effect of the immunotherapy was observed. Additional analyses are ongoing to further elucidate the correlation of immunologic efficacy and clinical benefit. Clinical trial information: NCT02514213

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c15-148: Phase I/II trial of concurrent chemohormonal therapy using enzalutamide and cabazitaxel in patients with metastatic castration resistant prostate cancer (mCRPC).

Presented Saturday, June 2, 2018

Authors:

Julie Nicole Graff, Tomasz M. Beer, Joshi J. Alumkal, Dustin Kreitner, Delia Petreaca, George V. Thomas, Heather H. Cheng; VA Portland Health Care System, Knight Cancer Institute, Oregon Health & Science University, Portland, OR; Knight Cancer Institute, Oregon Health & Science University, Portland, OR; OHSU Knight Cancer Institute, Portland, OR; University of Washington, Seattle, WA

Abstract Disclosures

Background:

The management of mCRPC has been both enhanced and complicated by the rapid emergence of at least five new agents that can lengthen survival. While great strides have been made in developing new agents for mCRPC, response rates and duration have remained modest, and men ultimately succumb to their disease. Historically, combined chemo-hormonal therapy has not improved outcomes for patients with prostate cancer, but earlier trials were hindered by lack of efficacious chemotherapy and weaker hormonal agents. In this study, we aim to determine if potential synergistic effects between two newer and more effective agents can be identified and exploited for therapeutic effect, and to obtain correlative biological information that may offer predictive and response value.

Methods:

An initial 3-12 study subjects will be treated with cabazitaxel at 25 mg/m² on day 1 and enzalutamide 160 mg daily every 21 days. These subjects will be permitted to continue on cabazitaxel and enzalutamide until progression and will be included in the final analysis of efficacy. The trial will proceed to phase II stage at the dose of 25 mg/m² if 0/3 or 1/6 patients receiving 25 mg/m² had DLT. The dose de-escalation will happen if \geq 2/3 or \geq 2/6 patients receiving 25 mg/m² had DLT. The trial will proceed to Phase II stage at the dose of 20 mg/m² if 0/3 or 1/6 patients receiving 20 mg/m² had DLT. In the absence of treatment delays due to adverse events, treatment with cabazitaxel and enzalutamide will continue for 6-10 cycles. Patients

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may then continue enzalutamide monotherapy on a 28-day cycle until progression or limiting toxicity. For the phase I portion of this trial an initial 3 study subjects were treated with cabazitaxel at 25 mg/m² on day 1 and enzalutamide 160 mg daily every 21 days; no DLTs occurred. These subjects will be permitted to continue on cabazitaxel and enzalutamide until progression and will be included in the final analysis of efficacy. The phase II patients are treated with 25 mg/m2 cabazitaxel and 160 mg enzalutamide. The trial is open at 2 sites and managed by the Prostate Cancer Clinical Trials Consortium (PCCTC). Clinical trial information: NCT02522715

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c15-160: Enzalutamide (ENZA) plus CC-115 in men with metastatic castrationresistant prostate cancer (mCRPC): A phase 1b Prostate Cancer Clinical Trials Consortium study.

Presented Saturday, June 2, 2018

Authors:

Dana E. Rathkopf, Karen A. Autio, Emmanuel S. Antonarakis, Heather H. Cheng, Gabrielle Arauz, Annelise Slack, Melanie Hullings, Howard I. Scher, Felix Y Feng, Karen E. Knudsen; Memorial Sloan Kettering Cancer Center, New York, NY; Johns Hopkins Sidney Kimmel Comprehensive Cancer Center, Baltimore, MD; University of Washington, Seattle, WA; Sidney Kimmel Comprehensive Cancer Center at Johns Hopkins University; Memorial Sloan-Kettering Cancer Center, New York, NY; University of California San Francisco, San Francisco, CA; Sidney Kimmel Cancer Center at Thomas Jefferson University, Philadelphia, PA

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Abstract Disclosures

Background:

Studies in PTEN-deficient prostate cancer (PC) models have shown additive anti-tumor activity when ENZA is combined with PI3K pathway inhibition due to modulation of reciprocal feedback loops. In addition, interplay between AR and DNA-PK regulates hormone-dependent DNA repair and PC progression. This phase Ib trial aims to optimize therapy for mCRPC with the combination of ENZA and the dual mTOR/DNA-PK inhibitor CC-115.

Methods:

This was a phase Ib multicenter trial (NCT02833883) for first-line mCRPC patients. Treatment was fixed dose ENZA (160 mg PO QD) with escalating doses of CC-115 (5 mg and 10 mg PO BID) using a 3 x 3 design. The primary endpoints were safety, PK and the recommended phase 2 dose (RP2D) of the combination. Secondary endpoints were PSA response, time on study and exploratory correlates using tumor biopsies, CTCs and ctDNA.

Results:

16 patients were treated: 9 in dose escalation and 7 in dose expansion, for a total of 13 patients treated at the RP2D of CC-115 10 mg PO BID. There were no drug-drug interactions. Median time on study was 26 (18-74+) weeks (wks), and 9 patients remain on active treatment. All evaluable patients had a > 50% PSA response, and 60% of patients achieved a ≥90% decline. The most common AEs were low grade fatigue (31%) and diarrhea (25%). At the RP2D, 8/13 (62%) patients developed rash: grade 3 (n = 6), grade 2 (n = 1) and grade 1 (n = 1) prompting dose reduction. 12 patients had baseline tissue analysis by IHC and/or NGS: 6 men had PTEN inactivation and 3 had DNA damage response and repair (DDR) alterations. Median time on study for those with PTEN deletions was 25 wks (7-57+), and was 29 wks (28-41+) for those with DDR alterations. Data on ctDNA and CTC biomarkers is pending.

Conclusions:

The combination of ENZA and CC-115 is safe and active in mCRPC, as demonstrated by all evaluable patients achieving a > 50% PSA decline and 60% achieving a \geq 90% PSA decline. Due to a higher than expected incidence of rash, the protocol was amended to continue with CC-115 at 7.5 mg PO BID for the phase 2 expansion. Funding: Celgene and Gateway for Cancer Research. Clinical trial information: NCT02833883

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ORIGINAL ARTICLE

Androgen receptor mutations in patients with castration-resistant prostate cancer treated with apalutamide

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Background: Mutations in the androgen receptor (AR) ligand-binding domain (LBD), such as F877L and T878A, have been associated with resistance to next-generation AR-directed therapies. ARN-509-001 was a phase I/II study that evaluated apalutamide activity in castration-resistant prostate cancer (CRPC). Here, we evaluated the type and frequency of 11 relevant AR-LBD mutations in apalutamide-treated CRPC patients.

Patients and methods: Blood samples from men with nonmetastatic CRPC (nmCRPC) and metastatic CRPC (mCRPC) pre- or post-abiraterone acetate and prednisone (AAP) treatment (≥6 months' exposure) were evaluated at baseline and disease progression in trial ARN-509-001. Mutations were detected in circulating tumor DNA using a digital polymerase chain reaction-based method known as BEAMing (beads, emulsification, amplification and magnetics) (Sysmex Inostics' GmbH).

Results: Of the 97 total patients, 51 had nmCRPC, 25 had AAP-naïve mCRPC, and 21 had post-AAP mCRPC. Ninety-three were assessable for the mutation analysis at baseline and 82 of the 93 at progression. The overall frequency of detected AR mutations at baseline was 7/93 (7.5%) and at progression was 6/82 (7.3%). Three of the 82 (3.7%) mCRPC patients (2 AAP-naïve and 1 post-AAP) acquired *AR* F877L during apalutamide treatment. At baseline, 3 of the 93 (3.2%) post-AAP patients had detectable *AR* T878A, which was lost after apalutamide treatment in 1 patient who continued apalutamide treatment for 12 months.

Conclusions: The overall frequency of detected mutations at baseline (7.5%) and progression (7.3%) using the sensitive BEAMing assay was low, suggesting that, based on this assay, AR-LBD mutations such as F877L and T878A are not common contributors to *de novo* or acquired resistance to apalutamide.

ClinicalTrials.gov identifier: NCT01171898.

Key words: apalutamide, ARN-509, castration-resistant prostate cancer, androgen receptor, mutations

Introduction

Castration-resistant prostate cancer (CRPC) is the lethal form of the disease that carries a poor prognosis [1, 2]. Molecular profiling

studies have shown that androgen receptor (AR) overexpression is associated with resistance to conventional antiandrogens, and preclinical experiments confirm that AR overexpression contributes

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to CRPC progression [3]. This insight and the demonstration that androgen ligands persist in CRPC patient tumors despite medical castration led to the eventual clinical development of novel androgen-AR axis–signaling inhibitors, including most recently, apalutamide [4, 5].

Although the majority of patients respond to these nextgeneration AR-targeted agents, the durability of response is limited [6], and only a subset benefit from sequential AR-directed therapies [7-10]. Several potential mechanisms have been proposed to explain resistance to these agents, including DNA alterations in the AR gene, the production of AR mRNA splice variants such as AR-V7 [11, 12], increased mitogen-activated protein kinase signaling and alternative signaling pathways [3]. Point mutations in the AR ligand-binding domain (AR-LBD) have also been associated with resistance to AR-targeted therapy [13-20], including AR F877L and AR T878A (formerly AR F876L and AR T877A) [21], which have been associated with resistance to apalutamide, enzalutamide or the androgen biosynthesis inhibitor abiraterone acetate (hereafter abiraterone), respectively. Additionally, although all AR mutations alter the specificity of ligand binding, there are 2 types of AR mutations, those that convert AR antagonists to agonists (e.g. F877L, W742L/C) and those that result in broadened ligand specificity and a 'promiscuous AR' that can bind to other endogenous steroids [17].

To evaluate the relationship of AR-LBD mutations and resistance to next-generation antiandrogens, Balbas et al. [14] screened for human prostate cancer cell populations with persistent AR transcriptional activity, proliferative ability and tumorigenic potential in the presence of enzalutamide using an AR-regulated enhanced green fluorescent protein reporter and a randomly mutagenized AR library. These investigators identified a novel mutation, AR F877L, that spontaneously arose in cells with prolonged treatment with enzalutamide and apalutamide [14]. Joseph et al. [18] and Korpal et al. [19] confirmed these findings with AR F877L-expressing prostate cancer cell lines in castrated mice. Neither enzalutamide nor apalutamide inhibited tumor growth in the AR F877L-expressing tumors, but both drugs exhibited robust antitumor activity in wild-type ARexpressing tumors [18, 19]. Based on these preclinical data, Joseph et al. [18] used the BEAMing (beads, emulsification, amplification and magnetics) technique to evaluate serial circulating tumor DNA (ctDNA) samples from 29 patients with metastatic CRPC (mCRPC) treated on a phase I study of apalutamide. As expected, AR F877L was not found in pretreatment samples but the mutation was detected in 3 (10%) post-apalutamide patients with a rising prostate-specific antigen (PSA), suggesting a possible mechanism for acquired treatment resistance [18]. There is biochemical evidence based on engineered cell line models that enzalutamide is only a weak partial agonist of AR F877L, but a strong partial agonist of the double mutant AR F877L/T878A [22, 23].

The *AR* T878A mutation has been associated with resistance to abiraterone in a xenograft model [15], which was subsequently detected in metastatic tumor biopsies from CRPC patients relapsing on the CYP17A1 inhibitors abiraterone or ketoconazole [16]. In a recent study, men harboring the *AR* T878A mutation in ctDNA showed inferior PSA response rates and shorter overall survival with abiraterone compared with men with a wild-type AR gene [24]. These studies and others underscore the need to

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further investigate predictive biomarkers for resistance to ARtargeted therapies.

The aim of the present study was to evaluate the frequency of F877L, T878A and other AR-LBD mutations at baseline and disease progression in nonmetastatic (nm) and mCRPC patients who were abiraterone plus prednisone naïve (AAP-naïve) or who had previously received abiraterone plus prednisone (post-AAP) [25, 26]. Eleven somatic AR-LBD mutations were evaluated at baseline and disease progression in ctDNA using BEAMing, a digital polymerase chain reaction (PCR)-based method (supplementary Table S1, available at *Annals of Oncology* online).

Methods

Patients with nmCRPC and mCRPC were enrolled in a phase II trial of apalutamide (ARN-509-001) [25, 26]. All patients had pathologically confirmed prostate cancer, had been medically or surgically castrated (serum testosterone of \leq 50 ng/dl) and had an Eastern Cooperative Oncology Group performance status of 0–1. Patients were excluded if they had received prior enzalutamide, ketoconazole or chemotherapy for mCRPC or had distant metastases with nmCRPC. Patients in the mCRPC cohort had disease progression based on either PSA progression (\geq 2 ng/ml within 2 weeks of study enrollment) or radiographic progression (\geq 2 new bone lesions, Prostate Cancer Working Group 2 criteria) [27] and had no prior exposure to abiraterone plus prednisone (i.e. AAP-naïve cohort) or received \geq 6 months of abiraterone plus prednisone treatment before disease progression (i.e. post-AAP cohort).

Plasma samples were sent to Sysmex Inostics' GmbH (Hamburg, Germany) analytical facility on dry ice; samples were stored at -70 °C until they were analyzed. Samples were thawed at room temperature for 15–30 min before DNA preparation. BEAMing (Sysmex Inostics' GmbH), which combines emulsion PCR using magnetic beads coated with gene-specific primers to detect and quantify known mutations in ctDNA [28], was used to detect 11 possible somatic AR-LBD mutations in the patient samples (i.e. 11 of >30 known AR-LBD mutations available to assay via BEAMing at the time of the analysis) (supplementary Table S1, available at *Annals of Oncology* online). These 11 mutations affect 6 key amino acid residues (V716, W742, H875, F877, T878 and M896). Detection, quantification and validation are discussed in the supplementary methods, available at *Annals of Oncology* online).

Results

Baseline data (N = 97) were similar among cohorts, with the exception of percentage of black and Asian patients, baseline PSA and Gleason score (supplementary Table S2, available at Annals of Oncology online). Ninety-three of 97 (96%) patients in the phase II study were assessable for the AR mutation analysis at baseline (nmCRPC, n = 50; AAP-naïve mCRPC, n = 24; post-AAP mCRPC, n = 19; 82 of the 93 (88%) patients assessable at baseline were assessable for the mutation analysis at progression (nmCRPC, n = 47; AAP-naïve mCRPC, n = 20; post-AAP mCRPC, n = 15). The median (range) treatment duration was 26.9 (0.03-37.84) months for the nmCRPC cohort, 20.97 (2.63-37.54) months for the cohort with AAP-naïve mCRPC and 4.87 (1.28-23.2) months for those with post-AAP mCRPC. A low frequency of AR mutations was detected in the overall patient population (Table 1). AR F877L and AR T878A mutations were found in more than one patient, and these are the focus of this report.

Table 1. Summ	ary of overall androgen receptor	mutation status		
AR point mutation ^b	Associated drug resistance	Baseline ^a N = 93	Progression 'acquired' <i>N</i> = 82	Total baseline and progression 'acquired' <i>N</i> = 93
		n (%)	n (%)	n (%)
F877L ^c	Enzalutamide [14, 18, 19] Apalutamide [14, 18]	2 (2.2)	3 (3.7)	5 (5.4)
T878A ^d	Abiraterone [15, 16]	3 (3.2)	1 (1.2)	4 (4.3)
W742C ^e	Bicalutamide [17]	1 (1.1)	0	1 (1.1)
V716T	Flutamide [17]	0	1 (1.2)	1 (1.1)
H875Y	Flutamide [20] Abiraterone [13]	1 (1.1)	1 (1.2)	2 (2.2)

^aFour nmCRPC patients were excluded from the efficacy analysis as they were later determined to have metastases on their screening scans. ^bAR M896T and AR M896V were not detected.

^cThree possible nucleotide changes (T \rightarrow C, C \rightarrow A and C \rightarrow G).

 $^d Two$ possible amino acid changes (T \rightarrow A and T \rightarrow S).

^eTwo possible amino acid changes (W \rightarrow C and W \rightarrow L).

AR, androgen receptor.

Table 2. Androgen receptor F877L and T878A mutation status^a in individual patients treated with apalutamide in the nmCRPC, AAP-naïve and post-AAP cohorts

Cohort	Patient ID#	<i>AR</i> mutation ^b	Mutation fraction at baseline ^c	Cycle at which mutation fraction at progression detected	Mutation fraction at progression ^{d,e}	12-Week PSA change ^f	Treatment duration (months) ^g
nmCRPC	1	F877L	(0.02%)	8	(0.3%)	-92.2%	6.9
AAP-naïve	2	F877L	-	22	(0.721%)	-77.7%	24.9
	3	F877L	(0.032%)	11	(0.41%)	-66.9%	11.0
	4	F877L	-	9	(0.18%)	-97.3%	8.0
Post-AAP	5	F877L	-	4	(0.04%)	+55.9%	3.4
	6	T878A	(0.84%)	4	(5.46%)	+112.7%	2.8
	7	T878A	(0.07%)	14	-	-62.7%	12
	8	T878A	(1.96%)	6	(0.4%)	-90.1%	4.8
	9	T878A	-	10	(0.02%)	-80.8%	23.2

^aA plasma sample was deemed positive for a given mutation if the percentage of mutant beads was above the cutoff (0.02%).

^bNo F877L/T878A double mutants were detected.

^cNumber of mutation positive patients at baseline (F877L, n = 2/93; T878A, n = 3/93).

^dNumber of mutation positive patients at progression (F877L, n = 5/82; T878A, n = 3/82).

^eDisease progression on apalutamide was defined as evidence of both PSA progression (\geq 25% and \geq 2 ng/ml above PSA nadir confirmed \geq 3 weeks later or \geq 2 ng/ml above baseline PSA after 12 weeks) and radiographic progression (soft tissue metastases by modified Response Evaluation Criteria In Solid Tumors 1.0) seen on computed tomography/magnetic resonance imaging scans and/or bone metastases by ^{99m}Tc-methylene diphosphate bone scans by Prostate Cancer Working Group 2 criteria, and clinically by the occurrence of a skeletal-related event, pain progression, or worsening of disease-related symptoms requiring new systemic anti-prostate cancer therapy.

^fMedian 12-week PSA change in F877L mutation negative patients (n = 86) was -79.8% (range, -99.9 to +175). Median 12-week PSA change in T878A mutation negative patients (n = 87) was -81.2% (range, -99.9 to +175).

^gMedian treatment duration in F877L mutation-negative patients (n = 92) was 19.6 months (range, 0.03–37.8). Median treatment duration in T878A mutation-negative patients (n = 93) was 18.4 months (range, 0.03–37.8).

-, undetected. AAP, abiraterone acetate plus prednisone; AR, androgen receptor; mCRPC, metastatic castration-resistant prostate cancer; PSA, prostate-specific antigen.

AR F877L

Two of the 93 (2.2%) patients harbored the *AR* F877L mutation at baseline at a mutation frequency of < 0.05%, and both were subsequently found to have a PSA decline in response to

apalutamide (Table 2; Figure 1A and B). One of these patients was in the nmCRPC cohort (12-week PSA change, –92.2%; treatment duration, 6.9 months) and the other was in the AAP-naïve cohort (12-week PSA change, –66.9%; treatment duration,

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Figure 1. PSA changes in patients with androgen receptor F877L mutations detected at baseline [(A) Pt ID#1, (B) Pt ID#3] and at progression on apalutamide [(C) Pt ID#5, (D) Pt ID#2]. AA, abiraterone acetate; PSA, prostate-specific antigen.

11.0 months). Both patients had detectable *AR* F877L and an increase in the mutation frequency at the time of progression.

Three additional patients [3/82 (3.7%)] were found to have the mutation at progression that had not been detected at baseline (Table 2); the PSA trajectory is shown in Figure 1C–E. The single patient in the post-AAP cohort who acquired *AR* F877L demonstrated no PSA decline (12-week PSA change, +55.9%; treatment duration, 3.4 months) and had a relatively low mutation frequency of 0.04% (Table 2; Figure 1C). The other 2 patients with acquired *AR* F877L were both in the AAP-naïve cohort with 12-

week PSA changes of –97.3% and –77.7%, treatment durations of 8.0 and 24.9 months, respectively, and mutation frequencies of 0.18% and 0.72%, respectively (Table 2; Figure 1D and E, respectively).

AR T878A

Three of 93 (3.2%) patients had the *AR* T878A mutation at baseline (Table 2); all had previously received at least 6 months of abiraterone and demonstrated similar baseline characteristics.

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Figure 2. PSA changes in patients with androgen receptor T878A mutations detected at baseline [(A) Pt ID#7, (B) Pt ID#8, (C) Pt ID#6] and at progression on apalutamide [(D) Pt ID#9]. AA, abiraterone acetate; PSA, prostate-specific antigen. Baseline characteristics for these patients are shown in Table 3.

Two had a PSA decline while on treatment with apalutamide, including 1 who had lost the mutation by the time of progression on apalutamide (Figure 2A; Table 3) (12-week PSA change, -62.7%; treatment duration, 12.0 months), and a second who had a decreased mutation fraction from 1.96% at baseline to 0.4% at progression (Figure 2B; Table 3) (12-week PSA change, -90.1%; treatment duration, 4.8 months). The third patient had an increased mutation fraction from 0.84% at baseline to 5.46% at progression and had no PSA decline (12-week PSA change, +112.7%; treatment duration, 2.8 months) (Figure 2C; Table 3). The PSA kinetics increased for these patients after AR T878A detection at progression (Figure 2A-D). One post-AAP patient acquired the AR T878 mutation at progression at a relatively low frequency of 0.02%. This patient had a PSA decline in response to apalutamide (12-week PSA change, -80.8%; treatment duration, 23.2 months) (Figure 2D; Table 3).

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The survival benefits seen with agents that target the ARsignaling pathway have transformed the management of mCRPC. Nevertheless, one-third of patients do not respond to second-generation AR-targeted therapies, and the majority of those who initially respond, will acquire resistance to these Table 3. Baseline demographics and disease characteristics of post-AAP patients with T878A mutations at baseline corresponding to patients shown in Figure 2 (per Figure 2A–C) and progression on apalutamide (per Figure 2D)

Patient	A (Pt ID#7)	B (Pt ID#8)	C (Pt ID#6)	D (Pt ID#9)
Age	83	64	74	58
Race	White	White	White	White
Baseline PSA (ng/ml)	58.4	1315.2	64.1	12.0
ECOG PS	1	1	1	0
Gleason score	4+5	4+3	4+3	N/A

AAP, abiraterone acetate plus prednisone; ECOG PS, Eastern Cooperative Oncology Group performance status; PSA, prostate-specific antigen.

agents. The optimal treatment of these patients, and how best to sequence available life-prolonging therapies, have not been established due to the inability to identify patients most likely to respond (or not respond) to specific AR-targeted drugs. This demonstrates the need for predictive molecular biomarkers to better inform treatment selection [11, 12, 24, 29]. Here, we report results of ctDNA sequencing using the BEAMing assay on samples from a phase II study of apalutamide in 3 distinct cohorts

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(nm, metastatic AAP-naïve, and metastatic post-AAP). The assay was selected because of its increased sensitivity versus an AR exon 8 sequencing approach used by others [13].

Overall, we tested 5 mutations derived from 11 possible amino acid alterations in 5 codons (supplementary Table S1, available at *Annals of Oncology* online) for which the assay was designed, including: F877L (n=5), T878A (n=4), W742C (n=1), V716M (n=1) and H875Y (n=2). The most common (occurring in more than one subject) were *AR* F877L and *AR* T878A, LBD mutations associated in laboratory models and in the clinic with resistance to enzalutamide and apalutamide (*AR* F877L) [14, 18, 19] and abiraterone (*AR* T878A) [15, 16].

The frequency of AR F877L mutations (i.e. copies of mutant AR per genomic equivalent) increased in the mCRPC cohort after exposure to apalutamide, suggesting the possibility of preexisting clones that underwent positive selection with treatment. The 2 patients with the AR F877L mutations at baseline had a 12-week PSA decline of >50% after treatment with apalutamide. Notably, both had a relatively low frequency of the mutation at baseline (<0.05%) that increased at the time of progression. Another AAP-naïve mCRPC patient remained on study for 24.9 months and acquired the AR F877L mutation at progression (mutation frequency, 0.72%), suggesting a possible mechanism for secondary resistance. AR F877L was not detected in any post-AAP mCRPC patients at baseline. One post-AAP patient acquired the AR F877L mutation at progression on apalutamide; however, this patient had a low frequency of the mutation (0.04%) and was only on study for 3.4 months with a rising PSA, potentially suggesting a method of resistance other than development of AR F877L in the setting of prior AAP exposure.

All patients in our study who harbored the AR T878A mutation were in the mCRPC post-AAP cohort, consistent with the results of a recent analysis showing that AR T878A was associated with resistance to abiraterone [13] and consistent with prevalence reported in prior studies [13, 16], whereas AR T878A was never detected in patients with nmCRPC or in those in the AAP-naïve mCRPC cohort. One of the patients who lost the AR T878A mutation at progression initially had a PSA elevation but subsequently experienced a robust PSA decline and was on treatment for 12 months until treatment discontinuation due to PSA, radiographic and clinical progression. The decrease or loss of the AR T878A mutation observed in 2 of the 3 post-AAP patients who received treatment with apalutamide suggests 3 possibilities: apalutamide may have selectively inhibited the clone with this mutation and restored sensitivity to AR-directed treatment; discontinuation of abiraterone may have removed the evolutionary selection pressure that encouraged this AR mutation to emerge during abiraterone treatment; or discontinuation may have removed selective advantage of progesterones with the availability of endogenous steroids.

Blood samples were collected from 93 patients at baseline and from 82 patients at progression using a BEAMing assay designed to detect 11 selected AR-LBD mutations. These mutations were found at a relatively low incidence and frequency. Potential limitations of the analysis include the use of only one assay (limited to one assay per study sample availability) predesigned to detect 11 AR-LBD mutations already known to be associated with resistance to AR signaling-directed therapies. There may be other as of yet not well defined AR-LBD mutations that contribute to resistance. For example, the clinical significance of emergence of *AR* L702H in patients

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treated with exogenous glucocorticoids was not known when this study was designed [30]. Larger, prospective studies using assays that can detect mutations as well as other alterations in the receptor such as the AR splice variants [12, 31] to more completely address the question of the role of AR-LBD mutations in both de novo and acquired resistance would require a different type of blood sample. Given the high sensitivity of the BEAMing assay, it is likely that the AR F877L and AR T878A mutations are not major contributors to de novo or acquired resistance with apalutamide. It is also possible that the presence of AR F877L and AR T878A mutations in apalutamide-treated patients is an epiphenomenon associated with clonal selection pressures rather than being a driver of apalutamide resistance. Notably, however, preclinical data strongly suggest that these AR mutations confer resistance to AR-targeting agents. Ultimately, an integrated analysis of tumor-specific mRNA and DNA would be required to study the full complement of AR aberrations in men receiving novel hormonal therapies.

Conclusions

Although AR F877L has previously been associated with resistance to apalutamide and enzalutamide, patients with CRPC who were treated with apalutamide in our study had a low rate of *de novo* acquisition of the *AR* F877L mutation [3 of 82 patients (4%)] even using the sensitive BEAMing method. Not surprisingly, in patients without prior exposure to second-generation AR antagonists, *AR* F877L was detected at a low frequency at baseline [2 of 93 (2%)], and the presence of these mutations did not preclude PSA declines with apalutamide. The increased frequency of the mutation at the time of progression does suggest that *AR* F877L mutation may contribute to apalutamide resistance, although the frequency of these mutations in patients progressing on apalutamide in this study was low.

Second-line therapy with apalutamide in 2 post-AAP patients resulted in either a decrease or a loss of the preexisting *AR* T878A mutation while on therapy. Given the low frequency of the *AR* F877L and *AR* T878A mutations, they are unlikely to play a dominant role in the mechanism of primary or acquired resistance to apalutamide in CRPC patients.

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Disclosure

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Original Study



Effect of Visceral Disease Site on Outcomes in Patients With Metastatic Castration-resistant Prostate Cancer Treated With Enzalutamide in the PREVAIL Trial

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Abstract

We assessed outcomes from men with metastatic castration-resistant prostate cancer that had spread to the liver and/or lungs in the PREVAIL clinical trial of enzalutamide in patients who had not received docetaxel chemotherapy. Compared with placebo, enzalutamide lengthened the time it took for the cancers to grow (according to changes in scans), prostate-specific antigen to rise, or patients to require chemotherapy. Background: The Multinational Phase 3, Randomized, Double-Blind, Placebo-Controlled Efficacy and Safety Study of Oral MDV3100 in Chemotherapy-Naive Patients With Progressive Metastatic Prostate Cancer Who Have Failed Androgen Deprivation Therapy (PREVAIL) trial was unique as it included patients with visceral disease. This analysis was designed to describe outcomes for the subgroup of men from PREVAIL with specific sites of visceral disease to help clinicians understand how these patients responded to enzalutamide prior to chemotherapy. Patients and Methods: Prespecified analyses examined the coprimary endpoints of radiographic progression-free survival (rPFS) and overall survival (OS) only. All other efficacy analyses were post hoc. The visceral subgroup was divided into liver or lung subsets. Patients with both liver and lung metastases were included in the liver subset. Results: Of the 1717 patients in PREVAIL, 204 (12%) had visceral metastases at screening (liver only or liver/lung metastases, n = 74; lung only metastases, n = 130). In patients with liver metastases, enzalutamide was associated with an improvement in rPFS (hazard ratio [HR], 0.44; 95% confidence interval [CI], 0.22-0.90) but not OS (HR, 1.04; 95% CI, 0.57-1.87). In patients with lung metastases only, the HR for rPFS (0.14; 95% CI, 0.06-0.36) and the HR for OS (0.59; 95% CI, 0.33-1.06) favored enzalutamide over placebo. Patients with liver metastases had worse outcomes than those with lung metastases, regardless of treatment. Enzalutamide was well tolerated in patients with visceral disease. Conclusions: Enzalutamide is an active first-line treatment option for men with asymptomatic or mildly symptomatic chemotherapy-naive metastatic castration-resistant prostate cancer and visceral disease. Patients with lung-only disease fared better than patients with liver disease, regardless of treatment.

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Introduction

Nearly all patients with recurrent prostate cancer or de novo metastatic disease treated with androgen deprivation therapy eventually develop castration-resistant prostate cancer (CRPC), the lethal form of this disease.^{1,2} Survival of patients with metastatic CRPC (mCRPC) is usually < 3 years, with > 26,000 deaths predicted in the United States alone in 2016.³⁻⁷ Patients with mCRPC with visceral disease, most commonly in the liver and/or lung, are thought to have a particularly poor prognosis, and the presence of liver metastases is associated with the shortest survival.^{3,4,8,9}

During the drug development process, patients with mCRPC have been previously categorized by docetaxel chemotherapy exposure, the first drug to improve overall survival (OS) for men with mCRPC in phase III trials.^{10,11} Studies of systemic agents in the post-docetaxel setting have generally included men with visceral disease.¹²⁻¹⁴ However, phase III trials in the pre-docetaxel setting have excluded these patients because of the widespread belief that docetaxel, rather than an investigational agent, is the preferred treatment option for patients with visceral disease given their poor prognosis.^{15,16} The Multinational Phase 3, Randomized, Double-Blind, Placebo-Controlled Efficacy and Safety Study of Oral MDV3100 in Chemotherapy-Naive Patients With Progressive Metastatic Prostate Cancer Who Have Failed Androgen Deprivation Therapy (PREVAIL) trial (ClinicalTrials.gov number: NCT01212991) challenged this view by enrolling patients with visceral disease, provided they were otherwise eligible based on performance criteria (ie, an Eastern Cooperative Oncology Group performance status [ECOG PS] of 0 or 1 and a score of 0 to 3 on Brief Pain Inventory Short Form question 3).⁵ PREVAIL was designed with the expectation that minimally symptomatic men with good ECOG PS would be followed carefully with imaging studies and could receive an investigational therapy or placebo and still receive chemotherapy after discontinuing the study medication.

In PREVAIL, enzalutamide significantly improved OS and radiographic progression-free survival (rPFS) relative to placebo in the overall population of men with chemotherapy-naive mCRPC.⁵ A prespecified subgroup analysis of PREVAIL data revealed that treatment with enzalutamide reduced the risk of the composite endpoint of radiographic progression or death by 72% (hazard ratio [HR], 0.28; 95% confidence interval [CI], 0.16-0.49) but not risk of death (HR, 0.82; 95% CI, 0.55-1.23) in patients with visceral disease, defined as a combined population with baseline disease in the liver and/or lung, with or without metastases to the bone or lymph nodes.¹⁷ Outcomes for patients with lymph node-only disease were also analyzed in this subgroup analysis.¹⁷ The current analysis of PREVAIL determines how outcomes with enzalutamide versus placebo treatment were affected by the specific site of visceral disease (ie, liver metastases vs. lung-only metastases). Moreover, this analysis provides information on the natural history of chemotherapy-naive patients with mCRPC and liver or lung-only visceral disease treated in the placebo arm.

Patients and Methods

Study Design and Participants

The PREVAIL study design, eligibility criteria, and conduct have been fully described elsewhere.⁵ Patients were randomized to

either oral enzalutamide 160 mg/day or placebo until the occurrence of unacceptable adverse events, or confirmed radiographic progression and the initiation of chemotherapy or an investigational agent. The study was approved by the independent review board at each participating site, and was conducted in compliance with the ethical principles originating in or derived from the provisions of the Declaration of Helsinki and the Good Clinical Practice Guidelines of the International Conference on Harmonisation. All patients provided written informed consent before participating in the trial.

Presence of visceral disease (liver and/or lung) was determined radiographically (computed tomography scan or magnetic resonance imaging) by the treating physician and did not require confirmation by biopsy. For all efficacy analyses, the visceral subgroup was divided into liver and lung subsets. Patients with both liver and lung metastases were included in the liver subset because of the previously described inferior survival outcomes of patients with liver versus lung-only involvement.^{3,4,8,9}

The coprimary endpoints of rPFS and OS were prospectively evaluated in the liver and lung subsets along with the exploratory analysis of the following endpoints (all were secondary endpoints in PREVAIL except where indicated): time to initiation of chemotherapy, time to prostate-specific antigen (PSA) progression, time to decline on the Functional Assessment of Cancer Therapy–Prostate questionnaire (FACT-P; exploratory endpoint), confirmed PSA response (\geq 50% PSA decline from baseline), and best overall tissue response determined by investigator assessment using Response Evaluation Criteria In Solid Tumors version 1.1. The coprimary endpoint rPFS was defined as time from randomization to first objective evidence of radiographic disease progression assessed by a blinded independent central review facility or death from any cause within 168 days after treatment discontinuation, whichever occurred first.

Statistical Analysis

The Kaplan-Meier product limit method was used to estimate distributions of the time to events. HRs and their 95% CIs were estimated using an unstratified Cox regression model. A 2-sided, unstratified log-rank test was used to compare rPFS and OS between enzalutamide and placebo. The primary analysis was by intention-to-treat, defined as those patients with measurable disease at screening who were then randomized to one of the treatment arms.

Cochran-Mantel-Haenszel score tests were used to compare the proportion of enzalutamide- and placebo-treated patients with a confirmed \geq 50% reduction in PSA from baseline to PSA nadir and objective response, with corresponding 2-sided 95% CIs calculated using the Clopper-Pearson method.

Incidence data were used to assess the safety and tolerability of enzalutamide and placebo. To adjust for differences in duration of study treatment between the enzalutamide and placebo groups, adverse events (AEs) were also evaluated using event-rate calculations (events per 100 patient-years).

The results presented herein are based on a cutoff date of September 16, 2013, except for rPFS, which was based on a data cutoff date of May 6, 2012.

Results

Patients and Treatment

In PREVAIL, 1717 patients were randomized to treatment: 872 to enzalutamide and 845 to placebo (See Supplemental Figure 1 in the online version). Overall, 204 patients had visceral disease at baseline: 98 (11%) in the enzalutamide group and 106 (13%) in the placebo group (Table 1). Among patients with visceral disease, liver metastases (in 36% of patients) were less frequent than lung metastases (in 64% of patients). Six (0.7%) patients in the enzalutamide group and 3 (0.4%) in the placebo group had both liver and lung metastases and were included in the liver subset.

In the visceral subgroup, patient demographics and disease characteristics were generally similar between treatment arms (Table 1). Liver and lung subsets were well-balanced between each other and the full population with respect to patient age, ECOG PS, median Gleason score, baseline levels of hemoglobin and albumin, baseline pain, and presence of bone disease. A greater proportion of patients in the liver subset than those in the lung subset and full population had more than 20 bone metastases (Table 1). Patients with liver metastases also had higher baseline levels of lactate dehydrogenase, alkaline phosphatase, and PSA than those with lung metastases and those in the full population.

In both the liver and lung subsets, the duration of treatment was longer with enzalutamide than placebo (Table 2). However, the duration of enzalutamide and placebo treatment was shorter in the liver subset than the lung subset and full population.

Efficacy

Coprimary Endpoints. Treatment with enzalutamide versus placebo reduced the risk of radiographic progression or death by 56% in patients with liver metastases and by 86% in patients with lung metastases (Figure 1). The HR in the lung subset (0.14) was similar to that in the full population (0.19).⁵ The HR in the smaller subset of patients with liver metastases favored enzalutamide (0.44), although the magnitude of benefit was less than in the lung subset or the full population. In both treatment groups, median rPFS was shorter in patients with liver metastases than in those with lung metastases.

Treatment with enzalutamide versus placebo was not associated with a reduced risk of death in the subsets of patients with liver and/ or lung metastases (Figure 2). In the liver subset, median OS was 18.9 months (interquartile range [IQR], 10.7-26.2 months) with enzalutamide and 14.8 months (IQR, 8.9 months to not yet reached [NYR]) with placebo, both considerably shorter than that observed in either the lung subset or full population.⁵ Median OS with enzalutamide in the lung subset (32.4 months; IQR, 20.9 months to NYR) was identical to that of patients in the full population receiving enzalutamide (32.4 months; IQR, 22.0 months to NYR⁵), and indicated some improvement in median OS over placebo (26.0 months; IQR, 14.8 months to NYR) in this subset of patients.

A post hoc test of the interaction between treatment and visceral status was not significant for rPFS (P = .2231) or OS (P = .4755).

Secondary and Exploratory Endpoints. In both the liver and lung subsets, treatment with enzalutamide versus placebo was associated with improvements in all secondary endpoints (Figure 3), including delaying time to initiation of chemotherapy (by approximately 15 and 18 months, respectively), which was similar to that in the full population (approximate delay of 17 months). In both visceral subsets, treatment with enzalutamide was associated with delaying time to PSA progression. Confirmed PSA response rates (\geq 50% decline) with enzalutamide were 51% in the liver subset (0% with placebo) and 94% in the lung subset (3% with placebo). In the full population, PSA response rates were 78% with enzalutamide and 3% with placebo.⁵ The small subset of patients with liver metastases fared worse than those with lung metastases, who had benefits on secondary endpoints consistent with the full population. Enzalutamide did not delay time to FACT-P decline in the visceral subsets versus placebo, which was not the case in the full population.⁵

In patients with measurable disease at baseline, best overall softtissue response rate with enzalutamide was 29% (10 of 34 patients) in the liver subset and 73% (27 of 37 patients) in the lung subset, and 3% (1 of 30 patients) and 0% (0 of 50 patients), respectively, with placebo. Six patients with visceral disease—2 (6%) with liver metastases and 4 (11%) with lung metastases—achieved a complete response with enzalutamide. Radiographic images showing the disappearance of liver and lung lesions in 2 patients with a complete response to enzalutamide are shown in Supplemental Figure 2 (in the online version).

Safety

The incidence of any AE, grade 3 or 4 AEs, and serious AEs in the visceral subgroup were similar to those in the full study population (See Supplemental Table 1 in the online version). The incidence rate of the most common AEs of fatigue, back pain, constipation, and arthralgia were each lower with enzalutamide than placebo; among specific AEs, rates of hypertension (11 vs. 8 per 100 patient-years) and cardiac AEs (19 vs. 15 per 100 patient-years) were higher with enzalutamide, which was consistent with findings in the full population (See Supplemental Table 1 in the online version).

Subsequent Therapies

More patients in the placebo arms of the nonvisceral and visceral subgroups received chemotherapy (either docetaxel or cabazitaxel) as the first subsequent therapy after progression (Table 3).

Discussion

The PREVAIL trial included patients with visceral disease who were asymptomatic or minimally symptomatic, had ECOG PS of 0 or 1, and were chemotherapy-naive. Men in the placebo arm also represent the first prospectively followed group with CRPC and visceral disease stratified by specific anatomical site to be reported.

It is important for clinicians to understand how the subgroup of men with baseline visceral disease located at common sites of metastasis did with second-line hormone therapy prior to chemotherapy. A prior analysis showed that enzalutamide versus placebo reduced the risk of rPFS but not OS in the 204 PREVAIL patients with baseline visceral disease at any site.¹⁷ Our analysis extends these findings by assessing enzalutamide efficacy specifically by the site of metastasis. Although patients with liver metastases had delayed radiographic progression and improvements on all progression and response endpoints, including complete responses in 2 (6%) patients, enzalutamide treatment did not improve OS in that subset.

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	Liver Met	astases	Lung Met	astases	Full Study P	opulation
Parameter	Enzalutamide (n $=$ 40)	Placebo (n = 34)	Enzalutamide (n = 58)	Placebo (n = 72)	Enzalutamide (n $= 872$)	Placebo (n = 845)
Median age, y (IQR)	74.0 (70.0-81.5)	70.0 (65.0-75.0)	73.0 (66.0-78.0)	71.0 (65.0-76.5)	72.0 (66.0-78.0)	71.0 (65.0-77.0)
ECOG PS, n (%)						
0	22 (55)	23 (68)	37 (64)	44 (61)	584 (67)	585 (69)
-	18 (45)	11 (32)	21 (36)	28 (39)	288 (33)	260 (31)
Baseline pain score on BPI-SF Q3, n (%) ^a						
0-1	22 (56)	24 (73)	38 (66)	41 (57)	569 (66)	567 (68)
≥2	17 (44)	9 (27)	20 (35)	31 (43)	290 (34)	273 (33)
Median lactate dehydrogenase, U/L (IQR)	204.5 (176.5-307.0)	218.5 (190.0-324.0)	180.5 (154.0-212.0)	190.0 (170.0-221.0)	185.0 (164.0-218.0)	185.0 (164.0-217.0)
Median alkaline phosphatase, U/L (IQR)	112.0 (77.5-168.0)	126.5 (77.0-298.0)	91.5 (71.0-119.0)	89.0 (70.0-131.0)	94.0 (70.0-138.0)	86.0 (68.0-126.0)
Median PSA, ng/mL (IQR)	83.9 (35.5-259.1)	104.3 (30.5-289.7)	70.2 (16.5-152.2)	51.2 (13.7-156.3)	54.1 (17.7-130.9)	44.2 (17.0-132.2)
Median hemoglobin, g/L (IQR)	128.5 (116.5-137.0)	127.0 (120.0-134.0)	130.0 (121.0-137.0)	130.0 (124.0-139.0)	130.0 (123.0-138.0)	131.0 (123.0-138.0)
Median albumin, g/L (IQR)	37.5 (36.0-41.5)	37.0 (35.0-39.0)	39.0 (36.0-41.0)	38.0 (36.0-40.0)	38.0 (36.0-40.0)	39.0 (36.0-40.0)
Median Gleason score (IQR)	8.0 (7.0-9.0)	7.0 (7.0-9.0)	7.0 (7.0-8.0)	7.0 (7.0-9.0)	8.0 (7.0-9.0)	8.0 (7.0-9.0)
Gleason score ≥ 8 at initial diagnosis, n (%) ^a	22 (56)	15 (47)	21 (38)	34 (49)	424 (51)	423 (52)
Bone disease, n (%)	34 (85)	27 (79)	46 (79)	57 (79)	741 (85)	690 (82)
>20 bone metastases, n (%)	10 (25)	13 (38)	7 (12)	14 (19)	145 (17)	150 (18)
Measurable soft-tissue disease, n (%)	34 (85)	30 (88)	37 (64)	50 (69)	396 (45)	381 (45)
Baseline use of corticosteroids, n (%)	3 (7.5)	2 (5.9)	3 (5.2)	2 (2.8)	35 (4.0)	36 (4.3)
Prior antiandrogen use, n (%)	36 (90)	31 (91)	46 (79)	64 (89)	760 (87)	730 (86)
Prior radical prostatectomy, n (%)	12 (30)	8 (24)	15 (26)	14 (19)	226 (26)	225 (27)

Abbreviations: BPI-SF 03 = Brief Pain Inventory Short Form question 3; EC0G PS = Eastern Cooperative Oncology Group performance status; IQR = interquartile range; PSA = prostate-specific antigen. ^aSome patients had missing baseline values. Percentages were calculated based on all patients with baseline values.

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Table 2 Duration of Study Drug Treatment in the PREVAIL Visceral Subgroups and Full Population							
	Liver Me	tastases	Lung Me	tastases	Full Study	Population ^a	
Parameter	Enzalutamide $(n = 40)$	Placebo $(n = 34)$	Enzalutamide $(n = 58)$	Placebo $(n = 72)$	Enzalutamide $(n = 871)$	Placebo $(n = 844)$	
Duration of treatment, mo							
Median (IQR)	9.6 (3.6-17.6)	3.4 (2.1-4.4)	15.5 (10.6-20.4)	3.9 (2.1-6.9)	16.6 (10.1-21.1)	4.6 (2.8-9.7)	
Mean (SD)	10.5 (8.15)	4.8 (4.67)	15.6 (8.21)	5.3 (4.32)	15.8 (7.64)	7.0 (6.05)	
Patients with ${\geq}12$ months of treatment duration, %	32	8.8	55	4.2	68	18	
Treatment ongoing at data cutoff date, %	20	0	36	2.8	42	7.2	
Median OS follow-up, mo (IQR)	22.9 (17.4-27.2)	25.1 (20.5-27.8)	22.8 (18.2-29.2)	23.6 (20.9-27.5)	22.2 (18.5-26.7)	22.4 (18.5-26.4)	

Abbreviations: IQR = interquartile range; OS = overall survival; SD = standard deviation. ^aOne patient in each treatment group was enrolled but never treated.

The lack of an effect on survival may have been because of the small number of patients with liver metastases in PREVAIL.

We focused on subsets of patients with liver and lung metastases because these were the most common sites of visceral disease, and we determined that these sites affected rPFS and OS, as well as secondary and exploratory endpoint measures. Patients with liver metastases had a distinctly worse outcome than those with lung metastases. Moreover, patients with lung-only visceral metastases had outcomes similar to patients without any visceral metastases and the overall PREVAIL study population.⁵ These findings confirm the poorer prognosis associated with liver metastases regardless of enzalutamide or placebo treatment, which is consistent with prior reports for other agents.^{3,4,8,9} We observed that a significant proportion of patients in the visceral and nonvisceral placebo arms were able to receive treatment with chemotherapy after progression on study, supporting the initial reasoning that placebo use in this population would not prevent subsequent treatment with chemotherapy.

Our results suggest a need to better understand the underlying biology of metastatic tumors with a predilection to the liver that leads to inferior treatment responses and outcomes in patients with CRPC regardless of the treatment prescribed. For those with lungonly metastases, improvements in rPFS, OS, and secondary endpoints were similar to those observed in the overall PREVAIL population. These findings suggest that the category of "visceral disease" should be divided into lung-only and liver and not analyzed separately, at least in this population of chemotherapy-naive men with mCRPC.

There is limited information on efficacy outcomes for chemotherapy-naive patients with mCRPC with visceral disease treated with systemic therapies other than chemotherapy. In the TAX 327 study, docetaxel plus prednisone improved survival compared with mitoxantrone plus prednisone in men with mCRPC.¹⁰ An updated survival analysis that combined all patients who received chemotherapy in TAX 327 showed that patients with visceral disease (liver or lung sites not specified), who comprised 23% of the overall study population, died earlier than those without visceral disease.¹⁸ A subsequent retrospective analysis that evaluated outcomes by site of visceral disease showed PSA response rates of 22% and 31% in patients with liver or lung metastases and radiographic response rates of 6% and 7%, respectively.⁴ In comparison, patients with liver or lung metastases treated with enzalutamide in

Figure 1 Kaplan-Meier Estimates of Radiographic Progression-free Survival in Patients With Metastatic Castration-resistant Prostate Cancer Who Participated in the Phase III PREVAIL Trial and Had Metastatic Liver (A) or Lung (B) Disease



Abbreviations: CI = confidence interval; HR = hazard radio; IQR = interquartile range; NYR = not yet reached.



Abbreviations: CI = confidence interval; HR = hazard ratio; IQR = interquartile range; NYR = not yet reached.

our analysis had PSA response rates of 51% and 94% and radiographic response rates of 29% and 73%, respectively. Complete responses were observed in individual patients with liver (6%) or lung (11%) metastases. Although the TAX 327 and PREVAIL trial populations and designs are not directly comparable and they were conducted more than a decade apart, our analysis suggests that enzalutamide has substantial clinical activity in chemotherapy-naive patients with mCRPC with visceral disease, regardless of the site of visceral involvement.

Several strengths and limitations of our analysis should be noted. PREVAIL was the first phase III study of chemotherapy-naive men with mCRPC with minimal or no symptoms to include patients with visceral disease. Liver and lung subsets were prospectively defined in terms of number and sites of involvement as recommended by the Prostate Cancer Clinical Trials Working Group 2.¹⁹ However, because presence of visceral disease (liver and/or lung) was determined radiographically by the treating physician and did not require confirmation by biopsy, it is possible that some of the lesions were not accurately attributed. Although enzalutamide was effective in chemotherapy-naive patients with mCRPC with visceral disease, it is likely that other agents that target androgen receptor signaling, such as abiraterone acetate, may also be efficacious. This assertion remains unresolved as the Phase 3, Randomized, Double-blind, Placebo-Controlled Study of Abiraterone Acetate (CB7630) Plus Prednisone in Asymptomatic or Mildly Symptomatic Patients With Metastatic Castration-Resistant Prostate Cancer (COU-302) trial excluded men with visceral disease.¹⁵ Finally, the total number of patients with liver or lung metastases was small compared with the nonvisceral

Figure 3 Secondary Efficacy Outcomes in the PREVAIL Visceral Subgroups and Full Population Patients, n Median, mo (IQR) Median, mo (IQR) Hazard Ratio ENZA/PBO **ENZA** PBO (95% CI) Time to initiation of chemo - liver mets 40/34 20.7 (10.4-NYR) 5.5 (3.2-15.4) 0.37 (0.19-0.71) Time to initiation of chemo - lung mets 58/72 26.0 (15.0-NYR) 8.5 (5.0-15.0) 0.25 (0.15-0.43) Time to initiation of chemo - full population 872/845 28.0 (15.3-NYR) 10.8 (4.9-28.8) 0.35 (0.30-0.40) Time to PSA progression - liver mets 40/34 8.3 (5.6-11.1) 3.0 (2.8-3.7) 0.25 (0.11-0.56) 0.11 (0.06-0.22) Time to PSA progression - lung mets 58/72 14.5 (8.3-24.8) 2.8 (2.8-3.7) Time to PSA progression - full population 872/845 11.2 (5.7-NYR) 2.8 (2.8-4.6) 0.17 (0.15-0.19) Time to FACT-P decline - liver mets 40/34 22.0 (2.8-NYR) 3.0 (1.0-11.1) 0.47 (0.22-1.00) Time to FACT-P decline - lung mets 58/72 11.1 (2.7-22.1) 5.6 (2.8-13.8) 0.65 (0.37-1.15) Time to FACT-P decline - full population 872/845 11.3 (2.8-NYR) 5.6 (2.7-16.6) 0.62 (0.54-0.72) ò 0.5 15 2.0 10 Favors Favors Enzalutamide

Abbreviations: Chemo = chemotherapy; Cl = confidence interval; ENZA = enzalutamide; FACT-P = Functional Assessment of Cancer Therapy–Prostate questionnaire; IQR = interquartile range; mets = metastases; NYR = not yet reached; PBO = placebo; PSA = prostate-specific antigen.

 Table 3
 All Subsequent Postbaseline Antineoplastic Therapy Use for Metastatic Castration-resistant Prostate Cancer in PREVAIL

	Nonvisceral Subgr	roup (n = 1513)	Visceral Subgroup (n $=$ 204)			
Parameter	Enzalutamide (n $=$ 774)	Placebo (n $=$ 739)	Enzalutamide (n $=$ 98)	Placebo (n $=$ 106)		
Patients with $\geq\!\!1$ postbaseline therapy listed below	307 (40)	516 (70)	44 (45)	78 (74)		
Antineoplastic therapy						
Abiraterone acetate	157 (20)	340 (46)	22 (22)	45 (43)		
Cabazitaxel	40 (5.2)	93 (13)	11 (11)	17 (16)		
Docetaxel	255 (33)	412 (56)	31 (32)	67 (63)		
Enzalutamide	5 (0.6)	29 (3.9)	4 (4.1)	8 (7.5)		
Sipuleucel-T	11 (1.4)	7 (0.9)	1 (1.0)	3 (2.8)		
Patients taking ≥ 1 investigational drug	38 (4.9)	69 (9.3)	4 (4.1)	12 (11)		

All data are shown as n (%).

subgroup, and PREVAIL was not designed or powered to detect treatment differences within these subsets. Our interpretations of results must therefore be considered exploratory.

Conclusions

Our analysis has relevance for clinical practice by addressing a knowledge gap in the literature regarding the outcomes of men with asymptomatic or minimally symptomatic mCRPC and visceral disease involving the liver and/or lung who were treated with enzalutamide or placebo. Enzalutamide is a reasonable therapeutic option in such patients and appears to be well-tolerated, with a safety profile similar to that observed in the full PREVAIL population. Because of the poorer outcomes in patients with liver metastases than in those with lung metastases observed in this and other studies,^{3,4,8,9} it is critical to identify tumor and microenvironment influences that may be responsible. Elucidating the biological differences between metastatic sites of CRPC may enable the development new drug combinations that further improve upon the efficacy of enzalutamide.

Clinical Practice Points

- Enzalutamide significantly decreases the risk of radiographic progression and death, delays the initiation of chemotherapy, and improves health-related quality of life in chemotherapy-naive men with asymptomatic or minimally symptomatic metastatic prostate cancer progressing on androgen-deprivation therapy.
- The PREVAIL trial of the oral androgen-receptor inhibitor enzalutamide versus placebo was unique in that it did not exclude patients with visceral disease. Our analysis revealed that enzalutamide improved rPFS in patients with liver and/or lung disease.
- Enzalutamide may be considered to be an active first-line treatment option in patients with mCRPC, including those with visceral involvement, delaying the need for chemotherapy.

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BHR Pharma, Dendreon, Emergent BioSolutions, Ferring, Genentech, Medivation, Orion Corporation, Pfizer, and Sanofi, has received institutional research funding from Algeta/Bayer, Aragon Pharmaceuticals, AstraZeneca, Dendreon, Emergent BioSolutions, Exelixis, Genentech, Medivation, Millennium, Oncogenex, Sanofi, and Teva, and has received travel expenses from AbbVie, Amgen, Astellas Pharma, Bayer, Dendreon, Emergent BioSolutions, Ferring, Genentech, Johnson & Johnson, Medivation, Ockham, Orion Pharma, Pfizer, Sanofi, and Teva. Y.L. has served as an advisor for Astellas, Bristol-Myers Squibb, Ipsen, Janssen, Roche, and Sanofi, and has received institutional research funding from Sanofi and travel expenses from Astellas, Bristol-Myers Squibb, and Sanofi. H.M. and S.B.N. are former employees of and hold stock in Medivation. D.P. is an employee of Astellas Pharma. C.N.S. has received institutional research funding or honoraria from Astellas, Bayer, Cougar Biotechnology (now Janssen Oncology), Medivation, Sanofi, Genzyme, Ipsen, and Roche/Genentech. B.T. has received grants from Astellas, Ferring, and Sanofi, personal fees from Astellas, Bayer, Ferring, Medivation, and Sanofi, and nonfinancial support from Astellas.

Supplemental Data

Supplemental table and figures accompanying this article can be found in the online version at http://dx.doi.org/10.1016/j.clgc. 2017.02.007.

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Enzalutamide for mCRPC With Visceral Disease



Abbreviation: ITT = intent-to-treat. *Randomization was stratified by study site. †Majority discontinued due to rising prostate-specific antigen. ‡Liver only or liver and lung metastases.

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Screening

Week 61



Abbreviation: PSA = prostate-specific antigen.

Enzalutamide for mCRPC With Visceral Disease

Supplemental Table 1 Summary of AEs in the PREVAIL Visceral Subgroup (Liver and Lung Subsets Combined) and Full Population					
	Visceral Sub	group, n (%)	Full Study Population, n (%) ^a		
Parameter	Enzalutamide $(n = 98)$	Placebo $(n = 106)$	Enzalutamide $(n = 871)$	Placebo $(n = 844)$	
AE					
Any AE	94 (96)	98 (93)	844 (97)	787 (93)	
Any grade 3-4 AE	47 (48)	38 (36)	374 (43)	313 (37)	
Any serious AE	35 (36)	33 (31)	279 (32)	226 (27)	
Most common AEs ^b					
Fatigue	28 (29)	26 (25)	310 (36)	218 (26)	
Back pain	25 (26)	24 (23)	235 (27)	187 (22)	
Constipation	26 (27)	20 (19)	193 (22)	145 (17)	
Arthralgia	17 (17)	12 (11)	177 (20)	135 (16)	
Specific AEs					
Hypertension	11 (11)	4 (3.8)	117 (13)	35 (4.1)	
Cardiac AEs	12 (12)	7 (6.6)	88 (10)	66 (7.8)	
Alanine aminotransferase elevation	2 (2.0)	2 (1.9)	8 (0.9)	5 (0.6)	
Seizure	0	1 (0.9)	1 (0.1) ^c	1 (0.1)	
AE, event rate per 100 patient-years of exposure					
Fatigue	28.8	50.0	29.9	43.0	
Back pain	26.1	53.9	23.6	42.5	
Constipation	25.3	40.4	18.5	28.4	
Arthralgia	20.9	23.1	18.6	29.5	
Hypertension	11.3	7.7	10.8	6.6	
Cardiac disorders	19.2	15.4	10.3	14.8	

Abbreviation: AE = adverse event. ^aOne patient in each treatment group was enrolled but never treated. ^bAt least 20% on enzalutamide and \geq 2% more than placebo in the safety population. ^cThis seizure occurred after the data cutoff date.

JOURNAL OF CLINICAL ONCOLOGY

ORIGINAL REPORT

Targeting Androgen Receptor and DNA Repair in Metastatic Castration-Resistant Prostate Cancer: Results From NCI 9012

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ASSOCIATED CONTENT



on page 1017 Appendix



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Purpose

To determine whether cotargeting poly (ADP-ribose) polymerase-1 plus androgen receptor is superior to androgen receptor inhibition in metastatic castration-resistant prostate cancer (mCRPC) and whether ETS fusions predict response.

Α В S Т R Α С Т

Patients and Methods

Patients underwent metastatic site biopsy and were stratified by ETS status and randomly assigned to abiraterone plus prednisone without (arm A) or with veliparib (arm B). Primary objectives were: confirmed prostate-specific antigen (PSA) response rate (RR) and whether ETS fusions predicted response. Secondary objectives were: safety, measurable disease RR (mRR), progression-free survival (PFS), and molecular biomarker analysis. A total of 148 patients were randomly assigned to detect a 20% PSA RR improvement.

Results

A total of 148 patients with mCRPC were randomly assigned: arm A, n = 72; arm B, n = 76. There were no differences in PSA RR (63.9% v72.4%; P = .27), mRR (45.0% v52.2%; P = .51), or median PFS (10.1 v11 months; P = .99). ETS fusions did not predict response. Exploratory analysis of tumor sequencing (80 patients) revealed: 41 patients (51%) were ETS positive, 20 (25%) had DNA-damage repair defect (DRD), 41 (51%) had AR amplification or copy gain, 34 (43%) had PTEN mutation, 33 (41%) had TP53 mutation, 39 (49%) had PIK3CA pathway activation, and 12 (15%) had WNT pathway alteration. Patients with DRD had significantly higher PSA RR (90% v 56.7%; P = .007) and mRR (87.5% v38.6%; P = .001), PSA decline $\geq 90\%$ (75% v25%; P = .001), and longer median PFS (14.5 v8.1 months; P = .025) versus those with wild-type tumors. Median PFS was longer in patients with normal PTEN (13.5 v 6.7 months; P = .02), TP53 (13.5 v 7.7 months; P = .01), and PIK3CA (13.8 v 8.3 months; P = .03) versus those with mutation or activation. In multivariable analysis adjusting for clinical covariates, DRD association with PFS remained significant.

Conclusion

Veliparib and ETS status did not affect response. Exploratory analysis identified a novel DRD association with mCRPC outcomes.

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INTRODUCTION

Despite a high response rate (RR) to androgen deprivation (AD), a majority of patients with metastatic prostate cancer (PCa) will experience progression to castration resistance. Advances in understanding the biology and progression mechanisms to castration resistance led to development and approval of novel androgen receptor (AR) -targeted therapies: abiraterone acetate plus prednisone (AAP) and enzalutamide.^{1,2} Both prolong survival in metastatic castration-resistant prostate cancer (mCRPC) irrespective of prior docetaxel.^{3,4} However, many patients exhibit de novo resistance to both therapies, and resistance invariably occurs in responders, warranting a search for better treatments.⁵⁻⁸

Several studies have shown that AR regulates components of DNA-repair pathways, and conversely, several enzymes involved in DNA repair can modulate AR activity.⁹⁻¹⁵ An important example is

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poly (ADP-ribose) polymerase-1 (PARP1), an enzyme with essential roles in recognition and repair of single-strand DNA breaks through base excision repair process.¹⁶ Several cancers, including CRPC, exhibit increased PARP1 expression and/or activity.¹⁶⁻¹⁹ Compelling data implicate PARP1 in mediation of DNA-repair responses to alkylators, cellular survival in BRCA-deficient cells, and AR-mediated PCa cell proliferation.^{16,20-23} Specifically, preclinical studies using PARP1 inhibitors (eg, veliparib, olaparib) in PCa showed that PARP1 activity was required for maximal AR function.¹⁶ In vivo, PARP1 inhibition with veliparib was as effective as castration in preventing tumor growth, and even greater inhibition was achieved with combination veliparib and castration.¹⁶

Canonic ETS gene fusions (androgen-responsive promoters driving ETS transcription factor overexpression) are present in > 50% of patients with PCa. ERG, the predominant ETS gene fusion product, physically interacts with PARP1.²⁴⁻²⁶ PARP1 is required for full ERG activity and its downstream oncogenic functions. ERG-positive xenografts are preferentially sensitive to PARP1 inhibitors.²⁶

On the basis of these data, we hypothesized that in patients with mCRPC, cotargeting AR and PARP1 would result in a better RR than AAP and the combination would be most effective in patients with ETS fusion–positive tumors.

PATIENTS AND METHODS

Patients

Eligible patients had mCRPC, Eastern Cooperative Oncology Group performance status of 0 to 2, testosterone < 50 ng/dL, normal organ function, no prior exposure to AAP, and up to two prior chemotherapy regimens. Complete eligibility criteria are outlined in the Study Protocol. All patients provided written informed consent per institutional and federal guidelines.

Study Design, Treatment, and End Points

This was a biomarker-stratified and randomized phase II multicenter trial (Fig 1). The primary objectives were to evaluate whether AAP plus veliparib is superior to AAP, as reflected by prostate-specific antigen (PSA)



Fig 1. CONSORT diagram. (*) Safety evaluable. (†) Defined as having received two cycles of therapy or removed because of toxicity; five patients who received < two cycles did so by patient choice. (‡) Sequencing completed for all patients with sufficient extra tissue from biopsy required for sequencing.

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Downloaded from ascopubs.org by UNIVERSITY WASHINGTON on December 6, 2018 from 128.095.104.109 Copyright © 2018 American Society of Clinical Oncology. All rights reserved. RR (\geq 50% decline), and whether ETS gene fusion predicts response. Other end points included measurable disease RR (mRR), progression-free survival (PFS), toxicities, and exploratory tumor molecular analysis.

All patients underwent metastatic disease biopsy (unless metastatic archival tissue was available). ETS status was determined by immunohistochemistry (IHC) for ERG and in situ hybridization (ISH) –based assays for ETV1 fusions,^{27,28} conducted in a College of American Pathologists/Clinical Laboratory Improvement Amendments–accredited laboratory. The study was activated before AAP approval in prechemotherapy setting. Eligible patients were stratified by prior ketoconazole and ETS fusion status (positive or negative) and randomly assigned to AA 1,000 mg per day plus prednisone 5 mg twice per day (arm A) or AAP plus veliparib 300 mg twice per day (arm B), for days 1 to 28. Arm B patients underwent lead-in treatment with AAP, followed on day 8 by veliparib, in cycle 1 only. Treatment was continued until radiographic/clinical disease progression, intercurrent illness, unacceptable adverse events (AEs), withdrawal of consent, or death.

Assessments

Patients underwent baseline disease assessments and then every 12 weeks with bone scan, computed tomography or magnetic resonance imaging of abdomen/pelvis, and x-ray or computed tomography of chest for the first year. For patients who have completed ≥ 1 year of therapy, imaging can be done every 4 months, and for patients who have completed ≥ 2 years of therapy, imaging can be done every 6 months. Irrespective of duration on therapy, imaging can be done sooner than the specified intervals as clinically indicated. PSA was assessed at baseline and on day 1 of each cycle. AEs were graded according to Common Terminology Criteria for Adverse Events (version 4.0).

Tumor Sequencing

Extra tumor tissue for sequencing was available for 87 patients; 80 of 87 were response evaluable (four patients received < two cycles of treatment, three patients were never treated, one was ineligible, and two withdrew consent). Their baseline characteristics are detailed in Appendix Tables A1 and A2 (online only). Flash-frozen biopsies were processed for genomic DNA and total RNA isolation using Qiagen AllPrep Kit (Hilden, Germany) and then underwent targeted exon sequencing and capture transcriptome analysis at University of Michigan (Ann Arbor, MI), as previously detailed.^{29,30}

Statistical Analysis

Biomarker-stratified design³¹ was used to determine a PSA RR difference between arms A and B and between arms by ETS fusion (positive ν negative strata). The trial was designed to accrue 148 response-evaluable patients randomly assigned at a one-to-one ratio to arms A and B to provide 80% power at a one-sided 5% significance level to detect an improvement of 20% in PSA RR between arms with a χ^2 test of proportions, assuming a PSA RR of 30% in arm A (based on data available at time of study design).¹ Response-evaluable patients were those receiving at least two therapy cycles or those removed from study because of toxicity before completing two cycles. The PSA RR difference between treatment groups by ETS fusion status was an interaction test with a significance threshold of .15 from a logistic model (trial design details provided in protocol).

The primary outcome of confirmed PSA RR (complete or partial response) was analyzed with χ^2 tests to test differences between treatment arms and differences within a biomarker stratum between treatment arms. Confirmed PSA RR was modeled to test ETS fusion status as prognostic using a logistic model with ETS status as the only covariate and as predictive using logistic models testing interaction of treatment arm and ETS. Similar models were used for mRR. Both prognostic and predictive models were used in the exploratory analyses for each sequencing biomarker including DNA-damage repair defect (DRD). Secondary end point PFS was reported using Kaplan-Meier methods and associated log-rank tests.

Exploratory analysis for prognostic biomarkers with association with PFS was reported using product-limit estimates and log-rank tests. Cox models were used to test biomarkers as predictive of PFS with models including an interaction of treatment arm and biomarker status. An unplanned analysis using a multivariable Cox model for PFS was used to explore biomarker associations with PFS after controlling for clinical covariates by adding the biomarker to the model including the clinical covariates. Each biomarker was modeled separately. All analyses were completed using SAS software (version 9.4; SAS Institute, Cary, NC).

RESULTS

Patient Characteristics

From May 2012 through December 2015, 190 patients with mCRPC were enrolled at 12 centers (Table 1); 185 eligible patients underwent metastatic biopsy (soft tissue, n = 89; bone, n = 96); 159

Table 1. Baseline Patient Demographic and Clinical Characteristics by Treatment Arm					
		No. (%)			
Characteristic	Arm A: Abiraterone (n = 74)	Arm B: Abiraterone + Veliparib (n = 79)	Ρ		
Age, years Median Range	69 50-90	68 47-85	.35		
Race White Black Other	61 (82.4) 9 (12.2) 4 (3.4)	74 (93.7) 3 (3.8) 2 (2.5)	.09		
Performance status 0 1 2	46 (62.2) 28 (37.8) 0	50 (63.3) 28 (35.4) 1 (1.3)	.93		
PSA, ng/mL Median Range	32.7 0.8-1,557.6	36.4 0.04-1,074.4	.67		
Cancer pain present	23 (31.1)	26 (33.0)	.81		
Bone Lymph node Visceral Other	64 (86.5) 45 (60.8) 13 (17.6) 13 (17.6)	68 (86.1) 53 (67.1) 21 (26.6) 16 (20.3)	.94 .42 .18 .67		
Previous treatments Chemotherapy Docetaxel/cabazitaxel Other Enzalutamide	16 (20.8) 11 (14.9) 5 (6.8) 2 (2.7)	23 (30.3) 17 (21.5) 6 (7.6) 2 (2.5)	.29 .99		
Sipuleucel-T Experimental agent	22 (29.7) 19 (25.7)	13 (16.5) 15 (19.0)	.05 .32		
Strata: ETS fusion and ketoconazole use ETS fusion positive* ETS fusion negative Previous ketoconazole	25 (33.8) 49 (66.2) 8 (10.8)	28 (35.4) 51 (64.6) 9 (11.3)	.83		
No. of treatment cycles Median Range	9 1-46	9 1-50	.68		
Overall survival Median 95% Cl	30.6 28.4 to NR	32.3 28.4 to NR			

Abbreviations: NR, not reached; PSA, prostate-specific antigen. *ETS fusion determined by immunohistochemistry/in situ hybridization.
patients (86%) had adequate tissue; 35% were ETS positive; 153 patients (white, 88%; black, 8%; median age, 68 years; median PSA, 35.4 ng/mL) were randomly assigned to arm A (AAP; n = 74) or arm B (AAP + veliparib; n = 79; Fig 1).

Safety

Because of bothersome low-grade AEs, veliparib dose was reduced to 200 mg twice per day for cycle 1, and if tolerated, dose was escalated to 300 mg twice per day for subsequent cycles. Distribution of grade \geq 3 AEs irrespective of attribution was similar between arms. Overall, therapy was well tolerated (Appendix Table A3, online only); hyperglycemia was the only high-grade treatment-related AE that occurred in > 5% of patients in either arm (arm A, 9%; arm B, 5%). In arm A, 20% of patients (n = 15) had grade 3 treatment-related AEs, and one patient had grade 4 hyperglycemia. In arm B, 24% of patients (n = 19) had grade 3 treatment-related AEs, one patient had grade 4 thrombocytopenia, and one patient had grade 5 cardiac arrest possibly treatment related. Any-grade AEs that were significantly more frequent (P < .05) in arm B versus arm A were fatigue, lymphopenia, nausea, and vomiting; edema occurred more frequently in arm A than arm B.

Efficacy

Of the 153 randomly assigned and treated patients, 148 were response evaluable; five (3%) were not evaluable (four patients chose to stop treatment within one cycle, and one had > 4-week treatment delay). There was no statistically significant difference between arms in confirmed PSA RR (arm A, 63.9%; arm B, 72.4%; P = .27), mRR (arm A, 45.0%; arm B, 52.2%; P = .51), or median PFS (arm A, 10.1 months; arm B, 11 months; P = .99; Table 2; Appendix Fig A1A). Furthermore, ETS fusion status did not predict PSA, mRR, or PFS (Appendix Fig A1B).

DRD and Additional Prognostic Biomarkers

For 87 patients, extra biopsy tumor tissue was analyzed by next-generation sequencing; 80 of 87 were treated and response evaluable (arm A, n = 33; arm B, n = 47). Sequenced patients' characteristics compared with those of patients who did not have tumor sequencing and their baseline characteristics by treatment arm are listed in Appendix Tables A1 and A2. Overall, the groups were fairly comparable, except for site of disease (bone v soft tissue [eg, lymph node, visceral disease]), which affected the site of biopsy: in the sequenced cohort, a majority (75%) were soft tissue biopsies, whereas in the nonsequenced population, a majority (70%) had bone biopsies. This is not surprising, considering tumor yield is known to be better with soft tissue biopsy. The tumor yield likely affected the difference between the two groups in the proportion of patients with ETS-positive tumors, which was higher in the sequenced group.

ETS fusion status was also analyzed by sequencing to evaluate concordance with the IHC/ISH methods used. Agreement between methods was observed for 72 (90%) of 80 patients (Appendix Table A4, online only); 41 patients (51.3%) were ETS positive by sequencing.

Sequencing classified patients into three categories of DNArepair status (Fig 2A): wild type (WT; n = 55 [68.75%]), biallelic DRD (n = 20 [25%]), and monoallelic DRD (n = 5 [6.25%]). Patients with DRD had alterations in *BRCA1*, *BRCA2*, *ATM*, *FANCA*, *PALB2*, *RAD51B*, or *RAD51C*, with *BRCA2* being the most frequently detected (Fig 2A). Notably, these genes represent major players in the homologous recombination (HR) pathway, which functions along with the nonhomologous end-joining (NHEJ) pathway to repair DNA double-strand breaks.¹⁵ Additional genes of interest were also significantly altered, including *AR* (n= 41 [51%]), *TP53* (n = 33 [41%]), *PTEN* (n = 34 [42.5%]), and *PIK3CA* (n = 39 [49%]). Alterations were also annotated for AR-related genes and the WNT pathway.

	Overall (n = 148) No. (%)		E	TS Positive (n = 52)			_			
			_	No. (%)			1	No. (%)	_	
Response	Abiraterone	Abiraterone + Veliparib	P	Abiraterone	Abiraterone + Veliparib	Р	Abiraterone	Abiraterone + Veliparib	P	Interaction P
PSA outcomes	(n = 72)	(n = 76)		(n = 25)	(n = 27)		(n = 47)	(n = 49)		
PSA response (CR/ PR)	46 (63.9)	55 (72.4)	.27	15 (60.0)	19 (70.4)	.43	31 (66.0)	36 (73.5)	.42	.89
CR	12 (16.7)	12 (15.8)		4 (16.0)	3 (11.1)		8 (17.0)	9 (18.4)		
PR	34 (47.2)	43 (56.6)		11 (44.0)	16 (59.3)		23 (48.9)	27 (55.1)		
Stable disease	19 (26.4)	15 (19.7)		7 (28.0)	7 (25.9)		12 (25.5)	8 (16.3)		
Progressive disease	7 (9.7)	6 (7.9)		3 (12.0)	1 (3.7)		4 (8.5)	5 (10.2)		
Measurable disease	(n = 40)	(n = 46)		(n = 15)	(n = 19)		(n = 25)	(n = 27)		
RECIST response (CR/PR)	18 (45.0)	24 (52.2)	.51	6 (40.0)	10 (52.6)	.46	12 (48.0)	14 (51.9)	.78	.69
CR	1 (2.5)	0(0)		0 (0)	0 (0)		1 (4.0)	0 (0)		
PR	17 (42.5)	24 (52.2)		6 (40.0)	10 (52.6)		11 (44.0)	14 (51.9)		
Stable disease	14 (35.0)	12 (26.1)		5 (33.3)	6 (31.6)		9 (36.0)	6 (22.2)		
Progressive disease	8 (20.0)	8 (17.4)		4 (26.7)	3 (15.8)		4 (16.0)	5 (18.5)		
Not evaluable	0 (0)	2 (4.4)		0 (0)	0 (0)		0 (0)	2 (7.4)		



Fig 2. Landscape of molecular alterations, DNA-repair status, and survival in this cohort of patients with metastatic castration-resistant prostate cancer (mCRPC). (A) Next-generation sequencing of tumor tissues identified alterations in different genes for each patient (n = 80) as depicted in the matrix, called by each allele. Three groups of patients were determined based on DNA-damage repair defect (DRD) status, represented at the top by black (biallelic DRD), gray (monoallelic DRD), or white boxes (wild-type [VVT] DRD). Above this, maximum percent decreases in prostate-specific antigen (PSA) levels throughout treatment are graphed for each patient, and those with confirmed PSA responses are noted with dark blue bars. Progression-free survival (PFS; months), treatment (abiraterone [A/ABI], veliparib [V/VEL]), and ETS fusion status are also indicated at the top of the matrix for each patient. (B) Matrix of DRD status associated with *PTEN* alterations. Patients along the top in black correspond to patients in this study, and patients in green represent cases from an additional mCRPC cohort.²⁹ (C) PFS curves are shown for patients with WT/monoallelic or biallelic DRD status. LOH, loss of heterozygosity.

Outcome analysis combined WT and monoallelic DRD patients, because the DRD status of the latter group is considered nondeleterious, and compared them with biallelic DRD patients. Prognostic covariates (metastatic site, performance status, PSA, pain, and prior therapies) were similar between DRD and WT groups except for prior sipuleucel-T therapy (DRD, n = 1 [5%] v WT, n = 16 [29%]).



Fig 2. (Continued)

Unexpectedly, we uncovered a novel, significant association between DRD and overall outcome/response. Patients with DRD tumors had significantly higher confirmed PSA RR (90% v 56.7%; P = .007; Table 3; Fig 2A), PSA decline of \ge 90% (75% v 25%; P = .001; Appendix Fig A2, online only), mRR (87.5% v 38.6%; P = .001; Table 3), and median PFS (14.5 v 8.1 months; P = .025; Fig 2C; depicted by treatment arm in Fig 3) compared with patients with WT tumors.

Analysis of Clinical and Molecular Variables

Exploratory biomarker analysis revealed three additional biomarkers associated with longer median PFS (Appendix Tables A5 and A6, online only). Significantly better overall outcomes were identified in patients with normal *PTEN* (13.5 v 6.7 months in those with mutation; P = .02), normal *TP53* (13.5 v 7.7 months in those with mutation; P = .01), or nonactivated PIK3CA pathway (13.8 v 8.3 months in those with activation; P = .03; Appendix Table A5, online only). Multivariable analysis including clinical and biomarker variables individually revealed DRD and TP53 as biomarkers separately associated with PFS after controlling for clinical covariates (Table 4). We also noted that mutation or loss of *PTEN* seemed to be almost mutually exclusive with DRD (Fig 2A).

Exceptional Responders

Several patients had exceptional and durable responses to therapy. These were patients in either arm with PFS > 24 months and PSA decline > 90%. On the basis of these criteria, 19 exceptional responders (arm A, n = 8; arm B, n = 11) were identified; their characteristics are listed in Appendix Table A7 (online only). Nine of 19 had tumor sequencing: four had biallelic DRD, one had monoallelic DRD, and four had WT tumors (Fig 2A; Appendix Table A8, online only).

DISCUSSION

This prospective metastatic tissue–based biomarker-stratified trial stratified patients with mCRPC by ETS fusion status and then randomly assigned them to AAP with or without veliparib. Preclinical data suggested that targeting PARP1 would synergize with AR inhibition, and ETS fusion–positive tumors would be preferentially sensitive to PARP1 inhibition.^{13,16,26} However, the addition of veliparib did not affect response, nor did ETS status predict response. There was no difference between arms in the rate of exceptional responders (AAP, n = 8; AAP + veliparib, n = 11). ETS fusion concordance between IHC/ISH and sequencing was 90%. ERG/ETS failure to predict response may have been a result of the high prevalence of defects in DRD genes (approximately 25% of patients), which was not known at time of study design.

Exploratory metastatic tissue sequencing analysis uncovered a novel finding. Several patients had alterations in genes involved in DNA repair, particularly those implicated in the HR pathway; DRD was significantly associated with better response and PFS irrespective of treatment arm. Prior studies demonstrated mechanistic connections between AR and DNA repair in prostate cancer models,⁹⁻¹⁵ but ours is the first report, to our knowledge, to show the association of DRD with outcome in patients with mCRPC treated with AAP with higher PSA RR, mRR, and PFS compared with patients with WT tumors. However, additional studies are needed for confirmation, because this trial was not designed specifically to test DRD predictive power with AR-targeted therapy. A recent trial in mCRPC showed that DRD was associated with high RRs to a different PARP1 inhibitor (olaparib), but there was no control arm of an AR-targeted agent.³²

	Progn	ostic Biomarker			DRD (n = 20)		DNA-Re	oair WT/Monoalle (n = 60)	lic	
	No	. (%)		No	. (%)		No	. (%)		
Response	DRD	DNA-Repair WT/ Monoallelic	P	Abiraterone	Abiraterone + Veliparib	Ρ	Abiraterone	Abiraterone + Veliparib	Ρ	Interaction P
PSA PSA response 95% CI, %	(n = 20) 18 (90.0) 76.9 to 100	(n = 60) 34 (56.7) 44.1 to 69.2	.007	(n = 7) 6 (85.7) 59.8 to 100	(n = 13) 12 (92.3) 77.8 to 100	1.0	(n = 26) 12 (46.2) 27.0 to 65.3	(n = 34) 22 (64.7) 48.6 to 80.8	.15	.97
Measurable disease RECIST response 95% CI, %	(n = 16) 14 (87.5) 59.5 to 98.3	(n = 44) 17 (38.6) 24.1 to 54.0	.001	(n = 5) 4 (80.0) 44.9 to 100	(n = 11) 10 (90.9) 73.9 to 100	1.0	(n = 19) 7 (36.8) 15.2 to 58.5	(n = 25) 10 (40.0) 20.8 to 59.2	.83	.64

bbreviations: DRD, DNA-damage repair defect; PSA, prostate-specific antigen; RECIST, Response Evaluation Criteria in Solid Tumors; WT, wild type.

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Fig 3. Survival by DNA-repair status and treatment arm. Progression-free survival (PFS) curves are shown by treatment arm for patients with wild-type (WT)/monoallelic or biallelic DNA-damage repair defect (DRD), as determined by next-generation sequencing of tumors shown in Figure 2 of the main manuscript: (A) abiraterone/prednisone; (B) abiraterone/prednisone plus veliparib.

AR plays a major role in promoting double-strand DNA break repair.^{12,13} As such, AR blockade alone would be expected to compromise DNA repair. This concept is supported by our data, wherein tumors defective in DNA repair were sensitized to AAP. Given this recently realized redundancy in function (eg, capacity of both PARP1 inhibitors and AR blockade to suppress DNA repair), it is not unexpected that PARP1 inhibitors did not add to AR blockade.

Our results also raise the question of how DNA repair alterations may be associated with better outcomes with AR-targeted therapy. Recent studies have shown that AR directly regulates genes involved in DNA-damage responses that allow prostate cancer cells to enhance DNA repair, decrease DNA damage, and continue cycling.^{10,12,13,15} Conversely, castration or treatment with antiandrogens leads to decreased expression of DNA-repair enzymes and therefore increased DNA damage and decreased cellular survival; in particular, inhibition of AR signaling has been shown to inhibit the expression of genes primarily involved in the NHEJ pathway of double-strand DNA break repair.¹¹⁻¹⁴ Disruption of NHEJ in the context of an underlying HR defect (the alterations identified in this trial cohort) could induce a synthetic lethality via disruption of both of the major repair pathways for doublestranded DNA breaks, thus explaining why patients with HR deficiencies fare better with AAP treatment. Furthermore, as described in this report, AR directly increases DNA-damage response effectors, and in turn, many DNA-damage response proteins directly modulate AR activity, including BRCA1 and BRCA2, two HR factors altered in several of the DRD patients.^{33,34} Without functional BRCA1 or BRCA2 cofactors, it can be hypothesized that these patients may have had altered AR transcriptional activity compared with WT patients. Further analysis of the sequencing data herein uncovered a positive association with outcome for patients with normal expression of PTEN and TP53 or nonactivated

	Table 4. Multivariable Analysis of PFS by Biomarker Status (n = 80)													
	_		Marker Sta	atus		Cox N	lodel							
		Not Normal		Normal		Univariable	Multivariable*							
Biomarker	No. (%)	Median PFS (months) (95% Cl)	No. (%)	Median PFS (months) (95% Cl)	Log-Rank P	Hazard Ratio (95% CI)	Hazard Ratio (95% CI)							
DRD v WT/monoallelic	20 (25)	14.5 (11.0 to 19.5)	55 (69)	8.0 (5.4 to 13.0)	.02	0.52 (0.29 to 0.93)	0.51 (0.27 to 0.97)							
TP53 (mutated v normal)	33 (41)	7.7 (5.3 to 8.8)	47 (59)	13.5 (8.2 to 16.6)	.01	1.88 (1.14 to 3.12)	2.52 (1.30 to 4.89)							
PTEN (mutated v normal)	34 (43)	6.7 (4.1 to 11.3)	46 (57)	13.5 (8.2 to 16.6)	.02	1.82 (1.11 to 3.01)	1.61 (0.92 to 2.82)							
PIK3CA (activated v normal)	39 (49)	8.3 (5.4 to 13.3)	41 (51)	13.8 (8.2 to 16.6)	.03	1.74 (1.05 to 2.87)	1.45 (0.79 to 2.68)							
SPOP (mutated v normal)	5 (6)	NR (2.8 to NR)	75 (94)	8.8 (7.8 to 13.6)	.06	0.28 (0.07 to 1.15)	0.54 (0.09 to 3.40)							
CHD1 (mutated v normal)	4 (5)	NR (2.6 to NR)	76 (95)	8.8 (7.8 to 13.6)	.09	0.31 (0.07 to 1.29)	0.39 (0.09 to 1.71)							
AR (amplified/mutated v normal)	41 (51)	8.8 (5.4 to 13.5)	39 (49)	11.0 (8.0 to 16.6)	.17	1.41 (0.86 to 2.31)	1.34 (0.80 to 2.23)							
ZFHX3 (mutated v normal)	6 (8)	10.0 (2.1 to 13.8)	74 (92)	10.3 (8.0 to 13.8)	.20	1.74 (0.74 to 4.09)	1.44 (0.57 to 3.63)							
RB1 (mutated v normal)	9 (11)	8.8 (1.9 to 23.7)	71 (89)	10.3 (8.0 to 13.8)	.46	1.32 (0.62 to 2.78)	1.47 (0.66 to 3.28)							
ETS (positive <i>v</i> negative)	41 (51)	8.2 (5.4 to 14.5)	39 (49)	13.3 (8.2 to 13.8)	.48	1.19 (0.73 to 1.95)	1.24 (0.45 to 3.38)							
WNT (activated <i>v</i> normal)	12 (15)	12.4 (2.7 to 23.7)	68 (85)	10.3 (8.0 to 13.6)	.91	0.96 (0.5 to 1.85)	0.88 (0.44 to 1.74)							

Abbreviations: DRD, DNA-damage repair defect; NR, not reached; PFS, progression-free survival; WT, wild type.

*Multivariable model includes age, baseline prostate-specific antigen, race, Eastern Cooperative Oncology Group performance status, treatment arm, prior chemotherapy, prior ketoconazole, fusion status stratum, and biomarker of interest.

PIK3CA pathway. However, multivariable analysis including clinical and biomarker variables individually revealed DRD and TP53 as biomarkers separately associated with PFS after controlling for clinical covariates. Expanded analysis of DRD and PTEN from an additional mCRPC cohort²⁹ demonstrated that DRD patients had significantly less aberrations in PTEN, whereas patients with WT DNA repair all had PTEN loss or aberration. The mutual exclusivity between DRD and PTEN could further explain why patients with WT DNA repair had worse outcome with therapy. PTEN loss has been associated with more aggressive prostate cancers, and preclinical models have suggested that PTEN loss/PIK3CA pathway activation can alter AR transcriptional activity and lead to hormonal therapy resistance.^{35,36} Directly related to our results, in retrospective analyses of patients with mCRPC receiving AAP in the postdocetaxel setting, PTEN loss was associated with shorter overall survival from time of initiation of AAP treatment.³⁷

In contrast to findings presented here, a recent study proposed that patients with germline DRD have decreased time from androgen-deprivation therapy initiation to castration resistance and worse outcome with first-line hormonal therapy once CRPC develops.³⁸ Important differences in these two studies are evident and could account for discrepancies. In our trial, DRD was determined by metastatic tumor tissue sequencing, the gold standard for detecting alterations. The contrasting study did not analyze tumor tissue but rather defined DRD through targeted germline sequencing. The WT DNA repair patients with whom the DRD patients were compared were only classified as such through germline sequencing, thus not accounting for those WT germline patients who may have acquired somatic DRD events. Indeed, the authors proceeded to sequence cell-free DNA, but only from those patients who were first determined to have germline DRD; these patients totaled 21 in comparison with the 80 tumors sequenced in our study. Finally, the patients with mCRPC in the previous study were treated with enzalutamide or AAP; in contrast, patients in our trial all received AAP.

There are several limitations in our study. The analyses of the biomarkers from sequencing were unplanned and exploratory and included a convenient sample of 80 of 148 patients who had extra biopsy tissue. The sequenced cohort included more soft tissue biopsies compared with patients who were not sequenced. This is not surprising, considering the known fact that the tissue yield is better from soft tissue metastases. The tumor tissue yield also likely affected the difference in the rate of ETS-positive tumors between the two cohorts. The multivariable modeling included many covariates for the sample size, so caution should be taken when interpreting these results. Additionally, there was not a correction for multiple comparisons in this study. Additional validation is needed for the exploratory findings.

In conclusion, this metastatic tissue biomarker-stratified, randomized trial in mCRPC showed that the approach is feasible. Despite robust preclinical supporting evidence, the addition of veliparib to AAP did not affect response, nor did ETS fusion predict response. Nonetheless, exploratory analysis led to the novel and unexpected finding that DRD was associated with improved outcomes with AAP treatment, possibly through induction of a synthetic lethality in the context of HR defects. Interestingly, DRD was also generally associated with normal PTEN status. Normal PTEN, normal TP53, and nonactivated PIK3CA signaling were significantly associated with improved outcome overall. These hypothesis-generating observations are being evaluated in a follow-up DRD-preselected randomized trial (AAP v olaparib v combination). These results highlight the complexity of mCRPC, importance of the totality of the biologic context, and need for informative clinical trial designs.

AUTHORS' DISCLOSURES OF POTENTIAL CONFLICTS OF INTEREST

Disclosures provided by the authors are available with this article at jco.org.

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Targeting Androgen Receptor and DNA Repair in Metastatic Castration-Resistant Prostate Cancer: Results From NCI 9012

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Appendix



Fig A1. Progression-free survival (PFS) in patients with metastatic castration-resistant prostate cancer treated with abiraterone (A) or abiraterone plus veliparib (A + V) and stratified by ETS gene fusion status. (A) PFS curves are shown for all 148 response-evaluable patients treated with abiraterone/prednisone alone (n = 72) or in combination with veliparib (n = 76). (B) PFS curves are shown for each treatment arm stratified by ETS gene fusion status (determined by immunohistochemistry or in situ hybridization).



Fig A2. Depth of prostate-specific antigen (PSA) decline by DNA-damage repair defect (DRD) status. WT, wild type.

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	No	o. (%)	
Characteristic	Sequenced (n = 80)	Not Sequenced (n = 68)	Ρ
Age, years			.44
Median	68	68	
Range	50-85	55-90	
Race			.67
White	69 (86.3)	62 (91.2)	
Black	7 (8.8)	4 (5.9)	
Other	4 (5.0)	2 (2.9)	
Performance status			.88
0	50 (62.5)	43 (63.2)	
1	29 (36.3)	25 (36.8)	
2	1 (1.3)	0	
°SA, ng/mL			.59
Median	36.8	31.0	
Range	0.04-1,557.6	0.5-940.7	
Cancer pain present	28 (35.0)	18 (26.5)	.26
Sites of disease			
Bone	66 (82.5)	62 (91.2)	.12
Lymph node	62 (77.5)	33 (48.5)	< .00
Visceral	20 (25.0)	14 (20.6)	.52
Other	15 (18.8)	13 (19.1)	.95
Previous treatment			
Chemotherapy	25 (31.3)	13 (19.1)	.09
Docetaxel/cabazitaxel	17 (21.3)	10 (14.7)	
Other	8 (10.0)	3 (4.4)	
Enzalutamide	2 (2.5)	2 (2.9)	.99
Sipuleucel-T	19 (23.8)	15 (22.1)	.85
Experimental agent	18 (22.5)	16 (23.5)	.88
Strata: ETS fusion and ketoconazole use			< .00
ETS fusion positive*	39 (48.8)	13 (19.1)	
ETS fusion negative	41 (51.3)	55 (80.9)	
Previous ketoconazole	10 (12.5)	6 (8.8)	.60
Treatment arm			.05
Abiraterone	33 (41.3)	39 (57.4)	
Abiraterone + veliparib	47 (58.8)	29 (42.7)	
No. of treatment cycles			.79
Median	9	9	
Range	2-50	1-46	
PSA response rate, %	65.0	72.1	.36
Measurable disease	60 (75.0)	26 (38.2)	< .00
Objective response, %	51.7	42.3	.43
PFS, months			.47
Median	10.3	10.8	
95% CI	8.0 to 13.8	8.2 to 13.7	
OS, months			.90
Median	32.3	30.6	
95% CI	24.1 to NR	28.1 to NR	

	N	o. (%)	_
Characteristic	Abiraterone (n = 33)	Abiraterone + Veliparib (n = 47)	F
Age, years			.2
Median	70	68	
Range	50-80	52-86	
Race			.6
White	27 (81.8)	42 (89.4)	
Black	4 (12.1)	3 (6.4)	
Other	2 (6.1)	2 (4.3)	
Performance status			.5
0	19 (57.6)	31 (66.0)	
1	14 (42.4)	15 (31.9)	
2	0	1 (2.1)	
PSA, ng/mL			.8
Median	35.2	39.2	
Range	2-1,557.6	0.04-785.8	
Cancer pain present	14 (42.4)	14 (29.8)	.2
Sites of disease			
Bone	15 (45.5)	27 (57.5)	.2
Lymph node	24 (72.7)	38 (80.9)	.3
Visceral	6 (18.2)	14 (29.8)	.1
Other	6 (18.2)	9 (19.2)	.9
Previous treatments			
Chemotherapy	9 (27.3)	16 (34.0)	.5
Docetaxel/cabazitaxel	5 (15.2)	12 (25.5)	
Other	4 (12.1)	4 (8.5)	
Enzalutamide	1 (3.0)	1 (2.1)	.g
Sipuleucel-T	12 (36.4)	7 (14.9)	.0
Experimental agent	8 (24.2)	10 (21.3)	.7
Strata: ETS fusion and ketoconazole	- ()		.6
use			
ETS fusion positive	17 (51.5)	22 (46.8)	
ETS fusion negative	16 (48.5)	25 (53.2)	
Previous ketoconazole	5 (15.2)	5 (10.6)	.7
No. of treatment cycles			.5
Median	9	9	
Range	2-39	2-50	
Confirmed PSA response	18 (54.6)	34 (72.3)	.1
Measurable disease response	11 (45.8)	20 (55.6)	.4
PFS, months			.8
Median	8.8	11.0	
95% CI	6.7 to 13.8	7.4 to 13.8	
OS, months			_
Median	29.4	32.3	
05% 01	17.4 to NB	2/1.1 to NB	

						No.	(%)					
		Arm A	A: Abirater	one (n =	- 74)		Ar	m B: Abir	aterone +	Velipari	ib (n =	79)
			Grad	е					Grad	е		
AE	1	2	3	4	5	Total	1	2	3	4	5	Total
ALT increased	8 (11)	1 (1)	3 (4)	0 (0)	0 (0)	12 (16)	4 (5)	0 (0)	2 (3)	0 (0)	0 (0)	6 (8)
Alkaline phosphatase increased	3 (4)	2 (3)	0 (0)	0 (0)	0 (0)	5 (7)	2 (3)	4 (5)	2 (3)	0 (0)	0 (0)	8 (10)
Anemia	9 (12)	1 (1)	1 (1)	0 (0)	0 (0)	11 (15)	10 (13)	4 (5)	2 (3)	0 (0)	0 (0)	16 (20)
Anorexia	3 (4)	0 (0)	0 (0)	0 (0)	0 (0)	3 (4)	5 (6)	5 (6)	0 (0)	0 (0)	0 (0)	10 (13)
Arthralgia	1 (1)	0 (0)	0 (0)	0 (0)	0 (0)	1 (1)	1 (1)	0 (0)	1 (1)	0 (0)	0 (0)	2 (3)
AST increased	14 (19)	2 (3)	0 (0)	0 (0)	0 (0)	16 (22)	6 (8)	2 (3)	0 (0)	0 (0)	0 (0)	8 (10)
Atrial fibrillation	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	1 (1)	0 (0)	0 (0)	1 (1)
Cardiac arrest	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	1 (1)	1 (1)
Confusion	1 (1)	0 (0)	0 (0)	0 (0)	0 (0)	1 (1)	0 (0)	0 (0)	1 (1)	0 (0)	0 (0)	1 (1)
Dehydration	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	2 (3)	1 (1)	0 (0)	0 (0)	3 (4)
Diarrhea	4 (5)	1 (1)	0 (0)	0 (0)	0 (0)	5 (7)	10 (13)	2 (3)	0 (0)	0 (0)	0 (0)	12 (15)
Dizziness	2 (3)	0 (0)	0 (0)	0 (0)	0 (0)	2 (3)	7 (9)	1 (1)	0 (0)	0 (0)	0 (0)	8 (10)
Edema limbs	13 (18)	2 (3)	0 (0)	0 (0)	0 (0)	15 (20)	5 (6)	0 (0)	0 (0)	0 (0)	0 (0)	5 (6)
Ejection fraction decreased	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	1 (1)	0 (0)	0 (0)	1 (1)
Fatique	18 (24)	2 (3)	0 (0)	0 (0)	0 (0)	20 (27)	31 (39)	8 (10)	0 (0)	0 (0)	0 (0)	39 (49)
Glucose intolerance	0 (0)	0 (0)	1 (1)	0 (0)	0 (0)	1 (1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)
Headache	6 (8)	0 (0)	0 (0)	0 (0)	0 (0)	6 (8)	5 (6)	1 (1)	1 (1)	0 (0)	0 (0)	7 (9)
Heart failure	0 (0)	0 (0)	1 (1)	0 (0)	0 (0)	1 (1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)
Hot flashes	8 (11)	1 (1)	0 (0)	0 (0)	0 (0)	9 (12)	16 (20)	0 (0)	0 (0)	0 (0)	0 (0)	16 (20)
Hyperglycemia	3 (4)	1 (1)	6 (8)	1 (1)	0 (0)	11 (15)	6 (8)	2 (3)	4 (5)	0 (0)	0 (0)	12 (15)
Hypertension	2 (3)	6 (8)	3 (4)	0 (0)	0 (0)	11 (15)	3 (4)	2 (3)	3 (4)	0 (0)	0 (0)	8 (10)
Hypokalemia	6 (8)	0 (0)	0 (0)	0 (0)	0 (0)	6 (8)	7 (9)	1 (1)	1 (1)	0 (0)	0 (0)	9 (11)
Hypophosphatemia	3 (4)	4 (5)	1 (1)	0 (0)	0 (0)	8 (11)	2 (3)	4 (5)	1 (1)	0 (0)	0 (0)	7 (9)
Hypotension	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	1 (1)	0 (0)	0 (0)	1 (1)
Insomnia	4 (5)	0 (0)	0 (0)	0 (0)	0 (0)	4 (5)	8 (10)	2 (3)	1 (1)	0 (0)	0 (0)	11 (14)
Lymphocyte count decreased	3 (4)	1 (1)	1 (1)	0 (0)	0 (0)	5 (7)	6 (8)	8 (10)	1 (1)	0 (0)	0 (0)	15 (19)
Nausea	5 (7)	0 (0)	0 (0)	0 (0)	0 (0)	5 (7)	29 (37)	12 (15)	1 (1)	0 (0)	0 (0)	42 (53)
Pain	0 (0)	1 (1)	0 (0)	0 (0)	0 (0)	1 (1)	2 (3)	1 (1)	1 (1)	0 (0)	0 (0)	4 (5)
Platelet count decreased	2 (3)	1 (1)	0 (0)	0 (0)	0 (0)	3 (4)	5 (6)	1 (1)	1 (1)	1 (1)	0 (0)	8 (10)
Bespiratory thoracic and mediastinal disorders-other	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	1 (1)	0 (0)	0 (0)	1 (1)
Sinus tachycardia	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	1 (1)	0 (0)	0 (0)	1 (1)
Syncope	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	1 (1)	0 (0)	0 (0)	1 (1)
Thromboembolic event	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	2 (3)	0 (0)	0 (0)	2 (3)
Vomiting	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	12 (15)	5 (6)	0 (0)	0 (0)	0 (0)	17 (22)
Maximum grade for patient	27 (36)	15 (20)	15 (20)	1 (1)	0 (0)	58 (78)	24 (30)	28 (35)	19 (24)	1 (1)	1 (1)	73 (92)

	ETS Status b No.	y Sequencing (%)
ETS Status by Trial Methods*	Negative	Positive
Negative	36 (45.0)	5 (6.25)
Positive	3 (3.75)	36 (45.0)
Agreement	72 (90) of 80

	Biomarke	er Status	
Response/PFS	Not Normal	Normal	Р
Confirmed PSA response	No.	(%)	
ETS (positive [n = 41] v negative [n = 39])	25 (61.0)	27 (69.2)	.44
DNA repair (defect $[n = 20] v$ WT/monoallelic $[n = 60]$)	18 (90.0)	34 (56.7)	.007
AR (amplified/mutated [n = 41] v normal [n =39])	25 (61.0)	27 (69.2)	.44
<i>TP53</i> (mutated [n = 33] <i>v</i> normal [n = 47])	20 (60.6)	32 (68.1)	.49
PTEN (mutated $[n = 34] v$ normal $[n = 46]$)	17 (50.0)	35 (76.1)	.016
PIK3CA pathway (activated [n = 39] v normal [n = 41])	22 (56.4)	30 (73.2)	.12
WNT pathway (activated $[n = 12] v$ normal $[n = 68]$)	8 (66.7)	44 (64.7)	.99
RB1 (mutated $[n = 9] v$ normal $[n = 71]$)	6 (66.7)	46 (64.8)	.99
CHD1 (mutated $[n = 4] v$ normal $[n = 76]$)	3 (75.0)	49 (64.5)	.99
SPOP (mutated $[n = 5] v$ normal $[n = 75]$)	4 (80.0)	48 (64.0)	.65
ZFHX3 (mutated [n = 6] v normal [n = 74])	3 (50.0)	49 (66.2)	.42
Measurable disease response			
ETS (positive $[n = 31] v$ negative $[n = 29]$)	15 (48.4)	16 (55.2)	.60
DNA repair (defect $[n = 16] v WT/monoallelic [n = 44])$	14 (87.5)	17 (38.6)	.001
AR (amplified/mutated $[n = 29]$ vnormal $[n = 31]$)	13 (44.8)	18 (58.1)	.31
<i>TP53</i> (mutated $[n = 24] v$ normal $[n = 36]$)	10 (41.7)	21 (58.3)	.21
PTEN (mutated $[n = 28] v$ normal $[n = 32]$)	12 (42.9)	19 (59.4)	.20
PIK3CA pathway (activated $[n = 29] v$ normal $[n = 31]$)	13 (44.8)	18 (58.1)	.31
WNT pathway (activated $[n = 8] v$ normal $[n = 52]$)	3 (37.5)	28 (53.9)	.47
RB1 (mutated $[n = 4]$ v normal $[n = 56]$)	2 (50.0)	29 (51.8)	.99
CHD1 (mutated $[n = 3] v$ normal $[n = 57]$)	2 (66.7)	29 (50.9)	.99
SPOP (mutated $[n = 4] v$ normal $[n = 56]$)	3 (75.0)	28 (50.0)	.61
ZFHX3 (mutated [n = 5] v normal [n = 55])	3 (60.0)	28 (50.9)	.99
PFS, months	Median (95% CI)	
ETS (positive $[n = 41] v$ negative $[n = 39]$)	8.2 (5.4 to 14.5)	13.3 (8.2 to 13.8)	.48
DNA repair (defect [n = 20] v WT/monoallelic [n = 60])	14.5 (11.0 to 19.5)	8.1 (5.5 to 11.0)	.025
AR (amplified/mutated $[n = 41] v$ normal $[n = 39]$)	8.8 (5.4 to 13.5)	11.0 (8.0 to 16.6)	.17
TP53 (mutated $[n = 33] v$ normal $[n = 47]$)	7.7 (5.3 to 8.8)	13.5 (8.2 to 16.6)	.01
PTEN (mutated $[n = 34] v$ normal $[n = 46]$)	6.7 (4.1 to 11.3)	13.5 (8.2 to 16.6)	.02
PIK3CA pathway (activated $[n = 39] v$ normal $[n = 41]$)	8.3 (5.4 to 13.3)	13.8 (8.2 to 16.6)	.03
WNT pathway (activated $[n = 12] v$ normal $[n = 68]$)	12.4 (2.7 to 23.7)	10.3 (8.0 to 13.6)	.91
RB1 (mutated $[n = 9]$ v normal $[n = 71]$)	8.8 (1.9 to 23.7)	10.3 (8.0 to 13.8)	.46
CHD1 (mutated $[n = 4] v$ normal $[n = 76]$)	NR (2.6 to NR)	8.8 (7.8 to 13.6)	.09
SPOP (mutated $[n = 5] v$ normal $[n = 75]$)	NR (2.8 to NR)	8.8 (7.8 to 13.6)	.06
ZEHX3 (mutated $[n = 6] v$ normal $[n = 74]$)	10.0 (2.1 to 13.8)	10.3 (8.0 to 13.8)	.20

Abbreviations: NR, not reached; PFS, progression-free survival; PSA, prostate-specific antigen.

	Marke	er Not Normal		N	larker Normal		
Response/PFS	Abiraterone	Abiraterone + Veliparib	Ρ	Abiraterone	Abiraterone + Veliparib	Ρ	Interaction P
Confirmed PSA response	No.	(%)		No	o. (%)		
ETS (positive [n = 41] v negative [n = 39])	8 (44.4)	17 (73.9)	.05	10 (66.7)	17 (70.8)	.78	.27
DNA repair (defect [n = 20] vWT/monoallelic [n = 60])	6 (85.7)	12 (92.3)	1.0	12 (46.2)	22 (64.7)	.15	.97
AR (amplified/mutated [n = 41] v normal [n = 39])	9 (47.4)	16 (72.7)	.097	9 (64.3)	18 (72.0)	.72	.45
PTEN (mutated $[n = 34] v$ normal $[n = 46]$)	5 (35.7)	12 (60.0)	.16	13 (68.4)	22 (81.5)	.31	.78
TP53 (mutated [n = 33] v normal [n = 47])	9 (60.0)	11 (61.1)	.95	9 (50.0)	23 (79.3)	.036	.18
PIK3CA pathway (activated [n = 39] v normal [n = 41])	6 (40.0)	16 (66.7)	.10	12 (66.7)	18 (78.3)	.41	.60
WNT pathway (activated [n = 12] v normal [n = 68])	3 (42.9)	5 (100.0)	.08	15 (57.7)	29 (69.1)	.34	.95
Measurable disease response	No.	(%)		No	o. (%)		
ETS (positive [n = 31] v negative [n = 29])	6 (42.9)	9 (52.9)	.58	5 (50.0)	11 (57.9)	.68	.94
DNA repair (defect [n = 16] vWT/monoallelic [n = 44])	4 (80.0)	10 (90.9)	1.00	7 (36.8)	10 (40.0)	.83	.64
AR (amplified/mutated [n = 29] v normal [n = 31])	4 (36.4)	9 (50.0)	.70	7 (53.9)	11 (61.1)	.69	.81
PTEN (mutated $[n = 28] v$ normal $[n = 32]$)	5 (45.5)	7 (41.2)	.82	6 (46.2)	13 (68.4)	.21	.31
<i>TP53</i> (mutated [n = 24] <i>v</i> normal [n = 36])	5 (50.0)	5 (35.7)	.68	6 (42.9)	15 (68.2)	.18	.14
PIK3CA pathway (activated [n = 29] v normal [n = 31])	5 (45.5)	8 (44.4)	.96	6 (46.2)	12 (66.7)	.25	.41
WNT pathway (activated $[n = 8] v$ normal $[n = 52]$)	0 (0.0)	3 (75.0)	.14	11 (55.0)	17 (53.1)	.90	.97
PFS, months	Median	(95% CI)		Mediar	n (95% CI)		
ETS (positive $[n = 41] v$ negative $[n = 39]$)	7.7 (2.7 to 19.5)	11.0 (7.4 to 17.9)	.29	13.8 (8.2 to 16.6)	11.0 (5.5 to 13.8)	.33	.20
DNA repair (defect [n = 20] ν WT/monoallelic [n = 60])	16.6 (13.5 to 19.5)	13.8 (8.2 to 32.9)	.93	8.2 (3.9 to 10.3)	8.1 (5.3 to 13.6)	.79	.89
AR (amplified/mutated [n = 41] v normal [n = 39])	8.3 (2.8 to 16.6)	8.8 (5.4 to 13.8)	.87	10.3 (6.7 to NR)	11.0 (6.4 to 17.9)	.60	.52
PTEN (mutated $[n = 34] v$ normal $[n = 46]$)	6.7 (2.6 to 19.5)	6.9 (2.8 to 13.6)	.55	13.5 (7.8 to 16.6)	13.8 (8.1 to 19.2)	.69	.40
TP53 (mutated [n = 33] v normal [n = 47])	8.3 (3.9 to 13.8)	5.7 (2.8 to 8.8)	.30	13.5 (2.7 to 16.6)	13.8 (8.2 to 17.9)	.84	.31
PIK3CA pathway (activated [n = 39] v normal [n = 41])	8.3 (2.6 to 19.5)	11.0 (5.3 to 13.6)	.62	13.8 (7.7 to 16.6)	13.8 (7.4 to 22.2)	.77	.51
WNT pathway (activated [n = 12] v normal [n = 68])	8.3 (1.9 to 23.7)	16.5 (5.4 to 32.9)	.74	8.8 (5.4 to 13.8)	11.0 (7.4 to 13.8)	.85	.80

NOTE. Markers included but too small of a mutation/aberrant representative sample size by treatment arm for analysis: *RB1, CHD1, SPOP*, and *ZFHX3*. Abbreviations: NR, not reached; PFS, progression-free survival; PSA, prostate-specific antigen.

		Hazard Ratio (95% CI)	
	Unadjusted	Univariable Analysis	Multivariable Cox Model
Covariate	All Patients	Sequenced Patients Only	Sequenced Patients Only
Clinical			
Treatment arm			
Abiraterone + veliparib v abiraterone	1.00 (0.70 to 1.44)	1.04 (0.62 to 1.72)	1.00 (0.58 to 1.72)
ETS fusion status			
Positive v negative	1.06 (0.72 to 1.56)	1.19 (0.73 to 1.95)	1.05 (0.60 to 1.83)
Prior ketoconazole	1.96 (1.11 to 3.46)	1.62 (0.79 to 3.31)	1.57 (0.74 to 3.36)
Age	1.02 (1.00 to 1.05)	1.04 (1.002 to 1.07)	1.04 (1.00 to 1.08)
Race			
Black <i>v</i> white	0.87 (0.44 to 1.73)	0.58 (0.23 to 1.44)	0.49 (0.18 to 1.34)
Other v white	0.65 (0.24 to 1.78)	0.35 (0.09 to 1.44)	0.29 (0.07 to 1.31)
Performance status			
Symptomatic <i>v</i> normal	2.00 (1.37 to 2.92)	2.27 (1.35 to 3.80)	2.02 (1.16 to 3.53)
Baseline PSA (log transformed)	1.13 (1.00 to 1.27)	1.09 (0.92 to 1.29)	1.02 (0.88 to 1.19)
Previous chemotherapy	2.09 (1.39 to 3.13)	2.19 (1.31 to 3.66)	2.00 (1.12 to 3.54)
Previous enzalutamide	5.48 (1.98 to 15.2)	Inf (2.0 to Inf)	—
Biomarkers*			
DNA repair (defect v WT/monoallelic)		0.52 (0.29 to 0.93)	0.51 (0.27 to 0.97)
AR (amplified/mutated v normal)		1.41 (0.86 to 2.31)	1.34 (0.80 to 2.23)
TP53 (mutated v normal)		1.88 (1.14 to 3.12)	2.52 (1.30 to 4.89)
PTEN (mutated v normal)		1.82 (1.11 to 3.01)	1.61 (0.92 to 2.82)
PIK3CA pathway (activated v normal)		1.74 (1.05 to 2.87)	1.45 (0.79 to 2.68)
WNT pathway (activated <i>v</i> normal)		0.96 (0.50 to 1.85)	0.88 (0.44 to 1.74)
RB1 (mutated v normal)		1.32 (0.62 to 2.78)	1.47 (0.66 to 3.28)
CHD1 (mutated v normal)		0.31 (0.07 to 1.29)	0.39 (0.09 to 1.71)
SPOP (mutated v normal)		0.28 (0.07 to 1.15)	0.54 (0.09 to 3.40)
ZFHX3 (mutated v normal)		1.74 (0.74 to 4.09)	1.44 (0.57 to 3.63)
ETS fusion by sequencing (positive v negative)		1.19 (0.73 to 1.95)	1.24 (0.45 to 3.38)

Abbreviations: PFS, progression-free survival; PSA, prostate-specific antigen. *Biomarkers were added separately and individually to the multivariable model containing clinical covariates.

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	RECIST Comments	1 hepatic mass had 80% exotorion in size, and other hepatic mass decreased in size by 76%; 1 LN termed	to normal; I. I.N. decreased by two hinds retroperitoneal LNs retrometic near LNs nortisegt pulmonery nortisegt pulmonery nortice remained stable;	progression by new liver metas tases Lateral external illiac LN mass; progression in 1 A mono.	2 masses reduced approximately 40% each;	LN shark by 56% Pubic ramus-associated	Lung nodule went from 11 at baseline to 0 at 2-month scan: LNs decreased from first scan through 19.5-month	acon when CR R was attimed; CR was confirmed 3 months after instal CR 122 months on trial 1 LN immitted tables; 2 decreted; patient continued receiving A after departial after departial	remained stable in follow- up 1 nodule reduced by 40%; 1 LN reduced to normal;	1 LN docreased and remained sible 1 LN reduced from 33 to 11, and other LN reduced from 14 to 6								
	Type of Lesion	2 hepatic masses and 2 illac LNs	5 LNs	1 LN	2 masses; 1 LN	1 mass	Left upper lung nodule and 3 LNs	3 LNs		2 LNs								
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ARTICLE



Post prostatectomy outcomes of patients with high-risk prostate cancer treated with neoadjuvant androgen blockade

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Abstract

Background Patients with high-risk prostate cancer have an increased likelihood of experiencing a relapse following radical prostatectomy (RP). We previously conducted three neoadjuvant androgen-deprivation therapy (ADT) trials prior to RP in unfavorable intermediate and high-risk disease.

Methods In this analysis, we report on the post-RP outcomes of a subset of patients enrolled on these studies. We conducted a pooled analysis of patients with available follow-up data treated on three neoadjuvant trials at three institutions. All patients received intense ADT prior to RP. The primary endpoint was time to biochemical recurrence (BCR). BCR was defined as a PSA ≥ 0.2 ng/mL or treatment with radiation or androgen-deprivation therapy for a rising PSA < 0.2 ng/mL.

Results Overall, 72 patients were included of whom the majority had a Gleason score ≥ 8 (n = 46, 63.9%). Following neoadjuvant therapy, 55.7% of patients (n = 39/70) had pT3 disease, 40% (n = 28) had seminal vesicle invasion, 12.9% (n = 9) had positive margins, and 11.4% (n = 8) had lymph node involvement. Overall, 11 (15.7%) had tumor measuring ≤ 0.5 cm, which included four patients (5.7%) with a pathologic complete response and seven (10.0%) with residual tumor measuring 0.1–0.5 cm. Compared to pretreatment clinical staging, 10 patients (14.3%) had pathologic T downstaging at RP. The median follow-up was 3.4 years. Overall, the 3-year BCR-free rate was 70% (95% CI 57%, 90%). Of the 15 patients with either residual tumor ≤ 0.5 cm or pathologic T downstaging, no patient experienced a recurrence.

Conclusion In this exploratory pooled clinical trials analysis, we highlight that neoadjuvant therapy prior to RP in unfavorable intermediate and high-risk patients may potentially have a positive impact on recurrence rates. Larger studies with longer follow-up periods are warranted to evaluate the impact of neoadjuvant hormone therapy on pathologic and long-term outcomes.

Rana R. McKay, Bruce Montgomery, Adam S. Kibel, and Mary-Ellen Taplin contributed equally to this work.

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Introduction

Despite generally outstanding results for radical prostatectomy (RP), patients with high-risk prostate cancer (PC) have an increased risk of biochemical recurrence (BCR) and

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PC mortality despite treatment [1]. Biochemical recurrence may not be indolent since approximately one-third of men with high-risk disease who suffer a BCR will die of PC within 10 years [2]. While adjuvant and salvage therapies can improve outcomes for patients with local recurrences, the overall relapse rate is still unacceptably high, in part due to occult systemic disease and radiation resistance. Consequently, novel strategies that integrate multimodality therapy are warranted to improve cure for high-risk patients.

Neoadjuvant systemic therapy is a widely accepted paradigm for the treatment of malignancies including breast [3], bladder [4, 5], and esophageal [6, 7]. Neoadjuvant therapy offers the potential for systemic control of microscopic metastases, while optimally treating the primary disease [8]. In some cases, neoadjuvant therapy may facilitate resection and provide prognostic information with an in vivo assessment of treatment sensitivity [8]. A key principal of neoadjuvant therapy is that local response correlates with long-term survival. In breast cancer, pathologic complete response (pCR) has been used as a surrogate for long-term survival resulting in FDA approval of pertuzumab [9]. Additionally, residual cancer burden (RCB), a method to quantify residual disease after neoadjuvant chemotherapy for breast cancer that incorporates number and size of nodal metastases and percent cellularity of the primary tumor bed, has been shown to correlate with long-term survival [10].

Historically, androgen-deprivation therapy (ADT) is the primary systemic therapy for men with PC [11]. The utilization of neoadjuvant ADT prior to RP was evaluated in the 1990's and while initially demonstrated improvements in the rate of organ-confined disease and decreased positive surgical margins, there was no benefit in recurrence rates [12–23]. These studies were underpowered to detect significant differences between disease-free survival (DFS) and overall survival (OS) given limited reporting of these endpoints, lack of long-term follow-up, and inclusion of primarily low and intermediate-risk patients [24].

These studies primarily utilized treatment with luteinizing hormone-releasing hormone (LHRH) agonizts and/or first-generation anti-androgens. Treatment with LHRH agonists and first-generation anti-androgens results in incomplete suppression of tissue androgen, which is hypothesized to be another possible explanation for the lack of efficacy of these former studies [25]. While serum androgens are reduced by approximately 90% with standard ADT, tissue androgens only decline by 75%, providing rationale for more complete androgen blockade [25].

The development of more potent hormonal agents provides the opportunity to investigate these therapeutic options in the neoadjuvant setting. In addition to LHRH suppression, further androgen receptor (AR) axis suppression can be achieved by targeting CYP17-mediated

	Prostate tissue testosterone and DHT levels	Pathologic complete response rate
	24 weeks	6-months
Bicalutamide 3: Goserelin + Dutasteride + Bicalutamide + Ketoconazole (1:1:1)	 1: 12 weeks Abiraterone acetate/ 24 weeks LHRH agonist 2: 24 weeks Abiraterone acetate/ 24 weeks LHRH agonist (1:1) 	1: Enzalutamide 2: Enzalutamide + Leuprolide + Dutasteride (1:1)
	Positive biopsies ≥ 3 AND Gleason score ≥ 7 OR PSA > 10 ng/mL OR PSA velocity > 2 ng/mL/year	Positive biopsies \geq 3 AND PSA > 10 ng/mL OR Gleason score \geq 7 (4

Prostate tissue DHT levels

Primary endpoint

neoadjuvant therapy

3-months

Goserelin + Dutasteride 2:

cT1-T3 AND PSA < 40 ng/dL

35

July 2006–December 2009

NCT00298155)

TAPS(27

28

September 2009–June

2011

NCT00924469)

Veo-Abi(26)

AND Gleason 7-10

Goserelin + Dutasteride +

Duration of

Arms

Selection criteria

Patients enrolled

Summary of neoadjuvant trials

Table 1 Study

Enrollment period

PSA prostate-specific antigen, DHT dihydrotestosterone, LHRH luteinizing hormone-releasing hormone

+ 3); T4 excluded

52

March 2012-November

2013

Neo-Enza(28) NCT01547299) androgen synthesis (ketoconazole, abiraterone) or with AR inhibition (enzalutamide). Abiraterone and enzalutamide improve OS in metastatic castration-resistant PC. We hypothesized that intense ADT can improve outcomes in high-risk localized PC and have published three neoadjuvant studies utilizing these hormonal agents [26–28]. Herein, we report on the post-RP outcomes of patients with available follow-up data enrolled on these studies.

Patients and methods

Patients

We conducted a pooled analysis of patients treated on three neoadjuvant trials at three institutions: Dana-Farber/Brigham and Women's Cancer Center, University of Washington, and Beth Israel Deaconess Medical Center (Table 1). Post-RP follow-up, including frequency of clinic visits, prostate-specific antigen (PSA) and radiographic evaluations, was not predefined on the studies given funding restrictions. Given that long-term follow up after RP was not mandated, patients included were those with available PSA and follow-up data. Clinical, laboratory, and radiographic data following RP were obtained. The decision to initiate adjuvant or salvage therapy was at the discretion of the treating physician. Informed consent was obtained from all subjects. This study was approved by the Institutional Review Board at each institution.

Statistical analysis

The primary endpoint was time to BCR, defined as the time from RP to BCR, censored at the last PSA follow-up for those without progression. BCR was defined as a PSA ≥ 0.2 ng/mL, with a second confirmatory level ≥ 0.2 ng/mL, or treatment with salvage radiation therapy or ADT for a rising PSA that was < 0.2 ng/mL at the time of therapy initiation. A secondary endpoint included time to metastasis (TTM), defined as the time of RP to the first evidence of metastasis on imaging, censored at the date of last PSA or imaging follow-up for those without progression. The distributions of time to BCR or TTM were estimated using the Kaplan–Meier method.

Median time to BCR and BCR-free rate at 2 and 3 years along with 95% confidence interval (CI) were summarized in overall cohort and by pathological response groups. Two pathological outcomes were analyzed: (1) minimum residual disease (MRD) defined as tumor in the RP specimen measuring ≤ 0.5 cm, and (2) improved pathologic T stage compared to clinical staging defined by the American Joint Committee on Cancer (AJCC) staging system at baseline. Patients who had an improvement in T stage either between T stage categories or within T stage categories were counted as having downstaging. The subgroup analyses of BCR by pathological response groups were explorative with limited statistical power; no formal comparison was provided.

Time to testosterone recovery was estimated by the Kaplan–Meier method. The recovery time was calculated from the date of RP to testosterone > 200 ng/dL, or censored at the last sample date if testosterone had not reached a normal level. If patients received ADT prior to testosterone recovery, their time to testosterone recovery was censored at the date of ADT initiation.

We conducted a descriptive exploratory analysis to evaluate the predicted pathologic RP outcomes of matched patients with comparable high-risk features planned to undergo RP alone. Using the Memorial Sloan Kettering Cancer Center (MSKCC) pre-RP nomogram (https://www. mskcc.org/nomograms/prostate/pre-op), we used the baseline parameters of patients in our cohort to determine the predicted pathologic outcomes including extracapsular extension, seminal vesicle invasion, and lymph node involvement of RP alone. No formal test could be made for this descriptive comparison.

Results

Baseline characteristics

Overall, 72 patients (50% of those enrolled on the trials) were included (Table 2). The median PSA prior to neoadjuvant therapy was 8.3 ng/mL. The majority of patients had a Gleason score ≥ 8 (n = 46, 63.9%). Fifty-two patients (72.2%) had high-risk disease by NCCN criteria.

Pathologic RP outcomes

Of the 72 patients, 70 (97.2%) had pathologic data available (Table 3). Two patients discontinued study treatment early and subsequently received RP at outside hospitals. The majority of patients (n = 39, 55.7%; 95% CI: 43%, 68%) had pT3 disease at RP and eight patients (11.4%; 95% CI: 5%, 21%) had lymph node involvement. The rates of seminal vesicle involvement and positive margins were 40% (n = 28; 95% CI: 28–52%) and 12.9% (n = 9; 95% CI: 6%, 23%), respectively.

Overall, 11 (15.7%; 95% CI: 8%, 26%) had tumor measuring ≤ 0.5 cm at largest cross section dimension in the RP specimen, including four patients (5.7%) with a pCR and seven (10.0%) with residual tumor measuring 0.1–0.5 cm. Of the patients with residual tumor measuring ≤ 0.5 cm, eight (72.7%) were treated on the Neo-Abi trial and three (27.3%) on the Neo-Enza trial.

Table 2 Baseline patient anddisease characteristics

	analysis cohort ($N = 72$)						
		TAPS $(n = 35)$		Neo-Abi (n	= 58)	Neo-Enza (n = 52)
	N (%)	Included N (%)	Excluded N (%)	Included N (%)	Excluded N (%)	Included N (%)	Excluded N (%)
Total N	72	4	31	41	17	27	25
Institution							
BIDMC	7 (10)	—	—	—	—	—	—
DF/BWCC	48 (67)	_	_	_	—	_	_
UW	17 (24)	_	_	_	_	_	_
Gleason score							
Gleason 7	26 (36)	1 (25)	24 (77)	15(37)	3 (18)	10 (37)	10 (40)
3 + 4	5 (7)	_	_	_	_	_	_
4 + 3	21 (29)	_	_	_	_	_	_
Gleason 8-10	46 (64)	3 (75)	7 (23)	26(63)	14 (82)	17 (63)	15 (60)
3 + 5	3 (4)	_	_	_	_	_	_
4 + 4	18 (25)	_	_	_	_	_	_
4 + 5	16 (22)	_	_	_	_	_	_
5 + 4	6 (8)	_	_	_	—	_	_
5 + 5	3 (4)	_	_	_	_	_	_
Clinical T stage							
T1	20 (28)	1 (25)	9 (29)	13 (32)	3 (18)	6 (22)	8 (32)
T2	37 (51)	2 (50)	16 (52)	24 (59)	6 (35)	11 (41)	13 (52)
Т3	12 (17)	1 (25)	6 (19)	3 (7)	7 (41)	8 (30)	4 (16)
Unknown	3 (4)	0	0	1 (2)	1 (6)	2 (7)	0
NCCN risk group							
	20 (28)	1 (25)	—	12 (29)	1 (6)	7 (26)	4 (16)
Intermediate							
High	52 (72)	3 (75)	—	29 (71)	16 (94)	20 (74)	21 (84)
	Median (IQR)	Median by treatment arm (range)	_	Median by treatment arm (range)	_	Median by treatment arm (range)	_
PSA at Baseline (ng/mL)	8.3 (5.0–14.2)	11.9/5.8/ 7.9 (-)	—	12.1/6.4 (2–316.6)	_	10.9/12.8 (0.6–61.1)	_
Median age at RP, years	59 (54–63)	62/66/60 (-)	—	55/60 (50–74)	—	61/60 (46–75)	_

Original trial cohorts

Current

-denotes not available

BIDMC Beth Israel Deaconess Medical Center, *DF/BWCC* Dana-Farber/Brigham and Women's Cancer Center, *UW* University of Washington, *NCCN* National Comprehensive Cancer Network, *NA* not available, *IQR* interquartile range, *PSA* prostate-specific antigen, *RP* radical prostatectomy

Compared to pretreatment clinical staging, ten patients (14.3%; 95% CI: 7%, 25%) had pathologic T downstaging at RP, including four patients (5.7%) with downstaging from T3 to pT2, four patients (5.7%) with downstaging from T1/T2 to pT0 and two patients (2.9%) with change in subcategories. Six patients achieved both tumor measuring ≤ 0.5 cm and pathologic T downstaging. Overall, 15

patients (20.8%; 95% CI: 13%, 33%) had either tumor measuring ≤ 0.5 cm or pathologic T downstaging at RP.

MSKCC pre-RP nomogram prediction

The predicted rates of extracapsular extension, seminal vesicle invasion, and lymph node involvement for matched

	Curr anal coho (n =	rent ysis ort = 70)	Orig	Original trial cohorts					
			TAI $(n =$	TAPS $(n = 32)$		Neo-Abi $(n = 56)$		Neo-Enza $(n = 48)$	
	Ν	%	N	%	N	%	N	%	
Pathologic T s	tage								
pT0	4	5.7	2	6.3	4	7.1	1	2.1	
pT2	27	38.6	21	65.6	22	39.3	15	31.3	
pT3	39	55.7	9	28.1	30	53.6	32	66.7	
Pathologic T d	lown-s	stage ^a							
Yes	10	14.3	—	—	—	—	—	—	
No	57	81.4	—	—	—	—	—	—	
Unknown	3	4.3	_	—	_	—	—	_	
Pathologic N S	Stage								
N0	61	87.1	—	—	46	82.1	41	85.4	
N1	8	11.4	—	—	10	17.9	7	14.6	
Unknown	1	1.4	—	—	0	0	0	0	
Positive marging	n								
Yes	9	12.9	—	—	8	14.3	9	18.8	
No	61	87.1	—	—	48	85.7	39	81.3	
Seminal vesicl	e invo	lvemen	t						
Yes	28	40.0	5	15.6	17	30.4	16	33.3	
No	42	60.0	27	84.4	39	69.6	32	66.7	
Largest cross s	section	dimens	sion						
≤0.5 cm	11	15.7	_	—	_	—	_	—	
>0.5 cm	55	78.6	—	—	—	—	—	—	
Unknown	4	5.7	_	—	_	—	_	—	
Pathologic con	nplete	respons	e						
Yes	4	5.7	2	6.3	4	7.1	1	2.1	
No	66	94.3	30	93.7	52	92.9	47	97.9	

Table 3 Pathologic outcomes at radical prostatectomy

Improved from T1c to pT0 (N = 2), T2a to pT0 (N = 1), T2b to pT2a (N = 1), T2c to pT0 (N = 1), T3 to pT2 (N = 1), T3a to pT2a (N = 2), T3a to pT2c (N = 1), T3b to pT3a (N = 1)

-denotes not available

^aDownstaging of clinical T stage as defined by AJCC staging system at diagnosis to pathologic T stage at radical prostatectomy

patients undergoing RP alone were 78%, 23%, and 25%, respectively. The predicted 3-year BCR-free rate was 50%.

Time to BCR, TTM, and OS

Overall, the median follow-up post-RP was 3.4 years (range 0.1–7.0): 5.7 years for TAPS, 4.3 years for Neo-Abi, and 2.6 years for Neo-Enza. Twenty-three patients had a BCR and median time to BCR was 5.1 years (95% CI: 4.4, not reached) (Fig. 1a). The 2-year BCR-free rate was 75% (95% CI: 63%, 84%) and 3-year rate was 70% (95% CI: 57%, 80%). Five



Fig. 1 Kaplan–Meier estimates of BCR (panel **a**) for the total cohort. Time to BCR by pathologic T downstaging (yes vs. no) (**b**) and largest cross section dimension (≤ 0.5 cm or > 0.5 cm) (**c**)

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Pathologic parameter	N. ^a	Number of events	Median, year (95% CI)	BCR free rate		
				2-Year (95% CI)	3-Year(95% CI)	
All patients	72	23	5.1 (4.4, NR)	75% (63%, 84%)	70% (57%, 80%)	
Pathologic T downstagin	ng					
Yes	10	0	NR	100%	100%	
No	57	20	5.1 (3.3, NR)	74% (60%, 84%)	67% (52%, 79%)	
Largest cross section dir	nension					
≤0.5 cm	11	0	NR	100%	100%	
>0.5 cm	55	20	5.1 (3.3, NR)	74% (60%, 84%)	67% (52%, 79%)	

NR not reached

^aExclude patients who did not have pathologic parameters because surgery was done at outside hospitals or tumor measures (i.e., T stage or Largest Cross Section Dimension) were not available from the original trials

patients (6.9%) developed metastases and median TTM was not reached. The 3-year metastasis-free survival was 95% (95% CI: 0.86, 0.98). Overall, there was one death from PC and 3-year OS rate was 98% (95% CI: 88%, 100%).

Time to BCR by pathologic parameters

In an exploratory analysis evaluating time to BCR by pathologic T downstaging, no patient with pathologic T downstaging (n = 10) had a BCR and median time to BCR was not reached (Table 4, Fig. 1b). Similarly, there were no recurrences in patients with a residual tumor ≤ 0.5 cm (n = 11) (Table 4, Fig. 1c). Median follow-up was 2.7 (range 0.6, 5.0) years in those with residual tumor ≤ 0.5 cm or pathologic T downstaging (n = 15).

Testosterone recovery

Post-RP testosterone data were available for 47 patients from two institutions. Overall, median time to testosterone recovery from RP was 4.0 months (95% CI: 3.4–4.9). The cumulative testosterone recovery rate was 31% (95% CI: 20%, 47%) by 3-months, 77% (95% CI: 63, 88%) by 6-months, and 88% (76, 96%) by 1-year, respectively.

Forty out of 47 patients had testosterone recovery, of whom 27 (67%) were BCR-free at last follow-up. The BCR-free rate at 2-years post testosterone recovery was 73% (95% CI: 55%, 85%). Four patients with low testosterone were lost to follow-up and were censored at the last testosterone test date. Three patients who received ADT prior to testosterone recovery were censored at time of ADT initiation.

Discussion

This exploratory analysis was designed to investigate the post-RP outcomes of patients treated with intense

neoadjuvant androgen deprivation. We demonstrate that at a median of three years following RP, 70% of patients remain disease free. Furthermore, no patient with pathologic T downstaging or residual tumor ≤ 0.5 cm experienced a recurrence. While our series is limited by the small number of patients and low failure events, neoadjuvant therapy prior to RP in unfavorable intermediate and high-risk patients may potentially have a positive impact on recurrence rates. These data are hypothesis generating and larger randomized studies with longer follow-up are needed to evaluate the benefit of neoadjuvant hormone therapy.

Currently, RP alone is insufficient for many patients with high-risk PC. Historic trials have evaluated the role of neoadjuvant hormonal therapy. The largest randomized trial included 547 men with cT1-T2 randomized to leuprolide and flutamide for three or eight months before RP [20]. Eight months of therapy was associated with improved preoperative PSA, lower positive surgical margin rate, and higher organ-confined disease rate [20]. Although the pCR rate was higher in the eight month group compared to the three-month group (9.3% vs. 5.1%), this was not statistically significant [20]. A meta-analysis including ten studies of neoadjuvant ADT prior to RP demonstrated statistically significant improvements in pathologic parameters at RP, however, these did not correspond to improved DFS or OS [24].

The more contemporary clinical trials included in this meta-analysis evaluate more potent androgen blockade beyond LHRH therapy and first-generation anti-androgens. This is the first report of the post-RP outcomes data of patients enrolled on these studies. While neoadjuvant ADT remains under investigation, our data highlight that a subset of patients may have a favorable response to treatment. This is consistent with recent data from the Systemic Therapy in Advancing or Metastatic PC: Evaluation of Drug Efficacy (STAMPEDE) trial evaluating abiraterone in patients never previously treated with hormone therapy [29]. Of the 1917 patients randomized, 27% had newly diagnosed high-risk locally advanced disease [29]. Overall, abiraterone added to ADT was associated with a 37% improvement in OS compared to ADT alone (hazard ratio (HR) 0.63; 95% CI: 0.52–0.76, p < 0.001) [29]. The benefit of abiraterone was seen in those with non-metastatic (HR = 0.71) and metastatic disease (HR = 0.65) [29].

Additionally, there is an increasing interest in surgery as part of an integrated multimodal treatment paradigm for patients with locally advanced or oligometastatic PC [30]. Radical surgery to remove the primary in metastatic disease has been associated with improved survival in several solid tumors including colorectal [31] and renal cell carcinoma [32]. With regards to PC, though prospective studies are lacking, a number of retrospective studies have demonstrated the potential benefit of RP in patients with advanced disease [30]. A Surveillance Epidemiology and End Results-based study compared the survival of 8185 men with metastatic PC receiving RP, brachytherapy or no local treatment, and demonstrated an improvement in 5-year OS with local treatment [33]. The safety and efficacy of RP in very-high risk or oligometastatic PC is being investigated in a single arm phase 1/2 clinical trial (NCT02971358). Additional randomized trials will be necessary to evaluate the role of multimodal therapy for locally advanced or metastatic PC.

In our cohort, 11% of patients were observed to have microscopic lymph node involvement at RP. These results are comparable to historic studies documenting rates of nodal involvement at ~10% in high-risk patients undergoing RP [34]. Additionally, in the exploratory analysis evaluating predicted pathologic outcomes of matched patients having undergone RP alone, the predicted rate of nodal involvement was 25%. Although patients did not have clinical lymph node involvement at baseline in our cohort, whether microscopic lymph node involvement was present at baseline is unknown. Direct comparisons cannot be made between these analyses, which highlight the differences between clinical and pathologic staging.

The impact of the pathologic response on long-term outcomes in PC has not been established. In our study, the pCR rate was low, though a subset of patients experienced pathologic T downstaging or MRD. Interestingly, there were no recurrences in these patients. It is possible that pathologic response may correlate with long-term clinical benefit, however, the duration of follow-up was short. Our analysis was exploratory and not powered to investigate the association of pathologic and survival outcomes.

In this analysis, we defined MRD as a residual tumor \leq 0.5 cm. However, this definition does not account for tumor volume and cellularity. In the Neo-Abi trial, we investigated the significance of MRD defined as RCB (tumor volume corrected for tumor cellularity) \leq 0.25 cm³ [26]. The rates of

RCB ≤ 0.25 cm³ ranged from 44–52%. Similar results were seen on the Neo-Enza trial with rates of RCB ≤ 0.25 cm³ of 36–74%. Consensus criteria for the measurement and reporting of pCR and MRD are important in the planning and interpretation of future neoadjuvant trials.

Despite more effective blockade of the androgen axis, the rate of testosterone recovery in our cohort was 85% and median time to testosterone recovery was 4 months. The short recovery time may be related to the young age of our population. We anticipate additional recovery with longer follow-up. Historic trials of neoadjuvant ADT evaluating variable durations of ADT ranging from 3-8 months did not report on testosterone recovery. For reference, we previously evaluated the efficacy of a LHRH agonist, bicalutamide with or without bevacizumab administered for six months in recurrent PC [35]. The rate of testosterone recovery in the ADT only cohort of this study was 71% and median time to testosterone recovery was 10.1 months. Although direct comparisons cannot be made, it appears that testosterone recovery following 6-months of potent androgen blockade was not inferior to that with standard ADT.

In our cohort, the 3-year BCR-free rate was 70% post-RP with eight patients receiving adjuvant radiation therapy or ADT. Using the MSKCC pre-RP nomogram, the predicted 3-year BCR-free rate was 50% for matched patients undergoing RP alone. Numerous questions remain regarding the long-term impact of neoadjuvant therapy on rates of BCR, need for salvage therapy, metastasis development, and OS. Although promising, the significance of our observation on BCR is indeterminate and the benefits can only truly be determined by a phase 3 trial.

Despite neoadjuvant therapy, the majority of patients had residual disease, underscoring the need to identify and target resistance in these patients. We previously demonstrated that persistent intraprostatic tissue androgens and continued AR activity in residual tumor cells may drive resistance [26, 27]. These data suggest that more potent AR inhibition or potentially longer therapy may be warranted. We are investigating these questions in two subsequent neoadjuvant studies. One study, which recently completed accrual, is evaluating the combination of abiraterone and enzalutamide (NCT02268175). The other study, currently open to accrual, is a two-part phase 2 study evaluating neoadjuvant and adjuvant abiraterone and apalutamide, a potent AR antagonist (NCT02903368). Additional correlative analyses are evaluating the genomic and expression profiles of baseline prostate biopsy and RP tissue for biomarkers of exceptional responders and resistance.

This post-hoc exploratory analysis has several limitations. Although patients were enrolled on prospective clinical trials, post-RP follow-up was variable between patients and data were collected retrospectively. Direct comparisons between the three trials is limited given differences in baseline patient and disease characteristics and small sample size. The endpoint of T downstaging at RP is weak given that clinical T stage at baseline was compared to pathologic T stage at RP. The analysis evaluating predicted pathologic outcomes is limited and direct comparisons cannot be made to our cohort. Furthermore, the endpoint of 3-year BCR is short and number of failure events was low.

Our subset analysis from three contemporary multicenter trials evaluating neoadjuvant intense ADT, demonstrates a favorable BCR compared to MSKCC nomogram predicted BCR. Ultimately, a randomized phase 3 study will be necessary to challenge the current treatment paradigm for men with unfavorable intermediate and high-risk disease and prove the value of neoadjuvant/adjuvant intense ADT. The development of such a study poses challenges in terms of the best choice of an intermediate clinical endpoint that is a surrogate for OS and funding. Our preliminary data support that pCR plus MRD (≤ 0.5 cm tumor or RCB < 25%) could be an endpoint that will correlate with BCR and ultimately freedom from metastasis. Despite these challenges, conduct of future neoadjuvant/adjuvant studies is needed to improve the current standard of care for these patients.

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Compliance with ethical standards

Conflict of interest RRM received research funding from Bayer and Pfizer. QDT is supported by an unrestricted educational grant from the Vattikuti Urology Institute, a Clay Hamlin Young Investigator Award from the Prostate Cancer Foundation and a Genentech BioOncology Career Development Award from the Conquer Cancer Foundation of the American Society of Clinical Oncology. RBM received research support from Jansen, Medivation and ESSA. ASK receives advisory board honorarium from Janssen, Bayer, and Sanofi-Aventis. MET receives research funding and advisory board honorarium from Janssen, Medivation.

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Platinum Priority – Prostate Cancer Editorial by Rahul Aggarwal on pp. 694–695 of this issue

Clinical Outcome of Prostate Cancer Patients with Germline DNA Repair Mutations: Retrospective Analysis from an International Study

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Abstract

Background: Germline DNA damage repair gene mutation (gDDRm) is found in >10% of metastatic prostate cancer (mPC). Their prognostic and predictive impact relating to standard therapies is unclear. **Objective:** To determine whether gDDRm status impacts benefit from established therapies in mPC. **Design, setting, and participants:** This is a retrospective, international, observational study. Medical records were reviewed for 390 mPC patients with known gDDRm status. All 372 patients from Royal Marsden (UK), Weill-Cornell (NY), and University of Washington (WA) were previously included in a prevalence study (Pritchard, NEJM 2016); the remaining 18 were gBRCA1/2m carriers, from the kConFab consortium. Australia.

Outcome measurements and statistical analysis: Response rate (RR), progression-free survival (PFS), and overall survival (OS) data were collected. To account for potential differences between cohorts, a mixed-effect model (Weibull distribution) with random intercept per cohort was used.

Results and limitations: The gDDRm status was known for all 390 patients (60 carriers of gDDRm [gDDRm +], including 37 gBRCA2m, and 330 cases not found to carry gDDRm [gDDRm-]); 74% and 69% were treated with docetaxel and abiraterone/enzalutamide, respectively, and 36% received PARP inhibitors (PARPi) and/ or platinum. Median OS from castration resistance was similar among groups (3.2 vs 3.0 yr, p = 0.73). Median docetaxel PFS for gDDRm+ (6.8 mo) was not significantly different from that for gDDRm- (5.1 mo), and RRs were similar (gDDRm+= 61%; gDDRm-= 54%). There were no significant differences in median PFS and RR on first-line abiraterone/enzalutamide (gDDRm+= 8.3 mo, gDDRm-= 8.3 mo; gDDRm+= 46%, gDDRm-= 56%). Interaction test for PARPi/platinum and gDDRm+ resulted in an OS adjusted hazard ratio of 0.59 (95% confidence interval 0.28–1.25; p = 0.17). Results are limited by the retrospective nature of the analysis. **Conclusions:** mPC patients with gDDRm appeared to benefit from standard therapies similarly to the overall population; prospective studies are ongoing to investigate the impact of PARPi/platinum.

Patient summary: Patients with inherited DNA repair mutations benefit from standard therapies similarly to other metastatic prostate cancer patients. © 2018 European Association of Urology. Published by Elsevier B.V. This is an open access article under

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1. Introduction

Inherited mutations in DNA damage repair (DDR) genes associate with an increased risk of developing prostate, breast, ovarian, and other cancers [1,2]. We previously described enrichment of such mutations in metastatic prostate cancer (mPC), with 11.8% of these men harbouring germline DNA damage repair gene mutation (gDDRm) [3]. Mutations in *BRCA2* were most prevalent (5.3%), with these data leading to a change in National Comprehensive Cancer Network (NCCN) guidelines, now recommending germline testing for all men with mPC [4]. Studies in mPC as well as in other diseases support tailored therapeutic approaches for this molecularly defined subset of patients [5–8].

Characterisation of the genomic landscape of prostate cancer has led to the identification of clinically actionable molecular alterations [9,10]. This renders an opportunity for a new classification of this common disease, beyond traditional anatomical and histological considerations, based on the prognostic and predictive significance of some of these alterations for treatment stratification.

Prior studies stated the role of germline *BRCA2* mutations are an independent poor prognostic factor for localised prostate cancer, associated with a more aggressive phenotype, increased rates of developing metastatic disease, and shorter survival from the disease [11,12]. However, when focusing on patients with mPC, the prognostic and predictive roles of gDDRm are unclear. Prior case series have reported conflicting data with regard to the relative benefit derived for patients carrying gDDRm from standard of care therapies (taxanes, abiraterone acetate, enzalutamide) [13–15].

Herein, we retrospectively reviewed the clinical outcome of mPC patients with and without gDDRm. We included 372 patients from three institutions enrolled in a previously published prevalence study of gDDRm (Royal Marsden, UK; Weill-Cornell, NY; University of Washington, WA); in order to increase the number of gDDRm carriers in this analysis, we included an additional cohort of 18 known g*BRCA1/2*m carriers with mPC from the kConFab consortium (Australia).

2. Patients and methods

All patients included had previously been tested for gDDRm. Germline mutations were called based on a panel of 20 genes summarised in Supplementary Table 1. For all the 372 cases from the three UK and US sites, these data had been published in a prior report, including sequencing and bioinformatics methodology [3]. In the original study, patients were not selected on the basis of family history, age, or any knowledge of genetic background. The remaining 18 patients were an independent cohort of known germline BRCA1/2 germline mutation carriers from Australia. Patient medical records were retrospectively reviewed, and patients had received treatment according to local guidelines. Baseline characteristics (demographic characteristics, age, Gleason score, prostate-specific antigen [PSA] and presence of metastatic disease at diagnosis, treatment exposure, and survival data) were collected. Response data (defined as a 50% PSA fall from baseline and/or radiological response according to RECIST) and progression-free survival (PFS; defined as the time from start of a treatment to RECIST/PSA progression or start of a new therapy for clinical progression) for abiraterone, enzalutamide, and docetaxel were annotated.

To account for potential differences between the cohorts, a mixedeffect parametric survival model (Weibull distribution) with random intercept per cohort was used to study correlations with clinical outcome. Multivariate analyses adjusted for age, Gleason score, metastatic disease at diagnosis, and prior radical treatment at diagnosis (either radical prostatectomy or radiotherapy). Fisher's exact test was used to study response rates to each therapy. A test for interaction was pursued for an exploratory subgroup analysis assessing the impact of PARP inhibitors (PARPi) and/or platinum therapy on patient outcome. Kaplan–Meier curves were used to represent time to event data.

3. Results

3.1. Baseline characteristics and treatment exposure

Clinical data were available for 390 patients including 330 not found to carry gDDRm (gDDRm-) and 60 cases with presence of gDDRm (gDDRm+). The distribution of genes mutated per case within the gDDRm+ group was as follows: BRCA2: 37; ATM: seven; CHEK2: four; BRCA1, PALB2, RAD51D: two each; others: seven (one patient had both ATM and CHEK2 mutations; Supplementary Tables 2 and 3). There were no significant differences in baseline characteristics based on gDDRm status (Table 1), including age at diagnosis (median of 62.6 vs 64.9 yr for gDDRm+ vs gDDRm-). Overall, 74% and 69% of patients received, respectively, docetaxel and novel androgen receptor signalling inhibitors (ARSIs: abiraterone acetate, enzalutamide) for metastatic castration-resistant prostate cancer (mCRPC). Based on the cross resistance demonstrated between abiraterone acetate and enzalutamide, in this analysis we considered only the first exposure to either abiraterone acetate or enzalutamide. Of note, 28/60 (47%) gDDRm+ and 113/330 (34%) gDDRmpatients also received treatment with PARPi and/or platinum chemotherapy, treatments that are not currently routinely used for prostate cancer care, reflecting the research focus of the involved academic groups.

3.2. Prognosis of patients with gDDRm

Overall survival (OS) was similar in the two subgroups, with 296 death events (75% of the study population), median OS from castration resistance was 3.0 yr for gDDRm+ (interquartile range [IQR] 2.4–5.6), 3.0 yr for gBRCA2+ (IQR 2.5– 5.4), and 3.2 yr for gDDRm– (IQR 1.7–5.5; log-rank test p = 0.73). In multivariate analysis, age at diagnosis (per 10 yr older, adjusted hazard ratio [aHR] 1.45, 95% confidence interval [CI] 1.21–1.73; p < 0.001), and Gleason score ≥ 8 (aHR 1.54, 95% CI 1.16–2.04; p = 0.003), but not germline mutations (aHR 0.93, 95% CI 0.63–1.37; p = 0.72) were associated with worse survival. When looking specifically at the impact of germline *BRCA2* mutations, these were also not associated with a significantly different prognosis (aHR 0.83, 95% CI 0.50–1.36, p = 0.45; Table 2 and Fig. 1).

3.3. gDDRm and docetaxel

On docetaxel chemotherapy, gDDRm did not associate with significantly different PFS (HR 0.86, 95% CI 0.61–1.20, p = 0.37); similar results were observed when evaluating

Table 1 – Baseline characteristics	of the study populat	on (<i>n</i> = 390)
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	Patients with any germline mutation (<i>n</i> = 60)		Patients withou mutation (1	ut germline 1 = 330)	p value ^a
	Ν	%	Ν	%	
Gleason score					
5–7	15	28.9	105	37.5	0.27
8-10	37	71.2	175	62.5	
Metastatic disease at diagnosis					
No	34	58.6	173	53.7	0.57
Yes	24	41.4	149	46.3	
Received radical treatment					
No	22	36.7	140	42.4	0.48
Yes	38	58.5	190	57.6	
Docetaxel					
No	16	26.7	88	26.7	1.00
Yes	44	73.3	242	73.3	
Abiraterone and/or enzalutamid	e				
No	18	30	101	30.6	1.00
Yes	42	70	229	69.4	
PARPi and/or platinum					
No	32	53.3	217	65.8	0.08
Yes	28	46.7	113	34.2	
Radium-223					
No	52	86.7	296	90.2	0.37
Yes	8	13.3	32	9.8	
	Median	Q1-Q3	Median	Q1-Q3	p value ^b
Age at diagnosis (yr)	62.6	55.3-66.2	62.4	57.7-68.5	0.24
PSA (ng/dl)	17.2	7.7–109.6	33.0	9.8-148.3	0.34

PARPi = PARP inhibitors; PSA = prostate-specific antigen.

^a Fisher's exact test.

^b Wilcoxon rank sum test.

germline *BRCA2* mutation carriers alone (HR 0.96, 95% CI 0.64–1.43, p = 0.83). Kaplan–Meier curves for PFS on docetaxel are shown in Figure 2. Response rate to docetaxel was 61% and 54% for gDDR+ and gDDR– patients, respectively (Fisher's exact p = 0.48, Supplementary Table 4); this resulted in an odds ratio of response to docetaxel of 1.33 (95% CI 0.66–2.69; p = 0.43) for patients carrying gDDRm compared with gDDRm– patients.

3.4. gDDRm and ARSIs (abiraterone, enzalutamide)

PFS on first ARSI (either abiraterone or enzalutamide) for mCRPC was not significantly different for patients with or without gDDRm (HR 0.93, 95% CI 0.65–1.32, p = 0.67), with similar median PFS for gDDRm+ (8.3 mo) and gDDRm– (8.3 mo; Fig. 2). Patients with *BRCA2* mutations also had similar PFS to the overall population (HR 1.09, 95% CI 0.72–1.67, p = 0.66). Response rates to the first ARSI were 46% and 56% for gDDRm+ and gDDRm– patients, respectively (Fisher's exact p = 0.28, Supplementary Table 4), resulting in a nonsignificant trend towards a lower chance of response for gDDRm+ (odds ratio 0.65, 95% CI 0.32–1.32, p = 0.23).

3.5. PARPi and platinum in patients with gDDRm

In this cohort, 141 (36%) patients had received PARPi and/or platinum chemotherapy, including 28/60 (47%) gDDRm+ cases. We explored the potential interaction of these

Table 2 – Overall survival from castration resistance and progression-free survival to standard therapies

		aHR (MVA)	95% CI	p value			
OS from castration resista	nce						
Any gDDRm+		0.93	0.63-1.37	0.72			
Age at diagnosis (per 10	yr)	1.45	1.22-1.73	< 0.001			
Gleason 8-10		1.54	1.16-2.04	0.003			
Metastatic disease		1.22	0.84-1.75	0.30			
Radical treatment		1.50	1.03-2.18	0.03			
	HR	95	5% CI	p value			
PFS docetaxel							
Any gDDRm +	0.86	0.61	l – 1.20	0.37			
Only gBRCA2m+	0.96	0.64	4–1.43	0.83			
PFS first line of ARS therap	ру						
Any gDDRm +	0.96	0.69	9–1.35	0.83			
Only gBRCA2m+	1.10	0.72	2–1.67	0.67			
aHR = adjusted hazard	ratio;	ARS = andro	gen receptor	signal;			
CI = confidence interval;	gDDRm	= germline Di	NA damage re	pair gene			
mutation; MVA = multivariate analysis; PSA = prostate-specific antigen.							
Results from a mixed-effe	Results from a mixed-effect survival model (Weibull distribution) with						
random intercept per coho	ort.						

treatments and gDDRm on survival from castration resistance in this cohort.

There was no statistically significant impact from PARPi/ platinum on OS for the overall population (aHR 0.97, 95% CI 0.73–1.31; p = 0.88). The hazard of death based on the presence of gDDR mutations once adjusted for exposure to



Fig. 1 – Kaplan–Meier curves for survival from date of castration resistance and from initial diagnosis based on the presence of gDDRm and specifically for gBRCA2m carriers. CRPC = castration-resistant prostate cancer; gDDRm = germline DNA damage repair gene mutation; IQR = interquartile range.

PARPi/platinum indicated no statistically significant difference in risk of death (aHR 1.23; 95% CI 0.73–2.07; p = 0.44).

An interaction test between gDDRm+ and PARPi/platinum therapy revealed an aHR of 0.59 (95% CI 0.28–1.25; p = 0.17). These data suggest that the association of gDDRm status and survival could have been impacted by the exposure to PARPi/platinum. Nevertheless, with this size of the gDDRm+ subgroup, no statistically significant differences were observed in this cohort and the null hypothesis could not be excluded. Survival curves illustrating the impact of PARPi/platinum by gDDRm status are shown in Figure 3.

4. Discussion

In this study, we retrospectively reviewed clinical outcome of lethal prostate cancer patients according to their gDDRm status [3]. Overall, we did not observe significant differences in response rate and PFS from docetaxel and ARSIs based on gDDRm status, suggesting that gDDRm+ carriers derive benefit from these therapies similarly to the overall population. These data are of major interest to the clinical community at this time in view of changes in NCCN guidelines in 2018 recommending germline testing for all men suffering from mPC [4].

Prior analyses interrogating this question have reported conflicting results. A recent retrospective study including 319 patients (22 gDDRm+, 16 being germline BRCA2 mutation carriers) reported shorter OS and worse outcome from abiraterone/enzalutamide treatment, but not from docetaxel for mCRPC patients with gDDRm [13]. Preliminary results of a prospective clinical trial of abiraterone and the PARP inhibitor veliparib suggested conversely that prostate cancer patients with DDR defects (here including germline and somatic alterations) may actually be more likely to respond to abiraterone acetate therapy [16]. Differences in the baseline characteristics, genes included in each analysis, and distribution and prevalence of mutations between study populations may have accounted for these differences. The retrospective nature of ours and other studies is a significant limitation, and prospective validation is required in ongoing studies [15]. Data from breast cancer studies also suggest that patients with germline BRCA1/2 mutations derive significant benefit from taxane-based chemotherapy [17].

A notable distinction of our patient cohort was the substantial proportion of patients treated with PARP inhibitors and/or platinum chemotherapy, which are not part of the standard of care for prostate cancer. This has to be taken into account when comparing the survival analysis in this study to others, since the introduction of these treatments may have impacted outcome. The use of such therapies should not, however, have impacted response data to the specific standard therapies presented here, since these were largely administered prior to the PARP inhibitor or platinum therapy. We observed a trend towards prolonged OS in gDDRm+ patients receiving PARPi/platinum. This interaction was not, however, statistically significant in this small gDDRm+ cohort, and may be a chance finding or have been impacted by other unrecognised confounding factors [7,8].

Another limitation of our study is the focus on germline, to the exclusion of somatic only, mutations [9,18,19]. It is estimated that 20-25% mPC have somatic inactivation of a DNA repair gene, but just less than half of these carry a germline mutation. Hence, it is likely that a substantial proportion of our cases in the gDDRm- group harboured somatic DDR defects and that some but not all the gDDRm+ cases would have had somatic inactivation of the second allele. Moreover, the lack of somatic DNA data for this cohort also prevented us from analysing the impact of other concurrent genomic events influencing prostate cancer progression, such as AR, TP53, or RB1 aberrations. Studies assessing clinical outcome to specific therapies incorporating somatic genomic data are ongoing and will be fundamental to shape precision medicine strategies in mCRPC and complement ongoing clinical trials of DNA repair targeting agents in CRPC. These studies and prospective clinical trials will also need to control for other







Dashed lines indicate the 95%Cl limits. Cl = confidence interval; CRPC = castration-resistant prostate cancer; gDDR = germline DNA damage repair; gDDRm = germline DNA damage repair gene mutation; IQR = interquartile range; PARPi = PARP inhibitor. metastatic castration-resistant prostate cancers. 3 - Kaplan-Meier curves depicting survival ы. Б

potential prognostic factors not assessed in this retrospective study.

5. Conclusions

The data presented here suggest that mPC patients with inherited mutations in DDR genes, including those with BRCA2 mutations, can derive similar benefit from standard of care therapies in terms of both response rate and PFS. Based on the limitations described, we acknowledge that this study may not be sufficient to fully inform clinical decisions; in view of the discrepancies identified among different retrospective analyses, prospective studies are now needed evaluating the impact of germline DNA repair mutations in advanced prostate cancer, beyond their clear importance to prompt family cascade counselling. Nevertheless, our overall data indicate that detection of gDDRm should not preclude mPC patients from receiving taxanes, abiraterone, and enzalutamide as standards of care. Pivotal clinical trials of PARPi are ongoing for prostate cancer sufferers with germline and somatic DDRm, and may offer additional therapy options for this group of patients.

Author contributions: Johann S. de Bono had full access to all the data in the study and takes responsibility for the integrity of the data and the accuracy of the data analysis.

Study concept and design: Mateo, Cheng, Beltran, Rubin, Nelson, de Bono. *Acquisition of data:* Mateo, Cheng, Beltran, Xu, Pritchard, Rescigno, Perez-Lopez, Sailer, Kolinsky, Balasopoulou, Bertan, Thorne, Sandhu.

Analysis and interpretation of data: Mateo, Cheng, Beltran, Dolling, Mossop.

Drafting of the manuscript: Mateo, Cheng, Beltran, Rubin, Nelson, de Bono. Critical revision of the manuscript for important intellectual content: Mateo, Cheng, Beltran, Dolling, Xu, Pritchard, Mossop, Rescigno, Perez-Lopez, Sailer, Kolinsky, Balasopoulou, Bertan, Carreira, Montgomery, Nanus, Tagawa, Thorne, Sandhu, Rubin, Nelson, de Bono.

Statistical analysis: Dolling, Mossop.

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Administrative, technical, or material support: Balasopoulou, Thorne. Supervision: Sandhu, Rubin, Nelson, de Bono.

Other: Patient recruitment: Mateo, Cheng, Beltran, Rescigno, Kolinsky, Nanus, Montgomery, Tagawa.

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Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at https://doi.org/10.1016/j.eururo.2018.01.010.

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Seminars article The resounding effect of DNA repair deficiency in prostate cancer

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Abstract

An estimated one-fifth or more of metastatic castration-resistant prostate cancer (mCRPC) harbor defects in genes involved in DNA repair pathway (e.g., *BRCA2, BRCA1*, and others). Early evidence suggests these alterations may be predictive of therapeutic response to PARP inhibitors and platinum chemotherapy, thought to reflect principles of synthetic lethality and are currently being investigated in an increasing number of prospective clinical trials. Other studies have examined these alterations as prognostic biomarkers and in association with response to currently available treatments. A smaller fraction of men (5%-10%) with mCRPC have evidence of microsatellite instability and defects in the DNA mismatch repair pathway, which may predict therapeutic response to immune checkpoint inhibitors. Loss of function of these 2 critical DNA repair pathways serves as new candidate predictive biomarkers for treatment strategies that represent net gains in the treatment toolbox for prostate cancer. Additionally, more than one-tenth of men with mCRPC carry genetic alterations of DNA repair in their germline DNA, which may indicate high- to moderate-penetrance heritable cancer risk and have important implications for family members. Cascade genetic testing of family can, in some cases, direct modified strategies for screening and prevention of multiple cancers. Further study in each of these arenas is ongoing, although the potential for resounding effect is clear. © 2018 Elsevier Inc. All rights reserved.

Keywords: Prostate Cancer; DNA repair; Biomarker; PARP inhibitor; Germline

New precision targets

The prostate cancer research field has recently witnessed a series of important discoveries revolving around genes critical to DNA repair and is beginning to harness the potential of these findings in earnest. In 2015, the Cancer Genome Atlas Research Network reported findings from 333 primary prostate cancers and the identification of 19% of primary tumors with mutations in DNA repair genes, including 3% in the homologous recombination repair gene, *BRCA2* [1]. In the same year, the International SU2C/PCF/AACR Prostate Cancer Dream Team applied exome sequencing to 150 metastatic biopsies and found approximately 20% of metastatic prostate cancers with alterations in genes critical to DNA repair, notably involving homologous recombination repair (*BRCA2, ATM*, and *BRCA1*)

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as well as mismatch repair (*MLH1* and *MSH2*) [2]. Other studies have validated the high prevalence of DNA repair alterations in metastatic castration-resistant prostate cancers (mCRPC) [3,4].

Deficiencies in specific DNA repair pathways have been characterized in other cancers where treatments exploit these deficiencies using principles of synthetic lethality (Fig). The basic rationale is that cancers with specific inactivation of one of a number of DNA repair pathways will render the cancer more reliant on the remaining intact repair pathways. However, drugs such as PARP inhibitors can inactivate one of the remaining DNA repair pathways, which is lethal in cancer cells (where there is insufficient DNA repair capacity to compensate), while being relatively less toxic in noncancerous cells (where there is sufficient remaining intact DNA repair capacity to compensate). These discoveries are major strides in the field, as they represent molecular subsets that may benefit from precision therapies and thus are promising candidate predictive biomarkers.

Homologous recombination deficiency

Following on the discovery that a significant proportion of mCRPC harbors defects in DNA repair was early,

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Fig. Schematic overview of major types of DNA damage, along with the corresponding DNA damage repair mechanisms, key genetic drivers, and treatment implications. Boxes denote components with particular new relevance to advanced prostate cancer. (Color version of figure is available online.)

biologically plausible evidence of clear therapeutic consequence-that not only PARP inhibitors but also platinum chemotherapy may have particular efficacy in prostate cancer with homologous recombination repair deficiency [5–7]: the TOPARP-A study showed that 14/16 (88%) of heavily pretreated patients with mCRPC who had defects in DNA repair genes had a response to the poly ADP ribosylase (PARP) inhibitor olaparib [5]. There are now a substantial number of clinical trials underway investigating PARP inhibitors in mCRPC with evidence of homologous DNA repair inactivation (Table).

In addition, several reports show notably improved response to platinum chemotherapy in patients with metastatic prostate cancer containing inactivating mutations of BRCA2, germline and somatic-only. In our case series from the University of Washington and Fred Hutchinson Cancer Center, 3 heavily pretreated patients observed to have exceptional responses to addition of carboplatin chemotherapy (up to 30 mo of PSA-progression-free survival) underwent tumor next generation sequencing and all were found to have evidence of biallelic inactivation of BRCA2. Notably, 2 patients had underlying germline BRCA2 pathogenic mutations [6]. In another single-institutional study of 141 men treated with at least 2 cycles of carboplatin and docetaxel for mCRPC, pathogenic germline BRCA2 variants were observed in 8/141 men (5.7%; 95% CI, 2.5%-10.9%). Six of 8 BRCA2 mutation carriers (75%) experienced PSA declines >50% within 12 weeks, compared with 23 of 133 noncarriers (17%; absolute difference, 58%; 95% CI, 27%-88%; P < 0.001) [8]. There are also prospective clinical trials underway examining treatment with platinum chemotherapy for patients with mCRPC (Table).

Mismatch repair deficiency and microsatellite instability

In May of 2017, the U.S. Food and Drug Administration granted approval to pembrolizumab for patients with unresectable or metastatic solid tumors with progression or no alternative treatments that have microsatellite instability (MSI) or mismatch repair deficiency, agnostic of tissue/site indication-in this regard, the first FDA-approval of its kind. A small subset of advanced prostate cancers have been reported to have complex MSH2 or MSH6 structural rearrangements resulting in hypermutation [2,8]. Preliminary findings from a combination study adding pembrolizumab at time of resistance to enzalutamide revealed one exceptional responder with evidence of tumor MSI (www.clinicaltrials. gov; NCT02312557) [9]. Thus, MSI/mismatch repair deficient suggests that immune checkpoint inhibition may be another precision-guided treatment avenue for a subset of men with advanced prostate cancer. It remains to be determined whether the combination of enzalutamide and pembrolizumab exerts a different effect on prostate cancer compared to monotherapy with pembrolizumab alone, and whether there are therapeutic differences between different timing and sequences of combinations. Other novel approaches include combination of immune checkpoint inhibitors and PARPi, with the goal of forcing errors in tumor replication and potentially rendering greater tumor antigenicity and visibility to the immune system.

Therapeutic opportunities

These findings have proven exhilarating to the prostate cancer field that has eagerly awaited delivery on the Table

Selected trials in prostate cancers related to DNA repair

Phase	Title	Disease state		Clinicaltrials. gov
III	Study of olaparib (Lynparza) vs. enzalutamide or abiraterone acetate in men with metastatic castration- resistant prostate cancer (PROfound Study)	mCRPC	PROFOUND	NCT02987543
III	A study of rucaparib verses physician's choice of therapy in patients with metastatic castration-resistant prostate cancer and homologous recombination gene deficiency (TRITON3)	mCRPC	TRITON3	NCT02975934
Π	A phase 2 efficacy and safety study of niraparib in men with metastatic castration-resistant prostate cancer and DNA-repair anomalies	mCRPC	GALAHAD	NCT02854436
Π	A multicenter, open-label phase 2 study of rucaparib in patients with metastatic castration-resistant prostate cancer associated with homologous recombination deficiency	mCRPC	TRITON2	NCT02952534
Π	Response rate study of talazoparib in men with DNA repair defects and metastatic castration-resistant prostate cancer who previously received taxane-based chemotherapy and progressed on at least 1 novel hormonal agent (enzalutamide or abiraterone acetate/prednisone)	mCRPC		NCT03148795
Π	Olaparib in men with high-risk biochemically recurrent prostate cancer following radical prostatectomy, with integrated biomarker analysis	BCR		NCT03047135
Π	Abiraterone/prednisone, olaparib, or abiraterone/prednisone + olaparib in patients with metastatic castration-resistant prostate cancer with DNA repair defects	mCRPC	BRCAaway	NCT03012321
Ι	A safety and pharmacokinetics study of niraparib plus an androgen receptor-targeted therapy in men with metastatic castration-resistant prostate cancer (BEDIVERE)	mCRPC	BEDIVERE	NCT02924766
Pilot	Docetaxel and carboplatin in treating patients with metastatic, hormone resistant prostate cancer containing inactivated genes in the BRCA 1/2 pathway	mCRPC	ABCD	NCT02598895
Π	The BARCODE 2 study - the use of genetic profiling to guide prostate cancer treatment (BARCODE2)	mCRPC	BARCODE-2	NCT02955082
Π	Docetaxel and carboplatin for patients with mCRPC and DNA-repair deficiencies	mCRPC	V-ABCD	NCT02985021
Π	Pembrolizumab in treating patients with metastatic castration-resistant prostate cancer previously treated with enzalutamide	mCRPC		NCT02312557
II	Study of pembrolizumab (MK-3475) in participants with metastatic castration-resistant prostate cancer	mCRPC	KEYNOTE-199	NCT02787005
Ib/II	Study of pembrolizumab (MK-3475) combination therapies in metastatic castration-resistant prostate cancer	mCRPC	KEYNOTE-365	NCT02861573

promise of precision oncology: we now have new candidate predictive biomarkers (homologous recombination deficiency, mismatch repair deficiency/MSI) for new treatments and a clear view of net gains in the therapeutic toolbox. Currently, clinical trials incorporating these targeted agents alone and in combination with other agents for prostate cancer are ongoing and in development (Table, www. clinicaltrials.gov).

Mechanisms of resistance

Synthetic lethality in homologous recombination deficient cancers has been extensively explored in ovarian and breast cancers, and some mechanisms of resistance to PARPi and platinum have been described, including reversion mutations (i.e., secondary mutations restoring open reading frames) [10–13]. Indeed, several reports in prostate cancer patients have already described reversion mutations of mutations in BRCA2 and PALB2 in the plasma ctDNA as a mechanism of resistance to PARPi and platinum [14,15] (Cheng et al. JCO PO, in press; Carneiro et al., JCO PO, in press). These reports are sobering in that, as with AR-targeting agents, the drive to resistance is a persistent force though the ability to detect resistant clones early may offer opportunities to triage to clinical trials to prevent development of resistance, such as through combination approaches.

Germline implications

There is little question that the new relevance of DNA repair deficiency in advanced prostate cancer has led to an abundance of new opportunities and therapeutic directions. In 2016, a dedicated germline study of nearly 700 men with metastatic prostate cancer found 11.8% harboring pathogenic germline mutations associated with high- to moderate-penetrance cancer predisposition, including *BRCA2*, *BRCA1* along with a number of other less common DNA repair genes newly associated with prostate cancer [16]. This discovery that approximately half of these treatment-actionable genetic alterations lie in the germline DNA (and are therefore heritable) may be an equally ripe opportunity for the field.

We have long recognized that family history of prostate cancer is a major risk factor for developing prostate cancer. The genetic risk is composed of a combination of common risk and modifying alleles as well as, in some men, relatively rare mutations in moderate-high penetrance cancer risk genes such as *BRCA2*. Both are important, but knowledge of moderate-high penetrance genes carries management recommendations for carriers who may be at increased risk of multiple cancers (NCCN clinical practice guidelines for genetic/familial high-risk assessment: breast and ovarian, genetic/familial high-risk assessment: colorectal.).

A number of groups have now demonstrated the clear limitations of prior criteria (largely family history of cancer)

for identification of men with prostate cancer and singlegene, high- to moderate-penetrance cancer predisposition (*BRCA2*, *BRCA1*, etc.) [16,17]. Moreover, germline carriers of *BRCA2* pathogenic mutations have worse prostate-cancer specific outcomes [18–20]. Germline mutation carriers who are at risk for prostate cancer may be candidates for modified cancer screening [21,22], and those with localized prostate cancer might be considered for clinical trials of treatment intensification to improve outcomes.

The identification of carriers of rare germline pathogenic mutation carriers among those diagnosed with metastatic prostate cancer can also facilitate cascade genetic testing (genetic testing of at-risk family members where each first degree relative has a 50% chance of inheriting the same risk variant), and with it more informed and tailored cancer risk management in these relatives. Alternate approaches are being explored in universal screening of colon and endometrial cancer patients for Lynch Syndrome [23], and similarly in hereditary breast and ovarian cancer syndrome [24,25].

Concerted efforts to determine best approaches to implementation of cascade genetic testing of family members are underway, and more work is needed to understand newer, less characterized variants and genes with respect to clarification of prostate cancer risk, consequent measures for early detection and prevention of not only prostate, but potentially also breast, ovarian, colon, and endometrial cancers, among others. New dedicated clinics and clinical trials are opening to address delivery, characterize risk, and improve management approaches.

Summary

Many new investigative areas and opportunity have arisen from recent discoveries around DNA repair in advanced prostate cancer: precision therapy opportunities (PARPi, platinum, immune-checkpoint inhibitors, and new combination approaches), liquid tumor biopsies in the form of circulating tumor cells and cell-free circulating tumor DNA, research and clinical considerations around germline pathogenic variants in DNA repair genes that could translate to improved management of the next generation (cancer risk management in family members). The full extent of affect will not be realized for a long time to come, but will undoubtedly lead to better outcomes for prostate cancer patients and their families.

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Metastatic Castration-Sensitive Prostate Cancer: Optimizing Patient Selection and Treatment

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OVERVIEW

The treatment landscape for metastatic castration-sensitive prostate cancer (mCSPC) has rapidly evolved over the past 5 years. Although androgen-deprivation therapy (ADT) is still the backbone of treatment, the addition of docetaxel or abiraterone acetate has improved outcomes for patients with mCSPC and become standard of care. With multiple treatment options available for patients with mCSPC, treatment selection to optimize patient outcomes has become increasingly difficult. Here, we review the clinical trials involving ADT plus docetaxel or abiraterone and provide clinicians with guidelines for treatment. Although surgery and/or radiation are standard of care for localized, intermediate- and high-risk prostate cancer, these treatments are not routinely used as part of initial treatment plans for patients with de novo mCSPC. Recent clinical data are challenging that dogma, and we review the literature on the addition of surgery and radiation to systemic therapy for mCSPC. Finally, the standard of care for oligometastatic prostate cancer (a subset of mCSPC with limited metastase) has not been established compared with that for some other cancers. We discuss the recent studies on metastasis-directed therapy for treatment of oligometastatic prostate cancer.

prostate cancer accounts for one in every five cancer diagnoses, making it the most common cancer in men, and metastatic prostate cancer is the second most common cause of cancer-related deaths in men in the United States.¹ The incidence of prostate cancer began to decline in 2000, and it has more rapidly declined since the U.S. Preventive Services Task Force changed its recommendations for prostate-specific antigen (PSA) screening in 2008 and 2011.^{1,2} However, over the same period in the United States, the incidence of metastatic prostate cancer is increasing, with at least one study showing a 72% higher incidence of mCSPC cases in 2013 than in 2004.^{3,4} Whether the increase in mCSPC is specifically related to changes in screening recommendations is unknown; however, this increase is concerning because mCSPC is generally considered to be incurable. Although localized prostate cancer has a 5-year survival rate of 100%, mCSPC has a 5-year survival rate of 29.8%.⁵

The treatment of mCSPC has significantly changed over the past 5 years. The backbone of treatment of mCSPC is ADT to deprive prostate cancer cells of growth-stimulating androgens.⁶ In 2013, the results of a phase III study of continuous versus intermittent ADT (SWOG9346) questioned the role of intermittent ADT. Further incremental progress in the outcome of patients with mCSPC came from the addition of novel agents, docetaxel or abiraterone, to ADT for more aggressive up-front treatment of metastatic prostate cancer. Since 2015, two clinical trials, CHAARTED and STAMPEDE arm C, demonstrated that up-front docetaxel plus ADT improves overall survival (OS) in patients with mCSPC.^{7,8} Then, in 2017, two clinical trials, LATITUDE and STAMPEDE arm G, showed that up-front abiraterone plus prednisone plus ADT improves OS to a similar degree as docetaxel plus ADT did.^{9,10} These clinical trials improved the prognosis for patients with mCSPC for the first time; however, they also present clinicians with a challenge to optimize treatment selection for individual patients among ADT alone, ADT plus docetaxel, and ADT plus abiraterone. To date, no head-to-head comparisons of ADT plus docetaxel versus ADT plus abiraterone are formally published. Additionally, a logical clinical question to ask is, what is the value of adding both docetaxel and abiraterone to standard castration therapy? Currently, there are no data to support this approach.

We begin by discussing the agents available for ADT and efficacy of different dosing regimens. We then more closely analyze the evolving treatment paradigm for mCSPC, including ADT plus docetaxel, ADT plus abiraterone, and novel combinations currently being investigated. After reviewing

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the available data, we discuss considerations for selection of the optimal treatment regimen for individual patients with mCSPC. Finally, we review the role for addition of surgery and/or radiotherapy to systemic therapy in de novo mCSPC and multimodality therapy for oligometastatic prostate cancer.

EVOLVING TREATMENT PARADIGM OF METASTATIC CASTRATION-SENSITIVE PROSTATE CANCER

Androgen-Deprivation Therapy

In mCSPC, prostate cancer cells need high levels of androgens to drive cancer growth.¹¹ Accordingly, approximately 90% of patients with mCSPC will respond to initial treatment with ADT.¹² ADT for mCSPC works by decreasing testicular production of androgens.¹³ There are multiple mechanisms of action to block testicular production of androgens, including orchiectomy, luteinizing hormone-releasing hormone (LHRH) agonists to prevent luteinizing hormone secretion, and LHRH antagonists to decrease luteinizing hormone secretion. Two LHRH agonists, leuprolide and goserelin, are approved in the United States, whereas degarelix is the only LHRH antagonist approved there. The first-generation antiandrogens flutamide, nilutamide, and bicalutamide are not recommended as monotherapy for mCSPC; however, they are frequently used when LHRH agonists are initiated to prevent testosterone flare.¹⁴ Until 2015, combined androgen blockade with an LHRH agonist and a first-generation antiandrogen was commonly used to treat mCSPC. Combined androgen blockade with first-generation antiandrogens can be considered, but data supporting the

PRACTICAL APPLICATIONS

- ADT plus docetaxel for six cycles is considered a standard of care for high-volume mCSPC based on the CHAARTED, STAMPEDE arm C, and GETUG-AFU 15 clinical trials.
- ADT plus abiraterone acetate continued until disease progression is considered a standard of care for all patients with mCSPC based on the LATITUDE and STAMPEDE arm G clinical trials.
- Predictive biomarkers are needed to select patients for ADT plus docetaxel versus ADT plus abiraterone. Until those are identified, ADT plus docetaxel may be considered for patients with mCSPC who have more than four metastases, have a good performance status, desire shorter total treatment time, or have concerns for prescription drug costs; ADT plus abiraterone acetate may be suggested to patients who have fewer than four sites of metastases or are unable/unwilling to tolerate the potential toxicity of chemotherapy.
- Multiple phase III clinical trials are investigating novel combinations of ADT and androgen axis inhibitors, including enzalutamide, apalutamide, darolutamide, and orteronel without corticosteroids in mCSPC.
- Clinical studies suggest that addition of surgery and/or radiotherapy to systemic treatment may have a role in the treatment of newly diagnosed mCSPC, and clinical trials are investigating this hypothesis.

benefits are small. Furthermore, second-generation androgen receptor (AR) antagonists or androgen synthesis inhibitors may negate the observed benefits (Fig. 1).

Recent investigations have studied the optimal dosing schedule of ADT to balance efficacy with patient quality of life. In a phase III clinical trial of 3,040 men with newly diagnosed metastatic hormone-sensitive prostate cancer (mHSPC), SWOG studied whether intermittent ADT is noninferior to continuous ADT.¹⁵ All patients were initially treated with 7 months of continuous ADT then randomly assigned to continuous or intermittent ADT if they had an ongoing PSA response. The coprimary endpoints for SWOG 9346 were noninferiority of intermittent ADT with respect to OS and quality of life 3 months after randomization. Unsurprisingly, intermittent ADT was associated with improved quality of life 3 months after randomization but not later because of the variable period of time "off therapy." However, intermittent ADT was not found to be noninferior to continuous ADT with respect to OS (5.8 years vs. 5.1 years; hazard ratio [HR], 1.10; 95% CI, 0.99-1.23) but rather the result was inconclusive. However, SWOG 9346 raised concerns about intermittent ADT, thus perpetuating continuous ADT as the favored therapy for mCSPC.

Analyses of several clinical trials have suggested that more aggressive up-front treatment could translate to improved outcomes for patients with mCSPC. In a subgroup analysis of 1,345 patients from SWOG 9346, lower PSA values after 7 months of continuous ADT were predictive of improved median OS.¹⁶ Specifically, the 383 (25%) patients with a PSA greater than 4 ng/mL had a median OS of 13 months, whereas the 602 (45%) patients with a PSA less than 0.2 ng/mL had a median OS of 75 months. A follow-up analysis from the PR-7 trial, in men with biochemically recurrent prostate cancer, found that lower testosterone levels were predictive of improved cancer-specific survival and time to castration-resistant prostate cancer (CRPC).¹⁷ These studies suggested that deeper androgen blockade could improve clinical outcomes for patients with mCSPC.¹⁸

Androgen-Deprivation Therapy Plus Docetaxel

To date, three clinical trials have investigated the efficacy of ADT plus docetaxel: CHAARTED, STAMPEDE arm C, and GETUG-AFU 15. CHAARTED was a phase III clinical trial that randomly assigned 790 men with mCSPC to receive ADT plus docetaxel or ADT alone.⁷ Docetaxel without daily prednisone was administered every 3 weeks for a total of six cycles. The primary outcome, median OS, was 13.6 months longer for patients treated with ADT plus docetaxel than for patients receiving ADT alone (57.6 months vs. 44.0 months, respectively; HR 0.61; 95% CI, 0.47–0.80). Of note, a substantial number of patients in the ADT-alone arm never received docetaxel at CRPC before death. ADT plus docetaxel also improved median time to progression compared with ADT alone (20.2 months vs. 11.7 months; HR 0.61; 95% Cl, 0.51-0.72). Docetaxel has a significant toxicity profile that differs from that of ADT, and 29.3% of patients treated with ADT plus docetaxel reported any grade 3/4 adverse events. The most frequently reported grade 3/4 adverse

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events were neutropenia (12.1%) and fatigue (4.1%). To determine whether ADT plus docetaxel should be used in all patients with mHSPC or only higher-risk patients, CHAARTED performed a subgroup analysis of median OS by extent of disease present.¹⁹ Investigators found that only patients with high-volume disease, defined as the presence of visceral metastases or at least four bone lesions with one or more beyond the vertebral bodies and pelvis, benefit from ADT plus docetaxel (median OS, 51 months vs. 34 months; HR 0.63; 95% CI, 0.50–0.79), whereas low-volume patients have similar outcomes with ADT alone or with docetaxel (median OS, 64 months vs. not reached; HR 1.04; 95% CI, 0.70–1.55).

GETUG-AFU 15, conducted before CHAARTED, was a phase III clinical trial that randomly assigned 385 men with mCSPC to receive ADT alone or ADT plus docetaxel.²⁰ Median OS was not significantly improved in the ADT plus docetaxel arm compared with ADT alone (58.9 months vs. 54.2 months; HR 1.01; 95% CI, 0.75–1.36). Furthermore, before use of granulocyte colony-stimulating factor, four treatment-related deaths occurred in the ADT plus docetaxel arm. After publication of CHAARTED, a follow-up analysis of GETUG-AFU 15 reported median OS by volume of disease, which was collected retrospectively.²¹ A nonsignificant trend toward improved OS was seen in high-volume disease (39.8 months vs. 35.1 months; HR 0.78; 95% CI, 0.56–1.09), and no difference in OS was observed for low-volume

disease (not reached vs. 83.4 months; HR 1.02; 95% Cl, 0.67–1.55).²²

With discordant findings between CHAARTED and GETUG-AFU 15, STAMPEDE arm C sought to further explore whether ADT plus docetaxel improves survival for patients with mCSPC. STAMPEDE randomly assigned 2,962 men with locally advanced or mHSPC to receive ADT alone (arm A); ADT plus zoledronic acid (arm B); ADT plus docetaxel (arm C); or ADT, docetaxel, and zoledronic acid (arm E).8 Similar to CHAARTED, ADT plus docetaxel significantly improved median OS compared with ADT alone in STAMPEDE arm C (81 months vs. 71.3 months; HR 0.78; 95% CI, 0.66–0.93). ADT plus docetaxel also improved median failure-free survival compared with ADT alone (37 months vs. 20 months; HR 0.61; 95% Cl, 0.53-0.70). As was seen in the other trials, more patients in the ADT plus docetaxel arm reported grade 3/4 adverse events than did those receiving ADT alone (39% vs. 17%), and one treatment-related death occurred in the ADT plus docetaxel cohort. Unfortunately, STAMPEDE did not report outcomes by volume of disease.

In a meta-analysis that included CHAARTED, STAMPEDE arm C/E, and GETUG-AFU 15, ADT plus docetaxel was confirmed to significantly improve median OS (HR 0.77; 95% Cl, 0.68–0.87) and median failure-free survival (HR 0.64; 95% Cl, 0.58–0.70) compared with ADT alone.²³ These trials and subsequent meta-analysis established ADT plus docetaxel as a standard of care for fit patients with high-volume mCSPC.



FIGURE 1. Androgen Synthesis Pathway Throughout Body With Drugs Targeting Androgen Synthesis

Abbreviations: AR, androgen receptor; GnRH, gonadotropin-releasing hormone; HSP, heat shock protein; SARD, selective androgen receptor degrader.

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ADT Plus Abiraterone Acetate Plus Prednisone

Similar to docetaxel, abiraterone acetate was initially approved for the treatment of mCRPC.^{24,25} Abiraterone is a nonsteroidal, irreversible inhibitor of CYP17A1, so it inhibits gonadal and extragonadal androgen synthesis. To date, two clinical trials studying abiraterone in mCSPC have been reported, LATITUDE and STAMPEDE arm G; one study, PEACE-1, is still ongoing. LATITUDE was a phase III clinical trial that randomly assigned 1,199 men with mCSPC to receive ADT plus abiraterone (1,000 mg daily) and prednisone (5 mg daily) or ADT alone.⁹ To be included in the trial, men with mCSPC needed to have at least two high-risk prognostic factors, including a Gleason score of 8 or higher, presence of at least three bone lesions, or measurable visceral metastases. LATITUDE was powered to measure two primary endpoints: median OS and radiographic progression-free survival. ADT plus abiraterone significantly improved median OS (not reached vs. 34.7 months; HR 0.62; 95% CI, 0.51-0.76) and median radiographic progression-free survival (33.0 vs. 14.8 months; HR 0.47; 95% CI, 0.39-0.55). Regarding toxicity, grade 3/4 adverse events were more common in the ADT plus abiraterone arm (63% vs. 48%). The most frequently reported grade 3/4 adverse events in the abiraterone arm were mineralocorticoid-related hypertension (20%), hypokalemia (11%), and increased alanine aminotransferase levels (5%).

Interestingly, in 2017, STAMPEDE arm G, which was simultaneously presented with LATITUDE at the ASCO annual meeting, showed similar benefits with upfront abiraterone. STAMPEDE arm G was a phase III clinical trial that included multiple cohorts of patients with advanced prostate cancer, including mCSPC, node-positive disease, or high-risk locally advanced disease.¹⁰ In total, 1,917 men with advanced prostate cancer were randomly assigned to receive ADT plus 1,000 mg of abiraterone plus 5 mg of prednisolone or ADT alone. Of these 1,917 men, 941 had newly diagnosed mCSPC. In the overall cohort, ADT plus abiraterone demonstrated a strong OS advantage compared with ADT (83% vs. 76%; HR 0.63; 95% CI, 0.52–0.76) and better 3-year failure-free survival (75% vs. 45%; HR 0.29; 95% Cl, 0.25-0.34). In patients with mCSPC, the effect of ADT plus abiraterone on OS and failure-free survival remained true. As was seen in LATITUDE, the incidence of grade 3/4 adverse events was higher in the ADT plus abiraterone group than in the ADTalone group (47% vs. 33%). On the basis of the results from the LATITUDE and STAMPEDE arm G clinical trials, ADT plus abiraterone acetate and prednisone is now considered a standard of care for mCSPC regardless of the disease volume status. However, follow-up for nonmetastatic prostate cancer is not adequate to determine the benefit.

A third phase III clinical trial evaluating ADT plus abiraterone is in progress. PEACE-1 will randomly assign 916 patients with mCSPC to one of four arms: ADT with or without docetaxel, ADT with or without docetaxel and abiraterone and prednisone, ADT with or without docetaxel and radiotherapy, or ADT with or without docetaxel and abiraterone and prednisone. PEACE-1 will help us better understand whether docetaxel and abiraterone can have synergistic effect in mCSPC.

OPTIMAL CURRENT TREATMENT PARADIGM

Because clinical trials investigating ADT plus docetaxel and ADT plus abiraterone had very similar outcomes and headto-head, prospective comparisons were not performed, clinicians face a new challenge optimizing treatment selection for patients with mCSPC. Furthermore, predictive biomarkers are not available in the clinic to help guide treatment selection. Although the efficacy of these regimens is similar, the toxicity profiles, cost, and duration of treatment can help guide selection between docetaxel and abiraterone.

Analysis of the individual trials shows that the disease volume may help tailor treatment selection.²⁶ In CHAARTED and GETUG-AFU 15, men with low-volume disease did not benefit with docetaxel. However, none of the trials with abiraterone have categorized men according to the volume status of the disease and thus have not shown lack of benefit in any given subset of patients.²⁷ We recommend that docetaxel be considered for patients with high-volume disease, and abiraterone can be recommended to all regardless of disease volume (Table 1). Table 1 shows considerations for the treating physician choosing between ADT plus abiraterone and ADT plus docetaxel.

In regard to toxicity, the frequency of grade 3 to 5 adverse events was similar between ADT plus docetaxel and ADT plus abiraterone plus prednisone. However, the profile of adverse events significantly differs between the two drugs. Docetaxel may cause bone marrow suppression, infections, and neuropathy, whereas abiraterone may cause mineralocorticoid-induced hypertension, hypokalemia, and elevated liver enzyme levels. In general, most patients better tolerate abiraterone than docetaxel. The duration of treatment also differs significantly between the reported regimens of docetaxel and abiraterone in mCSPC. Docetaxel is given once every 3 weeks for a total of six cycles, which is generally around 15 weeks of total treatment. In contrast, abiraterone is recommended daily until time of progression, which generally occurs after several years of treatment with abiraterone. Finally, the expense to the patient of abiraterone and docetaxel differs significantly. When only cost per cycle and number of cycles given are considered, the six cycles of docetaxel cost the same as 3- to 4-month treatment

TABLE 1. Attributes of Treatment That Favor ADT Plus Abiraterone or ADT Plus Docetaxel

Attribute	Favors Abiraterone	Favors Docetaxel
Efficacy in HVD	Х	х
Efficacy in LVD	Х	
Toxicity	Х	
Treatment duration		Х
Cost		х

Abbreviations: ADT, and rogen-deprivation therapy; HVD, high-volume disease; LVD, low-volume disease.

TABLE 2. Ongoing and Recently Reported Phase III Clinical Trials Evaluating Novel Androgen Axis Inhibitors in Metastatic Hormone-Sensitive Prostate Cancer

Trial Name	Arms	No. of Patients	Primary Endpoint	ClinicalTrials.gov Identifier	Anticipated Read Out
PEACE-1	ADT ± doce, ± RT, ± abi	916	rPFS, OS	NCT01957436	2020
SWOG-1216	ADT + TAK-700 vs. bicalutamide	1,304	OS	NCT01809691	2020
ARASENS	ADT + doce + ODM-201 vs. placebo	1,300	OS	NCT02799602	2022
ENZA-MET	ADT ± doce + enza vs. NSAA	1,100	OS	NCT02446405	2020
ARCHES	ADT ± doce + enza vs. placebo	1,100	rPFS	NCT02677896	2023
STAMPEDE ARM J	ADT ± doce, ± RT, ± abi + enza	1,800	OS	NCT00268476	2020
TITAN	ADT ± doce + apa vs. placebo	1,000	rPFS, OS	NCT02489318	2021

Abbreviations: ADT, androgen-deprivation therapy; doce, docetaxel; RT, radiotherapy; abi, abiraterone acetate; rPFS, radiographic progression-free survival; OS, overall survival; enza, enzalutamide; NSAA, nonsteroidal androgen antagonist; apa, apalutamide.

with abiraterone. Additionally, there is frequently a high copay with abiraterone (an oral drug) compared with docetaxel (an intravenous drug).^{28,29} This is a simplistic analysis that does not account for many components of cost-effectiveness; however, a formal cost-effectiveness analysis has yet to be done. Thus, docetaxel may be favored over abiraterone for patients or in countries where cost factors heavily into the treatment decision.

In summary, ADT plus docetaxel may be considered for patients who desire shorter total treatment time or when there are cost considerations. ADT plus abiraterone can be considered in patients who have low-volume disease, desire to avoid possible chemotherapy toxicity, or want to minimize facility visits for docetaxel administration. Finally, patient-specific comorbidities may guide treatment selection, for example, avoiding docetaxel in frail patients at high risk for myelosuppression and those with neuropathy and avoiding abiraterone plus prednisone in those with liver disease, diabetes, and osteoporosis.

NOVEL COMBINATIONS BEING INVESTIGATED FOR METASTATIC CASTRATION-SENSITIVE PROSTATE CANCER

With the knowledge that deeper androgen signaling blockade leads to improved outcomes in mCSPC and the recent success of docetaxel and abiraterone, several novel combinations of ADT plus androgen axis inhibitors are under investigation. Enzalutamide is a second-generation antiandrogen that binds to the AR with higher affinity than bicalutamide and prevents nuclear translocation of the AR (Fig. 1).³⁰ Enzalutamide is approved as any-line treatment of mCRPC.^{31,32} Two phase III clinical trials are evaluating ADT plus enzalutamide in patients with mCSPC: ENZA-MET and ARCHES (Table 2). ENZA-MET (NCT02446405) will randomly assign 1,000 patients with mCSPC to receive ADT with or without docetaxel plus enzalutamide or ADT with or without docetaxel plus a nonsteroidal androgen antagonist. ENZA-MET is anticipated to read out in 2020, and it will tell us whether ADT plus enzalutamide is more efficacious than standard ADT and whether ADT plus enzalutamide has a synergistic effect with docetaxel. ARCHES (NCT02677896) aims to answer the same clinical questions. ARCHES is also randomly assigning 1,100 patients to receive ADT with or without docetaxel plus enzalutamide or ADT with or without docetaxel plus placebo. Unfortunately, neither of these trials is comparing ADT plus enzalutamide to ADT plus abiraterone or docetaxel, which are now considered standard of care.

Apalutamide (ARN-509) is another second-generation antiandrogen that is an irreversible AR antagonist. Recently, in the SPARTAN trial in men with M0 CRPC, apalutamide showed improved survival outcomes; however, it is not currently approved for prostate cancer.³³ ADT plus apalutamide is being studied for mCSPC in the phase III TITAN clinical trial (NCT02489318). Previously, a phase II clinical trial of apalutamide in mCRPC demonstrated acceptable safety and efficacy to warrant further investigations in mCSPC and mCRPC.³⁴ TITAN is randomly assigning 1,000 patients with mCSPC to receive ADT with or without docetaxel plus apalutamide versus ADT alone (Table 2). TITAN will answer the question of whether addition of apalutamide to standard-of-care treatment may improve survival outcomes in mCSPC.

Darolutamide (ODM-201) is a next-generation antiandrogen that has a higher affinity for the AR than does enzalutamide or apalutamide.³⁵ Darolutamide is not currently approved for the treatment of prostate cancer. However, a phase I/II clinical trial in 134 men with progressive mCRPC found darolutamide to have an acceptable safety profile.³⁶ ARASENS (NCT02799602) is a phase III clinical trial in mCSPC that will randomly assign 1,300 men to receive ADT plus docetaxel and either darolutamide or placebo (Table 2). ARASENS is expected to read out in 2022.

Orteronel (TAK-700) is unique from the other novel androgen axis inhibitors discussed because it is a reversible CYP17 inhibitor that has more specificity for 17,20 lyase than 17 hydroxylase. Preclinical studies demonstrated that orteronel significantly reduces testosterone and androstenedione levels in cell lines and rats, resulting in smaller prostates.^{37,38} Although phase III clinical trials in mCRPC showed no OS benefit with orteronel, a phase II trial in patients with nonmetastatic prostate cancer and biochemical recurrence

Downloaded from ascopubs.org by UNIVERSITY WASHINGTON on November 28, 2018 from 128.095.104.109 Copyright © 2018 American Society of Clinical Oncology. All rights reserved. found that orteronel decreased PSA by greater than 30% in most patients and that 16% achieved a PSA less than 0.2 ng/mL at 3 months.³⁹⁻⁴¹ A phase III clinical trial, SWOG-1216, is investigating ADT plus orteronel (without prednisone) compared with ADT plus bicalutamide in 1,304 patients with mCSPC (NCT01809691).

THE ROLE OF LOCALIZED THERAPY IN METASTATIC CASTRATION-SENSITIVE PROSTATE CANCER

Prostate radiation or radical prostatectomy (RP) are not currently recommended for the treatment of patients with de novo metastatic prostate cancer. In some advanced malignancies, such as metastatic renal cell carcinoma, patients experience a survival benefit from cytoreductive surgery, which is considered a standard of care for these patients.⁴² This has led to increased interest in the role of local therapy for mCSPC. Although reported studies have important limitations, early results for this approach in mCSPC are intriguing and warrant further investigation.

Initially, two hypothesis-generating, retrospective Surveillance, Epidemiology, and End Results (SEER) database studies found that local therapy combined with systemic therapy improved survival in metastatic prostate cancer. In the first SEER analysis, 8,185 patients with stage IV prostate cancer were identified between 2004 and 2010.43 Of these 8,185 patients, 245 patients (3.0%) had an RP performed, and 129 patients (1.6%) were treated with prostate brachytherapy. The remaining, untreated patients were significantly older (p < .001) and less likely to have a Gleason score of 7 or lower (p < .001). Five-year OS and cancer-specific survival were higher in patients receiving RP (67.4% and 75.8%, respectively) and brachytherapy (52.6% and 61.3%) than in those receiving no local treatment (22.5% and 48.7%; p < .001). Another SEER study used a propensity score analysis to ensure that the observed effect of radical prostatectomy or brachytherapy were attributable to treatment instead of baseline cohort differences.⁴⁴ The authors confirmed that RP and brachytherapy improve CSS compared with no definitive treatment. Because of their use of the SEER database, both studies had substantial limitations, including not accounting for whether patients received ADT and the fact that less than 5% of their total cohorts received definitive therapy.⁴⁵ A third retrospective study used the National Cancer Database to confirm the findings from previous SEER studies.⁴⁶ Of 6,382 men with newly diagnosed mCSPC in this database, 538 men (8.4%) were treated with ADT plus radiotherapy, and the remaining men were treated with ADT alone. Men treated with ADT plus radiotherapy had significantly improved OS in multivariate analysis (HR 0.62; 95% CI, 0.55–0.71).

To address the limitations of the prior SEER studies, a study linked SEER outcomes to Medicare data.⁴⁷ This study design allowed the authors to account for medical comorbidities, receipt of ADT, and type of radiotherapy given (palliative, localized intensity-modulated radiation, or conformal radiation). In the multivariate analysis accounting for these factors, prostate cancer–specific mortality was improved for RP (HR 0.48; 95% CI, 0.27–0.85) and intensity-modulated radiation (HR 0.38; 95% CI, 0.24–0.61). Because the three prior studies came from the U.S. SEER database, a retrospective study of the Munich Cancer registry also looked at the effect of RP on survival for mCSPC.⁴⁸ Of the 1,538 men with mCSPC, 75 men (5%) received RP, and this group had improved 5-year OS compared with the no-surgery arm (55% vs. 21%; p < .01). Finally, a case-control series of 140 men with mCSPC randomly assigned 38 men to prostate radiotherapy.⁴⁹ Patients who received prostate radiotherapy had improved 3-year OS compared with the other groups (69% vs. 43%; p = .004), and no grade 3 or worse genitourinary adverse events were reported.

In summary, RP and local radiotherapy have shown potential to improve survival in patients with mCSPC.⁵⁰ However, the design of reported studies (i.e., retrospective or case-control series) and inconsistent findings indicate that randomized clinical trials are needed before definitive therapy is routinely used in the management of newly diagnosed mCSPC. A phase II clinical trial randomly assigning 180 men with mCSPC to ADT with or without localized therapy (NCT01751438) is underway and should begin to address this hypothesis. As clinical trials investigate these questions, investigators must consider how the significant morbidity associated with definitive therapy weighs against the benefits of treatment.

METASTASIS-DIRECTED THERAPY FOR OLIGOMETASTATIC PROSTATE CANCER

Although no consensus definition exists, oligometastatic prostate cancer is often defined as at least three or five metastases.⁵¹ To date, it is unclear whether patients with oligometastatic prostate cancer should be treated differently than patients with high-volume disease.

Multiple retrospective studies initially suggested that metastasis-directed therapy is safe, feasible, and efficacious in patients with oligometastatic prostate cancer. In a singlecenter study of 40 patients with fewer than two bone metastases in the spine, stereotactic body radiation therapy (SBRT) to the metastatic lesions was associated with an estimated local disease control rate of 95.5% at 6, 12, and 24 months.⁵² Another single-center study of 21 patients with oligometastatic disease involving the bone (19 patients), lymph nodes (one patient), or liver (one patient) found that SBRT had 100% local control at 5 months and that 53% of patients had an undetectable PSA.53 These studies were followed by a multicenter retrospective study of 119 patients that confirmed SBRT is efficacious in oligometastatic prostate cancer.⁵⁴ Then, two retrospective studies demonstrated that SBRT delays the initiation of ADT for patients with oligometastatic disease.55,56

With multiple retrospective studies suggesting that metastasis-directed therapy may be efficacious for oligometastatic prostate cancer, a phase II clinical trial, STOMP, sought to validate the role for metastasis-directed therapy.⁵⁷ In STOMP, 62 patients with biochemical recurrence after

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definitive therapy or fewer than three extracranial metastatic lesions were randomly assigned to surveillance or metastasisdirected therapy (either SBRT or surgery). The median ADTfree survival for surveillance was 13 months compared with 21 months for the metastasis-directed therapy arm (HR 0.60; 95% CI, 0.40–0.90). Quality of life was similar in the two arms at baseline, 3 months, and 12 months. Two ongoing phase III clinical trials, CORE and PCX IX, will provide overall survival data for metastasis-directed therapy. CORE (NCT02759783) is randomly assigning 206 patients with oligometastatic prostate, breast, and non–small cell lung cancer to standard of care or standard of care plus SBRT. In contrast, PCX IX (NCT02685397) is randomly assigning 130 patients with oligometastatic CRPC to an LHRH agonist plus enzalutamide or to LHRH agonist plus enzalutamide plus SBRT.

CONCLUSION

ADT plus docetaxel and ADT plus abiraterone are the contemporary standard treatment of mCSPC. ADT plus docetaxel may be considered for patients with mCSPC who have good performance status, have high-volume

disease, desire shorter total treatment time, or have concerns of prescription drug costs. ADT plus abiraterone acetate may be suggested for men with cancer of any volume and who desire to minimize hospital visits associated with chemotherapy infusions. Patient-specific comorbidities may guide treatment selection as well; for example, abiraterone plus prednisone may be avoided in those with diabetes, liver disease, osteoporosis, or difficult-to-control hypertension, and docetaxel may be avoided in those with neuropathy or at high risk for myelosuppression. Eventually, we need predictive biomarkers to optimize treatment selection between these current and emerging therapies. We also anticipate that treatment of mCSPC will continue to rapidly evolve. Multiple novel androgen axis inhibitors are being investigated in combination with ADT for treatment of mCSPC. On the basis of retrospective and casecontrol series data, local therapy for de novo mCSPC has the potential to augment current systemic therapies. Finally, for patients with oligometastatic prostate cancer, metastasis-directed therapy combined with systemic therapy is promising.

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JAMA Oncology | Original Investigation

Radiographic Progression-Free Survival as a Clinically Meaningful End Point in Metastatic Castration-Resistant Prostate Cancer The PREVAIL Randomized Clinical Trial

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IMPORTANCE Drug development for metastatic castration-resistant prostate cancer has been limited by a lack of clinically relevant trial end points short of overall survival (OS). Radiographic progression-free survival (rPFS) as defined by the Prostate Cancer Clinical Trials Working Group 2 (PCWG2) is a candidate end point that represents a clinically meaningful benefit to patients.

OBJECTIVE To demonstrate the robustness of the PCWG2 definition and to examine the relationship between rPFS and OS.

DESIGN, SETTING, AND PARTICIPANTS PREVAIL was a phase 3, randomized, double-blind, placebo-controlled multinational study that enrolled 1717 chemotherapy-naive men with metastatic castration-resistant prostate cancer from September 2010 through September 2012. The data were analyzed in November 2016.

INTERVENTIONS Patients were randomized 1:1 to enzalutamide 160 mg or placebo until confirmed radiographic disease progression or a skeletal-related event and initiation of either cytotoxic chemotherapy or an investigational agent for prostate cancer treatment.

MAIN OUTCOMES AND MEASURES Sensitivity analyses (SAs) of investigator-assessed rPFS were performed using the final rPFS data cutoff (May 6, 2012; 439 events; SA1) and the interim OS data cutoff (September 16, 2013; 54O events; SA2). Additional SAs using investigator-assessed rPFS from the final rPFS data cutoff assessed the impact of skeletal-related events (SA3), clinical progression (SA4), a confirmatory scan for soft-tissue disease progression (SA5), and all deaths regardless of time after study drug discontinuation (SA6). Correlations between investigator-assessed rPFS (SA2) and OS were calculated using Spearman ρ and Kendall τ via Clayton copula.

RESULTS In the 1717 men (mean age, 72.0 [range, 43.0-93.0] years in enzalutamide arm and 71.0 [range, 42.0-93.0] years in placebo arm), enzalutamide significantly reduced risk of radiographic progression or death in all SAs, with hazard ratios of 0.22 (SA1; 95% CI, 0.18-0.27), 0.31 (SA2; 95% CI, 0.27-0.35), 0.21 (SA3; 95% CI, 0.18-0.26), 0.21 (SA4; 95% CI, 0.17-0.26), 0.23 (SA5; 95% CI, 0.19-0.30), and 0.23 (SA6; 95% CI, 0.19-0.30) (P < .001 for all). Correlations of rPFS and OS in enzalutamide-treated patients were 0.89 (95% CI, 0.86-0.92) by Spearman ρ and 0.72 (95% CI, 0.68-0.77) by Kendall τ .

CONCLUSIONS AND RELEVANCE Sensitivity analyses in PREVAIL demonstrated the robustness of the PCWG2 rPFS definition using additional measures of progression. There was concordance between central and investigator review and a positive correlation between rPFS and OS among enzalutamide-treated patients.

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Corresponding Author: Michael J. Morris, MD, Memorial Sloan Kettering Cancer Center, 1275 York Ave, New York, NY 10065 (morrism @mskcc.org). verall survival (OS) is the benchmark for regulatory drug approval for patients with advanced cancer. Since 2010, 5 agents have achieved the milestone of prolonging OS for men with metastatic castration-resistant prostate cancer (mCRPC), and these agents have transformed the management of the disease.¹⁻⁸ The availability of these effective therapies, although clinically beneficial to patients, can have a secondary effect of blunting the impact of an investigational agent on OS by virtue of postprotocol exposures. Consequently, development efforts focusing on OS are likely to shift to more advanced and heavily pretreated clinical settings. End points short of survival that represent clinical benefit and can independently support regulatory approval will be necessary to ensure that effective drugs are available to improve outcomes for patients across all stages of disease.

To address this, the Prostate Cancer Clinical Trials Working Group 2 (PCWG2) developed a set of consensus criteria in 2008 regarding clinical trial conduct for contemporary studies in men with mCRPC.⁹ The PCWG2 stressed the importance of time-to-event measures that are not affected by posttreatment therapies and that could be strongly linked to clinical outcomes that were indicative of a worsening disease status, including deteriorations in quality of life, a need for a change in anticancer therapy, and, ultimately, death from disease. One such end point, radiographic progression-free survival (rPFS), is not affected by postprotocol treatments, but it has been difficult to quantify because of the lack of standardization of the outcome measure itself.

The PCWG2 sought to establish a definition for rPFS that would ensure that a drug was not working before therapy was discontinued. One definition proposed by PCWG2 was a "2 + 2" rule, which stated that progression not be declared early in a patient's treatment course unless at least 2 new lesions were seen on the first on-treatment scan, followed by at least 2 additional lesions on the second posttreatment scan. The rule was designed to control for tumor flare, a paradoxical worsening of the bone scan attributed to bone healing as a result of a favorable antitumor effect.^{9,10} The central hypothesis was that the continuous development of new lesions on sequential scans was an indication that the cancer was continuing to grow and spread as opposed to healing.

To enable the clinical validation of the PCWG2-proposed bone scan progression measure, a quantitative and reproducible bone scan assay was developed, analytically validated, and subsequently used as an integral part of the case report forms of serial, prospectively conducted, large phase 3 studies using androgen receptor (AR)-directed therapy.^{7,11,12} The progression biomarker was used first in the COU-AA-302 study of abiraterone acetate plus prednisone in chemotherapy-naive patients with mCRPC as a component of the definition of rPFS, which was a co-primary end point of the study.¹² PREVAIL, a phase 3, randomized, double-blind, placebo-controlled study evaluating the efficacy and safety of enzalutamide in chemotherapy-naive patients with mCRPC,⁷ was another trial that used rPFS as a co-primary end point with OS, allowing for further validation of the bone scan assay based on the PCWG2 criteria. As previously reported, PREVAIL demonstrated that enzalutamide therapy decreased the risk of death by 29% (haz-

Key Points

Question What is the clinical relevance of the Prostate Cancer Clinical Trials Working Group 2 (PCWG2) definition of radiographic progression-free survival (rPFS)?

Findings In a series of prespecified sensitivity analyses of rPFS in the PREVAIL randomized clinical trial of 1717 men with chemotherapy-naive metastatic castration-resistant prostate cancer, enzalutamide significantly reduced the risk of radiographic progression or death. Using 2 different statistical methods, rPFS and overall survival were found to be positively correlated.

Meaning The PCWG2 definition of rPFS is a robust end point that is clinically meaningful and associated with overall survival.

ard ratio [HR], 0.71; 95% CI, 0.60-0.84; P < .001) and the risk of radiographic progression by 81% (HR, 0.19; 95% CI, 0.15-0.23; P < .001).⁷

A series of sensitivity analyses (SAs) were included in the trial design of PREVAIL to evaluate how robust and clinically meaningful the rPFS result signified.^{7,13} These prespecified analyses examined the impact of additional measures of progression, including skeletal-related events (SREs), initiation of radiotherapy and or new antineoplastic therapy, and unequivocal clinical progression, on the primary rPFS analysis. The goals of these SAs were to confirm the clinical relevance of the PCWG2 rPFS definition, to further examine concordance between central and investigator assessment using the bone capture data assay form, and to examine the correlation between rPFS and OS.

Methods

The PREVAIL study design has previously been described,⁷ and the trial protocol is available in Supplement 1. This study was conducted in accordance with the Declaration of Helsinki and was approved by the ethics committee at each participating center. All patients provided written informed consent before enrollment.

Randomization and Masking

Patients were assigned 1:1 to receive enzalutamide 160 mg or placebo using a centrally administered, randomized permutedblock method and stratified by study site. All patients, investigators, site personnel, and sponsor personnel involved in the conduct of the study were blinded to treatment assignment.

Primary Assessment of rPFS

The co-primary end points of PREVAIL were OS and rPFS, in which rPFS was defined as the time from randomization to first objective evidence of radiographic disease progression assessed by blinded independent central review or death from any cause within 168 days after treatment discontinuation, whichever occurred first. Radiographic disease progression was evaluated using a modified form of the PCWG2 guidelines for bone disease⁹ and Response Evaluation Criteria in Solid Tumors, version 1.1, for soft-tissue disease.¹⁴

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A separate investigator assessment of imaging was performed at each site using a bone scan worksheet adapted from the Prostate Cancer Clinical Trials Consortium.¹¹ As specified, progression in bone (≥2 new lesions on radionuclide bone scan) observed at week 9 necessitated 2 or more additional new lesions on a confirmatory scan at least 6 weeks later; radiographic disease progression in bone observed after week 9 necessitated 2 or more new lesions relative to the week 9 scan, confirmed on a subsequent scan at least 6 weeks later. Radiographic disease progression in soft tissue did not require a confirmatory scan.¹⁴

Sensitivity Analysis of rPFS

Six SAs (SA1-SA6) based on investigator assessments were performed (eTable 1 in Supplement 2).

Statistical Analysis and Censoring Procedures

The final intention-to-treat analysis of rPFS was performed by the independent central review facility after 439 events (data cutoff, May 6, 2012), and the interim intention-to-treat OS analysis was performed after 540 events (data cutoff, September 16, 2013).

In all analyses, patients who were not known to have had an rPFS event at the time of data cutoff were censored at the date of last assessment. In the primary analysis, SA1, and SA2, patients were censored for rPFS if, prior to objective evidence of disease progression, there was a change in tumor scan modality, initiation of a new antineoplastic treatment and/or radiation therapy for prostate cancer, SRE, treatment discontinuation, 2 or more consecutive missed tumor assessments, or death after 168 days following treatment discontinuation without progression. In SA4, patients who discontinued study drug primarily because of clinical progression before objective evidence of radiographic disease progression were considered to have clinical progression on the date of the last dose of study drug. In SA5, patients with soft-tissue disease progression through week 13 without a confirmatory scan were censored at the date of earliest soft-tissue disease progression prior to week 13. In SA3 and SA6, the same censoring rules for the primary analysis applied, except that new SREs, any radiation therapy for prostate cancer, or new antineoplastic therapy (SA3) and all deaths (SA6) were considered rPFS events.

All data analyses were performed using SAS, version 9.1.3 (SAS Institute), as previously described.⁷ Estimates of medians and 95% CIs were determined using the Kaplan-Meier method. Hazard ratio relative to placebo (with less than 1.00 favoring enzalutamide) was determined using an unstratified Cox regression model with treatment as the only covariate. The analysis of rPFS was conducted using a 2-sided unstratified log-rank test with a type 1 error rate of .001.

Overall concordance between independent central review and investigator assessments (using SA1) of the intention-to-treat population was calculated as (concordance for progressive disease) + (concordance for nonprogressive disease). In addition, correlations between rPFS (using SA2) and OS were calculated using 2 methods: Spearman ρ and Kendall τ via Clayton copula.¹⁵⁻¹⁸

Results

Patient Disposition and Demographic and Clinical Characteristics

The primary results of PREVAIL have been published previously and showed that patient demographic and disease characteristics were similar between treatment arms at baseline.⁷ The mean age at baseline was 72.0 (range, 43.0-93.0) years in the enzalutamide arm and 71.0 (range, 42.0-93.0) years in the placebo arm.⁷ Patient disposition is presented in **Figure 1**. In all SAs presented here (except SA2), analyses were based on data from 832 patients in the enzalutamide arm all randomized patients were used in the analysis (enzalutamide arm, n = 872; placebo arm, n = 845). Results from all analyses are presented in **Table 1**.

Primary Analysis of rPFS

At the final cutoff date for primary rPFS analysis, 118 of 832 patients (14.2%) in the enzalutamide arm had an rPFS event, compared with 321 of 801 patients (40.1%) in the placebo arm. The majority of rPFS events resulted from radiographic progression (105 of 118 and 295 of 321 patients, respectively). Thirteen of 832 patients (1.6%) in the enzalutamide arm and 26 of 801 patients (3.2%) in the placebo arm died without radiographic progression. Enzalutamide reduced the risk of radiographic progression or death by 81% compared with placebo (HR, 0.19; 95% CI, 0.15-0.23; P < .001).⁷ Median time to an rPFS event was not reached (95% CI, 13.8 to not reached

Table 1. Summary of Radiographic Progression-Free Survival (rPFS) Sensitivity Analyses (SAs) (Intention-to-Treat Population)

No. (%)			
Sensitivity Analysis ^a	Enzalutamide (n = 832)	Placebo (n = 801)	 HR (95% CI)
Primary			
Total events ^b	118 (14.2)	321 (40.1)	
Radiographic progression	105 (12.6)	295 (36.8)	0.19 (0.15-0.23)
Death ^c	13 (1.6)	26 (3.2)	
SA1			
Total events ^b	117 (14.1)	296 (37.0)	
Radiographic progression	102 (12.3)	271 (33.8)	0.22 (0.18-0.27)
Death ^c	15 (1.8)	25 (3.1)	
SA2			
Total events ^{b,d}	387 (44.4)	502 (59.4)	
Radiographic progression	343 (39.3)	459 (54.3)	0.31 (0.27-0.35)
Death ^c	44 (5.0)	43 (5.1)	
SA3			
Total events ^b	161 (19.4)	409 (51.1)	
Radiographic progression	94 (11.3)	219 (27.3)	
Death ^c	9 (1.1)	24 (3.0)	
Initiated antineoplastic therapy	13 (1.6)	87 (10.9)	0.21 (0.10.0.20)
Initiated radiation therapy	2 (0.2)	5 (0.6)	0.21 (0.18-0.26)
SRE	15 (1.8)	21 (2.6)	
SRE, initiated antineoplastic therapy	2 (0.2)	6 (0.7)	
SRE, initiated radiation therapy	26 (3.1)	47 (5.9)	
SA4			
Total events ^b	120 (14.4)	299 (37.3)	
Clinical progression	17 (2.0)	67 (8.4)	0.21 (0.17.0.20)
Radiographic progression	92 (11.1)	205 (25.6)	0.21 (0.17-0.26)
Death ^c	11 (1.3)	27 (3.4)	
SA5			
Total events ^b	108 (13.0)	245 (30.6)	
Radiographic progression	92 (11.1)	205 (25.6)	0.23 (0.19-0.30)
Death ^c	16 (1.9)	40 (5.0)	
SA6			
Total events ^b	111 (13.3)	252 (31.5)	
Radiographic progression	92 (11.1)	205 (25.6)	0.23 (0.19-0.30)
Death	19 (2.3)	47 (5.9)	

Abbreviations: HR, hazard ratio; SRE, skeletal-related event.

^a SA1 was based on investigator's assessments using final rPFS cutoff; SA2, investigator's assessments using interim overall survival cutoff; SA3, SRE, initiation of radiation therapy, and new antineoplastic therapy; SA4, clinical progression; SA5, confirmatory scan requirement for progressive disease related to soft-tissue disease; and SA6, all deaths.

^b Based on the earliest contributing event (eTable 1 in the Supplement).

^c Deaths only counted as rPFS events if they occurred within 168 d of treatment discontinuation and in the absence of radiographic progression.

^d Includes all randomized patients (n = 872 for enzalutamide; n = 845 for placebo).

[NR]) in the enzalutamide arm and was 3.9 months (95% CI, 3.7-5.4 months) in the placebo arm (**Figure 2**A).⁷

Concordance Between Independent and Investigator Assessments of rPFS

Using the same censoring rules and final rPFS data cutoff date, there was a high level of agreement between investigator assessments of radiographic progression (SA1) and those obtained by independent central assessment (eTable 2 in Supplement 2). Agreement at the final rPFS analysis between independent and investigator assessments for progressive and nonprogressive disease was 87.6% (90.9% with enzalutamide and 84.0% with placebo). Results from the remaining SAs were consistent between investigator assessment and central review (eTable 3 in Supplement 2). The main difference in investigator and central assessment for the subset analyses was the identification of soft-tissue progression, which did not use a standardized data capture form and was consistently higher when assessed by central review (eTable 4 in Supplement 2).

Sensitivity Analyses of rPFS

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To remove the confounding factor of investigator assessment vs independent central review, and because SA1 differed from the primary analysis only in the use of investigator assessment, we used SA1 as the comparator. In SA1, enzalutamide treatment reduced the risk of radiographic progression or death by 78% compared with placebo (HR, 0.22; 95% CI, 0.18-0.27; P < .001) (Table 1). Median time to an rPFS event was 16.4 months (95% CI, 13.8 months to NR) in the enzalutamide arm and 5.5 months (95% CI, 5.2-5.6 months) in the placebo arm (Figure 2A).



Figure 2. Duration of Radiographic Progression-Free Survival (rPFS) in Primary Analysis, Sensitivity Analysis 1 (SA1), and SA2

A, Primary analysis and SA1 (intention-to-treat population, data cutoff May 6, 2012). B, SA2 (intention-to-treat population, data cutoff September 16, 2013).

SA2 included all randomized patients with an additional 16 months of data collection. As expected, the number of qualifying events increased substantially (Table 1). Enzalutamide therapy reduced the risk of radiographic progression or death by 69% (HR, 0.31; 95% CI, 0.27-0.35; P < .001). Median time to an rPFS event was 19.7 months (95% CI, 18.1-22.3 months) in the enzalutamide arm and 5.4 months (95% CI, 4.2-5.6 months) in the placebo arm (Figure 2B).

In SA3, in which SREs or any use of radiation or antineoplastic therapy were counted as rPFS events, there was an increase in the number of events, particularly in the placebo arm (Table 1). In both treatment arms, rPFS resulting from death decreased, whereas the bulk of the additional rPFS events were associated with new SREs and/or initiation of new antineoplastic therapies. Enzalutamide reduced the risk of radiographic progression or death by 79% (HR, 0.21; 95% CI, 0.18-0.26; P < .001). Median time to an rPFS event was 13.3 months (95% CI, 11.2-16.4 months) in the enzalutamide arm and 3.7 months (95% CI, 3.6-4.4 months) in the placebo arm (**Figure 3A**). In SA4, in which rPFS events included discontinuation of treatment resulting from clinical progression prior to objective evidence of radiographic disease progression, there was a modest increase in the number of qualifying events in both treatment arms (Table 1). Enzalutamide therapy reduced the risk of radiographic progression or death by 79% (HR, 0.21; 95% CI, 0.17-0.26; P < .001). Median time to an rPFS event was 14.2 months (95% CI, 13.8 months to NR) in the enzalutamide arm and 5.4 months (95% CI, 4.6-5.6 months) in the placebo arm (Figure 3B).

In SA5, in which progression related to soft-tissue disease required a confirmatory scan, there was a decrease in the number of qualifying events in both treatment arms. Although the number of radiographic progression events decreased in both treatment arms, the number of deaths remained the same in the enzalutamide arm and increased in the placebo arm (Table 1). Enzalutamide treatment reduced the risk of radiographic progression or death by 77% (HR, 0.23; 95% CI, 0.19-0.30; P < .001). The median time to an rPFS event was 16.4 months (95% CI, 13.8 months to NR) in the enzalutamide arm and 5.7 months (95% CI, 5.5-8.2 months) in the placebo arm (Figure 3C).

The definition of rPFS in the primary analysis included death from any cause within 168 days of treatment discontinuation. In SA6, any death was considered an rPFS event, regardless of length of time after study drug discontinuation, which resulted in a modest decrease in the number of qualifying events in both treatment arms (Table 1). The number of radiographic progression events decreased in both treatment arms. As expected, the number of deaths increased in both treatment arms, although the increase was modest in the enzalutamide arm. Enzalutamide therapy reduced the risk of radiographic progression or death by 77% (HR, 0.23; 95% CI, 0.19-0.30; P < .001). Median time to an rPFS event was 15.0 months (95% CI, 13.8 months to NR) in the enzalutamide arm and 6.0 months (95% CI, 5.5-8.2 months) in the placebo arm (Figure 3D).

Correlation of rPFS and OS

At the planned interim analysis for OS, there were 540 deaths and 889 investigator-assessed rPFS events. Treatment with enzalutamide resulted in a 29% decrease in the risk of death compared with placebo (HR, 0.71; 95% CI, 0.60-0.84; P < .001).⁷ Using SA2, rPFS was positively associated with OS among all patients and patients in each treatment arm using 2 different methods (**Table 2**). Spearman ρ was 0.72 (95% CI, 0.67-0.76) among all patients, 0.89 (95% CI, 0.86-0.92) among enzalutamide-treated patients, and 0.53 (95% CI, 0.43-0.61) among placebo-treated patients. Kendall τ was 0.53 (95% CI, 0.49-0.57) among all patients, 0.72 (95% CI, 0.68-0.77) among enzalutamide-treated patients, and 0.37 (95% CI, 0.30-0.44) among placebo-treated patients.

Discussion

As more life-prolonging drugs are approved for the treatment of mCRPC, addressing the need for outcome measures that strongly correlate with survival or reflect clinical benefit in their



All intention-to-treat population; data cutoff, May 6, 2012

able 2. Correlation of Radiographic Progression-Free Survival With Overall Survival ^a						
	Correlation (95% CI)					
Method	Total (N = 1717)	Enzalutamide (n = 872)	Placebo (n = 845)			
Spearman p	0.72 (0.67-0.76)	0.89 (0.86-0.92)	0.53 (0.43-0.61)			
Kendall τ	0.53 (0.49-0.57)	0.72 (0.68-0.77)	0.37 (0.30-0.44)	^a The analysis data of September 16, 201		

own right is essential to ensure the timely development of drugs needed to further improve patient outcomes. Toward this objective, PREVAIL included in its design the co-primary end points of OS and rPFS.

The results of PREVAIL further confirmed the rigor of the PCWG2 definition of rPFS using a standardized bone scan data capture assay in patients with mCRPC. There was a high degree of concordance between the central and investigator reviews in both treatment arms. Notably, individual investigators were trained at each site using the bone scan data capture forms and the end result was a high level of reproducibility between readers, which highlights the clinical utility of this end point. The prespecified SAs in the PREVAIL study showed the impact of different clinical factors on rPFS, including SREs, initiation of radiotherapy and/or new antineoplastic therapy, and unequivocal clinical progression, which all confirmed the superiority of enzalutamide over placebo.

The PREVAIL analysis is the second to demonstrate a positive correlation between rPFS using the PCWG2 criteria and OS (Spearman ρ of 0.72 and Kendall τ of 0.53 for all patients). The rutoff was 13.

COU-AA-302 trial also demonstrated a correlation between rPFS and OS12; both studies used the PCWG2 definition of radiographic progression, involved patients with mCRPC who had not received chemotherapy, and involved treatment that targeted the AR axis. Both studies also found a high concordance between the central and investigator reads, validating the reproducibility of the analytically validated bone scan progression biomarker to document rPFS disease progression. Notably, there were only 188 progression events in the PREVAIL enzalutamide arm vs 542 in the COU-AA-302 abiraterone acetate plus prednisone arm. As a result, although the HR was high for the enzalutamide arm (0.19), the event rate was relatively low, a fact that may bias the analyses accordingly.

Because the distribution of data was not known up front, 2 different statistical methods were used that measured correlation in slightly different ways. Spearman ρ and Kendall τ rank correlations are both nonparametric tests, with no assumption about the distribution of data and often used for nonlinear monotonic relationships.¹⁹ Spearman ρ measures how the magnitude and direction of change of one end point

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corresponds to the magnitude and direction of change of the other end point, whereas Kendall τ only considers the direction of change. Consequently, Kendall τ generally results in a value closer to O (no correlation) than Spearman ρ does.²⁰ Results from both analyses in this study were consistent, with a positive correlation.

In our analysis, the lower correlation between rPFS and OS seen with placebo-treated patients than seen with enzalutamide-treated patients could be partly related to postprotocol exposure to life-prolonging therapy. Patients in the placebo arm received more postprotocol therapies than those in the enzalutamide arm (76% vs 44%), including docetaxel (57% vs 33%), abiraterone acetate (46% vs 21%), and enzalutamide (4% vs 1%).⁷

Limitations

PREVAIL and COU-AA-302 both studied drugs that target the AR signaling pathway and enrolled chemotherapy-naive patients with mCRPC. The use of a co-primary end point using both OS and rPFS in both studies was designed to clearly demonstrate clinical benefit; however, the studies were not designed

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to address rPFS as a surrogate for survival. In addition, the results based on end points from these AR-directed trials may not be applicable to biologic agents, bone microenvironmentdirected approaches, and non-AR-targeted therapies, whose impact on the tumor, and consequently on radiographic progression, has not yet been fully defined. It is anticipated that a one-size-fits-all end point that is general enough to encompass all therapies in all clinical scenarios will not be sufficient to enable regulatory approvals. As a result, the definition of rPFS as a clinically relevant end point may need to be adapted and, if so, revalidated accordingly to fit the disease, population, imaging modality, and treatment involved.

Conclusions

In this series of prespecified SAs of data from the PREVAIL trial of men with chemotherapy-naive mCRPC, the PCWG2 definition of rPFS was found to be a robust and clinically meaningful end point associated with OS in enzalutamide-treated patients.

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Evolving Intersection Between Inherited Cancer Genetics and Therapeutic Clinical Trials in **Prostate Cancer: A White Paper From the Germline Genetics** Working Group of the Prostate **Cancer Clinical Trials Consortium**

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summary

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Purpose Advances in germline genetics, and related therapeutic opportunities, present new opportunities and challenges in prostate cancer. The Prostate Cancer Clinical Trials Consortium Germline Genetics Working Group was established to address genetic testing for men with prostate cancer, especially those with advanced disease undergoing testing for treatment-related objectives and clinical trials.

Methods The Prostate Cancer Clinical Trials Consortium Germline Genetics Working Group met monthly to discuss the current state of genetic testing of men with prostate cancer for therapeutic or clinical trial purposes. We assessed current institutional practices, developed a framework to address unique challenges in this population, and identified areas of future research.

Results Genetic testing practices in men with prostate cancer vary across institutions; however, there were several areas of agreement. The group recognized the clinical benefits of expanding germline genetic testing, beyond cancer risk assessment, for the goal of treatment selection or clinical trial eligibility determination. Genetic testing for treatment selection should ensure patients receive appropriate pretest education and consent and occur under auspices of a research study whenever feasible. Providers offering genetic testing should be able to interpret results and recommend post-test genetic counseling for patients. When performing tumor (somatic) genomic profiling, providers should discuss the potential for uncovering germline mutations and recommend appropriate genetic counseling. In addition, family members may benefit from cascade testing and early cancer screening and prevention strategies.

Conclusion As germline genetic testing is incorporated into practice, further development is needed in establishing prompt testing for time-sensitive treatment decisions, integrating cascade testing for family, ensuring equitable access to testing, and elucidating the role of less-characterized germline DNA damage repair genes, individual gene-level biologic consequences, and treatment response prediction in advanced disease.

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recommendations are those of the author and are not necessarily endorsed by the Department of Defense.

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INTRODUCTION

Although the contribution of heredity to prostate cancer has long been known, the underlying genetic causes remained elusive. Recent discoveries reveal that a significant fraction of men with metastatic prostate cancer (mPC) carry germline mutations in DNA damage repair (DDR) genes, including *BRCA1*, *BRCA2*, and *ATM*.^{1,2} Compelling early findings suggest that germline and/ or somatic alterations in these and other DDR genes may predict response to poly (ADP-ribose) polymerase (PARP) inhibitors and platinum chemotherapy.³⁻⁵ Germline mutations in mismatch repair (MMR) genes (*MSH2*, *MSH6*, *MLH1*, and *PMS2*), which are associated with Lynch syndrome and development of tumors with defective DNA MMR or high microsatellite instability (MSI), may identify candidates for immunotherapy with programmed cell death protein 1 checkpoint inhibitors.⁶ In addition, response to other systemic therapies for prostate cancer may be influenced by the presence of a germline and/or somatic DDR gene mutation.⁷⁻¹⁰

Table 1. Selected Therapeutic Clinical Trials in Prostate Cancer With Relevance to Germline Gene
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Phase	Title	Disease State	Abbreviated Title	ClinicalTrials.gov Identifier
III	Study of Olaparib Versus Enzalutamide or Abiraterone Acetate in Men With Metastatic Castration-Resistant Prostate Cancer (PROfound Study)	mCRPC	PROfound	NCT02987543
III	A Study of Rucaparib Verses Physician's Choice of Therapy in Patients With Metastatic Castration-Resistant Prostate Cancer and Homologous Recombination Gene Deficiency (TRITON3)	mCRPC	TRITON3	NCT02975934
Π	A Phase 2 Efficacy and Safety Study of Niraparib in Men with Metastatic Castration-Resistant Prostate Cancer and DNA-Repair Anomalies	mCRPC	GALAHAD	NCT02854436
Π	A Multicenter, Open-Label Phase 2 Study of Rucaparib in Patients With Metastatic Castration-Resistant Prostate Cancer Associated With Homologous Recombination Deficiency	mCRPC	TRITON2	NCT02952534
Π	Response Rate Study of Talazoparib in Men With DNA Repair Defects and Metastatic Castration-Resistant Prostate Cancer Who Previously Received Taxane-Based Chemotherapy and Progressed on at Least 1 Novel Hormonal Agent (Enzalutamide and/or Abiraterone Acetate/Prednisone)	mCRPC		NCT03148795
II	Olaparib in Men With High-Risk Biochemically-Recurrent Prostate Cancer Following Radical Prostatectomy, With Integrated Biomarker Analysis	BCR		NCT03047135
Π	Abiraterone/Prednisone, Olaparib, or Abiraterone/Prednisone + Olaparib in Patients With Metastatic Castration-Resistant Prostate Cancer With DNA Repair Defects	mCRPC	BRCAaway	NCT03012321
Ι	A Safety and Pharmacokinetics Study of Niraparib Plus an Androgen Receptor-Targeted Therapy in Men With Metastatic Castration-Resistant Prostate Cancer (BEDIVERE)	mCRPC	BEDIVERE	NCT02924766
Pilot	Docetaxel and Carboplatin in Treating Patients With Metastatic, Hormone Resistant Prostate Cancer Containing Inactivated Genes in the BRCA 1/2 Pathway	mCRPC	ABCD	NCT02598895
II	The BARCODE 2 Study—The Use of Genetic Profiling to Guide Prostate Cancer Treatment (BARCODE2)	mCRPC	BARCODE-2	NCT02955082
II	Docetaxel and Carboplatin for Patients With mCRPC and DNA- Repair Deficiencies	mCRPC	V-ABCD	NCT02985021
II	Pembrolizumab in Treating Patients With Metastatic Castration Resistant Prostate Cancer Previously Treated With Enzalutamide	mCRPC		NCT02312557
II	Study of Pembrolizumab (MK-3475) in Participants With Metastatic Castration-Resistant Prostate Cancer	mCRPC	KEYNOTE-199	NCT02787005
Ib/II	Study of Pembrolizumab (MK-3475) Combination Therapies in Metastatic Castration-Resistant Prostate Cancer	mCRPC	KEYNOTE-365	NCT02861573

Abbreviations: BCR, biochemical recurrence; mCRPC, metastatic castration-resistant prostate cancer.



Fig 1. Framework for approaching genetic testing within the context of therapeutic decisions. (*) Currently primarily relevant to metastatic and high-risk localized prostate cancer, but likely will include earlier disease states in the future. GC, genetic counseling.

The current models for genetic counseling and testing were developed for assessment of individuals and families with suspicion for hereditary cancer syndromes and focused on risk assessment, cancer screening, and risk reduction (eg, salpingo-oophorectomy for female BRCA1/2 carriers). For prostate cancer, genetic counseling and testing practices are newly driven by a growing interest in identifying patients who are candidates for enrollment in biomarker-selected clinical trials. This treatment-driven ascertainment, where patients are referred for germline testing in part for therapy selection, presents unique opportunities and challenges for practitioners regarding appropriate delivery of elements of genetic counseling in a feasible manner.

The Prostate Cancer Clinical Trials Consortium is a group of researchers from 11 institutions working together to develop novel therapeutics and biomarkers, translating scientific discoveries to improve standards of care in prostate cancer. The Germline Genetics Working Group of the Prostate Cancer Clinical Trials Consortium was established in June of 2017 in response to the growing intersection between germline genetics and therapeutics. In this article, we outline the special considerations when genetic testing is used for therapeutic purposes in men with mPC and to suggest areas of future research. Although germline genetics may affect management decisions in early-stage prostate cancer, we focus here on advanced disease because of the current therapeutic and clinical trial implications, although many of the principles outlined apply to all stages of disease.

GERMLINE DNA REPAIR MUTATIONS IN RECURRENT AND METASTATIC PROSTATE CANCER

Prostate cancer has a significant heritable component, with 57% of the risk attributed to genetic factors.^{11,12} Mutations in high and moderately penetrant genes involved in DDR can be associated with varying degrees of increased predisposition to prostate cancer (Appendix

Table 2. Referral Criteria for Genetic Counseling forMen with Prostate Cancer

Criteria
Recommend genetic counseling if:
Metastatic prostate cancer (radiographic evidence or biopsy proven)
Prostate cancer Gleason score ≥ 7 AND family history:
One or more relatives with ovarian or breast cancer diagnosed at age ≤ 50 years OR
Two or more relatives on same side of family diagnosed with cancer, especially breast, ovary, pancreas, prostate (Gleason score \geq 7), colon, endometrial
Consider genetic counseling if:
High-risk or very high-risk localized prostate cancer
Any-risk prostate cancer AND family history:
Father, brother, or multiple family members with prostate cancer age ≤ 50 years OR
Relative with breast, ovarian, or pancreas cancer OR
Relative with Lynch syndrome–related cancer (colon, endometrial, gastric, ovarian, upper
tract urotnellal, pancreas, blie duct)

Adapted from National Comprehensive Cancer Network guidelines (https://www.nccn.org/professionals/physician_gls/default. aspx#genetics_screening; https://www.nccn.org/professionals/ physician_gls/default.aspx#genetics_colon; https://www.nccn. org/professionals/physician_gls/default.aspx#prostate). Table A1). In a landmark study, the incidence of inherited pathogenic DDR mutations in men with mPC was 11.8% (5.3% with mutations in BRCA2, 1.9% in CHEK2, and 1.5% in ATM).1 This prevalence was significantly higher compared with men with localized prostate cancer (11.8% v 4.6%; P < .001). In a second confirmatory study, the prevalence of germline pathogenic DDR mutations in unselected patients with recurrent or mPC was 14.0% (6.0% in BRCA2, 2.0% in CHEK2, and 2.0% in ATM), with an apparent enrichment in men with intraductal or ductal histologic features.13 An association between germline BRCA2 mutations and intraductal prostate cancer was also reported in a prior study.¹⁴

Germline *BRCA1/2* mutation carriers may have more aggressive disease at presentation and have a higher risk of recurrence and prostate cancer–specific mortality compared with noncarriers.¹⁵⁻¹⁷ In a retrospective case-case study of patients with low-risk localized prostate cancer and patients who died as a result of disease, the combined carrier rate of *BRCA1*, *BRCA2*, and *ATM* mutations was higher in lethal cases (6.1% v 1.4%; P < .001), and those with mutations had a shorter interval to death after diagnosis.¹⁸

Men with Lynch syndrome (due to germline mutations in MLH1, MSH2, MSH6, or PMS2) may also be at increased risk of prostate cancer; however, data are conflicting, with some studies showing a two- to five-fold increased risk and others showing no increased risk.¹⁹⁻²³ These risk ranges may be due to the different penetrance of Lynch genes; there is suggestion that prostate cancer risk is particularly elevated in MSH2 carriers.^{24,25} It is also likely that as screening for colorectal cancer improves, men with Lynch syndrome are living longer, and thus the incidence of older-onset cancers is increasing.25 Unfortunately, many patients with prostate cancer with germline MMR mutations do not meet traditional family history criteria.26 In men with Lynch syndrome, prostate cancer infrequently represents the index cancer; however, prostate tumors can lack MMR gene protein expression or show MSI.^{21,27} In a study of 451 patients with prostate cancer, 3% of patients had tumors with somatic alterations in MMR genes, which predicted for high mutation count.28 Identifying patients with mPC whose tumors harbor these features has become increasingly relevant, because the programmed cell death protein 1 immune checkpoint inhibitor pembrolizumab was approved by the US Food and Drug Administration for treatment of any cancer with deficient MMR or high MSI.²⁹

CLINICAL TRIALS USING GERMLINE MUTATIONS AS ELIGIBILITY CRITERIA

An increasing number of therapeutic clinical trials in prostate cancer are using presence of DDR mutations, including germline, as an eligibility requirement for enrollment, similar to advanced ovarian and breast cancers with germline BRCA1/2 mutations (eg, olaparib, rucaparib; Table 1). For example, the BRCAaway trial (Clinical Trials.gov identifier: NCT03012321) is a phase II randomized trial of the PARP inhibitor olaparib versus abiraterone versus the combination of the two agents in men with germline or somatic homologous recombination deficiency mutations. Additional trials are exploring the efficacy of rucaparib, niraparib, and olaparib as single agent for men with metastatic castration-resistant prostate cancer and a deleterious genomic alteration, either germline or somatic, in BRCA2, BRCA1, and other DDR genes (ClinicalTrials. gov identifiers: NCT02952534, NCT02975934, NCT02854436, NCT02987543). The TRIUMPH (Trial of Rucaparib in Patients With Metastatic Hormone-Sensitive Prostate Cancer Harboring Germline DNA Repair Gene Mutations) trial (Clinical Trials.govidentifier: NCT03413995) will enroll men with metastatic hormone-sensitive prostate cancer and a germline DDR gene pathogenic alteration, who will be treated with the PARP inhibitor rucaparib in the absence of hormonal therapy. It is anticipated that an increasing number of men with mPC will undergo genetic testing and that new trials will be designed and implemented for the germline DDR-deficient population.

CONTEXTUAL DIFFERENCES AND IMPORTANCE OF CONFIRMING PATIENT PRIORITIES

Next-generation sequencing has made germline testing more accessible and comprehensive, and broader cohorts of patients with cancer are being tested using large gene panels. These approaches have the potential to address two important but distinct objectives: first, treatment and clinical

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Title	Novel Approaches	ClinicalTrials.gov Identifier
Genetic Evaluation of Men—The GEM Registry	Prospective research registry of men with prostate cancer or at increased risk	NCT03076242
GENTleMEN: Genetic Testing for Men with Metastatic Prostate Cancer	Web-based consent and pretest counseling Web-based and phone-based post-test counseling Pathogenic and likely pathogenic mutation results are delivered by a genetic counselor over the phone and invited for in-person counseling	NCT03503097
Evaluating an Alternative Clinical Genetics Cancer Care Delivery Model: A Pilot Study of Patient Outcomes	Consenting by primary oncologist or urologist, same-day blood draw Standard pretest education and video Risk assessment and delivery of results by a genetic counselor by telephone	NCT02987543
ProGen: Genetic Counseling Processes and Outcomes Among Males with Prostate Cancer	Comparison of standard genetic counseling v video-based counseling with in-person counseling only for patients with germline mutations	NCT03328091

trial possibilities, and, second, inherited cancer risk. For providers, it is worth discussing and confirming patient goals before offering testing—for example, asking whether patients are interested primarily in treatment options, familial risk assessment, or both. Figure 1 provides a framework for genetic testing within the context of treatment decisions. Oncologist-driven genetic education is ideally in close collaboration with a cancer genetics service. Family history intake is critical and needs to be streamlined for oncology and clinical trial settings. Table 2 summarizes clinical criteria to consider for referral to genetic counseling.

This panel agrees that men with prostate cancer who undergo germline genetic testing for therapeutic or clinical trial options should receive pretest education on the implications of a positive result for themselves and for their families. Which genes should be included in testing may vary if the setting is treatment decision making versus risk assessment and risk management. For example, although at least *BRCA1/2* and MMR genes should be tested for men who meet criteria for the corresponding syndromes, additional genes, such as *ATM*, *CHEK2*, and *PALB2*, could be included for therapeutic decision making, especially in the clinical trial setting.^{4,30,31}

TUMOR-ONLY SEQUENCING MAY IDENTIFY GERMLINE MUTATIONS

Targeted next-generation sequencing of the tumor is also increasingly being used for treatment decision making and clinical trial eligibility determination. Although the goal of testing may be to identify treatment options, there is a possibility that somatic testing may identify germline mutations that are reflected in tumor sequence. In several recent studies of research somatic sequencing, germline mutations with clinical implications were identified.^{32,33} Tumor sequencing may even be more sensitive in detecting genetic syndromes, such as Lynch, than the traditional molecular tests.³⁴

Most commercial tumor assays do not specifically report whether a mutation is present in the germline, and some subtract the germline component, but the presence of well-described founder mutations may be highly suggestive. For example, the Ashkenazi Jewish *BRCA1/2* founder mutations (*BRCA1* 185delAG; *BRCA1* 5382insC; *BRCA2* 6174delT) are almost always germline, not somatic, events, and ordering providers should be familiar with them. Somatic tumor profiling can also identify increased mutation load and MSI, which can be associated with germline MMR mutations (Lynch syndrome).³⁵

Although it seems that most patients are interested in knowing secondary germline findings, they also expect their providers to offer decisionmaking guidance and clarify key information.^{36,37} This panel agrees that men with prostate cancer who undergo tumor-based genetic testing for therapeutic or clinical trial options should be educated about the potential for uncovering germline mutations, which may warrant referral to a cancer genetic specialist for confirmatory germline testing. This panel recommends that if a *BRCA1* or *BRCA2* mutation is identified on tumor-based testing, patients should be referred for discussion of dedicated, confirmatory germline testing. Moreover, if increased mutational load, a high MSI, or MMR deficiency is identified in tumor-only profiling, the patient's family history and personal history of other malignancies should be confirmed and reviewed with consideration for referral for dedicated confirmatory germline testing.

NEED FOR NEW GENETICS CARE DELIVERY MODELS

A major challenge is how best to integrate the workflow and provide the clinical support needed for responsible genetics care. The traditional clinical genetics cancer care delivery model—where patients are referred to a genetic counselor for in-person, pretest risk assessment and education and in-person post-test counseling—cannot meet the projected demand for testing of patients with prostate cancer, some facing time-sensitive treatment decisions. Even when testing is performed primarily for treatment selection, building in systems for those who are interested in testing of family members is of critical importance.

Current barriers to genetic testing have been described in the context of testing for cancer predisposition in hereditary breast and ovarian

Table 4. Challenges and New Research Directions

Challenge or Direction

Defining which patients should be offered germline genetic testing and at what point(s) in the diagnosis/treatment timeline
The role of less-studied germline DNA-damage repair genes for therapeutic decision making and clinical trial eligibility

- Best framework and workflows for rapid testing for time-sensitive therapeutic decisions
- Integration of cascade education and testing for family members

Ensuring historically underserved populations have access to genetic testing

cancer and Lynch syndromes. These barriers include process issues (referral to genetic counseling and testing, access, wait times, insurance coverage); physician knowledge, comfort, and time; patients' lack of awareness and understanding; and refusal of testing. With appropriate education, patients may be more interested in pursuing testing. For example, > 85% of patients with ovarian cancer reported willingness to be tested if there were therapeutic implications or benefit to family, and a majority believed that genetic testing should be offered before or at the time of diagnosis.³⁸

When testing for therapeutic decision making, the ability to undergo assessment and testing and receive results in a timely manner is of utmost

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Statement
General considerations when ordering germline testing
When feasible, genetic testing for therapeutic purposes should be performed in the setting of a research trial
Providers who choose to order germline testing themselves should be able to interpret test results (positive, negative, and variant of uncertain significance) and be prepared to initiate or refer for cascade testing of family members
Men diagnosed with an inherited genetic mutation should be referred for management of other associated cancer risks, and their blood relatives should be referred for cascade testing
Considerations during tumor-only genomic profiling
Men referred for tumor-only genomic profiling should be counseled on the potential for uncovering germline mutations, which may warrant referral to a genetic specialist for confirmatory germline testing
In tumor-only genomic profiling, pathogenic mutations in BRCA1 or BRCA2 should prompt referral for discussion of confirmatory germline testing
Men with prostate cancers with high microsatellite instability or mismatch repair deficiency or with tumor-only profiling with mutations <i>MSH2</i> , <i>MLH1</i> , <i>MSH6</i> , or <i>PMS2</i> should have an expanded family history to screen for Lynch syndrome or be considered for referral for genetic counseling
Considerations with germline testing for therapeutic purposes or clinical trial eligibility
If the purpose of testing is identifying potential therapeutic targets or determining eligibility for clinical trials, multigene panel testing (beyond <i>BRCA1/BRCA2</i>) is acceptable

If the purpose of testing is identifying potential therapeutic targets or determining eligibility for clinical trials, testing men without significant family history of prostate or other *BRCA* or Lynch syndrome-associated cancers is acceptable

importance. Newer approaches in cancer risk genetics include video- or phone-based pretest counseling and mainstreaming, an approach in which trained individuals provide standardized consenting and counseling before testing and genetics referral.³⁹ The ENGAGE (Evaluation of a Streamlined Oncologist-Led BRCA Mutation Testing and Counseling Model for Patients With Ovarian Cancer) study of oncologist-led BRCA1/2 mutation testing in women with ovarian cancer showed that this process is feasible, with high patient satisfaction.⁴⁰ These alternate genetic counseling delivery approaches need to be studied for provider feasibility and patient acceptability. Several trials at our sites are seeking to explore some of these new delivery models (Table 3).

SPECIAL CHALLENGES IN UNDERSERVED POPULATIONS

Intensive efforts are needed to ensure that genetic assessment is available to underserved populations, which include ethnic and racial minorities, people of low income, and those in rural areas, among others.41,42 Although rates of germline testing have not been studied in different ethnic and racial subgroups of men with prostate cancer, evidence shows that black and Hispanic women with breast cancer are substantially less likely to undergo genetic testing.43,44 Reasons for disparities in genetic testing may include differences in physician referrals, distrust and/or lack of understanding of genetics and cancer risk, fear of genetic discrimination on the part of insurers, and disproportionate financial and time burdens for patients with limited resources.44-50 Ensuring equitable access to genetic testing for black men with prostate cancer may be particularly important, because some preliminary studies show they may be more likely to have germline mutations in BRCA1 and BRCA2 than white men.⁵¹ This is compounded by the fact that black men have a 2.4 times greater risk of death from prostate cancer, are more likely to present with late-stage disease, and are significantly less likely to receive definitive treatment than non-Hispanic white men.52-55

Improving access to genetic testing in geographically remote areas, where availability of genetic counselors is scare, is also an active area of research. Telephone genetic consults, and other novel genetic assessment, education, and testing delivery methods, show promise.⁵⁶ To expand our knowledge and evidence of most effective testing strategies, men with prostate cancer should be offered genetic testing in the setting of clinical trials whenever feasible.

THE CRUCIAL RESPONSIBILITY OF CASCADE TESTING

Cascade testing is the systematic identification of individuals at risk for a hereditary condition through extension of genetic testing to biologic relatives. Although awareness of cascade testing is important in any situation where a germline mutation is identified, it can be particularly important when genetic testing is performed for therapeutic selection. In contrast to patients who pursue genetic testing because of familial cancer risk, those who undergo germline testing for therapy selection may be less aware of the potential implications to family members, because they were not necessarily tested because of an identified familial risk. Moreover, men with prostate cancer are often diagnosed when their children are adults, can pursue testing, and, if positive, undergo enhanced cancer screening or risk-reduction strategies.

There are several known barriers for a patient's communication of results to family members. In *BRCA1/2* screening studies, factors associated with of lack of communication include high worry about genetic risks, low interest or understanding of genomic information, and negative family history.⁵⁷⁻⁵⁹ Men and second-degree relatives are less likely to pursue genetic testing.⁵⁸ Thus, there is an opportunity through education to increase familial communication of results. This panel agrees that when germline testing is performed, the ordering provider should be knowledgeable and work with local cancer genetics experts to offer cascade testing for family members.

CONCLUSION AND FUTURE RESEARCH DIRECTIONS

Recent exciting discoveries in prostate cancer genetics and potential therapeutic interventions with PARP inhibitors and platinum chemotherapies have led to a rapid increase in germline testing for men with mPC. The traditional

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framework for genetic testing was developed for individuals believed to be at risk for inherited syndromes, but this model requires adaptation for men with mPC who are increasingly referred for genetic testing to aid in treatment decisions. In this article, we have highlighted special considerations with this treatment-driven ascertainment approach and described areas of research needs (Tables 4 and 5). As the field rapidly evolves, close collaboration between oncologists,

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urologists, clinical geneticists and counselors, researchers, and indeed, patients themselves, among others, will ensure that we develop the best practices to benefit patients with mPC and their families.

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Gene	Potential Treatment/Clinical Trials With Inclusion of Alteration (germline and/or somatic)	Level of Evidence Suggesting Predisposition to Prostate Cancer*	Predisposition Risk Conferred	Association With Aggressive Disease
BRCA2	Yes	А	RR, 3-8	Yes
BRCA1	Yes	А	RR, 2-4	Yes
ATM	Yes	С	Not established	Emerging
CHEK2	Yes	D		
PALB2	Yes	D		
RAD51D	Yes	D		
ATR	Yes	D		
NBN	Yes	С	Not established	
MLH1	Yes	В	Conflicting (RR, 1-6)	
MSH2	Yes	В	Conflicting (RR, 1-6)	
MSH6	Yes	В	Conflicting (RR, 1-6)	
PMS2	Yes	В	Conflicting (RR, 1-6)	
<i>HOXB13</i> (p.G84E)	No	А	OR, 2-8	

Table A1. Selected Genes Associated With Treatment Implications and Predisposition to Prostate Cancer

Abbreviations: OR, odds ratio; RR, relative risk.

*Adapted from Giri et al.³¹ Levels of evidence: (A) high-grade evidence: at least one prospectively designed study or three or more large validation studies or three or more descriptive studies; (B) moderate-grade evidence: two cohort or case-control studies; (C) emerging data: increasing data in support of association to prostate cancer, but not yet moderate-grade evidence; (D) low/insufficient: limited data or not studied in the context of prostate cancer.

Metastatic Hormone-Sensitive Prostate Cancer: Clinical Decision Making in a Rapidly Evolving Landscape of Life-Prolonging Therapy

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Background

The majority of men who die as a result of metastatic prostate cancer developed castration-resistant disease that progressed from an earlier hormone-sensitive state. In 2004, the first life-prolonging therapy, docetaxel (DOC), was approved by the US Food and Drug Administration for metastatic castration-resistant prostate cancer (mCRPC). Since 2010, five additional agents were approved for mCRPC on the basis of prolonging median overall survival (OS) by up to 5 months: sipuleucel-T, cabazitaxel, abiraterone plus prednisone (AAP), enzalutamide (ENZA), and radium-223.¹⁻⁷ Recent practice-changing trials have demonstrated that rationally intensifying treatment of metastatic hormone-sensitive prostate cancer (mHSPC), by advancing effective therapy for mCRPC to the hormone-sensitive state, has a bigger impact on OS. This treatment includes DOC (CHAARTED [Chemohormonal Therapy Versus Androgen Ablation Randomized Trial for Extensive Disease in Prostate Cancer] trial supported by STAMPEDE [Systemic Therapy in Advancing or Metastatic Prostate Cancer: Evaluation of Drug Efficacy] Arm C and GETUG-15). AAP (LATITUDE [Abiraterone Acetate Plus Prednisone in Patients With Newly Diagnosed High-Risk Metastatic Castration-Sensitive Prostate Cancer] with additional support from STAMPEDE Arm G), ENZA (ENZAMET [Enzalutamide in First-Line Androgen-Deprivation Therapy for Metastatic Prostate Cancer], with support from ARCHES [Enzalutamide Plus Androgen-Deprivation Therapy for Metastatic Hormone-Sensitive Prostate Cancer]), and apalutamide (APA; TITAN [Apalutamide Plus Androgen-Deprivation Therapy (ADT) Versus ADT in Patients With Metastatic Hormone-Sensitive Prostate Cancer] trial).8-14 The hazard ratios (HRs) for these agents in mHSPC are similar to those in mCRPC. Because OS is longer for mHSPC, however, these therapies have a larger absolute effect in this setting, with an unprecedented increase in median OS by more than 1 year. This supports the basic principle in oncology that advancement

of effective therapies to earlier stages of disease leads to better therapeutic impact, with four agents now demonstrating improved survival in this setting.

Although encouraging, these trials leave us with several unanswered questions: How do we best personalize therapy on the basis of clinical subgroups? What is the role of focal therapy in the setting of effective systemic therapy? How should we incorporate molecular characteristics into management?

Clinical Subgroups

Selection of which agent to use for mHSPC is guided in part by disease burden, which is based on conventional imaging (computed tomography and bone scan). For more than 30 years, it has been recognized that prognosis in mHSPC is informed by the extent of disease burden.¹⁵ The definitions of low volume/risk versus high volume/risk have varied, driven by metastases location¹⁵⁻¹⁷ and/or number¹⁸ of bone metastases. The CHAARTED trial was positive overall and supported androgen-deprivation therapy (ADT) plus DOC for patients with mHSPC.⁹ A priori stratification was based in part on disease volume, with high volume defined as either visceral metastases or four or morebone lesions with one or more lesions beyond the axial skeleton per conventional imaging. The improvement in OS from DOC was primarily driven by benefit in patients with high-volume disease (HR, 0.63); there was no significant impact on OS in patients with low-volume disease¹⁹ (HR, 1.04; Table 1). A similar result was seen in the post hoc analysis of GETUG-15.²⁰ CHAARTED was not powered for this subgroup analysis, however, and the subgroup was small. Post hoc analysis of STAMPEDE Arm C, expected to be reported later this year, will provide additional evidence.

In contrast, the benefit of the androgen receptor pathway inhibitors (ARPIs) AAP, ENZA, and APA seem to apply to all patients with mHSPC, regardless of disease burden. LATITUDE evaluated AAP in patients with high-risk disease (defined by Gleason score

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Trial	for Metastatic Hormon Clinical Trials Information	ne-Sensitive Prostate Cancer Comparator Arm	Control Arm	No. of Trial Participants	PFS, HR or EP	OS, HR or EP	First Author or Status
			Reported trials				
High volume/high risk							
Docetaxel							
CHAARTED	NCT00309985	ADT + DOC	ADT	513	0.58 (time to CRPC)	0.63	Kyriakopoulos ¹⁹
GETUG-15	NCT00104715	ADT + DOC	ADT	183	NA	0.78	Gravis ²⁰
STAMPEDE Arm C	NCT00268476	ADT + DOC	ADT	724	NA	TBD	James ¹⁰
ARPI							
LATITUDE	NCT01715285	ADT + AAP	ADT	955	NA	0.62	Fizazi ²¹
STAMPEDE Arm G	NCT00268476	ADT + AAP	ADT	473	0.31 (FFS)	0.54	Hoyle ²²
ENZAMET	NCT02446405	ADT + ENZA (± DOC)	ADT + NSAA (± DOC)	588	0.45	0.80	Davis ¹³
ARCHES	NCT02677896	ADT + ENZA (prior DOC allowed)	ADT (prior DOC allowed)	727	0.44 (rPFS)	TBD	Armstrong ²³
TITAN	NCT02489318	ADT + APA (prior DOC allowed)	ADT (prior DOC allowed)	660	0.53	0.68	Chi ¹⁴
RT							
STAMPEDE Arm H	NCT00268476	RT to prostate	ADT (+ DOC possible)	1,120	NA	1.07	Parker ²⁵
HORRAD	ISRCTN06890529	RT to prostate	ADT	272	NA	1.06	Boevé ²⁶
Low volume/low risk							
Docetaxel							
CHAARTED	NCT00309985	ADT + DOC	ADT	277	0.70 (Time to CRPC)	1.04	Kyriakopoulos ¹⁹
GETUG-15	NCT00104715	ADT + DOC	ADT	202	NA	0.9	Gravis ²⁰
STAMPEDE Arm C	NCT00268476	ADT + DOC	ADT	362	NA	TBD	James ¹⁰
ARPI							
LATITUDE	NCT01715285	ADT + AAP	ADT	243	NA	0.72	Fizazi ²¹
STAMPEDE Arm G	NCT00268476	ADT + AAP	ADT	428	0.24 (FFS)	0.66	Hoyle ²²
ENZAMET	NCT02446405	ADT + ENZA (± DOC)	ADT + NSAA (± DOC)	537	0.30	0.43	Davis ¹³
ARCHES	NCT02677896	ADT + ENZA (prior DOC allowed)	ADT (prior DOC allowed)	423	0.24 (rPFS)	TBD	Armstrong ²³
TITAN	NCT02489318	ADT + APA (prior DOC allowed)	ADT (prior DOC allowed)	392	0.36	0.67	Chi ¹⁴
			(continued on following pag	(ə			

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TABLE 1. Phase III Trials 1	or Metastatic Hormone Clinical Trials	e-Sensitive Prostate Cancer (co	ntinued)	No of Trial			Firet
Trial	Information	Comparator Arm	Control Arm	Participants	PFS, HR or EP	OS, HR or EP	Author or Status
RT							
STAMPEDE Arm H	NCT00268476	RT to prostate	ADT (+ DOC possible)	819	NA	0.68 (OS)	Parker ²⁵
HORRAD	ISRCTN06890529	RT to prostate	ADT	160	NA	0.68 (OS)	Boevé ²⁶
			Not-reported trials				
ARPI							
STAMPEDE Arm J	NCT00268476	ADT + AAP + ENZA (DOC)	ADT (DOC)	1,800		Primary EP	Completed accrual 2016
PEACE-1	NCT01957436	ADT + DOC + AAP (± RT)	ADT + DOC (± RT)	1,173	Coprimary EP	Coprimary EP	Completed accrual 2018
ARASENS	NCT02799602	ADT + DOC + darolutamide	ADT + DOC	1,303		Primary EP	Complete approximately 2022
SW0G-1216	NCT01809691	ADT + orterenel	ADT + bicalutamide	1,313		Primary EP	Complete approximately 2022
RT							
PEACE-1	NCT01957436	ADT + DOC ± AAP + RT	ADT + DOC ± AAP	1,173	Coprimary EP	Coprimary EP	Completed accrual 2018
PLATON	NCT03784755	SST + ablative therapy for all sites	SST + ablative therapy for prostate	410	Primary EP		Complete approximately 2025
SW0G-1802	NCT03678025	SST + definitive treatment of prostate	SST	1,273		Primary EP	Complete approximately 2028
Abbreviations: AAP, abir Docetaxel in Metastatic Cas Ablation Randomized Trial ENZAMET, Enzalutamide ir Local External Radiation TF Hizh-Risk Metastatic Castr	aterone acetate plus p tration-Sensitive Prosta for Extensive Disease n First-Line Androgen-C lerapy in Patients With ation-Sensitive Prostate	rednisone; ADT, androgen-dep te Cancer; ARCHES, Enzalutami in Prostate Cancer; ARPI, andr beprivation Therapy for Metastati Primary Diagnosed Metastasize. Cancer: NA, not available: NSA	ivation therapy; APA, apalutamic de Plus ADT for Metastatic Hormo ogen receptor pathway inhibitor; c Prostate Cancer; EP, end point; J Prostate Cancer; HR, hazard rat A. nonsteroidal anti-androgen: O	ie; ARASENS, ODM- ine-Sensitive Prostate CRPC, castration-res FFS, failure-free survi io; LATITUDE, Abirat S. overall survival: PF	201 in Addition to S Cancer; CHAARTED istant prostate canco val; HORRAD, Horm erone Acetate Plus F S. progression-free s	tandard Androg), Chemohormo er; DOC, docet ional Therapy V Prednisone in P survival: PLATO	gen-Deprivation Therapy and nal Therapy Versus Androgen axel; ENZA, enzalutamide; ersus Hormonal Therapy Plus atients With Newly Diagnosed N. Local Ablative Therapy for

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Metastatic Prostate Cancer: Evaluation of Drug Efficacy; TBD, to be determined; TITAN, Apalutamide Plus Androgen-Deprivation Therapy (ADT) Versus ADT in Patients With Metastatic Hormone-Sensitive

Prostate Cancer.

Hormone-Sensitive Oligometastatic Prostate Cancer; rPFS, radiographic progression-free survival; RT, radiotherapy; SST, standard systemic therapy; STAMPEDE, Systemic Therapy in Advancing or

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together with sites and number of metastases on conventional imaging) and showed survival improvement for these men.^{11,21} Post hoc subgroup analysis of LATITUDE by disease volume (CHAARTED definition) confirmed benefit across subgroups, although the P value for benefit in lowvolume disease was not significant. STAMPEDE Arm G included patients with metastatic high- or low-risk/volume disease (52%) and patients with high-risk nonmetastatic disease (48%) and was positive for OS in the whole population (HR, 0.63).¹² Post hoc analysis of patients with metastatic disease demonstrated improved OS in both high- and low-risk groups (LATITUDE definition; high-risk HR, 0.54; low-risk HR, 0.66). Similar results were seen in high- and low-volume disease (per CHAARTED definition).²² ENZAMET (HR, 0.67) and TITAN (HR, 0.68) were both positive in the overall patient population, with benefit seen in high- and low-volume disease for ENZA and APA, respectively (ENZA HRs, 0.80 and 0.43; APA HRs, 0.68 and 0.67). Thus, the totality of the data indicates that patients with lower disease burden also benefit from earlier AAP. Of note, in ENZAMET and TITAN, there seemed to be less benefit of an ARPI for patients who also received DOC, which likely had a greater effect on the HR for those with high-volume disease than with low-volume disease. These studies generally excluded patients with histologies other than adenocarcinoma; poor performance status; recent cardiac events; or, for the trials involving anti-androgens, prior seizure, and the balancing of risks and benefits is critical in considering therapy intensification in these patients.

Although subgroup evaluation of volume/risk is informative, more is needed to personalize therapy better. Patients with metastases only in the lung, for example, are considered high volume/risk as a result of having visceral metastases, yet they may actually have prolonged responses to ADT alone.²⁴ The evolution of imaging technologies is a major confounding factor in the context of both those with M1 disease by conventional imaging and those with MO disease by conventional imaging but M1 disease on nextgeneration imaging (eg, fluciclovine positron emission tomography or prostate-specific membrane antigen-targeted imaging). Trials to date have not incorporated nextgeneration imaging, and as such, how to factor in newer imaging for management decisions is not clear. Future trials should seek to refine subgroup definitions by incorporating newer imaging techniques and prospectively evaluating subgroup-specific therapy.

Focal Therapy

The role of local therapy to the prostate has been a subject of interest for decades but with no definitive data. The radiotherapy (RT) arm of STAMPEDE (Arm H) evaluated the impact of prostate RT in patients with mHSPC. After Arm H was fully accrued, the investigators annotated patients' volume of disease, having hypothesized that RT would be more beneficial in patients with low-volume mHSPC, and before analysis, specified these subgroups and powered Arm H accordingly. Improvement in failurefree survival with the addition of prostate RT was found for all patients (HR, 0.76). There was no OS benefit in the overall population (HR, 0.92), but patients with low-volume disease had an improved OS (HR, 0.68).²⁵ A similar effect was observed in the HORRAD (Hormonal Therapy Versus Hormonal Therapy Plus Local External Radiation Therapy in Patients With Primary Diagnosed Metastasized Prostate Cancer) trial for those with fewer than five metastases (HR, 0.68) and is summarized in a meta-analysis.^{26,27} In both trials, ADT alone was the treatment for the majority of patients; in STAMPEDE, 16% of patients received additional DOC.

The role of radiation to oligometastatic disease has been an area of significant interest as well. Many patients with lowvolume disease have oligometastatic disease by conventional imaging, and the question is whether they will benefit from RT to all sites of disease.²⁸ To date, trials that have evaluated metastasis-directed therapy have focused on delaying the initiation of ADT rather than on improvement in OS. This was true in STOMP (Surveillance or Metastasis-Directed Therapy for Oligometastatic Prostate Cancer Recurrence), which targeted up to three metastases seen on next-generation imaging (choline positron emission tomography-computed tomography), and in ORIOLE (Observation Versus Stereotactic Ablative Radiation for Oligometastatic Prostate Cancer), an ongoing trial that targets up to three metastases seen on conventional imaging.^{28,29} No definitive data support the survival benefit of this strategy, although several ongoing trials are evaluating the role of focal therapy in various settings. PEACE-1 is evaluating the role of local RT and/or AAP addition to ADT and DOC regardless of disease volume/risk, both for OS and for effect on local symptoms. The PLATON (Local Ablative Therapy for Hormone-Sensitive Oligometastatic Prostate Cancer) trial is comparing ablative therapy to the prostate versus to all sites of oligometastatic disease. Of note, patients in this trial are allowed to discontinue systemic therapy, which for the first time allows evaluation for cure with a combination systemic therapy and focal therapy approach. SWOG-1802 is testing the role of definitive therapy to the prostate, regardless of disease volume. The innovative design of SWOG-1802 offers definitive therapy only to those who are still responding to systemic therapy after 22 to 28 weeks, which thus spares those with primary refractory disease. It addresses whether the benefit of local prostate cancer control can be extended to more patients and whether treating the primary is relevant in an era of more-effective systemic therapy (akin to CARMENA [Clinical Trial to Assess the Importance of Nephrectomy], which replaces interferon with more-effective tyrosine kinase inhibitors).³⁰ In addition to improvements in survival, SWOG-1802 and PEACE-1 are evaluating treatment effects on quality of life.

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Molecular Characteristics

One way to improve upon risk stratification using diseasevolume/risk subgroups is to incorporate molecular characteristics. In mCRPC, defects in the tumor suppressor genes *PTEN*, *RB1*, and *TP53* are associated with aggressive-variant prostate cancer, and patients with these alterations may benefit from platinum-based therapy.^{31,32} Data suggest that loss of these genes also may inform risk in mHSPC because patients with intact tumor suppressor genes do well on ADT alone.³³ Similarly, decisions about the addition of local therapy to the prostate would be better personalized if they incorporated molecular characteristics of the disease. For example, the gene expression assay Decipher (Decipher Biosciences, San Diego, CA) predicts benefit from adjuvant or salvage RT.³⁴ Its performance in the metastatic setting is unknown.

To date, treatment of mHSPC is not biomarker targeted. The exception is the tissue agnostic indication in the United States for pembrolizumab for microsatellite instability-high or mismatch repair-deficient solid tumors. Numerous reports have cataloged the genomic landscape of localized prostate cancer or mCRPC.³⁵⁻⁴⁰ Those that examined mHSPC have suggested that the same genetic alterations are present in this disease state, with frequencies intermediate between localized disease and CRPC.^{33,41,42} These include loss of function of PTEN and DNA repair genes. (The major exception is androgen receptor alterations that arise only in mCRPC.) Early-phase trials have demonstrated in mCRPC the ability to target deficiency in DNA repair with poly (ADP-ribose) polymerase inhibitors or carboplatin and PTEN loss with phosphatidylinositol 3-kinase or AKT inhibitors.^{32,41-47} When moved to mHSPC (in patients with the appropriate genomic profile), these therapies may improve outcomes more dramatically.

Current Practice in Response to Available Data

Many physicians understandably are concerned about making major changes to their practice on the basis of subgroup analyses of the trials described herein, some of which are post hoc. It comes down to a desire for conclusive data versus a willingness to tolerate some imperfection and to make the best decision possible on the basis of the data available. The trials that generate these results took many years to conduct and the willing participation of thousands of patients internationally. The generation of conclusive

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⁴Institut Gustave Roussy, University of Paris Sud, Villejuif, France ⁵Manchester Cancer Research Centre, Manchester, United Kingdom data about the proper setting to use DOC, an ARPI, and/or RT to the prostate would require many more years and many more patients, a large cost for validating a result that already has high confidence.

We take a pragmatic approach to interpreting these newly available results and conclude that they are sufficient to change practice but do not preclude further studies to confirm their value moving forward. As part of our pragmatic approach, we propose that pending conclusive data in patients with low-volume oligometastatic mHSPC on conventional imaging, it is reasonable to consider intensified therapy with ADT + ARPI, radiation to the prostate, and potentially radiation to metastatic sites, with an acknowledgment that fewer data exist for the latter approach. Moreover, if the patient achieves an undetectable prostate-specific antigen with durable control (eg, more than 2 to 3 years), it is reasonable to halt systemic therapy, especially if adverse events that are metabolic and quality-of-life impairing emerge, and observe until biochemical progression. Not all these strategies are supported by level 1 evidence at this time and should be undertaken on the basis of informed shared decisions that balance risks/benefits. comorbidities. emerging data, and patient preferences. In the meantime, the trials that test these hypotheses should continue, and patients preferentially should be offered the opportunity to participate in these trials. Individual patient data registries or meta-analyses, which depend on a global willingness for data sharing, will provide greater granularity on outcomes by subgroup in the real world. These are planned or ongoing.

In conclusion, since 2015, there has been significant improvement in survival for patients with mHSPC, with an unprecedented "return on investment" from DOC and ARPIs. Refinement of clinical subgroups and incorporation of molecular characteristics will help to personalize therapy by identifying for whom and how to intensify therapy. Yet, we remain far from eradicating metastatic disease. Continued discovery and evaluation of novel therapeutic vulnerabilities and a better understanding of mechanisms of resistance are critical to transforming care. These efforts to expand the patient populations that experience an exceptional response to systemic therapy will convert metastatic prostate cancer from deadly to chronic on our way to potential cure.

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AUTHORS' DISCLOSURES OF POTENTIAL CONFLICTS OF INTEREST AND DATA AVAILABILITY STATEMENT

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AUTHORS' DISCLOSURES OF POTENTIAL CONFLICTS OF INTEREST

Metastatic Hormone-Sensitive Prostate Cancer: Clinical Decision Making in a Rapidly Evolving Landscape of Life-Prolonging Therapy

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Molecular profiling stratifies diverse phenotypes of treatment-refractory metastatic castration-resistant prostate cancer

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Metastatic castration-resistant prostate cancer (mCRPC) is a heterogeneous disease with diverse drivers of disease progression and mechanisms of therapeutic resistance. We conducted deep phenotypic characterization of CRPC metastases and patient-derived xenograft (PDX) lines using whole-genome RNA sequencing, gene set enrichment analysis, and immunohistochemistry. Our analyses revealed 5 mCRPC phenotypes based on the expression of well-characterized androgen receptor (AR) or neuroendocrine (NE) genes: AR-high tumors (ARPC), AR-low tumors (ARLPC), amphicrine tumors composed of cells coexpressing AR and NE genes (AMPC), double-negative tumors (i.e., AR⁻/NE⁻; DNPC), and tumors with small cell or NE gene expression without AR activity (SCNPC). RE1 silencing transcription factor (REST) activity, which suppresses NE gene expression, was lost in AMPC and SCNPC PDX models. However, knockdown of REST in cell lines revealed that attenuated REST activity drives the AMPC phenotype but is not sufficient for SCNPC conversion. We also identified a subtype of DNPC tumors with squamous differentiation and generated an encompassing 26-gene transcriptional signature that distinguished the 5 mCRPC phenotypes. Together, our data highlight the central role of AR and REST in classifying treatment-resistant mCRPC phenotypes. These molecular classifications could potentially guide future therapeutic studies and clinical trial design.

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Molecular profiling stratifies diverse phenotypes of treatment-refractory metastatic castration-resistant prostate cancer

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Metastatic castration-resistant prostate cancer (mCRPC) is a heterogeneous disease with diverse drivers of disease progression and mechanisms of therapeutic resistance. We conducted deep phenotypic characterization of CRPC metastases and patient-derived xenograft (PDX) lines using whole-genome RNA sequencing, gene set enrichment analysis, and immunohistochemistry. Our analyses revealed 5 mCRPC phenotypes based on the expression of well-characterized androgen receptor (AR) or neuroendocrine (NE) genes: AR-high tumors (ARPC), AR-low tumors (ARLPC), amphicrine tumors composed of cells coexpressing AR and NE genes (AMPC), double-negative tumors (i.e., AR⁻/NE⁻; DNPC), and tumors with small cell or NE gene expression without AR activity (SCNPC). RE1 silencing transcription factor (REST) activity, which suppresses NE gene expression, was lost in AMPC and SCNPC PDX models. However, knockdown of REST in cell lines revealed that attenuated REST activity drives the AMPC phenotype but is not sufficient for SCNPC conversion. We also identified a subtype of DNPC tumors with squamous differentiation and generated an encompassing 26-gene transcriptional signature that distinguished the 5 mCRPC phenotypes. Together, our data highlight the central role of AR and REST in classifying treatment-resistant mCRPC phenotypes. These molecular classifications could potentially guide future therapeutic studies and clinical trial design.

Introduction

The androgen receptor (AR) regulates cellular programs that promote the survival and proliferation of prostate cancer (PC) cells. Consequently, first-line treatment for metastatic PC centers on inhibiting AR activity through androgen deprivation therapy

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Submitted: February 20, 2019; Accepted: July 23, 2019; Published: September 16, 2019. Reference information: / Clin Invest. 2019;129(10):4492–4505. https://doi.org/10.1172/JCl128212. (ADT), resulting in the suppression of AR target genes and clinical remissions that generally last several years (1). However, ADT is not curative. PC recurs as castration-resistant prostate cancer (CRPC), typically with reactivated AR signaling. Second-generation AR pathway inhibitors (ARIs), such as enzalutamide (ENZ) and abiraterone (ABI), were designed to further repress AR signaling and are primarily used to treat CRPC. Although these agents extend survival, durable complete responses are rare and these therapies also eventually fail (2, 3).

Typically, the vast majority of metastatic CRPC (mCRPC) tumors progress with rising prostate-specific antigen (PSA/KLK3) levels despite standard of care treatment. Moreover, most mCRPC tumors are adenocarcinomas, which have robust AR program activity (4). Though rigorous epidemiological data are lacking, recent studies report that a substantial number of mCRPC tumors progressing on ARIs have lost AR signaling (5). Paralleling increased use of ARIs has been an increase in the proportion of treatment-resistant CRPC metastases that have AR-null phenotypes, i.e. tumors with diffuse small cell or neuroendocrine (NE) characteristics (SCNPC) or the recently described double-negative (DNPC) phenotype that lacks both NE and AR activity (5). A contemporary study evaluating the histology and molecular characteristics of 202 men with mCRPC found that 17% of the evaluable tumors were classified as SCNPC and this phenotype was associated with short-

ened survival (6). Notably, a subset of tumors exhibited discordance between the pathological assessment of SCNPC and gene expression programs. Other tumors exhibited mixed phenotypes of NE features concurrent with AR activity, raising questions of intratumoral heterogeneity due to mixtures of cell types (6).

In addition to histology, the classification of cancers into subtypes with distinct functional features has been supplemented with transcript profiles. For example, transcript signatures subdivide breast cancers into groups that exhibit distinct outcomes (7). This subclassification, based on gene expression levels, has also been applied to localized PC and shown to associate with treatment outcomes (8, 9). In this study, we sought to characterize the phenotypic diversity of treatment-refractory mCRPC using both histological assessments and gene expression profiling. In addition to SCNPC and DNPC, we identified adenocarcinomas that had high AR activity (ARPC), measurable but low AR activity (ARLPC), and amphicrine tumors comprised of cells exhibiting both AR and NE activity (AMPC). Notably, a subset of DNPC tumors exhibited squamous differentiation. We determined that the relationships of 2 major factors regulating cell differentiation states, AR and RE1 silencing transcription factor (REST), associated with these mCRPC subtypes. We generated a 26-gene transcriptional signature that could be clinically useful for classifying mCRPC phenotypes and prioritizing treatment.

Results

Treatment-refractory mCRPC exhibits diverse phenotypes. To assess the diversity of phenotypes present following resistance to therapeutics used to treat metastatic PC, we evaluated 98 tumors obtained at rapid autopsy from 55 men between 2003 and 2017. Patient demographics and clinical data are summarized in Supplemental Table 2; supplemental material available online with this article; https://doi. org/10.1172/JCI128212DS1. All patients received ADT. The median duration of treatment was 4.2 years (range, 0.3–15.1 years). Patients also received a variety of other drugs including docetaxel (n = 44; 80%), abiraterone (n = 8; 15%), enzalutamide (n = 4; 7%) or both abiraterone and enzalutamide (n = 17; 31%). Bone, lymph nodes, and liver were the most frequent sites of metastasis.

To provide an initial evaluation of phenotypic diversity, we used histological assessments and immunohistochemical (IHC) analysis of proteins associated with AR-active adenocarcinomas (AR and PSA) and NE differentiation (chromogranin A, CHGA; synaptophysin, SYP). We observed 5 distinct mCRPC phenotypes: adenocarcinomas with near-uniform expression of AR and PSA, and lack of CHGA and SYP expression, classified as ARPC; adenocarcinomas with weak or heterogeneous expression of AR and PSA, and negative for CHGA and SYP, classified as AR-low PC (ARLPC); tumors composed of cells that coexpress AR, PSA, CHGA, and SYP, classified as amphicrine PC (AMPC); tumors with small cell or neuroendocrine histology with CHGA and SYP expression and lack of AR and PSA expression, classified as small cell or neuroendocrine PC (SCNPC); and tumors lacking detectable expression of AR, PSA, CHGA, and SYP, classified as double-negative PC (DNPC; Figure 1A).

Transcriptome profiles associate with mCRPC phenotypes. Morphologic and IHC analyses are the gold standard for pathologic diagnosis. However, the assessment of transcriptional programs has

found utility in subclassifying breast tissue and cancers that exhibit similar histological characteristics (10, 11). We sought to develop a clearer understanding of the mCRPC disease continuum through transcriptome profiling by whole-genome RNA sequencing (RNA-Seq) of 98 mCRPC tumors. Patient metastases were first analyzed and segregated according to expression levels of a gene signature reflecting AR activity (AR panel; Figure 1B). The AR-regulated genes selected for the AR signature are well characterized in the literature and include KLK3, NKX3-1, SLC45A3, and TARP (12-14). Tumors were also analyzed and segregated depending on expression levels of NE-associated genes. We previously demonstrated that NE-associated genes can be separated into REST-repressed genes such as SYP, CHGA, SNAP25, and SRRM4 (NEURO I panel; ref. 15), and transcription factors that regulate NE differentiation, such as SOX2, POU3F2/BRN2, NKX2-1, and LMO3 (NEURO II panel; refs. 15-17). Applying the AR, NEURO I, and NEURO II gene expression sets to the mCRPC tumors clearly defined the 5 mCRPC subtypes (Figure 1B). ARPC tumors expressed AR-regulated genes but also showed heterogeneity with low expression of some NE genes. ARLPCs had attenuated AR expression with concomitant low expression of some AR-regulated genes. AMPCs expressed AR-associated genes and REST-repressed neuronal factors (NEU-RO I), but lacked expression of the NE-associated transcription factors (NEURO II). DNPC tumors were generally devoid of AR, NEURO I, and NEURO II panel genes. SCNPC tumors lacked AR expression and signaling but expressed both the NEURO I and NEURO II genes. Analysis of 62 corresponding tumor sites through IHC revealed that phenotypic determinations based on AR, PSA, CHGA, and SYP staining mirrored the phenotypic determinations made through RNA-Seq analysis (Supplemental Figure 1). Moreover, our rapid autopsy cohort included 34 patients, each with 2-3 metastatic sites characterized through RNA-Seq. This provided an opportunity to query the intertumoral phenotypic heterogeneity within patients. Of the 34 patients with 2-3 analyzed metastases, 5 patients (14.7%) displayed phenotypic differences between sites. However, this may underestimate the extent of heterogeneity, as 2-3 metastases generally represent a fraction of the total tumor burden. In addition, there can be intratumoral phenotypic heterogeneity that is not readily assessed through bulk RNA sequencing (Supplemental Figure 2).

To validate the results of the patient specimen analysis using an orthogonal system, we conducted RNA-Seq and IHC analyses on 18 CRPC LuCaP patient-derived xenograft (PDX) lines. The 5 distinct phenotypes were identified by IHC and accurately segregated according to the AR, NEURO I, and NEURO II gene expression profiles (Supplemental Figure 3, A and B).

To discover novel gene expression profiles for each of the mCRPC phenotypes, we cross-compared the patient metastases RNA-Seq data from the defined phenotypic cohorts (i.e., ARLPC, AMPC, DNPC, and SCNPC) relative to ARPC. This analysis generated a comprehensive list of unique and shared upregulated differentially expressed genes (vs. ARPC, up >3-fold and P < 0.05; Figure 1C and Supplemental Table 3). In addition, this analysis demonstrated that DNPC and SCNPC are markedly different from the other mCRPC phenotypes (806 and 1669 unique upregulated genes respectively; Figure 1C). Notably, the AR-null phenotypes (DNPC and SCNPC) share an additional 590 upregulated



Figure 1. Molecular profiling of mCRPC reveals a heterogeneous disease. (**A**) IHC of 5 mCRPC sites from patients using antibodies to AR, PSA, CHGA, and SYP. Scale bars: 20 μ M. (**B**) RNA-Seq heatmap of mCRPC specimens acquired through rapid autopsy from 2003–2017 (*n* = 98). REST-repressed NE genes are listed in the NEURO I panel (top), NE transcription factors are listed in the NEURO II panel (middle), and AR-associated genes are listed in the AR panel (bottom). Results are expressed as log₂ fragments per kilobase of transcript per million mapped reads (FPKM) and colored according to scale. (**C**) Venn diagram showing the number of unique and shared upregulated genes between phenotypes relative to ARPC (up >3-fold; *P* < 0.05). ARPC (AR-high prostate cancer; AR⁺/NE⁻), ARLPC (AR-low prostate cancer; AR⁻/NE⁺).

genes relative to the AR-expressing phenotypes (Figure 1C). Furthermore, ARLPC, and AMPC share gene expression profiles similar to ARPC (Figure 1C).

Gene Set Enrichment Analysis (GSEA) determined that the 806 upregulated genes unique to DNPC were enriched in Gene Ontology biological process terms for response to external biotic stimulus ($P = 4.5 \times 10^{-18}$), immune system process ($P = 3.5 \times 10^{-15}$), and cornification ($P = 5.5 \times 10^{-9}$). As expected, the 1669 upregulated genes unique to SCNPC were enriched for core neuronal activities such as nervous system process ($P = 7.5 \times 10^{-12}$) and regu-

lation of nervous system process ($P = 4.7 \times 10^{-10}$). Interestingly, the top processes for the 829 upregulated genes in common between SCNPC and DNPC included locomotory behavior ($P = 5.0 \times 10^{-07}$) and cell adhesion ($P = 2.1 \times 10^{-07}$), suggesting changes in metastatic potential common to AR-null phenotypes. The 229 upregulated genes unique to the ARLPC phenotype were enriched for processes in response to external biotic stimulus ($P = 3.3 \times 10^{-07}$) and regulation of inflammatory response ($P = 8.4 \times 10^{-06}$), while the 193 upregulated genes in common between ARLPC, DNPC, and SCN-PC phenotypes were significantly enriched in acute inflammatory



Figure 2. Disease progression is a continuum in mCRPC specimens. (A) IHC of different mCRPC sites from patient 13-084. Site PP7 (bone; ARPC), II2 (bone; ARLPC), PP7 (bone; DNPC), and H1 (liver, SCNPC). Primary antibodies were directed toward pan-cytokeratin, AR, PSA, CHGA, and SYP. Insets for AR and PSA staining are images of the same section using the ×400 objective lens. Original magnification 40×. (B) IHC of LuCaP 173.2 tumor sections from passages 2, 4, 7, 8, and 11 using a SYP antibody. Black arrows point to clusters of cells with SYP positivity. Magnification 100×. (C) RNA-Seq heatmap and NEURO score of LuCaP 173.1 and serial passages from LuCaP 173.2. Results are expressed as log, FPKM or as enrichment scores and are colored according to scale.

response ($P = 4.0 \times 10^{-11}$) and defense response ($P = 1.3 \times 10^{-06}$). Finally, GSEA determined that the 111 upregulated genes unique to AMPC were not involved in any significant processes. However, the 250 common upregulated genes between AMPC and SCNPC were involved in ancillary neuronal processes such as neurotransmitter transport ($P = 4.4 \times 10^{-10}$) and synaptic vesicle localization ($P = 6.5 \times 10^{-09}$). Importantly, analysis of the 250 significantly upregulated genes shared between SCNPC and AMPC using the MSigDB C3-Transcription Factor Target database showed that REST was the top transcription factor pathway altered in the gene set ($P = 4.2 \times 10^{-35}$; Supplemental Table 4). Taken together, these data support the use of AR, NEURO I, and NEURO II genes to segregate mCRPC phenotypes and identify biologically relevant pathways that emphasize the heterogeneity of mCRPC. *mCRPC phenotypes represent a disease continuum.* The relationships between different mCRPC phenotypes have not been clearly established though prior studies suggest that SCNPC is often derived from an AR-positive precursor, or share a common progenitor (18, 19). Thus, we investigated these relationships by studying the phenotypic progression of an individual with mCRPC and a complicated treatment history. At diagnosis in 2012, patient 13-084 had a PSA of 159 ng/mL and a prostate biopsy revealed an adenocarcinoma with a Gleason score of 4 + 5 = 9 and IHC demonstrating focal NE differentiation. He was treated with leuprolide and bicalutamide but ensuing CT and bone scans revealed numerous metastases in liver, lung, and bone. Platinum-based chemotherapy was initiated due to the possible presence of SCNPC with cycles of carboplatin/irinotecan (5 cycles) or cisplatin/irinotecan



Figure 3. REST splicing occurs in AMPC and SCNPC phenotypes. (A) Immunofluorescence of an AMPC LuCaP 77CR tumor using PSA (green) and SYP (red) antibodies. Sections were counterstained with DAPI (blue) and top panels represent LuCaP 77CR PDX sections stained with secondary antibody only. Scale bars: 20 µM. (**B**) Immunoblot of LuCaP PDX specimens probing for REST, AR, and SYP. ACTB was used as a loading control. Short, 10-second film exposure; long, 5-minute film exposure. (**C**) PCR of LuCaP PDX specimens using primers specific to REST shows the REST4 insertion sequence appearing in AMPC (LuCaP 77CR) and SCNPC (LuCaP 93, 145.2, and 173.1) but not in DNPC (LuCaP 173.2) or ARPC (LuCaP 86.2 and 73). (**D**) RNA-Seq heatmap of VCaP cells displaying NE-associated genes (NEURO I and NEURO II) and AR-associated genes. Results are expressed as log₂ FPKM and colored according to scale. (**E**) Immunoblot of C4-2B, VCaP, and LuCaP 93 whole-cell extracts using antibodies against AR, REST, SYP, and ACTB. ACTB was used as a loading control. (**F**) PCR of C4-2B, VCaP, and NCIH660 cells using primers specific to REST. The upper band represents the REST4 splice variant.

(3 cycles) leading to a PSA decline and stable disease for approximately 8 months. He subsequently received 2 cycles of capecitabine and gemcitabine with eventual PSA progression prior to death (Supplemental Figure 4). At autopsy in 2013, we recovered several metastatic tumors that exhibited different phenotypes, including ARPC, ARLPC, and DNPC sites in bone and SCNPC sites in the liver as determined by IHC (Figure 2A). We developed 2 PDX lines representing SCNPC (LuCaP 173.1) and DNPC (LuCaP 173.2) from acquired patient metastases (5). Previous reports have described the transdifferentiation of an AR-expressing adenocarcinoma PC PDX line to SCNPC (20). We therefore questioned whether the DNPC phenotype is a transition stage. We sought to test the hypothesis that sustained tumor growth through serial passaging of the DNPC LuCaP 173.2 PDX line would lead to SCNPC conversion. Indeed, serial passaging in intact mice of LuCaP 173.2 and staining for SYP expression through IHC showed that first passage PDX tumors were negative for SYP expression, whereas SYP-positive cells were detected by passage 4 and were maintained as a minor cell population through passage 9 (Figure 2B). RNA-Seq of LuCaP 173.2 from passages 2, 9, and 12 indicated that the NEURO I and NEURO II panels of genes were expressed at substantially higher levels in the later passages (Figure 2C). Furthermore, the NEURO scores of LuCaP 173.2 from passages 9 and 12 were similar to SCNPC LuCaP 173.1. These data suggest that mCRPC is a disease continuum, and that although the DNPC phenotype is generally stable, a small proportion of DNPC tumor cells possess an intrinsic plasticity that permits conversion to SCNPC.

The amphicrine phenotype and relationship with REST expression. Historically, SCNPC was considered to lack AR activity but recent studies have identified atypical tumors with NE features that express



Figure 4. REST knockdown in AR-expressing and AR-null CRPC cell lines. (A) Immunoblot of REST, AR, SYP, and ACTB using C4-2B, PC-3, and PacMet AR-null cells transfected with either REST siRNA (siREST) or negative control siRNA (siNCT). (B) AR activity scores assessed in C4-2B cells transfected with siNCT (n = 2) or siREST (n = 2) by RNA-Seq. (C) RNA-Seq heatmap of the 24 common upregulated genes (up >3-fold; P < 0.05) between C4-2B, PC-3, and PacMet AR-null cells transfected with siREST or siNCT. Log, mean-centered ratios of genes are depicted and colored according to scale. (D) Venn diagram describing the interrelationships of all upregulated genes (vs. siNCT; up >3-fold; P < 0.05) identified through RNA-Seq in siREST transfected cell lines.

AR and exhibit AR-mediated signaling (6). In addition, classification of the AMPC phenotype based on bulk RNA-Seq or IHC using single markers may be due to tumors comprised of multiple cell types (AR⁺/NE⁻ and AR⁻/NE⁺) or may be due to tumors comprised of individual cells expressing both AR and NE differentiation markers simultaneously. Thus, to establish the existence of AMPC cells in our clinical specimens (i.e., cells with both AR transcriptional output and neuroendocrine features; AR+/NE+), we stained LuCaP PDX tumors and patient metastases with immunofluorescent (IF) antibodies to PSA and SYP. AMPC LuCaP 77CR tumors contained numerous cells coexpressing PSA and SYP (Figure 3A). Though PSA and SYP coexpression normally occurred throughout LuCaP 77CR tumors, we also identified a subset of tumors with focal SYP expression (unpublished observations). Furthermore, we used IF to characterize 6 AMPC metastases from 4 patients. The patient tissues used for IF analysis were adjacent to the specimens used for RNA-Seq. Importantly, IF demonstrated clear PSA and SYP coexpression in patient tumor cells. However, patient 13-042 site M3 and patient 17-033 site I1 showed regions that were mixed of distinct populations of ARPC and SCNPC tumor cells (Supplemental Figure 5).

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Previously, we interrogated SCNPC patient tumors and PDX lines and determined that SCNPC is associated with loss of REST repressor activity (15). However, the role of REST in other mCRPC phenotypes has not been evaluated. Using representative PDX lines from ARPC (LuCaP 35CR and 96CR), AMPC (LuCaP 77CR), ARLPC (LuCaP 176), DNPC (LuCaP 173.2), and SCNPC (LuCaP 173.1 and 93), we found that full-length REST protein was decreased in both AMPC and SCNPC tumors (Figure 3B). Interestingly, we observed REST species with our REST C-terminus antibody at both approximately 120 KDa and approximately 200 KDa in PDX lysates from ARPC, ARLPC, and DNPC. Full-length REST protein is predicted to be 116 KDa but can be O-glycosylated and readily detected at approximately 200 KDa (21, 22). Additionally, the REST transcript has multiple splice variants that produce truncated proteins (23). Nevertheless, both REST proteins with intact C-terminus repressor domains were diminished in AMPC and SCNPC PDX models. Moreover, AMPC LuCaP 77CR showed robust expression of both AR and SYP protein, whereas ARLPC LuCaP 176 had low AR protein expression (Figure 3B).

Next, we examined alternative splicing of the REST transcript. The RNA splicing factor SRRM4 splices the REST transcript to REST4, resulting in the loss of the C-terminus repressor domain and diminished REST transcriptional repression (15, 24, 25). To examine SRRM4-mediated splicing of REST in mCRPC phenotypes, we conducted PCR using REST primers spanning the SRRM4 splice site and determined that REST4 splicing events occurred exclusively in AMPC and SCNPC LuCaP PDX models (Figure 3C). However, instead of a previously reported 62 bp inser-



Figure 5. DNPC can convert to a squamous phenotype. (**A**) H&E staining of mCRPC tissues from LuCaP 173.2 and patient 13-084. Black arrows point to squamous pearl structures. (**B**) Expression of squamous cell lung cancer associated genes from RNA-Seq of LuCaP 173.2 DNPC cells and squamous pearl (SP) cells isolated by laser capture microdissection. Results are expressed as log₂ FPKM and colored according to scale. (**C**) IHC of specimens from LuCaP 173.2 and patient 13-084 using KRT6 antibody or IgG as a negative control. (**D**) H&E staining (left panels) and KRT6 IHC (right panels) of DNPC tumor sections from patients 11-028 and 13-099. Scale bars: 20 μM.

tion into the REST transcript (25), band sequencing identified a 50 bp insertion, suggesting a mechanism of REST4 splicing in AMPC and SCNPC phenotypes similar to small cell lung cancer (26). Taken together, these data indicate that the AMPC phenotype arises from the loss of REST transcriptional repression.

To further support the existence of the AMPC phenotype, we interrogated the VCaP PC cell line, which exhibits an amphicrine-like transcript profile. RNA-Seq confirmed that VCaP cells express AR-associated genes and the REST-repressed NEURO I genes but do not express the NEURO II transcription factors that drive the SCNPC phenotype (Figure 3D). Immunoblot analysis determined that VCaP cells express considerable AR and SYP protein and have diminished full-length REST protein expression compared with C4-2B cells (Figure 3E). Immunofluorescence validated that both PSA and SYP are coexpressed in the same VCaP cell (Supplemental Figure 6) and PCR analysis of REST determined that REST transcripts are alternatively spliced to REST4, similar to neuroendocrine NCIH660 cells (Figure 3F). Notably, the growth of VCaP cells is inhibited by ADT or exposure to the AR antagonist enzalutamide (27). In addition, 22Rv1 cells also exhibit features of AMPC as they have attenuated REST expression and appreciable SYP and AR protein expression (28). Taken together, these results confirm the existence of AMPC cells in patient specimens and in CRPC models in vitro and in vivo, and suggest that the AMPC phenotype is still driven by AR activity and is responsive, at least transiently, to AR pathway repression.

REST knockdown in CRPC cells promotes an amphicrine phenotype. To examine the impact of the loss of REST activity in ARexpressing and AR-null cell lines, we conducted knockdown studies using siRNAs directed to REST (siREST) or a negative control (siNCT) in C4-2B, PC-3, and PacMet AR-null cells. PacMetUT1 cells were modified using CRISPR-Cas9-mediated editing to knockout AR expression and were characterized previously (5, 29). REST knockdown led to increases in the NE-associated protein SYP (Figure 4A). Interestingly, REST depletion in AR-expressing C4-2B cells did not alter AR protein expression or the magnitude of AR transcriptional output (Figure 4, A and B). However, this does not rule out the possibility that complete loss of REST could alter the AR transcriptional output. Transcript profiling by RNA-Seq and subsequent GSEA showed that REST ablation in C4-2B, PC-3, and PacMet AR-null cells led to significant upregulation of known REST-repressed genes (up >3-fold; P < 0.05). Furthermore, the REST pathway was the top altered pathway from the MSigDB C3-Transcription Factor Target database in all siREST transfected cell lines. Surprisingly, the number of genes significantly upregulated with REST knockdown was relatively low across all cell models and only 24 genes were in common between C4-2B, PC-3, and PacMet AR-null cells (Figure 4, C and D; Supplemental Table 5). The REST-repressed genes with increased expression following REST depletion included SYP, SNAP25, CHRNB2 (NEURO I Panel) as well as VGF, SCG3, and CHGB (Figure 4C). However, REST knockdown did not significantly alter the expression of transcrip-



Figure 6. Expression of squamous markers is associated with DNPC and ARLPC. RNA-Seq heatmap of patient specimens (*n* = 98) highlighting AR-regulated genes and genes associated with squamous pearl cells (SQUAM). Results are expressed as log, FPKM and colored according to scale.

tion factors and drivers of SCNPC such as *NKX2-1*, *POU3F2*, and *SOX2* (NEURO II panel) in either AR-expressing or AR-null CRPC cell lines (Supplemental Figure 7). Taken together, we determined that REST loss induces the expression of a limited set of NE-associated genes (NEURO I) and drives PC conversion to the AMPC phenotype with continued evidence of AR activity.

A subtype of mCRPC exhibits features of squamous cell carcinoma. While histologically characterizing the DNPC LuCaP 173.2 PDX model, we observed squamous pearls, which were evidence of focal squamous differentiation (Figure 5A). To determine if the squamous pearls occurred spontaneously during LuCaP 173.2 development or were native to the original malignancy, we evaluated tumors from patient 13-084 and identified squamous pearl structures in adjacent tumor sections of the rib bone metastasis that served as the origin of LuCaP 173.2 (Figure 5A). Squamous pearl cells from LuCaP 173.2 PDX tumors were then isolated using laser capture microdissection and subjected to RNA-Seq and GSEA. Transcriptome analysis determined that 880 genes were upregulated and 29 genes were downregulated in LuCaP 173.2 squamous pearl cells compared with surrounding DNPC tumor cells (FDR < 0.001; Supplemental Table 6). GSEA determined that many of the upregulated genes were enriched in other squamous cancer gene sets, such as RICKMAN_HEAD_AND_NECK (P < 0.0001; ref. 30). Importantly, KRT5, KRT6A, KRT6B, and DSG3 were recently highlighted through ROC curves as biomarkers to differentiate lung adenocarcinoma from lung squamous cell cancer (31). Indeed, our analysis showed that KRT5, KRT6A, KRT6B, and DSG3 were highly expressed in LuCaP 173.2 squamous pearl cells compared with surrounding DNPC tissue (Figure 5B). IHC using a primary antibody specific to KRT6 in LuCaP 173.2 and 13-084 tumor specimens revealed strong KRT6 staining only in tumor cells with squamous pearl morphology (Figure 5C).

Examination of 4 other patients with DNPC metastases identified squamous pearls with positive KRT6 staining in 2 patients: 11-028 and 13-099 (Figure 5D). Interestingly, patient 11-028 had an adenocarcinoma phenotype in the initial prostate biopsy and was subsequently treated with diethylstilbesterol (DES) for 13 months prior to cystoprostatectomy. At the time of cystoprostatectomy, histology and IHC revealed adenocarcinoma with focal basaloid and squamous differentiation in several sections of the prostate as well as a left axillary lymph node that was consistent with squamous carcinoma. The other 2 patients with KRT6-positive metastases, patients 13-084 and 13-099, had primary prostate cancers with no evidence of squamous differentiation, and subsequent hormone therapy led to the appearance of squamous mCRPC. Although DES and hormone therapies have been linked to the development of squamous cancer in the prostate with subsequent squamous metastases (32-36), this report provides evidence for hormone therapy-mediated conversion of ARPC to squamous DNPC at metastatic sites.

We compared the top significantly (FDR < 0.001) upregulated genes from the LuCaP 173.2 squamous pearl data set with the literature to identify genes with known roles in squamous cell differentiation or other squamous cancers. In addition to *KRT5*, *KRT6A*, *KRT6B*, and *DSG3*, we also found *IVL*, *SBSN*, *FGFBP1*, *SCEL*, *S100A7*, *MUC4*, *KRT14*, and *ANXA8* to be significantly overexpressed in other squamous cell types (37–44). Importantly, RNA-Seq heatmaps show that these genes are strikingly elevated in subsets of both ARLPC and DNPC patient specimens (Figure 6), suggesting that ARLPC and DNPC phenotypes could be transition states to squamous mCRPC. These results indicate that squamous cell conversion is not a rare occurrence in end-stage disease and should be considered an emerging phenotype following resistance to AR-directed therapy.

Transcript signatures define the molecular phenotypes of mCRPC. The variability in expression of any single marker, both at the biological level and technical level makes tumor classification by immunohistochemistry challenging. Transcript panels for tumor



Figure 7. Cluster analysis using AR, NE, and squamous gene expression profiles segregates mCRPC specimens and LuCaP PDX models into the different phenotypes. (**A**) RNA sequencing of mCRPC specimens acquired between 2003–2017 (n = 98; modified from Figure 1B). NE genes listed in the NEURO I and NEURO II panels, AR and AR-regulated genes are listed in the AR panel, and squamous associated genes are shown in SQUAM panel. Results are expressed as log₂ FPKM and colored according to scale. Multidimensional scaling and cluster analysis of (**B**) mCRPC specimens (n = 98) and (**C**) LuCaP PDX models using the 26-gene set depicted in A. The LuCaP analysis was conducted on 18 distinct PDX lines (n = 2 for each line). ARPC (AR⁺/NE⁻; green), ARLPC (AR¹/NE⁻; purple), DNPC (AR⁻/NE⁻; blue), AMPC/mixed (AR⁺/NE⁺; red), SCNPC (AR⁻/NE⁺; yellow).

classification have been explored as predictive and prognostic biomarkers for treatment decision-making (45, 46). We leveraged the data generated from the patient metastases and LuCaP PDX models to develop a 26-gene transcriptomic signature for defining treatment-refractory mCRPC phenotypes. Using the aforementioned AR, NEURO I, and NEURO II gene panels, as well as a squamous panel (SQUAM) that includes *KRT5*, *KRT6A*, *KRT6B*, and *FGFBP1*, we conducted multidimensional scaling (MDS) and cluster analysis of the patient metastases and LuCaP PDX models (Figure 7A and Supplemental Figure 3B). The MDS demonstrated clear distinction between the 5 mCRPC phenotypes (ARPC, ARLPC, AMPC, DNPC, and SCNPC) in both patient specimens and LuCaP PDX models (Figure 7, B and C).

We further evaluated our 26-gene signature using PolyA RNA-Seq landscapes from 270 CRPC metastases in the Stand Up To Cancer (SU2C) data set (47). Although the SU2C data set contains RNA-Seq from mCRPC tumors earlier in disease progression and from tumors that are responding to treatment, the transcriptional signature segregated the tumors into the 5 mCRPC phenotypes (Supplemental Figure 8, A and B). Interestingly, we detected expression of the squamous-associated genes in 2 DNPC tumors and 2 ARLPC tumors but also observed marked squamous marker



Figure 8. Schematic of the mCRPC disease continuum. The proposed mechanisms, molecular drivers, and cellular differentiation states following AR pathway inhibition therapy. ADT, androgen deprivation therapy; ABI, abiraterone; ENZ, enzalutamide; PC, hormone-sensitive prostate cancer; ARPC, AR-high prostate cancer; ARLPC, AR-low prostate cancer; SCNPC, small cell or NE prostate cancer; DNPC, double-negative prostate cancer; AMPC, amphicrine prostate cancer; SQUAPC, squamous prostate cancer.

expression in 4 ARPC tumors and 1 SCNPC tumor. Thus, removing the squamous genes from the analysis showed a more effective clustering of the tumors into their respective phenotypes (Supplemental Figure 8C). We do not know if the ARPC and SCNPC specimens with squamous aspects represent tumors containing 2 different phenotypes or single phenotypes.

Discussion

The clinical phenotyping of mCRPC has been limited to morphologic and immunohistochemical analyses. Although adenocarcinoma (AR and PSA) and NE (CHGA and SYP) biomarkers have provided some clarity for pathologic classification, the complexity of tumor heterogeneity, and the emergence of new treatment-resistant phenotypes have catalyzed a need for deeper understanding of the mCRPC disease continuum. Moreover, anaplastic tumors or aggressive variants are a clinically defined group of small cell metastatic/CRPC phenotypes with varying degrees of both AR expression (generally AR-null) and NE differentiation (48, 49). The classifications prompted a call for further elucidation of underlying mCRPC biology and more accurate nomenclature that limits confusion between research and medical fields (50). At the transcriptome level, expression signatures for classifying SCNPC have been demonstrated (51), but an encompassing signature that appreciates the spectrum of mCRPC phenotypes has not been identified. In this report, we interrogated end-stage mCRPC patient specimens and treatment-resistant LuCaP PDX models and demonstrated that transcriptome analysis in conjunction with IHC is a powerful method for phenotyping mCRPC in the current era. Our approach led to the characterization of 5 distinct mCRPC phenotypes (AR-high/ARPC, AR-low/ARLPC, amphicrine/ AMPC, double-negative/DNPC, and small cell or NE tumors lacking AR expression/SCNPC) and ultimately resulted in a clinically relevant 26-gene transcriptional signature to classify mCRPC biospecimens. Moreover, our data demonstrated that mCRPC is a disease continuum driven by AR, REST, and core SCNPC transcription factor programs; treatment-induced differentiation of DNPC to squamous cell carcinoma is an emerging mCRPC phenotype; AR-low and AR-null phenotypes share common pathways of resistance to AR pathway inhibition that could be exploited for clinical benefit; and loss of REST repressor activity is critical for driving conversion to the AMPC/mixed phenotype but only promotes rather than drives the SCNPC phenotype.

Observations made through our rapid autopsy program support a treatment-induced shift in mCRPC phenotypes with ARI therapies increasing the number of AR-null and AR-low metastases at end-stage disease (5). In addition, our patient, LuCaP PDX, and cell line data suggest that ARPC can transition to ARLPC, AMPC/mixed, DNPC/squamous, or SCNPC to bypass hormone or AR pathway suppression therapies. These results were further verified through our analysis of the SU2C cohort of CRPC metastases (47). Notably, DNPC is a proliferative AR-null intermediate that contains cells with the inherent plasticity and potential to convert to SCNPC or squamous mCRPC (Figure 8 and Supplemental Figure 9). Multiple cell line, murine model, and PDX reports have demonstrated that loss of tumor suppressor proteins, AR-directed therapies, and/or the tumor microenvironment contribute to CRPC cellular plasticity and ARPC to SCNPC transition (16, 20, 52-56). Moreover, Beltran et al. have established that subsets of NE tumors are clonally derived from ARPC (18). Of note, the genomic landscapes of intrapatient CRPC metastases are relatively similar (4). Thus, our analysis indicating that intertumoral phenotypic heterogeneity is not a rare occurrence argues that epigenetic, posttranscriptional, posttranslational, and microenvironment events can contribute to phenotypic diversity in mCRPC. Taken together, our data add further clinical support for the proposed mCRPC disease continuum and demonstrates that treatmentinduced selective pressures can change the phenotypic and molecular landscapes of mCRPC.

The analyses of DNPC tumors and the LuCaP 173.2 PDX model unexpectedly revealed the appearance of squamous cell pearls within the mass of DNPC tumor cells. RNA-Seq and staining for KRT6 confirmed the molecular nature of the squamous pearls. We hypothesize that only the most differentiated squamous carcinoma cells stain positive for KRT6 and display a cornified GSEA profile and that there exists a proliferating DNPC/squamous intermediary. Support for this hypothesis comes from RNA-Seq and IHC that shows ARLPC metastases and LuCaP 176 significantly enriched for squamous transcriptional profiles but negative for squamous pearl structures and KRT6 staining. The mechanisms of ARLPC/DNPC to squamous transition remain unclear, but future research examining the parallels between prostate and lung cancer lineage plasticity is warranted. For example, prostate and lung epithelial cells can be reprogrammed to small cell NE cancers through induction of the same transcription factor pathways (19). Moreover, lung adenocarcinomas can transition to squamous cell carcinomas through *LKB1*-loss (57). Our RNA-Seq data show no evidence *LKB1/STK11*-loss across patient samples but other mechanisms of adenocarcinoma-squamous differentiation are likely. We speculate that there are common molecular pathways driving lung and prostate cancer lineage switching. Taken together, our data demonstrate that treatment-induced ARPC-DNPC-squamous conversion is one potential pathway to bypass AR-suppression strategies.

There are currently no standard treatments for SCNPC, DNPC, and ARLPC phenotypes. However, RNA-Seq and GSEA between mCRPC phenotypes revealed biologically relevant pathways that could be further interrogated for therapeutic benefit. Significantly upregulated genes common to the AR-null and ARLPC phenotypes were enriched for cell adhesion processes, and delving into the pathway revealed CEACAM5 as a top hit. CEACAM5 has been identified as a surface marker of potential utility in directing chimeric antigen T cells in SCNPC (58), and our data reveal that this therapy could also be clinically effective against subsets of ARLPC and DNPC tumors. Moreover, upregulated genes common to ARLPC and AR-null phenotypes are enriched in immune system, inflammatory, and defense responses. Since the phenotype comparisons were relative to ARPC, these data support the notion that the immune cell content of ARLPC and AR-null tumors is strikingly different from that of ARPC tumors. Notably, DNPC-specific immune-related genes included IL8 and CXCR1, which have been reported to promote CRPC metastasis and angiogenesis (59), and genes such as TGFB and RUNX2, which support tumor growth in bone (60). Whether associated with the tumor cells, immune cells, or stromal cells, the presence of enriched immunomodulatory signaling pathways suggests that ARLPC, DNPC, and SCNPC tumors could be more receptive to immunotherapies.

Our group and others have previously demonstrated that loss of REST repressor activity promotes the SCNPC phenotype (15, 24, 61, 62). Here, we confirmed the existence of AMPC cells in vivo and in vitro and demonstrated that AMPC cells express a limited set of neuronal genes that are REST-repressed (NEURO I panel) and maintain AR signaling. Furthermore, transcriptome analysis of mCRPC and LuCaP PDX tumors and siRNA-mediated knockdown of REST in AR-expressing and AR-null cell lines provided compelling evidence that loss of REST repressor activity is critical for conversion to the AMPC/mixed phenotype but does not necessarily drive the SCNPC phenotype. We realize that siRNA treatments transiently relieve REST-mediated transcriptional repression, and that the impact of sustained REST-ablation remains to be determined. However, we hypothesize that epigenetic factors are preventing the expression of core SCNPC transcription factors (NEURO II panel of genes) that would permit SCNPC transdifferentiation in AR-null and AR-expressing cells with REST knockdown. Indeed, the epigenomes of NE and adenocarcinoma tumors are significantly different and EZH2 inhibitors have been shown to reactivate AR expression in some SCNPC models (18, 63). On the other hand, SRRM4-mediated splicing of REST and other neuronal regulators can drive ARPC-SCNPC transition (24). Our results demonstrated that SRRM4-mediated splicing of REST occurs in both AMPC and SCNPC PDX models and in AMPC VCaP cells, suggesting that SRRM4 expression alone is not sufficient to drive SCNPC conversion in all cases. Concordantly, overexpression of SRRM4 converted DU145 cells to a classical SCNPC phenotype but failed to do so in PC-3, 22Rv1, and LNCaP cells (64), implying that multiple hits to the cellular blueprint are required for complete lineage switching. Furthermore, REST directly represses SRRM4 expression and loss of REST activity has been proposed as a feed-forward mechanism for SCNPC conversion (25, 62). Whether loss of REST activity mediates increased SRRM4 expression or increased SRRM4 activity mediates loss of REST requires further examination. Nevertheless, our data clearly show that the homeostatic regulation of the SRRM4-REST axis is required for epithelial differentiation and function.

In summary, our comprehensive analysis of end-stage mCRPC highlights the use of AR and REST transcriptional programs to categorize mCRPC phenotypes in the abiraterone/enzalutamide era. In addition, the data generated in this report could be exploited through biopsy or blood-based biomarkers in future therapeutic studies to define inclusion criteria. This approach could stratify patients according to mCRPC phenotypes and account for the mCRPC disease continuum to implement targeted therapies.

Methods

Tissue acquisition. Biospecimens were obtained within 8 hours of death from patients who died of metastatic CRPC. Visceral metastases were identified at the gross level, bone biopsies were obtained according to a previously described template (65) from 16–20 different sites, and metastases were identified at a histological level. LuCaP PDX lines were established from specimens acquired at either radical prostatectomy or at autopsy, implanted, and maintained by serial passage in immune compromised male mice (66).

Cell lines. All cells were maintained at 37° C in humidified Steri-Cult CO₂ incubators (Thermo Fisher Scientific). C4-2B (gift from L. Chung, Cedars-Sinai Medical Center, Los Angeles, CA), PC-3 (ATCC), and PacMet AR-null cells (5) were maintained in RPMI-1640 Media (Gibco, Life Technologies) with 10% fetal bovine serum (Atlanta Biologicals). VCaP cells (ATCC) were maintained in DMEM (ATCC) with 10% fetal bovine serum (Atlanta Biologicals).

Transient transfections. Cells were suspended in Nucleofector Solution V (Lonza) and 5 μ L of 50- μ M ON-TARGETplus pooled REST siRNA or control siRNA (Dharmacon). Cell suspensions were electroporated using the Nucleofector II device (Lonza) and program T-027 and then replated in complete media. Forty-eight hours after transfection, cells were harvested for RNA or protein for subsequent analysis.

Immunohistochemistry. The antibodies used in this study are listed in Supplemental Table 1. Five-micron-thick sections of the TMAs were deparaffinized and rehydrated in sequential xylene and graded ethanol. Antigen retrieval was performed in 10 mM citrate buffer (pH 6.0) in a pressure cooker for 30 minutes. Endogenous peroxidase and avidin/biotin were blocked respectively (Vector Laboratories). Sections were then blocked with 5% normal goat-horse-chicken serum, incubated with primary antibody (Supplemental Table 1), incubated with biotinylated secondary antibody (Vector Laboratories), followed by ABC reagent (Vector Laboratories), and stable DAB (Thermo Fisher Scientific). All sections were lightly counterstained with hematoxylin and mounted with Cytoseal XYL (Richard Allan Scientific). Mouse or rabbit IgG was used as negative control. IHC scores were represented as values between 0–200 and were determined as previously described (15).

Immunofluorescence. Formalin-fixed, paraffin-embedded (FFPE) patient and LuCaP PDX tumors were prepared according to the above methods up to and including antigen retrieval. For cells in culture, VCaP cells were seeded on chamber slides (Nunc Lab-Tek; Thermo Fisher Scientific) in complete media 24 hours prior to fixing. Cells were fixed and permeabilized with ice-cold methanol for 10 minutes and then washed in PBS. Cells and sections were blocked for 1 hour with 5% normal goat-horse-chicken serum, incubated for 1 hour (cells) or overnight (sections) with primary antibodies in blocking buffer, washed, and then incubated with fluorescent secondary antibodies for 45 minutes in the dark. All incubations occurred at room temperature and antibodies used are listed in Supplemental Table 1. Slides were mounted using ProLong Gold Antifade Mountant with DAPI (Thermo Fisher Scientific) and then visualized and imaged at ×20 on an Olympus BX41 Fluorescence Microscope.

Immunoblot analysis. Protein extracts from LuCaP PDXs and cell lines were obtained using the Nuclear Extract Kit (Active Motif) according to the manufacturer's protocols. Quantification of total protein was determined using the ProStain Protein Quantification Kit (Active Motif) according to the manufacturer's protocols. Ten to twenty micrograms of total protein lysate was electrophoresed on 4%–15% Bis-Tris gels (Bio-Rad Laboratories) with 1× Tris/Glycine/SDS Buffer (Bio-Rad Laboratories). The proteins were transferred to PVDF that was blocked with 5% Blotting-Grade Blocker (Bio-Rad Laboratories) in TBS/0.1% Tween-20 and subsequently probed with primary and secondary antibodies (Supplemental Table 1). Proteins were visualized using Clarity Western ECL Substrate (Bio-Rad Laboratories).

RNA isolation. Total RNA was isolated from 98 tissue samples of CRPC metastases, which had been frozen in OCT (Tissue-Tek) with RNA STAT-60 (Tel-Test). Using an H&E-stained slide for each sample for orientation, 1-mm core punches of tumor were obtained. Alternatively, multiple sections enriched for tumor were cut using a Leica CM3050S cryostat. Total RNA was isolated from flash-frozen LuCaP PDX tissues or cell lines with RNA STAT-60 (Tel-Test) followed by purification with RNeasy Mini Kit (Qiagen) using the manufacturer's recommended in-solution DNase digestion (Qiagen). The purity and yield of the RNA were determined on a NanoDrop 2000 (Thermo Fisher Scientific). RNA integrity was assessed on a 2100 Bioanalyzer (Agilent Technologies).

PCR and sequencing. First-strand cDNA synthesis was performed with 1 µg RNA using an Advantage RT-for-PCR Kit (Clontech Laboratories). PCR was performed using either Platinum SYBR Green qPCR SuperMix-UDG (Invitrogen; real-time PCR) or HotStarTaq Plus Master Mix (Qiagen; PCR for sequencing) on a Rotor-Gene Q (Qiagen). PCR primers (Integrated DNA Technologies) specific for REST were adapted from Raj et al. (25). The REST 5' primer-GAGAACG-CCCATATAAATGTGAAC and 3' primer-CGGGTTACTTCATGTT-GATTAGAG were used. The PCR reaction parameters were as follows: 50°C for 2 minutes and 95°C for 2 minutes (one cycle), followed by 30 cycles (standard gels) or 40 cycles (band sequencing) at 95°C for 10 seconds, annealing/extension at T(m) for 30 seconds, and 72°C for 30 seconds; the final extension was 72°C for 7 minutes. REST and REST4 PCR products were visualized after electrophoresis on a 1.2% agarose gel. For sequencing, PCR product bands were dissected out and purified using the QIAquick Gel Extraction Kit (Qiagen). The purified product was then sequenced by Eurofins Genomics using their Standard Read sequencing chemistry.

RNA sequencing. RNA-Seq libraries were constructed from 1 µg total RNA using the Illumina TruSeq Stranded mRNA LT Sample Prep Kit according to the manufacturer's protocol. Barcoded libraries were pooled and sequenced on the Illumina HiSeq 2500 generating 50 bp paired end reads. Sequencing reads were mapped to the hg38 human using TopHat v2.1.0 (67). For PDX samples, sequences were also aligned to the mm10 mouse genome and those derived from potential contamination with mouse tissue were removed from the analysis as previously described (68). Gene level abundance was quantified from the filtered human alignments in R using the GenomicAlignments Bioconductor package (69). Differential expression was assessed using transcript abundances as inputs to the edgeR Bioconductor package in R (70). For edgeR analysis, genes filtered for a minimum expression level of at least 1 count per million reads (CPM) in at least 2 samples were used to calculate expression differences using an exact test with a negative binomial distribution, applying a significance level of 0.05 with Benjamin-Hochberg false discovery rate (FDR) adjustment. The RNA-Seq data from this report can be accessed through GEO at GSE126078 (https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi? acc=GSE126078).

Pathway analysis. Gene expression results were ranked by their edgeR statistics and used to conduct Gene Set Enrichment Analysis (GSEA) to determine patterns of pathway activity in different treatment groups. We used the curated pathways from within the MSig-DBv6.1. Gene ontology (GO) enrichment of Venn diagram groups was computed using GOrilla with default parameters (71). The target and background list option was used and gene sets with enrichment of P < 0.001 were considered significant.

Multidimensional scaling (MDS) plots. Specimens were classified according to expression of NEURO I, NEURO II, AR, and SQUAM gene signatures. ARPC and ARLPC phenotypes were differentiated based on AR or KLK3 expression (RNA-Seq) with ALRPC possessing an AR log₂ FPKM value less than 4.0 or a KLK3 log₂ FPKM value less than 2.0. Phenotypic groups were visualized using classical multidimensional scaling (MDS) calculated with the cmdscale function in R using the expression profiles of the 26 genes from the combined lists of NEURO I, NEURO II, AR, and SQUAM gene signatures. The distance metric was euclidean calculated by dist function on the columns (samples). The RNA-Seq data from the Stand Up To Cancer mCRPC cohort were accessed using dbGaP accession phs000915.v2.p2.

Statistics. Sample size for each experiment is indicated in the figure legends. Experiments were repeated a minimum of 2 times. Statistical analyses for RNA sequencing, pathway analyses, and MDS were performed as indicated using R software. The enrichment scores were calculated in R using the GSVA package using the 14 genes in the NEURO I and NEURO II gene sets for NEURO scores and a previously published set of AR-regulated genes for AR-activity scores (5, 72). Mean AR-activity scores in transfected C4-2B cells were graphed using GraphPad Prism software.

Study approval. All rapid autopsy tissues were collected from patients who had signed written informed consent under the aegis of the Prostate Cancer Donor Program at the University of Washington (73). The IRB of the University of Washington approved this study. All patient-derived xenograft experiments were approved by the University of Washington IACUC.

RESEARCH ARTICLE

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Author contributions

MPL, LGB, PSN, and CM conceived and designed the project. IMC, RC, and AK performed sequencing and bioinformatics analyses. MPL, LGB, LK, BL, YCY, and ACH conducted molecular and cell biology experiments. LDT and RMG provided pathology evaluation. HMN, EC, and CM provided biospecimens and patient-derived xenograft models. CSH, EYY, HHC, EAM, BM, MTS, DWL, and PSN consented patients for the rapid autopsy program and/or provided clinical expertise. MPL, PSN, and CM wrote the manuscript, and all authors reviewed and edited the manuscript.

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Original Study

Germline Genetic Testing in Advanced Prostate Cancer; Practices and Barriers: Survey Results from the Germline Genetics Working Group of the Prostate Cancer Clinical Trials Consortium

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Abstract

More than 10% of patients with advanced prostate cancer carry inherited genetic mutations that might amplify their response to targeted therapies, but barriers, including a shortage of genetic counselors, limit patient access to testing that would enable targeted therapy. This study of practices in nineteen US comprehensive cancer centers showed that a shortage of genetic counselors and 4 other barriers limit adoption of this important advance. Herein we also catalogue germline genetic testing practices and illuminate initiatives that might expand testing availability.

Background: Germline genetic testing increasingly identifies advanced prostate cancer (PCa) patients who are candidates for precision therapies. The Prostate Cancer Clinical Trials Consortium (PCCTC) established the Germline Genetics Working Group to provide guidance and resources to expand effective use of germline genetic testing. Materials and Methods: A 14-item questionnaire was e-mailed to academic oncologists at 43 PCCTC sites to collect information on germline genetic testing patterns, including patients considered, choice of assays, barriers slowing adoption, and actions to overcome barriers. Results: Twenty-six genitourinary oncologists from 19 institutions responded. Less than 40% (10 of 26) reported referring patients to a genetics department, whereas the remainder take personal responsibility for genetic testing and counseling; 16 (62%) consider testing all metastatic PCa patients,

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whereas 3 (12%) consider testing all patients with high-risk local disease; and 7 (27%) use multigene comprehensive pan-cancer panels, and 14 (54%) use smaller or targeted cancer gene panels. Barriers to widespread use are: (1) delayed or limited access to genetic counseling; (2) no insurance coverage; (3) lack of effective workflows; (4) insufficient educational materials; and (5) time and space constraints in busy clinics. The primary limitation was the <50% (19 of 43) response from PCCTC sites and no coverage of nonacademic cancer treatment facilities. **Conclusion:** Joint efforts by urologists, oncologists, genetics counselors, insurers, and cancer centers can accelerate implementation of integrated germline genetic services for personalized treatment and clinical trial eligibility for PCa patients.

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Introduction

A significant number of prostate cancer (PCa) cases have a heritable component. Germline DNA damage repair (DDR) defects are present in >10% of patients who develop metastatic PCa (mPCa), with defects in breast cancer (BRCA2) found in more than 5% and defects in BRCA1, ataxia-telangiectasia mutated (ATM), and checkpoint kinase 2 genes each found in 1% to 2%. Prevalence of germline mutations in DDR genes in men with mPCa exceeded the observed 5% prevalence in men with localized PCa and 3% prevalence in men without a known cancer diagnosis.^{1,2} In recent years, the treatment landscape for mPCa has been refined by the discovery of DDR deficiency as predictive biomarkers for response to targeted therapies. For example, the presence of homologous recombination deficiency might predict response to poly (adenosine diphosphate-ribose) polymerase inhibitors as well as to other DNA-damaging chemotherapy agents (platinum chemotherapy).³⁻⁶ Similarly, the presence of germline mutations in mismatch repair (MMR) genes might identify candidates for treatment with immune checkpoint inhibitors.7-10 Thus, it has become progressively important to assess practice patterns and needs regarding germline genetic testing and counseling for men with PCa. Urologists are increasingly ordering germline testing for their PCa patients in light of recent evidence that BRCA1/2 and ATM mutation status is associated with grade reclassification or PCa patients undergoing active surveillance.¹¹ Urology involvement in germline genetic testing will grow as the area evolves to include high-risk localized (HRL) and earlier disease states.¹²⁻¹⁴

The Germline Genetics Working Group (GGWG) of the Prostate Cancer Clinical Trials Consortium (PCCTC) was established in June 2017 in response to the need to better inform and advise clinicians of the increasing evidence that germline alterations in DDR genes might identify additional options for PCa therapy. The objectives of the GGWG are to work together with clinicians and researchers around topical challenges of treatment selection and eligibility for trials of investigational therapeutics, and to enable more streamlined and effective use of germline genetic testing in PCa patients in the face of a rapidly evolving genetics-informed therapeutic landscape.

In June 2018, the GGWG produced a white paper that presented a framework to address unique challenges and therapeutic opportunities regarding germline testing for precision therapy in patients with advanced PCa and identified areas of future research.¹⁵ In the white paper the GGWG recommended that clinicians: (1) consider expanding germline genetic testing beyond cancer risk assessment to inform treatment selection and eligibility for clinical trials; (2) work with genetic counselors to ensure pretest informed decision-making through education or counseling and post-testing counseling; and (3) where appropriate, ensure mechanisms for offering cascade germline genetic testing to family members. However, barriers and challenges to broader implementation of these recommendations require attention.

To elucidate practice patterns and challenges in germline genetic testing of PCa patients in oncology, the GGWG surveyed medical oncologists from institutions who were members of the PCCTC. Herein, we report survey data from responding oncologists from 19 PCCTC cancer centers identifying commonalities and differences in practice patterns. The survey results were used to support recommendations for addressing barriers to germline testing for men with PCa and are placed in the context of current National Comprehensive Cancer Network (NCCN) guidelines for genetic testing of PCa patients.

Materials and Methods

Survey

A 14-question survey was developed by the GGWG to capture data on the practice patterns and needs of oncologists at PCCTC institutions. The survey was refined after pilot testing and then distributed to oncologists at their institutions using RedCap, a Web-based survey tool, with an e-mail (December 20, 2017) asking members to complete the survey and to ask other investigators at their institutions to respond. A reminder e-mail was sent on January 16, 2018 to GGWG members who had not completed the survey. PCCTC principal investigators were reminded of the survey during 2 sequential monthly conference calls that took place between the 2 e-mail survey distributions (December 21, 2017 and January 8, 2018).

The survey questions offered multiple choice answer selections on personal practices around genetics services, on patient characteristics oncologists consider for germline testing (metastatic disease, advanced stage, family history), on cascade genetic testing processes, and on gene panels. The remainder were free-form questions asking for clarifications of answers to the multiple-choice questions and also asking participants to describe their approaches to integrating

Table 1Cancer Centers Providing Germline Genetic Testing Survey Responses					
Cancer	Responses				
Fred Hutc	3				
Johns Hoj Center	3				
Lurie Corr	2				
Rush Univ	2				
Weill Corr	2				
Beth Israe	1				
Carbone (1				
Dana-Fart	1				
Duke Com	1				
Jonsson (1				
Lineberge	r Comprehensive Cancer Center	1			
Masonic (1				
Memorial	1				
Moores C	ancer Center	1			
Oregon He Institute	1				
Sidney Kir University	1				
University Center	1				
Wayne Sta	1				
Yale Canc	1				

germline testing with therapeutic clinical trials and to cascade testing. The full survey is shown in Supplemental Appendix 1 in the online version).

Analysis

Data were gathered in the RedCap package and exported to a comma-separated value file. Data were imported into Excel (Version 16.18, Microsoft Corp, Redmond, WA), where they were summarized, tabulated, and graphed.

Results

Between December 20, 2017 and April 3, 2018, representatives of the 43 PCCTC participating and affiliate sites received the germline genetic testing current practice survey and an e-mail encouraging redistribution to institutional colleagues, and 26 PCa oncologists from 19 sites (44%) completed the survey (Table 1).

Personal Practices of PCa Oncologists Regarding Genetics Services for PCa Patients

Whereas 10 of 26 (38%) participating oncologists reported that they refer patients to a separate department for genetic testing and counseling, more than half reported taking personal responsibility for some or all genetic education and testing of their patients. Four (15%) reported personally performing pretest counseling, ordering germline testing, and performing post-test counseling. Those who reported using a combination of approaches generally referred to

Figure 1 Provider Considerations of Germline Testing Among Men With Prostate Cancer. (A) Men With Metastatic Prostate Cancer (PCa) Considered for Germline Testing. (B) Men With High-Risk Localized (HRL) and Biochemically Recurrent (BCR) PCa Considered for Germline Testing. (C) Factors Affecting Decision to Test. (D) Factors Affecting Decisions on Results



Abbreviations: + = positive results; GC = genetic counselor; N = no; NC = no post-test genetic counseling; NCCN = National Comprehensive Cancer Network; NT = no germline genetic testing; VUS = variant of uncertain significance; Y = yes.

Germline Genetic Testing in Prostate Cancer



comprehensive and limited) explained that lack of insurance or limited patient capacity to pay sometimes causes them to select a more limited panel (eg, Sites that listed multiple approaches genetic counselors for post-test counseling. Variation in practice appears to depend on factors such as: (1) patient's insurance coverage for genetic testing and counseling; (2) availability of testing and counseling resources within the oncology group; (3) testing and counseling resources in a separate genetics department; and (4) wait times for referrals.

Patients Considered for Germline Genetic Testing

Metastatic PCa. All 26 participating oncologists reported considering some mPCa patients for germline genetic testing: 16 (62%) reported considering all mPCa patients; 7 (27%) considered testing mPCa patients with a family history and/or who were eligible for clinical trials; and 3 (12%) considered testing only for patients with a family history for germline genetic testing (Figure 1A).

High-Risk Localized PCa Patients and Non-mPCa. More than half of the participating oncologists, 14 of 26 (54%), considered germline genetic testing for some PCa patients with HRL or nonmPCa (nmPCa), whereas 12 (46%) did not consider germline testing for these patients. Three (12%) reported testing all HRL/ nmPCa patients; 3 (12%) reported considering testing only for patients with a family history for germline genetic testing; and 8 (31%) reported considering testing only those with a family history of cancer (Figure 1B).

Operational Barriers Faced by Oncologists Considering Germline Genetic Testing for PCa Patients

On the basis of participant responses and free text comments, 5 barriers in streamlining genetic testing were identified: access to genetic counselors, insurance coverage and cost, clinic workflow, time and space availability, and access to resources for provider and patient education. Figure 1C shows the role of those operational barriers and the flow of considerations on whether to conduct germline genetic testing reported by responding oncologists, whereas Figure 1D shows how referral decisions are made on the basis of those results.

Reported Germline Testing Approaches

Participating oncologists reported their approaches for germline cancer predisposition testing. Seven of 26 (27%) reported using only "comprehensive pan-cancer panels," whereas 14 (54%) listed only "expanded cancer panels (eg, Lynch and *BRCA1/2* and hereditary breast and ovarian cancer genes)," and 4 others (15%) reported using more than 1 type of panel. One participant did not answer this question (Table 2).

Resources for Patients and Family Members Regarding Genetic Testing

The GGWG aggregated a list of Web sites that it has found valuable for educating patients and their families about germline genetic testing for PCa (Table 3). Two participants reported they are developing local resources (a video and an information sheet for patients).

Discussion

The relevance of germline genetic testing in PCa is emerging today as it did in breast cancer 3 decades ago, although in PCa it is

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Table 3 Web Resources for Educating PCa Patients and Families About Germline Genetic Testing							
Source	URL	Content					
Color	https://www.color.com/learn/can-cancer-be-inherited	Patient-friendly discussion and data about cancer due to inherited (germline) genetic mutations					
Dana Farber	https://www.dana-farber.org/cancer-genetics-and-prevention/ videos/	Videos explaining topics in cancer genetics and testing					
Invitae	https://www.invitae.com/en/patients/genetic-diagnosis/	Brief descriptions of genetic testing					
Memorial Sloan Kettering	https://www.mskcc.org/cancer-care/risk-assessment-screening/ hereditary-genetics/genetic-counseling/inherited-risk-prostate	Very brief discussion of inherited risk of PCa					
National Society of Genetic Counselors	https://www.nsgc.org/	Comprehensive guidance for patients, including help findi counselors					
Prostate Cancer Foundation	https://www.pcf.org/news/genetic-screening-guidelines-for- prostate-cancer/	High-level overview of genetics-related knowledge helpful to patients with PCa and their families					
	https://www.pcf.org/patient-resources/family-cancer-risk/ genetic-testing-prostate-cancer/	Recommendation to speak with physician about whether patients need genetic testing, with 5 more detailed subpages					
Sidney Kimmel Cancer Center of Thomas Jefferson University	https://prostategenetics.jeffersonhealth.org/	PCa-focused and patient-friendly, Web-based resource explaining genetic counseling, genetic testing, family hist genes, and cancer risks					

Abbreviation: PCa = prostate cancer.

accompanied by concurrent therapeutic relevance. These rapid and exciting changes have resulted in challenges illustrated by the 2018 PCCTC GGWG survey of medical PCa oncologists at academic institutions in the PCCTC consortium, around their practices in germline genetic testing of PCa patients. The survey identified common themes across 19 institutions as well as substantial

Table 4 Therapeutic and Delivery Model Clinical Trials in PCa With Relevance for Germline Genetic Eligibility Criteria						
Phase	Title	Disease State	Abbreviated Title	Clinicaltrials.gov		
Therapeutic Trials						
III	Study of Olaparib (Lynparza™) Versus Enzalutamide or Abiraterone Acetate in Men With Metastatic Castration-Resistant Prostate Cancer (PROfound Study)	mCRPC	PROFOUND	NCT02987543		
Ш	A Study of Rucaparib Versus Physician's Choice of Therapy in Patients With Metastatic Castration-resistant Prostate Cancer and Homologous Recombination Gene Deficiency	mCRPC	TRITON3	NCT02975934		
II	An Efficacy and Safety Study of Niraparib in Men With Metastatic Castration-Resistant Prostate Cancer and DNA-Repair Anomalies	mCRPC	GALAHAD	NCT02854436		
II	A Study of Rucaparib in Patients With Metastatic Castration-resistant Prostate Cancer and Homologous Recombination Gene Deficiency	mCRPC	TRITON2	NCT02952534		
II	A Study of Talazoparib in Men With DNA Repair Defects and Metastatic Castration-Resistant Prostate Cancer	mCRPC		NCT03148795		
II	Olaparib in Men With High-Risk Biochemically-Recurrent Prostate Cancer Following Radical Prostatectomy, With Integrated Biomarker Analysis	BCR		NCT03047135		
II	Abiraterone/Prednisone, Olaparib, or Abiraterone/Prednisone + Olaparib in Patients With Metastatic Castration-Resistant Prostate Cancer With DNA Repair Defects	mCRPC	BRCAaway	NCT03012321		
Pilot	Docetaxel and Carboplatin in Treating Patients With Metastatic, Castration Resistant Prostate Cancer Containing Inactivated Genes in the BRCA 1/2 Pathway	mCRPC	ABCD	NCT02598895		
II	Docetaxel and Carboplatin for Patients With mCRPC and DNA-Repair Deficiencies	mCRPC	V-ABCD	NCT02985021		
II	Trial of Rucaparib in Patients With Metastatic Hormone-Sensitive Prostate Cancer Harboring Germline DNA Repair Gene Mutations	mHSPC	TRIUMPH	NCT03413995		
Delivery Model Trials						
NA	Evaluating an Alternative Clinical Genetics Cancer Care Delivery Model: A Pilot Study of Patient Outcomes	PCa		NCT02917798		
NA	Genetic Evaluation of Men (GEM)	PCa	GEM Registry	NCT03076242		
NA	Genetic Counseling Processes and Outcomes Among Males With Prostate Cancer (ProGen)	PCa	ProGen	NCT03328091		
NA	Genetic Testing for Men With Metastatic Prostate Cancer	mPCa	GENTIeMEN	NCT03503097		

Abbreviations: BCR = biochemical recurrence; mCRPC = metastatic castration-resistant prostate cancer; mHSPC = metastatic hormone-sensitive prostate cancer; mPCa = metastatic prostate cancer; PCa = prostate cancer.

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variation in those practices. Five barriers to obtaining genetic testing were identified: lack of timely access to genetic counselors, lack of insurance coverage or high patient out-of-pocket costs, lack of integrated clinic workflow, time and space constraints, and insufficient resources for provider and patient education. Our survey showed that more than half of oncologists reported taking part or full responsibility for germline genetic testing and education/ counseling, despite the fact that most oncologists are not trained in genetic counseling.¹⁶ Nearly 40% (10 of 26) of the participating oncologists reported that among mPCa patients, they considered germline genetic testing mainly for patients with a family history of cancer and those who were eligible for a clinical trial with genetic eligibility criteria, rather than all mPCa patients. Germline testing results are increasingly important for consideration of clinical trial eligibility. PCCTC sites reported 10 therapeutic trials for PCa patients with relevance to germline mutations and 4 trials testing new models of genetics delivery in PCa (Table 4). Similarly, a little more than half of respondents reported considering germline genetic testing for patients with HRL PCa and nmPCa. These responses might reflect a period of limited resources and substantial logistical barriers and the need for triaging and prioritization of genetic counseling and testing until barriers can be better addressed.

At the time the survey was distributed, the NCCN guidelines did not include recommendations for germline testing for most PCa patients. On the basis of recent data of germline mutations in men with PCa, before all GGWG survey responses were returned, NCCN prostate guidelines (version 4.2018) were expanded to recommend consideration of germline genetic testing for most metastatic and HRL PCa patients.¹⁷ Thus, the survey captured change in action.

The current guidelines recommend consideration of germline testing for all patients with high-risk and very high-risk local disease, regional disease, and metastatic disease. Further, with more sensitive techniques for early identification of metastatic disease such as prostate specific membrane antigen, fluciclovine,¹⁸ and choline,^{19,20} more patients might be classified as metastatic than in the past, further increasing the numbers of patients to be considered for germline genetic testing. This expansion of patient populations to be considered for genetic testing, together with the barriers reflected in our findings, highlight the need for dedicated education and training for radiation oncologists, urologists, and medical oncologists. In the localized disease setting with risk levels that are very low, low, favorable intermediate, and unfavorable intermediate, the NCCN prostate guidelines suggest consideration for germline testing on the basis of a strong family history of PCa and/or other primary cancers, or for patients with a relative with a known familial cancer risk syndrome.

The current NCCN prostate guidelines also suggest that patients whose tumor testing is positive for microsatellite instability-high or deficient-MMR (indicating potential use of pembrolizumab in treatment for metastatic castration-resistant PCa (mCRPC), also be referred for genetic counseling to assess for the possibility of Lynch syndrome. Finally, the current NCCN guidelines recommend that physicians consider testing tumors of patients with mCRPC for germline and somatic mutations in *BRCA1*, *BRCA2*, *ATM*, partner and localizer of *BRCA2* and Fanconi anemia complementation group A genes.

Approximately half of survey participants indicated that they would refer patients for genetic counseling and dedicated confirmatory germline testing if a tumor mutation was potentially germline in nature (thus with family counseling implications²¹) consistent with the recommendation in the GGWG white paper.¹⁵ As tumor sequencing for targeted treatment opportunities increase in PCa, the likelihood of identifying mutations that are potentially germline might increase, raising the need for distinct workflows to address this specific clinical scenario.

Several respondents noted that patient willingness to undergo germline genetic testing could be affected by concerns about genetic discrimination for life, disability, and long-term care insurance. The Genetic Information Nondiscrimination Act (GINA) of 2008²² provides protection from genetic discrimination in health insurance and employment in most employment scenarios, but does not cover life insurance, long-term care, disability insurance, Indian Health Service, federal employees enrolled in the Federal Employee Health Benefits Plan, and other specific Veterans Administration or US military plans. Because of these gaps in protection by the GINA law and potential changes over time, patients approached about germline testing need to consider these issues and their own financial situations before proceeding with germline testing. Thus, providers and patients can benefit from educational and practiceready resources to help address the need to discuss genetic discrimination laws.

There are some limitations to consider in our results. Urologists were not surveyed, because metastatic disease has been a key driver of genetic testing up to the present time. However, because guidelines for testing are expanding to earlier-stage disease, including urologists in future surveys will add important information. Our analysis does not account for institutional limitations that might have informed physician decisions regarding whom to test. In addition, there were site-specific differences in clinical trial availability with germline genetic eligibility criteria, including in the nmPCa setting which would have influenced consideration of genetic testing for that group. Another limitation is the response rate (oncologists from only 19 of 43 PCCTC sites responded), and the composition of respondents being largely oncologists with specific focus on PCa in academic centers. Nevertheless, we believe that the general concepts around the clinical need for better integration of germline genetic testing in PCa care and the current barriers to implementation will be broadly applicable across oncology practice settings.

Conclusion

The NCCN and other professional organizations advocate informed decision-making for patients in the pretest setting.²³⁻²⁷ Research to improve delivery of pretest education and optimization of informed decision-making is key to streamlining genetic testing for men with PCa. In the post-test setting, discussion with a genetic counselor is important for patients with germline mutations,

variants of uncertain significance, and with no mutations but with a family history of cancer to ensure understanding of results and appropriate follow-up with regard to additional cancer screening and cascade testing recommendations. Physicians ordering genetic testing need to be well versed in cancer risk guidelines for screening, genetic results interpretation, GINA laws, and population-level cancer screening guidelines. Although referral to a genetic counselor is preferred when possible, there is a recognized shortage of genetic counselors that is predicted to worsen,^{28,29} suggesting a role for subspecialty oncologists with training in genetics as well as for genetics training for oncology providers who perform aspects of genetic counseling themselves.³⁰ Registries that include germline data, family history, treatments, and outcomes such as those being developed in the GEM (Genetic Evaluation of Men), GENTLle-MEN (Genetic Testing for Men With Metastatic Prostate Cancer), and ProGen (Genetic Counseling Processes and Outcomes Among Males With Prostate Cancer) trials, along with systems to address barriers to genetic testing, will help inform future guidelines and facilitate integrated genetic testing and counseling services into busy clinical practices.

Clinical Practice Points

- In the context of an evolving therapeutic landscape for men with mPCa and expanding NCCN guidelines for germline testing for patients with earlier stage disease, oncologists and urologists will increasingly need to consider incorporating genetic education, counseling, and germline testing for men with PCa.
- Providing guideline-concordant care now requires that practices and institutions prioritize including germline genetic testing as part of optimal care delivery.
- Physicians, advanced practice providers, genetic counselors, practice managers, and other team members must work in a concerted manner to overcome these barriers in practice- and resource-specific ways for this evolving care model.

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Disclosure

The authors have stated that they have no conflicts of interest.

Supplemental Data

The supplemental appendix accompanying this article can be found in the online version at https://doi.org/10.1016/j.clgc.2019. 04.013.

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Supplemental Appendix 1

Survey Questions and Germline Genetic Testing-Related Therapeutic Clinical Trials

- 1. What are your current personal practices around genetics services?
- 2. If you practice a combination of approaches, very briefly, how would you describe your general approach for an individual patient?
- 3. What prostate cancer patient population(s) are you currently considering for germline genetic testing? Select all that apply.
 - a. Men with metastatic PCa (all)
 - b. Men with metastatic PCa (trial candidates)
 - c. Men with metastatic PCa (with family history of cancer)
 - d. Men with high-risk localized or nonmetastatic PCa (all)
 - e. Men with high-risk localized or nonmetastatic PCa (trial candidates)
 - f. Men with high-risk localized or nonmetastatic PCa (with family history of cancer)
 - g. PCa patients with family history of PCa and other cancers
 - h. Other criteria (see next question)
- 4. If you are testing a combination of the groups listed above, very briefly, how would you describe your decision process for an individual patient?
- 5. What is your personal/institutional mechanism or system to integrate germline results with therapeutic clinical trials?
- 6. What is your personal/institutional mechanism for cascade testing of pathogenic/likely pathogenic germline mutation carriers?
- 7. Cascade genetic testing refers to offering genetics referral to relatives such as siblings and children of patients found to

carry a germline mutation (pathogenic variant) in a cancer risk gene. This might provide valuable information for family members regarding their own risk and options for cancer screening and prevention. Is the cascade genetic testing process in your practice systematized to attempt to capture screening for other cancers and to facilitate cascade testing of family members?

- 8. What is your general approach to germline cancer predisposition testing? (If you select more than one, please explain further in the question that follows.)
 - a. Specific individual genes (eg, BRCA1, BRCA2)
 - b. Limited prostate cancer-specific panel
 - c. Expanded cancer panel (eg, Lynch and *BRCA1/2* and hereditary breast and ovarian cancer genes)
 - d. Comprehensive, pan-cancer panel
 - e. Clinical trial-focused panel
 - g. Reflex, single-site if tumor sequencing suggests germline finding
- 9. Please add any comments or details about your approach here.
- Do you have any clinical trials around the delivery of genetic testing at your institution open or anticipated? (See Responses in Table 4.)
- 11. Do you have suggestions for patient/family resources to recommend to patients for more information?
- 12. What would be most immediately helpful to you as a resource for germline genetics that the PCCTC Working Group can help develop?
- 13. List any specific concerns, frustrations, worries, barriers, and challenges you would like to share around germline genetics and prostate cancer.
- 14. What is your name/institution?

Germline and Somatic Mutations in Prostate Cancer for the Clinician

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ABSTRACT

It is increasingly important for clinicians involved in the management of prostate cancer to understand the relevance of heritable (germline) mutations that, for select patients, affect prostate cancer risk and cancer biology, and acquired (somatic) mutations that occur in prostate cancer cells. In the advanced disease setting, mutations in homologous recombination repair genes (eg, BRCA1, BRCA2, ATM, CHEK2, PALB2) suggest candidacy for platinum chemotherapy and PARP inhibitor trials. Similarly, microsatellite instability and mismatch repair deficiency, which may arise in the setting of MLH1, MSH2, MSH6, and PMS2 mutations, suggest potential vulnerability to PD-1 inhibitors. Germline genetic testing has potential importance in the treatment and assessment of familial risk, and tumor-directed somatic sequencing may guide treatment decision-making. This review provides clinicians with knowledge of basic genetic terminology, awareness of the importance of family history of cancer (not limited to prostate cancer), contrasts between the different but potentially related objectives of germline versus somatic testing of tumor tissue, and indications for genetic counseling. Specific clinical scenarios, objectives of testing, and nature of the assays are reviewed. Germline and somatic mutations of known and potential relevance to prostate cancer are discussed in the context of treatment options, and algorithms to assist clinicians in approaching this area are proposed.

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^aDivision of Medical Oncology, University of Washington, and ^bDivision of Clinical Research, Fred Hutchinson Cancer Research Center, Seattle, Washington; ^cRobert H. Lurie Comprehensive Cancer Center of Northwestern University, Chicago, Illinois; and ^dHelen Diller Family Comprehensive Cancer Center, University of California, San Francisco, San Francisco, California. Expansion of genomic technologies and declining costs of next-generation sequencing (NGS) have led to rapid changes in germline and somatic genetic testing that must be considered in everyday clinical practice. Similar technology is used in direct-to-consumer "recreational" testing for understanding genealogic origins from an individual's DNA. Tests for primary prostate cancer to determine risk of recurrence and inform decisions regarding active surveillance are addressed elsewhere.1-3 This review focuses on testing ordered by medical providers to determine heritable risk of cancer and guide treatment options in the advanced disease setting, provides a framework for understanding current options and uses for genetic testing, and considers data supporting genetic testing recommendations in the latest version of the NCCN Clinical Practice Guidelines in Oncology (NCCN Guidelines) for Prostate Cancer, version 2.2019 (in this issue).4

Germline DNA refers to the constitutional DNA of an individual resulting from the unique combination of genetic material, half from mother (egg) and half from father (sperm). (A list of key terms and definitions is provided in supplemental eTable 1, available with this article at JNCCN.org). Germline DNA is present in every cell of the body, and specific genetic changes have a 50/50 chance of being passed on to biologic children. Germline genetic testing can identify presence of inherited pathogenic variants (also called *mutations*) in genes associated with cancer risk. Testing can be performed on lymphocyte DNA from blood or a combination of lymphocyte and buccal cells from saliva, because germline DNA is nearly identical in all nucleated cells of an individual. Identification of a germline mutation associated with cancer susceptibility should involve a genetic counselor to ensure that medical, psychologic, legal, and ethical consequences for the patient and relatives are explained. Germline testing also can have important implications regarding treatment options for some patients with cancer.

In prostate cancer, the percentage of patients with germline mutations in DNA repair genes ranges from

See JNCCN.org for supplemental online content.

4.6% in localized disease to 11.8% to 16.2% in metastatic disease.^{5,6} Patients with a strong pattern of cancers found on a comprehensive family history should be evaluated by a genetic counselor, who may recommend specific tests (Figure 1). In addition, if a germline mutation is identified, genetic counselors ensure appropriate education and testing for family members who may also carry the same gene mutation, a process known as "cascade genetic testing."

Sequencing DNA for tumor-acquired genetic changes (also referred to as *somatic mutations*) requires prostate tumor material: cancer-containing biopsies, surgical material, or, in some cases, circulating tumor cells or circulating tumor DNA (ctDNA) in the blood. Testing of tumor tissue from primary or metastatic sites or blood may help guide treatment options in the advanced disease setting. A number of specific mutations are summarized in Table 1, although the base of knowledge is evolving rapidly.

Somatic mutations observed in tumor tissue may change over time due to genetic instability and selective pressure from therapy. Thus, repeat testing of tumor DNA may be appropriate during the disease course. Findings in archival primary tissue obtained years earlier may differ from those in a metastatic site, although detection of certain relevant mutations is possible early in tumorigenesis. Other potential limitations include



Figure 1. Algorithm for inherited/germline and tumor/somatic mutation testing in men diagnosed with prostate cancer. Abbreviations: dMMR, mismatch repair deficiency; HRD, homologous recombination DNA repair; MSI-H, microsatellite instability-high; PV/LPV, pathologic variant or likely pathologic variant.

Table 1. Genes with Established or Emerging Potential Clinical Actionability, Germine vs Somatic							
Gene	Association With Increased PC Risk	Prevalence of Germline Mutations in mPC⁵	Prevalence of Germline Mutations in PC With Clinical Suspicion ¹¹	Consideration of DNA-Damaging Agents: PARPi Trials, Platinum ⁴⁰	Consideration of Immune Checkpoint Inhibitors: PD-1 Inhibitors		
ATM	Х	1.6%	2.0%	Х			
ATR		0.3%	Not evaluated				
BRCA1	Х	0.9%	0.7%	Х			
BRCA2	Х	5.4%	4.7%	Х			
BRIP1		0.2%	0.3%				
CDK12 (somatic only)		-	-		Х		
CHEK2	Х	1.9%	2.9%	Х			
FAM175A		0.2%	Not evaluated				
FANCA		_	Not evaluated	Х			
HOXB13 (germline only)	Х	Not evaluated	1.1%				
MLH1	Х	—	0.06%		Х		
MRE11A		0.14%	Not evaluated				
MSH2	Х	0.14%	0.69%		Х		
MSH6	Х	0.14%	0.45%		Х		
NBN	а	0.3%	0.32%	Х			
PALB2	а	0.4%	0.56%	Х			
PMS2	Х	0.3%	0.54%		Х		
RAD51C		0.14%	0.21%				
RAD51D		0.4%	0.15%				

Abbreviations: mPC, metastatic prostate cancer; PARPi, PARP inhibitors; PC, prostate cancer. *Emerging/Limited data.

variance in tumor content and purity, and sensitivity and specificity of detecting tumor-specific mutations. Tumor-based testing has the potential to identify germline mutations that have implications for inherited cancer predisposition.^{7,8} Tumor testing should never be used to substitute for germline testing because of the risk for false-positives and false-negatives due to variation in bioinformatics and reporting between commercially available tests. If somatic testing identifies a mutation in a gene associated with cancer predisposition (eg, BRCA2), referral to a genetic counselor for dedicated, confirmatory germline testing is indicated.

Family and Personal History of Cancer

Family history of cancer remains a foundation of genetic risk assessment, and inquiring about prostate and nonprostate cancers is critical to a complete assessment for possible inherited cancer risk (supplemental eTable 2).5 In particular, cancers of the breast (especially in men or those diagnosed at a young age), ovary, pancreas, and melanomas should be noted, given their known association with mutations in BRCA1/2.9 However, other cancers, such as mesothelioma, should also be noted.10 Importantly, family history is necessary but not sufficient for identifying all germline carriers.5

In a recent study of 3,607 men diagnosed with prostate cancer who underwent genetic testing between 2013 and 2018, 17.2% were found to have germline mutations and 37% would not have met criteria for testing from the NCCN Guidelines for Genetic/Familial High-Risk Assessment: Breast and Ovarian.9 However, the dates spanned a period when guidelines were changing (consideration of genetic testing in individuals with a personal history of metastatic prostate cancer was not incorporated until 2017), and therefore the tested population was likely influenced by clinical suspicion based on family history even if they did not meet contemporaneous testing guidelines.¹¹ The argument that all men with prostate cancer should be tested is thought-provoking, but costeffectiveness and actionability of widespread genetic testing in early, low-risk prostate cancer settings without other risk factors remain unclear, and short-term unintended consequences include clinical confusion and lowvield depletion of limited genetic counseling resources.

In contrast, clinical predictors of germline status, such as metastatic stage⁵ or intraductal histology,^{12,13} emerging data about ductal histology,^{14,15} and/or history of second or multiple primary cancers at younger age¹⁶ may help prioritize candidates for testing, because each has been independently associated with the presence of germline DNA repair mutations. The biochemically recurrent population is heterogeneous, although application of advanced modern imaging such as C-11 choline and F-18 fluciclovine PET scans may help distinguish patients with indolent versus occult metastatic disease. Figure 1 illustrates the interaction between clinical disease features, family history, and pathology to determine who should be offered germline and/or somatic testing and genetic counseling.⁴

Genetic Counseling

Genetic counselors play an essential role in many aspects of the genetic testing process, but particularly in educating patients and family members, deciding on appropriate testing when there is strong family history, guiding accurate communication of medical information to family, and addressing psychosocial aspects of testing.

Risk assessment and pretest genetic counseling have been performed traditionally by genetic counselors, but access and long wait times can hamper time-sensitive testing that may inform treatment options in advanced disease. Ongoing studies are exploring novel delivery models for genetic services to balance time sensitivity with responsibility for informed consent, pretest education, and posttest follow-up (ClinicalTrials.gov identifiers: NCT02987543, NCT3328091, and NCT03503097).

Figure 1 illustrates the points in care at which genetic counseling is essential: (1) when there is a strong family history of cancer to ensure appropriate testing is ordered and that posttest communication to family is accurate; (2) after a germline pathogenic variant (mutation) is identified to ensure cascade testing; (3) when somatic testing uncovers a mutation that is potentially germline in nature; or (4) if the patient displays any indication of stress, distress, or unanswered questions. Providers should work closely with their genetics colleagues to develop systems that address patient needs with thoughtful stewardship of local genetics resources.

Genetic Testing

Choice of which germline test to use is beyond the scope of this review, although a number of commercial tests are available and typically use blood or saliva. There is variation in insurance coverage and out-of-pocket costs, although with assistance programs and competitive pricing, patient costs can often be limited to several hundred dollars or less. If genetic testing is being performed in the context of advanced prostate cancer, *BRCA1*, *BRCA2*, *ATM*, *PALB2*, *CHEK2*, *MLH1*, *MSH2*, *MSH6*, and *PMS2* should be included due to potential treatment implications, although this list is expected to be refined over time. In specific research or clinical contexts, a larger gene panel may be appropriate. For example, *HOXB13* is a prostate cancer risk gene that does not have clear therapeutic implications in advanced disease at this time, but which should be included if heritable prostate cancer risk is part of the question.⁴ Similarly, the gene list to consider may be larger for a somatic tumor gene panel and extend beyond cancer risk genes.

Potential outcomes for germline testing include identification of a mutation (pathogenic or likely pathogenic variant), which may suggest additional prostate cancer treatment options and clinical trials and inform risk of other cancers. This result would also indicate a 50/50 chance that first-degree relatives inherited the same risk gene and thus would prompt a recommendation for the patient to share this information (including a copy of test results) with relatives and for referral of family members to genetic counseling for cascade genetic testing. Single-site testing for a specific mutation is typically covered by insurance and is less expensive.

Another potential outcome is a variant of uncertain significance (VUS), which indicates that available data in the field were insufficient to characterize the finding as either benign or pathogenic at the time of test interpretation. A VUS result should not be used to direct clinical management. Research studies are available to help reclassify VUS, and these can be discussed with a genetic counselor.¹⁷ In one study, 7.7% of VUS results were reclassified: 91% as benign/likely benign and 9% as pathogenic/likely pathogenic.¹⁸

An outcome could also be that no mutations were identified (a benign result). Failure to identify a single, inherited cancer risk—associated mutation does not obviate an increased risk of prostate cancer to family members if there is a strong family history. If testing is negative (benign, with no mutations) or identifies a VUS, the clinical family history should be used to guide cancer screening for family members. Although tempting, VUS—including and especially in *BRCA1/2*—should not be used for medical management, although follow-up with genetic counseling and consideration of research opportunities, such as registries and variant reclassification studies, are encouraged.

Individuals found to have germline pathogenic (or likely pathogenic) variants must see a genetic counselor for counseling, guidance on communication to family, and appropriate cascade genetic testing that extends genetic testing to other family members (https://www. nsgc.org/findageneticcounselor). Providers should also be aware that telehealth-, phone-, and new technologybased genetic counseling services may be an additional option for patients.

Prostate Cancer Risk

For germline BRCA2 mutation carriers, the relative risk of developing prostate cancer by age 65 years is estimated to be 2.5- to 8.6-fold compared with noncarriers.¹⁹ In a recent study, lifetime risk of prostate cancer by age 80 years was reported between 19% and 61%, and 7% and 26% for carriers of BRCA2 and BRCA1 mutations, respectively.20 Retrospective studies have shown that men with BRCA2 mutations present at a younger age with higher Gleason grade tumors, higher rates of nodal involvement and distant metastases at diagnosis, and higher prostate cancer-specific mortality.^{21,22} BRCA1,²³ ATM,²⁴ CHEK2,^{25,26} and PALB227 also are involved in homologous recombination DNA repair and have been associated with increased prostate cancer risk, although these germline mutations have fewer data available and suggest less apparent relative risk of developing prostate cancer compared with BRCA2.5,28 Germline mutations in the mismatch repair (MMR) genes MLH1, PMS2, MSH2, and MSH6 are associated with Lynch syndrome, an inherited condition that predisposes individuals to an increased risk of developing many different types of cancers, including colorectal, endometrial, and gastrointestinal, often at a young age.²⁹ Several studies suggest a modest increased risk of prostate cancer in patients with Lynch syndrome,^{30,31} and germline MMR gene mutations have been seen in the metastatic setting.⁵ HOXB13 G84E is a germline variant associated with increased risk of developing prostate cancer, but this variant is not clearly associated with increased disease aggressiveness nor should it influence treatment decision-making.32-34 Emerging data suggest that NBS1 (also called NBN),³⁵ FANCA,³⁶ and other DNA repair genes are associated with increased prostate cancer risk and choice of treatment, but further studies are needed before clinical action is warranted.

Screening Recommendations for Carriers of Pathogenic Germline Mutations

Screening recommendations have not been established for men with pathogenic germline mutations associated with increased prostate cancer risk. The ongoing IMPACT study is evaluating the role of targeted prostate-specific antigen (PSA) screening in men with *BRCA1/2* mutations (ClinicalTrials.gov identifier: NCT00261456). Preliminary results support yearly PSA screening in men with *BRCA2* mutations aged 40 to 69 years.³⁷ NCI's recently opened Men at High Genetic Risk for Prostate Cancer trial incorporates annual PSA testing and regular digital rectal examination and prostate MRI (NCT03805919). If clinical trial participation is not available, annual PSA measurement for carriers of high-risk mutations should begin at age 40 years (Figure 2). Men with PSA levels greater than the median age-adjusted PSA ranges^{3,38,39} may consider prostate biopsy, which may be MRI/ultrasound fusion—guided.

Therapeutic Implications of Genetic Testing

Prostate tumors can now be sequenced for mutations that may offer molecularly targeted therapeutic options.⁴ Archival tissue from the primary is often considered acceptable for studies of targeted agents when the biomarker in question is present, but archival tissue from a patient who has had multiple therapies may not reflect current tumor DNA status. Contemporary sampling of metastatic disease sites or cell-free ctDNA or circulating tumor cells may be more informative, although uninformative somatic testing, false-negatives, and limitations due to tumor purity must also be considered. Studies suggest that concordance with metastatic tissue can be good,⁴⁰ and that clinical selection and the timing of ctDNA draw at progression may improve diagnostic yield.⁴¹

Recent studies have resulted in major changes to consideration of germline testing in some patients with prostate cancer.^{5,6,13,15} Germline genetic testing is now recommended for all men with a family history of prostate cancer or intraductal histology and/or high- or very high-risk regional or metastatic prostate cancer.⁴ The decreasing cost of germline panel testing has made it more feasible to follow these guidelines for testing, although substantial issues remain regarding disparities in insurance coverage and access to genetic counseling.

The standards for somatic testing and reporting are less established than those for germline testing. Rapid changes in assays and clinical trials in progress make it difficult to recommend specific assays. A number of NGS sequencing panels are available and FDA-approved for somatic testing

For men with personal history of *BRCA1/2* mutation, Lynch syndrome, or mutations (ie, pathogenic variants) in prostate cancer-associated risk genes:

- Begin screening at age 40 y.
- Annual PSA and DRE.
- Men with a PSA level above the median for their age group are at higher risk for prostate cancer and aggressive prostate cancer. The higher above the median, the greater the risk.
- If PSA level is below age-adjusted median and no other indication for biopsy, repeat screening in 12 months.
- If PSA level is above age-adjusted median, recheck PSA in 6–12 months; if increased, consider extended pattern biopsy with mpMRI or TRUS-guidance.
- Upper limit age-adjusted median range PSA^{38,39}:
 - o Aged ≤49 y, PSA >1.5 ng/mL
 - Aged 50-59 y, PSA >2.0 ng/mL
 - Aged 60–69 y, PSA >2.5 ng/mL

Figure 2. Recommendations for prostate cancer early detection in carriers of high-risk mutations.

Abbreviations: DRE, digital rectal examination; mpMRI, multiparametric MRI; PSA, prostate-specific antigen; TRUS, transrectal ultrasound.

in CLIA-certified laboratories. Currently, somatic testing for homologous recombination gene mutations and microsatellite instability (MSI) and MMR deficiency (dMMR) should be considered due to potential treatment implications. In addition, some somatic NGS assays may also report alterations that, although investigational, may inform clinical trial candidacy: androgen receptor amplifications, *PTEN* deletions, PI3K/Akt/mTOR pathway alterations, and *TMPRSS2-ERG* gene fusions.

The definition of actionability for specific gene mutations in prostate cancer is emerging, and currently at least 2 classes of gene mutations should be considered (Table 1). Tumor and/or germline mutations in genes such as BRCA1, BRCA2, ATM, PALB2, FANCA, RAD51D, and CHEK2 may suggest candidacy for early use of platinumbased chemotherapy^{42,43} or enrollment in clinical trials testing PARP inhibitors,44 such as olaparib and rucaparib, which have been granted breakthrough designation by the FDA. Ongoing clinical trials are evaluating a number of PARP inhibitors for metastatic castration-resistant prostate cancer (mCRPC) and earlier disease states (ClinicalTrials.gov identifiers: NCT02854436, NCT02975934, NCT02987543, and NCT03148795). Retrospective and prospective studies to date have not shown that any FDA-approved treatment of mCRPC should be withheld from men with advanced prostate cancer and germline mutations.45-47

Tumor DNA evaluation for high MSI (MSI-H) or dMMR can be determined using immunohistochemistry or NGS methods demonstrating loss of function of *MLH1, MSH2, MSH6*, or *PMS2*, and is ideally validated for prostate cancer.^{48,49} Identification of tumor MSI-H or dMMR indicates potential eligibility for pembrolizumab in later lines of therapy for advanced disease.⁴

Importance of the Molecular Tumor Board

Because approaches to NGS testing of tumors have changed and continue to evolve quickly, interpretation of results for the busy clinician may be challenging. Many institutions have instituted molecular tumor boards in which relevant clinical information is presented alongside results of germline and/or somatic testing and is reviewed by a multidisciplinary team. These tumor boards should include expert interpretation of data by a molecular pathologist, medical oncologist with diseasespecific expertise, and genetic counselor, and may also include radiation and surgical oncologists. Such molecular tumor boards are increasingly available at comprehensive cancer centers with consultation for or participation by outside physicians because molecular pathology expertise is not yet widely available.

Conclusions

A summary of important points is available in eTable 3. Information about heritable (germline) and tumoracquired (somatic) mutations has increasing importance in the management of men with prostate cancer. Germline data can inform both patient and family risk for prostate and other cancers and drive more aggressive screening in men at high risk of developing prostate cancer. Somatic testing is performed to determine whether the tumor has actionable targets for therapy, and prior knowledge of germline mutations can help in the interpretation of the results. Molecular tumor boards are needed to best interpret results and to direct clinical management and trial opportunities for providers and patients. Partnership with genetic counselors is needed to assist patients and relatives with decisions regarding genetic testing, interpretation, and follow-up cascade testing for family members. Clinicians should be aware of how to integrate genomic testing into treatment paradigms, because this field is rapidly evolving.

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JOURNAL OF THE NATIONAL COMPREHENSIVE CANCER NETWORK

Supplemental online content for:

Germline and Somatic Mutations in Prostate Cancer for the Clinician

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eTable 1: Key Terms and Definitions eTable 2: Obtaining a Comprehensive Family History of Cancer eTable 3: Take-Home Points

eTable 1. Key Terms and Definitions

Cascade testing: Genetic counseling and testing in blood relatives of individuals who have been identified with specific genetic mutations; may include screening, counseling, or referral for a patient with a relative who has tested positive for a genetic mutation.

CTC: Circulating tumor cells. Tumor cells from the circulation (blood) that can be enumerated, measured, and/or evaluated.

ctDNA: Circulating tumor DNA. Typically measured from cell-free DNA in the plasma.

DDR: DNA damage response pathways. Includes homologous recombination, MMR, base excision repair, and others.

dMMR: Deficiency in mismatch repair. Refers to the inability to use a mechanism of correcting errors in DNA by detecting and replacing bases in the DNA that are paired incorrectly (mismatched bases). dMMR in the tumor may be associated with susceptibility to treatments, such as immune checkpoint inhibitors.

Genetic counseling: The evaluation and understanding of a family's risk for an inherited medical condition. A genetic counselor is a healthcare professional with specialized training in medical genetics and counseling.

Genetic testing: Laboratory methods to evaluate DNA of an individual to identify increased risks of specific conditions (eg, cancer), select treatment, or determine response to treatment.

Germline DNA: Constitutional DNA that is inherited from mother and father, present in nucleated cells of the body, such as lymphocytes, and may be passed on to children. Some genes may be shared with siblings.

HRD: Homologous recombination deficiency. Refers to the inability to use a common mechanism of repairing harmful breaks that occur on both strands of DNA, known as doublestrand breaks, through genetic recombination. Examples: BRCA2, BRCA1, PALB2.

MSI-H: Microsatellite instability. MSI-high refers to microsatellite instability, a measure of dMMR. Can result from defects in genes such as MLH1, MSH2, MSH6, or PMS2.

NGS: Next-generation sequencing. High-throughput DNA sequencing technologies. Millions or billions of DNA strands can be sequenced in parallel to yield more throughput. Practically, this allows multiple genes to be tested at the same time in gene "panels."

Pathogenic variant: A genetic alteration that increases an individual's susceptibility or predisposition to a certain disease or disorder (eg, prostate cancer). Development of prostate cancer is more likely, but not certain, when such a variant (or mutation) is inherited.

Somatic DNA: Acquired mutations and genetic changes to the germline DNA. Often refers to tumor-associated genetic changes that are not heritable.

VUS: Variant of uncertain significance. Typically refers to a genetic change in germline DNA where there is insufficient information available to know if it causes an increased susceptibility to cancer or not.

Abbreviations: CTC, circulating tumor cells; ctDNA, circulating tumor DNA; dMMR, mismatch repair deficiency; HRD, homologous recombination deficiency; MMR, mismatch repair; MSI, microsatellite instability; MSI-H, microsatellite instability-high; NGS, next-generation sequencing; VUS, variant of uncertain significance.
eTable 2. Obtaining a Comprehensive Family History of Cancer

- Detailed family history includes:
 - Parents
 - Children
 - Siblings/Half siblings
 - Grandparents and great-grandparents (specify maternal or paternal)
 - Nieces and nephews
 - Aunts and uncles (specify maternal or paternal)
 - Cousins (specify maternal or paternal)
 - Ethnicity/Country of origin
 - Consanguinity

Minimal data for each cancer-affected relative:

- Current age and age at diagnosis (if not known exactly, decades can be helpful)
- Age at and cause of death (especially if cancer-related)
- Type of cancer (note multiple primaries)
- Results of any prior genetic testing

Resources for collecting family history:

- CDC My Family Health Portrait, https://phgkb.cdc.gov/FHH/html/index.html
- Cancer.net, https://www.cancer.net/sites/cancer.net/files/cancer_family_history_questionnaire.pdf
- NCCN Guidelines for Genetic/Familial High-Risk Assessment: Colorectal (see algorithm page HRS-A; available online at NCCN.org).

Abbreviation: CDC, Centers for Disease Control and Prevention.

eTable 3: Take-Home Points

- Germline DNA is inherited from both biologic parents and is present in all cells in the body. It does not change over time, therefore repeat testing will typically be of limited value.
- Somatic (tumor) DNA is comprised of germline genetic material with additional acquired mutations; however, somatic testing platforms may or may not report suspected germline mutations (pathogenic variants).
- Tumor testing may suggest the need for, but should never replace, dedicated germline testing.
- Tumor evolution over time means repeat somatic testing may be of value.
- Germline testing can identify increased risk for heritable cancers.
- Germline DNA may have therapeutic implications for some patients.
- Tumor sequencing can be performed to find actionable mutations that may have therapeutic implications in advanced disease.
- Germline mutation testing should be offered to patients with a family history of prostate other cancers, or those with a personal history of high- and very high-risk localized prostate cancer, regional, or metastatic disease.
- All patients with pathogenic germline mutations should be referred to a genetic counselor.
- When there is a strong family history, genetic counseling is recommended before genetic testing whenever possible.
- If germline testing is negative or inconclusive (ie, there is no known cancer associated with the identified mutation) but there is a strong family history for cancers, referral to genetic counseling is indicated.
- Variants of uncertain significance (VUS; including in BRCA1/2) should not be used for medical management.
- Tumor DNA analysis should be performed at a time when a new therapy is under consideration.
- Intraductal histology has a higher association with actionable tumor and germline mutations.
- Genetic counselors can be found at https://www.nsgc.org/findageneticcounselor.
- Carriers of the BRCA1/2 mutation are at increased risk of prostate cancer before age 65 years, and prostate cancer in men with germline BRCA2 mutations occurs earlier and is more likely to be associated with prostate cancer mortality.
- Men with germline BRCA1/2 mutations may consider beginning shared decision-making about PSA screening at age 40 years and at annual intervals, factoring in age-adjusted median PSA values. Early detection clinical trials are recommended whenever possible.



Original Research

Radium-223 in combination with docetaxel in patients with castration-resistant prostate cancer and bone metastases: a phase 1 dose escalation/randomised phase 2a trial



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KEYWORDS

Castration-resistant prostate cancer; Radium 223 dichloride; Docetaxel; Combination treatment **Abstract** *Purpose:* Radium 223 dichloride (radium-223) is an alpha particle—emitting bonedirected therapy that prolongs overall survival in men with bone-predominant metastatic castration-resistant prostate cancer (mCRPC). Docetaxel is an antimicrotubule cytotoxic agent that improves survival in mCRPC. We investigated whether combining these potentially cross-sensitising agents to dually target tumour and bone would be safe and effective.

Patients and methods: Phase 1 was a dose escalation study to define a recommended phase 2 dose (RP2D) of docetaxel and radium-223. In phase 2a, patients were randomised 2:1 to the recommended combination regimen or docetaxel at a dose of 75 mg/m² every 3 weeks (q3w). Patients with bone-predominant mCRPC were eligible. End-points were safety, efficacy and treatment-related changes in serum and imaging biomarkers.

Results: Twenty patients were enrolled in phase 1; 53 patients were randomised in phase 2a: 36 to combination treatment and 17 to docetaxel alone. The RP2D for the combination was radium-223 55 kBq/kg every six weeks \times 5 doses, plus docetaxel 60 mg/m² q3w \times 10 doses. Febrile neutropenia was dose limiting. A higher rate of febrile neutropenia was seen in the docetaxel monotherapy arm (15% vs 0%); the safety profile of the treatment groups was otherwise similar. The combination arm had more durable suppression of prostate-specific antigen (median time to progression, 6.6 vs 4.8 months, respectively), alkaline phosphatase (9 vs 7 months) and osteoblastic bone deposition markers.

Conclusions: Radium-223 in combination with docetaxel at the RP2D was well tolerated. Exploratory efficacy data suggested enhanced antitumour activity for the combination relative to docetaxel alone. Comparative studies with end-points of clinical benefit are warranted. ClinicalTrials.gov number: NCT01106352.

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1. Introduction

Prostate cancer is bone-tropic, rendering it particularly susceptible to treatments that target bone formation and osteoblastic activity. The cancer-induced abnormal bone metabolism that places patients at risk of death and morbidity can also be leveraged to deliver lifeprolonging therapy.

Radium 223 dichloride (radium-223), a calcium mimetic alpha particle–emitting radiopharmaceutical, targets hydroxyapatite. It selectively accumulates in areas of increased bone turnover that surround meta-static lesions, where it emits four high-energy, short-range (<100 μ m) alpha particles with resulting minimal radiation effects on the adjacent bone marrow [1,2]. In preclinical models, it reduces abnormal bone production, tumour burden and dysregulated bone deposition [3,4]. Clinically, radium-223—given at a dose of 55 kBq/kg every 4 weeks for 6 doses—prolongs life and the time to first symptomatic skeletal event in patients with bone-predominant metastatic castration-resistant prostate cancer (mCRPC) and no known visceral metastases [5].

Docetaxel is a chemotherapeutic agent that interferes with microtubule dynamics and has a radiosensitising effect [6]. Docetaxel given at a dose of 75 mg/m² every 3 weeks (q3w) in combination with prednisone prolongs life in patients with mCRPC [7].

We hypothesised that combining bone-targeted alpha radiation therapy with chemotherapy in patients with mCRPC might be an effective treatment approach, predicated on the concepts of multicompartment targeting and possible cross-sensitisation in bone lesions [8]. We conducted a phase 1/2a study to investigate this combination.

2. Patients and methods

2.1. Patients

Eligible patients had progressive mCRPC with >2 bone metastases, testosterone <50 ng/dL, Karnofsky Performance Status of >70%, life expectancy of >6 months and adequate organ functionality (white blood cell count $>3 \times 10^{9}$ /L, with an absolute neutrophil count $>1.5 \times 10^{9}$ /L, a platelet count $>100 \times 10^{9}$ /L and haemoglobin \geq 10.0 g/dL; total bilirubin level \leq upper limit of normal (ULN) and aspartate aminotransferase and alanine aminotransferase concentrations $\leq 1.5 \times \text{ULN}$; creatinine $\leq 1.5 \times$ ULN and albumin > 30 g/L). The patients needed to have had two consecutive prostatespecific antigen (PSA) increases at least one week apart, with a minimum value of 2 ng/mL at screening, or two or more new bone lesions when analysed by bone scintigraphy. Those patients on a first-generation androgen inhibitor needed to progress through a 4-week withdrawal. The exclusion criteria included the following: visceral metastases, defined as >2 lung metastases and/or liver metastases that were >2 cm in size, symptomatic nodal disease and malignant lymphadenopathy >3 cm in shortaxis diameter. Patients should not have received >10

previous docetaxel doses or previous treatment with a bone-seeking radiopharmaceutical.

2.2. Study design

This two-part phase 1/phase 2a study, conducted at eight centres, seven in the United States and one in France, aimed to establish a recommended phase 2 dose (RP2D) of radium-223 in combination with docetaxel and to investigate safety and exploratory efficacy end-points at the RP2D.

In phase 1, between 9 and 18 patients were to be enrolled and treated according to a 3 + 3 design. The dose escalation scheme is shown in Fig. 1A. Doselimiting toxicity (DLT) was assessed during the 6-week period after the first radium-223 injection. DLT was defined as absolute neutrophil count $<0.5 \times 10^9$ /L for >7 days without fever despite granulocyte-colony stimulating factor support, grade ≥ 3 febrile neutropenia (after a protocol amendment), platelet count $<25 \times 10^9$ /L L for >7 days, grade ≥ 3 diarrhoea despite optimal medical management, grade ≥ 4 vomiting or constipation.

Radium-223 was started at a dose of 27.5 kBq/ kg (according to the National Institute of Standards and Technology [NIST] 2016 update [9]), every six weeks (q6w), and could be escalated to 55 kBq/kg (according to NIST 2016 update [9]). The starting dose of docetaxel was 75 mg/m² q3w, with a planned reduction to 60 mg/m^2 in the event of DLT. We prioritised achieving full-dose radium-223 over full-dose chemotherapy in the dose escalation scheme, given that there are survival data using docetaxel as part of combination therapy at its step-down dose but no survival data using a lower dose of radium-223 [10]. Radium-223 was administered every other chemotherapy dose rather than monthly to optimise the likelihood of patient acceptance and compliance by having only one day of treatment per cycle, at a dosing interval known to have favourable clinical effects [11]. The number of doses was capped at five in an abundance of caution to protect long-term marrow integrity in the event of enhanced toxicity that would not be detected by blood count assessments during treatment. In all cohorts, docetaxel was to be administered every 3 weeks and was to be continued in the absence of progressive disease or unacceptable toxicity. Docetaxel and radium-223 were administered on the same day, with docetaxel administered first, followed by radium-223 as soon as practically feasible. Prednisone 5 mg was given orally twice daily, continuously. Dexamethasone premedication was given before docetaxel dosing as per each institution's practice. Growth factor support was allowed only as secondary prophylaxis.

In phase 2a, using a schedule generated by an independent statistician, patients were randomly assigned centrally 2:1, using a block randomisation scheme (block size of three), via an interactive voice response system, to combination therapy or docetaxel alone, respectively. A preplanned early stopping rule applied in the event of significant toxicity in the combination arm. The treatment period was a maximum of 30 weeks (10 doses of docetaxel), followed by 22 weeks of follow-up.

The study was conducted in accordance with the Declaration of Helsinki and the International Conference on Harmonisation E6, Good Clinical Practice. The protocol and all amendments were approved by the independent ethics committee/institutional review boards at each site, and written informed consent was obtained from the patients before any assessments were performed.

2.3. Assessments

Adverse events (AEs) were coded according to the Medical Dictionary for Regulatory Activities version 13.0. Severity was graded according to the National Cancer Institute Common Terminology Criteria for Adverse Events version 4.0. The safety assessment period for AEs was from the start of study treatment to 6 weeks after the end of study treatment (8 weeks for serious AEs [SAEs]). Data on marrow sequelae and any second malignancies were collected up to 12 months after the start of study treatment. Exploratory efficacy assessments included on-treatment changes in bone alkaline phosphatase (bALP), total ALP (tALP), urinary C-telopeptide of type 1 (uCTX-1), N-terminal propeptide of procollagen type 1 (P1NP), pyridinoline cross-linked carboxyterminal telopeptide (ICTP), PSA and circulating tumour cells (CTCs).

2.4. Statistical considerations

The primary objectives were to establish a recommended dose of radium-223 combined with docetaxel and to investigate safety and explore efficacy at this dose level. The safety population included all patients who received treatment. To examine the antitumour effect of treatment in this exploratory study, the efficacy population comprised patients who received $\geq 40\%$ (2 infusions) of the specified number of radium-223 doses (combination arm) or docetaxel doses (docetaxel arm) and had no major protocol violations (per protocol population). No formal statistical testing was planned.

Exploratory efficacy end-points included time to PSA progression, time to bALP progression, time to tALP progression, time to first radiographic or clinical progression based on Response Evaluation Criteria in Solid Tumours (RECIST) [12] version 1.1 and Prostate Cancer Working Group 2 (PCWG2) [13] definitions and overall survival. Time-to-event end-points were measured from the first dose of study treatment. For this report, progression-free survival (PFS) events are defined as radiographic or clinical progression or death. Medians



Fig. 1. Study profile. (A) Dose escalation scheme.*A return to the very first dose cohort could be considered in the event of 0/3 or <2/6 DLTs at 55 kBq/kg radium-223 + 60 mg/m² docetaxel q3w. If then 2/3 or $\geq 2/6$ DLTs occurred at docetaxel 75 mg/m², the chosen regimen for the phase 2a cohort was to be radium-223 50 kBq/kg × 5 + docetaxel 60 mg/m² q3w × 10. (B) Phase 1 dose escalation cohorts. *One patient was replaced, unable to receive both combined doses of radium-223 and docetaxel because of docetaxel hypersensitivity. [†]Withdrew before receiving both doses of radium-223 to receive another treatment deemed necessary by the study sponsor. [‡]Withdrew after receiving both doses of radium-223, too ill to attend the 12-month follow-up visit. (C) Phase 2a safety and efficacy cohort.*25 patients in the combination arm received all planned radium-223 doses, 20 patients in the combination arm and 5 patients in the docetaxel arm vas stepped down to 60 mg/m². The study was completed through 12 months of follow-up from the start of treatment with 23 (70%) patients in the combination arm and 9 (69%) in the

for time-to-event variables were estimated using the Kaplan-Meier method. Changes in biomarkers over time were computed as the area under the bone marker curve. Based on the Lehmann alternative power function for a two-sided 0.05-level test, the planned 42 patients were to be randomised. Assuming for a given marker that the odds were 3:1 that a patient in the combination group had a greater area under the bone turnover curve relative to a patient in the docetaxel group, the power of the test was 0.78. *P* values for exploratory efficacy end-points have not been corrected for multiplicity of testing and are provided for information only.

3. Results

3.1. Phase 1 dose escalation

Seventeen patients were treated in the phase 1 dose escalation cohort, including three with visceral disease; patient disposition and baseline characteristics are summarised in Fig. 1B and Supplementary Table 1. No DLTs occurred among the first three patients treated at full-dose chemotherapy and half-dose radium-223 (27.5 kBq/kg), but two developed febrile neutropenia, which was not then specified as a DLT. The cohort was expanded to six patients; no DLTs or additional febrile neutropenia events were seen. Owing to febrile neutropenia in two of six patients, the docetaxel dose was reduced to 60 mg/m^2 in the second cohort, which also used radium-223 at a dose of 27.5 kBg/kg. No DLTs were seen in the first three patients enrolled in this cohort. Because it appeared that the docetaxel dose at 75 mg/m² was accounting for the neutropenic fevers, the radium-223 dose was escalated to 55 kBq/kg in the third cohort, holding the docetaxel dose at 60 mg/m^2 . No DLTs were seen in the first three patients enrolled at this dose level. However, one patient developed grade 3 neutropenia and another developed grade 4 neutropenia, both without fever or infection. After reviewing the safety data, it was decided to add three more patients to this cohort. No DLTs occurred in these patients. The third cohort dose (55 kBq/kg radium q6w \times 5 and 60 mg/m² docetaxel q3w \times 10) was consequently selected as the RP2D to be administered over 30 weeks. Haematological treatment-emergent AEs (TEAEs) occurring in phase 1 are shown in Supplementary Table 2.

3.2. Phase 2a cohort

3.2.1. Patients and treatment

Between December 19, 2012, and April 7, 2014, 53 patients were randomly assigned to receive combination therapy with docetaxel 60 mg/m² and radium-223 55 kBq/kg q6w \times 5 (n = 36) or docetaxel alone, at a standard dose of 75 mg/m² q3w \times 10 (n = 17, Fig. 1C, Supplementary Fig. 1); seven patients were found not to be eligible and were not treated. Baseline characteristics were similar between treatment groups (Table 1). Seven (15%) of 46 eligible patients had visceral metastases at baseline, five in the combination arm and two in the docetaxel arm.

3.2.2. Treatment exposure

The patients in the combination arm received a cumulative median of 1187 mg of docetaxel (range, 250-1520), versus 1270 mg (range, 643-1600) in the docetaxel monotherapy arm. The median number of docetaxel doses was 10 (range, 2-11) in the combination arm and 9 (range, 4-10) in the monotherapy arm. The median number of radium-223 doses in the combination arm was 5 (range, 1-5).

In the combination therapy arm, radium-223 and docetaxel administration was delayed in two patients because of TEAEs (cellulitis and osteoporosis), with docetaxel administration delayed in a further five patients (because of back pain, pain in extremity; oral abscess; pneumonia; toothache; diarrhoea, dehydration, pleural effusion, acute respiratory failure and pneumonia). There were three dose delays because of TEAEs in the docetaxel arm (hypotension; influenza-like illness, cough and melaena; cellulitis). In the combination arm, radium-223 and docetaxel were discontinued in 4 of 33 (12%) patients because of TEAEs (unilateral blindness; cerebrovascular accident; pneumonitis; asthenia and back pain), and docetaxel was discontinued in a further two (6%) patients (peripheral neuropathy; asthenia). In the docetaxel arm, 3 of 13 (23%) patients discontinued treatment because of TEAEs (febrile neutropenia; interstitial lung disease; peripheral neuropathy).

3.2.3. Safety

TEAE and TESAE incidence in the phase 2a safety population is summarised in Table 2 and Supplementary Table 3. Notably, there was less toxicity of any grade seen with combination therapy than docetaxel alone for neutropenia, febrile neutropenia, fatigue, dyspnoea, arthralgia and nausea. However, combination therapy was associated with more diarrhoea and back pain. The incidence of grade 3 or 4 TEAEs was low in both arms (Table 2), with the exception of neutropenia. Febrile neutropenia occurred in two patients (one grade 3 and one grade 4) in the docetaxel arm and none in the combination arm; growth factors were used to prevent or resolve neutropenia in four patients in the combination arm and two

docetaxel arm. [†]Received at least 40% of drug dose, no protocol violation. [¥]Including the one patient who was excluded from the per protocol population. [‡]All deaths occurred during follow-up and were due to disease progression. [§]3 patients entered hospice, and 1 had disease progression. PD, progressive disease; DLT, dose-limiting toxicity; ITT, intention to treat; q3w, every 3 weeks; q6w, every 6 weeks.

Table 1Baseline characteristics (phase 2a cohort).

Characteristic	Radium-223 $+$ docetaxel	Docetaxel
	N = 33	N = 13
Age, median (range), years	68 (49-82)	67 (55-82)
Weight, median (range), kg	87 (61-120)	78 (69–132)
Karnofsky Performance Status, median %, (range)	90 (70-100)	90 (70-100)
Albumin, median, g/L	43.0	43.0
Haemoglobin, median, g/L	122.0	121.0
PSA		
>ULN, N (%)	32 (97)	13 (100)
Median (range), ug/L	99 (3-1000)	43 (4-1042)
Total ALP		
>ULN, N (%)	20 (61)	10 (77)
Median (range), U/L	167 (62-1016)	186 (74-472)
Bone ALP		
>ULN, N (%)	23 (70)	11 (85)
Median (range), µg/L	36 (10-331)	47 (16-164)
LDH		
>ULN, N (%)	6 (18)	2 (15)
Median (range), U/L	191 (123–418)	190 (124-328)
Patients with visceral metastatic lesions, N (%)		× ,
Any	5 (15)	2 (15)
Lung	1 (3)	1 (8)
Liver	0	0
Other	4 ^a (12)	1 ^b (8)
Extent of disease (number of bone lesions), N (%)		
2-4	4 (12)	0
5-9	7 (21)	3 (23)
10-20	9 (27)	4 (31)
>20	13 (39)	6 (46)
Time since initial diagnosis, median (range), months	73 (7–292)	45 (12-274)
Time since bone metastases, median (range), months	23 (1-58)	10 (0-92)
Prior anticancer therapies, $N(\%)$		
Hormonal therapies		
Abiraterone + prednisone	25 (76)	8 (62)
Enzalutamide	3 (9)	5 (38)
Chemotherapy		
Docetaxel	2 (6)	0
Immunostimulants		
Sipuleucel-T	6 (18)	4 (31)
Bone-modifying agents, N (%)		
Bisphosphonates	13 (39)	5 (38)
Denosumab	12 (36)	3 (23)
Other, N (%)		
Radiation	24 (73)	9 (69)

ALP, alkaline phosphatase; LDH, lactate dehydrogenase; PSA, prostate-specific antigen; ULN, upper limit of normal.

^a Adrenal (2 patients), pleura, pancreas.

^b Adrenal.

patients in the docetaxel arm. There were no TEAEs of thrombocytopenia reported in either arm during the treatment period, and median platelet laboratory values were similar for both treatment groups between baseline and day 8 (Supplementary Fig. 2). There were no grade 5 TEAEs. No fractures were observed.

3.2.4. Efficacy

PSA declines of >50% occurred in 61% of patients in the combination arm and 54% of patients in the docetaxel arm (Supplementary Fig. 3A). Plots of PSA level relative to baseline from week 4 to end of treatment show similar profiles for both arms, but PSA suppression was more

pronounced with the combination arm (Supplementary Fig. 4A, Supplementary Table 4). A longer time to PSA progression was also observed with the combination arm (Fig. 2A; median, 6.6 vs 4.8 months).

The median PFS was 12.0 months in the combination arm and 9.3 months in the docetaxel arm (Fig. 2D). Twelve-month overall survival rates were similar (89% and 90%, respectively), although the high level of censoring precluded meaningful analysis. Disease progression based on RECIST and PCWG2 criteria is shown in Supplementary Table 5.

Changes in bone marker levels indicated a greater suppression of osteoblastic activity in the combination

Table 2 TEAEs in the phase 2a treatment period (any grade and grade 3 or 4): safety population.

TEAE	Any grade		Grade 3 or 4	
	Radium- 223 + docetaxel N = 33	Docetaxel $N = 13$	Radium- 223 + docetaxel N = 33	Docetaxel $N = 13$
Any	33 (100)	13 (100)	16 (48)	8 (62)
Haematological ^a				
Neutropenia	10 (30)	5 (38)	10 (30)	5 (38)
Anaemia	3 (9)	1 (8)	1 (3)	0
Leucopenia	2 (6)	2 (15)	2 (6)	2 (15)
Lymphopenia	1 (3)	0	1 (3)	0
Febrile neutropenia	0	2 (15)	0	2 (15)
Non-haematological ^b				
Fatigue	17 (52)	9 (69)	0	0
Nausea	16 (48)	8 (62)	0	0
Diarrhoea	15 (45)	5 (38)	1 (3)	0
Back pain	13 (39)	4 (31)	2 (6)	0
Alopecia	12 (36)	7 (54)	0	0
Peripheral oedema	12 (36)	5 (38)	0	1 (8)
Constipation	11 (33)	5 (38)	0	0
Decreased appetite	11 (33)	4 (31)	0	0
Peripheral neuropathy	10 (30)	4 (31)	0	0
Dysgeusia	7 (21)	8 (62)	0	0
Arthralgia	7 (21)	6 (46)	0	0
Dyspnoea	2 (6)	5 (38)	0	0
Gastrointestinal reflux disease	1 (3)	4 (31)	0	0

TEAEs, treatment-emergent adverse events.

Data are number of patients (%).

^a Selected because of their relevance to radium-223 and chemotherapy.

^b Any grade occurring in $\geq 25\%$ of patients in either treatment group.

arm (Supplementary Fig. 3B, 3C, 4B, C, Supplementary Table 4). For both tALP and bALP, a longer median time to progression was observed for combination arm patients than docetaxel arm patients (9.0 vs 6.9 and 9.3 vs 7.4 months, respectively; Fig. 2B and C).

P1NP showed a decline pattern favouring the combination similar to that for bALP (Supplementary Fig. 3D, 4D). The weighted median area under the time—activity curve for P1NP was substantially smaller for the combination arm (25.0 v 46.2 μ g*day/L), reflecting greater suppression of this marker (Supplementary Table 6).

Markers of osteoclastic activity, uCTX-1 and ICTP, showed similar patterns of decrease during treatment for combination arm and docetaxel arm patients (Supplementary Fig. 3E, 3F, Fig. 4E, F, Supplementary Table 6).

An antitumour treatment effect in both arms was suggested by the decrease in CTCs (Supplementary Table 7).

4. Discussion

To our knowledge, this trial is the first to explore the concept of dual targeting of osteoblastic bone and

cancer cells using two concurrent agents, radium-223 and docetaxel, both of which prolong survival in patients with mCRPC. The concept of targeting bone and tumour is not novel. Prior studies have examined docetaxel in combination with bone-targeting agents that are not known to prolong survival, namely, strontium-89 and rhenium-188-hydroxyethylidine diphosphonate [14,15]. These studies only used one or two doses of the bone-seeking radiopharmaceutical, rather than as a repetitively dosed regimen integrated with chemotherapy. Neither of these studies yielded data sufficiently promising to warrant advancement to phase 3. This study, however, used only life-prolonging agents in a regimen in which patients were exposed to both agents throughout the treatment. Although the combination arm used the step-down dose of docetaxel commonly applied in clinical practice, the cumulative exposure to docetaxel in the two arms of the phase 2a cohort was similar, and the combination was associated with less neutropenia, fatigue, and certain gastrointestinal toxicities. Another factor that may have contributed to the safety profile of the combination is that we administered five doses of radium q6w, rather than six doses every four weeks. Combination therapy appeared to increase the proportion of patients with substantial



Fig. 2. Kaplan–Meier plots for (A) time to PSA progression; (B) time to tALP progression; (C) time to bALP progression and (D) radiographic or clinical progression-free survival. *Per protocol population; intent-to-treat patients who received \geq 40% of specified number of radium-223 injections or docetaxel, per dose escalation study results, and have no major protocol violations. [†]As per Prostate Cancer Working Group 2 (PCWG2). PSA progression for patients with an initial PSA decline from baseline is defined as a PSA increase \geq 25% and \geq 2 ng/mL above nadir, confirmed \geq 3 weeks later; for those with no PSA decline from baseline, progression is defined as a PSA increase \geq 25% and \geq 2 ng/mL above baseline after 12 weeks. [‡]tALP/bALP progression for patients with an initial decline in tALP/bALP from baseline was defined as a tALP/bALP increase \geq 25% above the nadir, confirmed \geq 3 weeks later; for patients with no tALP/bALP decline from baseline, progression was defined as a tALP/bALP increase \geq 25% above the baseline after 12 weeks. [¥]Time to radiographic or clinical progression is a composite end-point encompassing time to first radiographic or clinical progression or death. bALP, bone alkaline phosphatase; CI, confidence interval; PSA, prostate-specific antiger; tALP, total alkaline phosphatase.

declines in levels of PSA and bone formation biomarkers relative to docetaxel alone and appeared to delay time to progression of these markers.

The safety of this combination is increasingly clinically relevant. Patients generally receive abiraterone or enzalutamide as first-line therapy for mCRPC, with chemotherapy reserved for second-line or beyond. After abiraterone or after enzalutamide therapy, patients frequently manifest both bony disease and soft tissue disease [16,17] and remain sensitive to chemotherapy despite the presence of molecular changes that may render tumours resistant to further androgen receptor (AR)-directed therapy [18]. We therefore have an increasing clinical need for a regimen that is non-AR directed and delivers potent therapy both systemically to the cancer cells and also to the osteoblasts surrounding metastatic bone lesions. Radium-223 and docetaxel appear to fulfil these criteria well. This trial suggests that such an approach is safe, with patients followed up for 1 year without the emergence of long-term safety concerns. It is unknown whether the combination prolongs overall survival compared with radium-223 or docetaxel alone, thus warranting further investigation.

5. Conclusions

This study showed that radium-223 (55 kBq/kg q6w) plus docetaxel (60 mg/m² q3w) was well tolerated and presented no greater safety concerns than docetaxel alone (75 mg/m² q3w). Exploratory efficacy data suggested enhanced antitumour activity in the combination arm. Based on these results, the radium-223/docetaxel combination will be further explored in a phase 3 trial in patients with bone metastatic CRPC (NCT03574571).

Role of the funding source

The study was designed by the funder in conjunction with the coordinating investigator (M.J.M.). The funder collected, analysed and interpreted the study data in collaboration with the authors and commissioned medical writing support for the drafting of the report. M.J.M. had the final responsibility for the decision to submit for publication.

Conflict of interest statement

M.J.M. discloses consultancy/advisory roles with Astellas Pharma, Bayer, Endocyte and Advanced Accelerator Applications and has received travel/accommodation expenses from Bayer and Endocyte, and his institution has received research funding from Bayer, Endocyte, Progenics and Sanofi; Y.L. discloses consultancy/advisory roles with Astellas Pharma, AstraZeneca, Janssen, Merck Sharp & Dohme, Pfizer, Roche, Seattle Genetics and Sanofi, and his institution has received research funding from Sanofi; C.J.S. declares stock ownership in relation to Leuchemix, consultancy/advisory roles with Astellas Pharma, AstraZeneca, Bayer, Genentech/Roche, Janssen Biotech, Pfizer and Sanofi and intellectual property interests in relation to Leuchemix and Exelixis, and his institution has received research funding from Astellas Pharma, Baver, Janssen Biotech, Sanofi and Sotio; K.F. has received honoraria from Bayer and Sanofi, discloses consultancy/advisory roles with Amgen, Astellas Pharma, Bayer, Janssen and Sanofi and has received travel/accommodation expenses from Amgen; C.J.R. has received honoraria from Astellas Pharma, Bayer and Janssen Oncology, discloses consultancy/advisory roles with Bayer, Ferring and Millennium and has received research funding from BIND Biosciences, Karyopharm Therapeutics and Novartis: D.H.S. declares participation in speakers' bureau for Bayer; E.S.A. has received honoraria from Astellas Pharma, AstraZeneca, Clovis Oncology, Dendreon, ESSA, Janssen Biotech, Medivation, Merck and Sanofi, discloses consultancy/advisory roles with Astellas Pharma, AstraZeneca, Clovis Oncology, Dendreon, ESSA, Janssen Biotech, Medivation, Merck and Sanofi, has an intellectual property interest in relation to Qiagen and has received travel/accommodation expenses from Dendreon, Medivation and Sanofi, and his institution has received research funding from Aragon Pharmaceuticals, Astellas Pharma, Astra-Zeneca, Clovis Oncology, Constellation Pharmaceuticals, Dendreon, Exelixis, Genentech, Janssen Biotech, Johnson & Johnson, Merck, Millennium, Novartis, Sanofi and Tokai Pharmaceuticals; N.P-.T. has nothing to disclose; D.D. has received travel/accommodation expenses from Bayer Healthcare and General Electric, and her institution has received research funding from Bayer Healthcare; H.A.J. has received honoraria from Astellas Pharma, Bayer Healthcare and Ipsen and has an intellectual property interest in relation to Cambridge University Press, and her institution has received research funding from GTx and Siemens Healthineers; H.V. discloses a consultancy role with MIM Software, outside the submitted work; O.P. is an employee of Bayer; C.L. is an employee of Bayer and

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Data availability statement

Availability of the data underlying this publication will be determined according to Bayer's commitment to the EFPIA/PhRMA 'Principles for responsible clinical trial data sharing'. This pertains to scope, time point and process of data access.

As such, on request from qualified scientific and medical researchers, Bayer commits to sharing patientlevel clinical trial data, study-level clinical trial data and protocols from clinical trials in patients for medicines and indications approved in the United States (US) and European Union (EU) as necessary for conducting legitimate research. This applies to data on new medicines and indications that have been approved by the EU and US regulatory agencies on or after January 01, 2014.

Interested researchers can use www. clinicalstudydatarequest.com to request access to anonymised patient-level data and supporting documents from clinical studies to conduct further research that can help advance medical science or improve patient care. Information on the Bayer criteria for listing studies and other relevant information is provided in the Study sponsors section of the portal.

Data access will be granted to anonymised patientlevel data, protocols and clinical study reports after approval by an independent scientific review panel. Bayer is not involved in the decisions made by the independent review panel. Bayer will take all necessary measures to ensure that patient privacy is safeguarded.

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Appendix A. Supplementary data

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Clinical Cancer Research

The Role of Lineage Plasticity in Prostate Cancer Therapy Resistance

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Abstract

Lineage plasticity has emerged as an important mechanism of treatment resistance in prostate cancer. Treatmentrefractory prostate cancers are increasingly associated with loss of luminal prostate markers, and in many cases induction of developmental programs, stem cell-like phenotypes, and neuroendocrine/neuronal features. Clinically, lineage plasticity may manifest as low PSA progression, resistance to androgen receptor (AR) pathway inhibitors, and sometimes small cell/neuroendocrine pathologic features observed on metastatic biopsy. This mechanism is not restricted to prostate cancer as other malignancies also demonstrate lineage plasticity during resistance to targeted therapies. At present, there is no established therapeutic approach for patients with advanced prostate cancer developing lineage plasticity or small cell neuroendocrine prostate cancer (NEPC) due to knowledge gaps in the underlying biology. Few clinical trials

Introduction

Lineage plasticity is a biological process that occurs during normal development and later as a mechanism that promotes cell survival when adapting to their environment, evading stress, or repairing tissues. Plasticity may manifest as reversible or irreversible changes in cellular "identity," whereby cells take on an alternative morphologic, phenotypic, or epigenetic state (1). In cancer, lineage plasticity facilitates carcinogenesis, metastasis, and treatment resistance (2). During therapy-related lineage plasticity, differentiated tumor cells acquire new phenotypes, in some cases reverting back to a more "stem-like" state followed by redifferentiating toward an alternative "cell fate" in order to bypass address questions in this space, and the outlook for patients remains poor. To move forward, urgently needed are: (i) a fundamental understanding of how lineage plasticity occurs and how it can best be defined; (ii) the temporal contribution and cooperation of emerging drivers; (iii) preclinical models that recapitulate biology of the disease and the recognized phenotypes; (iv) identification of therapeutic targets; and (v) novel trial designs dedicated to the entity as it is defined. This Perspective represents a consensus arising from the NCI Workshop on Lineage Plasticity and Androgen Receptor-Independent Prostate Cancer. We focus on the critical questions underlying lineage plasticity and AR-independent prostate cancer, outline knowledge and resource gaps, and identify strategies to facilitate future collaborative clinical translational and basic studies in this space.

therapeutic pressure. This versatility of cellular state is particularly prominent in cancer types with effective therapies that target major growth programs and lineage-directing factors (e.g., BRAF-mutant melanoma, EGFR-mutant lung cancer, AR-driven prostate cancer). In these cases, early "targetable" genomic alterations are often retained, but expression of the pressured target is suppressed. Despite preserving a molecular memory of their differentiated cancer cell precursor, alternative lineage programs facilitate subsequent tumor progression.

Prostate cancer is a malignancy driven by androgen receptor (AR) signaling, and AR-targeted therapies are commonly used to treat patients at all stages of the disease. Prostate tumors most frequently

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Translational Relevance

Lineage plasticity associated with loss of androgen receptor signaling dependence and the acquisition of alternative lineage programs occurs in up to 20% of advanced prostate cancer patients as a mechanism of treatment resistance, with important clinical and therapeutic implications. We discuss our current understanding of mechanisms underlying this process and outline a path toward the development of novel biomarkers and trials for this molecularly distinct subset of patients.

display an adenocarcinoma morphology reminiscent of normal luminal prostate architecture, with higher levels of disorganization associated with advanced tumor grade. Downstream markers of canonical AR activity, such as PSA, are used as clinical biomarkers to confirm a diagnosis of prostate cancer and for disease monitoring. Although several prostate cancer drugs are effective at lowering androgen levels and/or blocking the AR directly, metastatic prostate cancers universally develop treatment resistance (3). Acquired resistance is typically due to reactivation of AR signaling mediated, in part, by genomic mutation, amplification, or structural rearrangement of the AR gene itself. However, loss of AR expression and/ or downstream signaling occurs in an estimated 15% to 20% of castration-resistant tumors (4-6). In extreme cases, tumors may reprogram toward alternative pathways adopting features of neuroendocrine, neuronal, or other lineages. Clinically, these cancers are notable for attenuated AR signaling and a range of histologies of which the most common exhibit small cell neuroendocrine carcinoma characteristics. At present, the definition and mechanistic underpinnings of this subset remain ill-defined, and there are no established therapeutic approaches for small cell/NEPC or other phenotypes. Few clinical trials address lineage plasticity, and the outlook for patients remains poor.

To address the challenges resulting from lineage plasticity, the NCI organized a Workshop focused on Lineage Plasticity and Androgen Receptor-Independent Prostate Cancer. Five working groups were assembled prior to the workshop to formulate questions underlying basic, translational, and clinical knowledge gaps and to develop approaches to address them (Supplementary Information). This Perspective generated as a result of the workshop summarizes concepts, data, deficiencies, and opportunities that drive critical questions underlying lineage plasticity and ARindependent prostate cancer.

Gap 1: A Fundamental Understanding of How Lineage Plasticity Occurs

Lineage plasticity is a term that implies that cells are capable of reprogramming their identity by acquiring an alternative lineage state and that this process is at some point plastic, or reversible. Whether AR-independent treatment resistance is mediated through an intermediate stem-like state, an "epithelialmesenchymal transition" (EMT), or through direct transdifferentiation to acquire new characteristics and the extent of the reversibility of these processes are not well understood. Tumors with mixed or overlapping features expressing both AR and AR pathway genes as well as neuroendocrine markers ("hybrid" or "amphicrine" tumors), or those lacking both AR and neuroendocrine markers ("double negative" tumors) may further represent distinct disease states or a continuum (Fig. 1). Lineage programs such as gastrointestinal, squamous, and others have also been described (7). Identifying subsets within ARindependent disease provides expanding insights into the unique biology of AR-independent therapy resistance as well as potentially distinct therapeutics, such as the preferential activation of fibroblast growth factor signaling in "double negative" castrationresistant prostate cancer (CRPC; ref. 4).

The transition of prostate cancer away from a luminal epithelial phenotype is facilitated by genomic loss of the tumor suppressors *RB1* and *TP53*, leading to changes in stem cell, developmental, and EMT programs, mediated in part by the lineage pluripotency transcription factor SOX2 (8–10). Downregulation of REST (a transcription factor that normally silences the expression of neuron-specific genes in nonneuronal cells) through splicing



Figure 1.

Schematic of the proposed molecular events and transition states underlying lineage plasticity that occurs during CRPC progression from an AR-positive, ARdriven prostate adenocarcinoma (luminal phenotype) toward an AR-negative, AR-independent cellular state (e.g., small cell/neuroendocrine).

regulated by SRRM4 (11, 12), as well as activation of lineageassociated transcription factors such as N-myc (13, 14), Onecut2 (15, 16), and BRN2 (17), and derepression of developmental genes such as PEG10 (18) also occur. These changes in cellular programs associate with an increase in cellular proliferation and amplification or overexpression of cell-cycle regulators (e.g., aurora kinase, polo-like kinase; refs. 13, 19), leading to aggressive tumor growth and often visceral metastatic spread. Lineage tracing studies (20) have supported a luminal cell of origin of neuroendocrine prostate cancer cells that arise upon potent androgen blockade, supporting a "transdifferentiation" process. Important questions concerning the timing, cooperation, and feedback of the drivers of transdifferentiation processes and their relationships to oncogenic programs and AR silencing remain to be addressed. Further, identification of noncanonical AR programs associated with AR-positive, PSA low tumors as well as genes derepressed by AR inhibition could provide biological insights into other potential early mediators of lineage plasticity. Epigenetic modifications including changes in DNA methylation and upregulation of the polycomb complex gene enhancer of zeste 2 (EZH2) also play a role in silencing the luminal program and in reprogramming lineage (8, 10). Targeting epigenetic programs may result in some degree of reversibility or reversion back to a more luminal state. Metabolic shifts mediated in part by loss of PKC λ/ι (21), which support proliferation and epigenetic changes, as well as changes in tumor hypoxic state (15) are also observed during NEPC progression. A better understanding of the fundamental cellular and molecular interactions that drive lineage plasticity and the role of the tumor microenvironment, metabolic alterations, and changes in epigenetic state requires further focus and study. This will help to further refine the working definition of this cellular state in prostate cancer.

Working definition of lineage plasticity in prostate cancer

A progressive state of CRPC associated with the loss of AR-regulated lineage characteristics and in some situations the acquisition of new phenotypes (e.g., neuroendocrine features). Plasticity is driven by intrinsic and/or acquired alterations in the biological activities of tumor cells and the tumor microenvironment that involve metabolic, genetic, and epigenetic changes. The consequences of these changes comprise a gene expression profile/phenotype consistent with AR/androgen independence and sustained proliferation.

Open questions

- Is loss of canonical AR signaling equivalent to AR independence? For instance, could the presence of AR in cases with low AR signaling still drive a noncanonical program to sustain tumor growth?
- How many lineages are there and how do we best recognize and define them?
- What degree of reversibility underlies lineage plasticity? Could targeting epigenetic alterations completely revert back toward a luminal state, and/or do genetic factors "fix" tumors in an alternate state?
- What are the mechanisms and mediators of tumor microenvironment regulation that underlie lineage plasticity—aging, senescence, inflammation, metabolism, oncogenic, and nononcogenic biological processes; and the cellular dynamics of immune cells, fibroblasts, adipocytes, endothelial, and neuronal cells that effect this process?

- How do lineage determining transcription factors interact or cooperate during prostate cancer progression?
- What extent do factors related to the metastatic environment (e.g., liver, bone) and/or oncogene-associated or therapy-induced senescence contribute to lineage plasticity?

Gap 2: Determining the Temporal Contribution and Cooperation of Emerging Drivers

How AR-directed therapies affect clonal evolution, clonal selection, and the evolutionary bottlenecks that shape lineage plasticity is not well established. Mapping these processes have important clinical implications for biomarkers and therapeutics. For instance, hormone-naïve high-grade localized prostate cancers with low PSA levels may express neuroendocrine genes and harbor lower AR signaling (22), which may represent a high-risk patient population for developing lineage plasticity when later treated with AR pathway inhibitors. RB1 loss, with or without TP53 mutation or deletion, also occurs in a subset of prostate adenocarcinomas along the disease spectrum (23, 24), and may identify patients for aggressive surveillance and/or early intervention therapeutic strategies. The timing and cooperation of lineagederived transcription factors further shape downstream programs as well as the epigenetic landscape. Whether intermittent AR inhibition, potentially alternating with therapies that target these alterations to induce differentiation, could delay the onset of lineage plasticity or prevent its emergence due to reconstitution of the tumor ecosystem with luminal lineage cells is intriguing and requires further study.

Understanding how mixed CRPC tumors that express both AR and neuroendocrine (or other) markers respond to AR therapies, and whether double-negative and small cell NEPC share treatment vulnerabilities such as sensitivity to platinum chemotherapy have important clinical implications for therapy selection. Assessment of the impact of emerging therapies (and combination approaches) on the prevention or reversal of phenotype or for their impact on tumor kill will help refine treatment goals; the readouts from targeting epigenetic alterations or alternative splicing, for instance, may differ from the goals of targeting proliferation or downstream effects of fixed genomic events. Serial metastatic biopsies or liquid biopsies will be useful for understanding the sequence of aberrations in patients and, when combined with clinical features such as PSA trends and sites of radiologic progression, have the potential to improve the diagnosis of patients progressing through the various biological disease states and to help refine clinical endpoints. One proposed translational research strategy for identifying the context and impact of RB1 alterations is highlighted in Box 1.

Open questions

- What are the relationships between lineage drivers and oncogenic programs?
- Does the presence of *RB1* and/or *TP53* aberrations in *prostate* adenocarcinoma predispose patients toward developing lineage plasticity and small cell/neuroendocrine features?
- Is there an intermediate clinical state where intervention may be effective in preventing or reversing lineage plasticity?
- Do PSA dynamics adequately reflect AR signaling in patients?

Box 1. One of the proposed translational research strategies developed at the workshop to address the role and cooperation of *RB1* and *TP53* in driving lineage plasticity in prostate cancer and other Rb1-deficient tumors (e.g., small cell lung cancer, SCLC) and an approach toward the development of novel biomarker-driven therapeutics.

What are the vulnerabilities in NEPC versus SCLC and other RB-deficient cancers?

Aim 1: Develop a series of collaborating institutions with large clinical volumes of CRPC patients and clinical databases to determine clinical parameters associated with RB loss \pm TP53 loss and type of alteration (mutation; copy loss). Compare with other dual RB/p53 loss cancer types (SCLC).

Aim 2: Develop tissue and blood-based markers (IHC/ISH/ transcriptional/proteomic/metabolic signatures) that detect/ identify and associate with specific RB1 ± TP53 aberrations.

Aim 3: Develop isogenic models of RB \pm TP53 deficiency in prostate cancer backgrounds [cell lines, patient-derived xenograft (PDX), organoids] to assess: (i) molecular consequence for E2F and TP53 signaling, (ii) biological impact, and (iii) relevance for reflecting clinical observations as per Aim 1.

Aim 4: Utilize models developed in Aim 3 to screen for vulnerabilities/synthetic lethality using high-throughput strategies (e.g., CRISPR screening, FDA-approved compound screening) with the goal of establishing the foundation for the next phase of clinical testing

Aim 5: Refine strategies for accurately assessing RB and TP53 status in liquid biopsy, and develop longitudinal studies to determine the impact on progression from prostate cancer to CRPC to NEPC.

- How and when is the AR lost in the context of disease progression and how do specific therapeutics influence resistance pathways?
- Are there strategies to maintain cell differentiation and AR dependency while still restraining tumor growth?
- Do increased DNA damage response gene activities, or other specific transcriptional signatures contribute to the lineage plasticity program, and can these activities be exploited therapeutically?
- Are there synthetic lethal therapeutic approaches that may be exploited to target lineage plasticity and AR-independent prostate cancer?
- What degree of intratumoral heterogeneity is seen within and across metastases in individual patients?

Gap 3: Preclinical Models That Recapitulate Biology of the Disease and the Recognized Phenotypes

Preclinical models that represent the prostate cancer disease spectrum are essential for understanding biology and for the

Box 2: Glossary

AR signaling (canonical): androgen receptor signaling that occurs through ligand (androgen)-mediated or ligand-independent means, resulting in activation of downstream programs critical for prostate growth, development, and function

AR signaling independent or AR indifferent: sustained growth of prostate tumor cells that is not driven by or reliant on downstream canonical AR signaling

Cellular identity or differentiation: a means of classifying cells based on their phenotype or physiologic function

Cellular determination: the process by which a cell becomes specialized to perform a specific function

Clonality: cells that share a common ancestry

Differentiation: the process by which a stem cell or progenitor cell matures into a cell with a specific identity. Dedifferentiation is when a differentiated cell loses its matured cellular identity to become less mature and more stem-like

Double-negative prostate cancer: a subset of castrationresistant prostate cancer that does not express the AR and also does not express neuroendocrine markers

Epigenome/epigenetics: changes in gene expression and cellular phenotype caused by mechanisms other than changes in DNA

Epithelial–Mesenchymal Transition: a process by which epithelial cells lose their cell–cell adhesion and gain migratory and invasive properties to become more like mesenchymal cells, which may facilitate cancer growth and metastatic spread

Embryonic stem cells: pluripotent stem cells that have the potential to differentiate into multiple cell types and are capable of self-renewal

Lineage determining transcription factors: proteins that bind to DNA, either alone or in cooperation with other partners, to control transcriptional output of a cell type to regulate its phenotype and functional characteristics

Lineage reprogramming: the conversion of a mature, terminally differentiated cell type into another mature cell type with or without undergoing dedifferentiation

Lineage tracing: A method that delineates all progeny produced by a single cell or a group of cells

Multipotent: Potential of a cell to form different lineages

Plasticity: Ability of a cell to convert from one cell type to another. This may refer to the potential of a differentiated cell to dedifferentiate and then redifferentiate into a new state

Progenitor: ancestor cell that gives rise to a specific type of differentiated cell

Neuroendocrine: cells that are neural and endocrine in structure or function. In the pathologic classification of neoplasms, this designation is typically based on tumor morphology rather than function. Well-differentiated neuroendocrine tumors (e.g., carcinoids) and poorly differentiated neoplasms (e.g., small cell carcinoma) have distinct biology and may arise in various anatomic sites

Pluripotent: A cell that is capable of developing into any cell type

Small cell carcinoma: morphologic definition based on pathologic review of tumor hematoxylin and eosin–stained slides demonstrating small blue cells, high-grade features, scant cytoplasm, and distinct nuclear features (i.e., fine chromatin, lacking prominent nucleoli). Protein expression of classical neuroendocrine markers such as chromogranin or NSE may be present but is not required

Stem-like: cells that possess characteristics similar to normal stem cells, such as the ability to give rise to other cell types within a tumor

Transdifferentiation: reprogramming of a differentiated cell of one lineage into a differentiated cell of another lineage

development of novel therapeutics. Currently, the number and types of cell lines that recapitulate lineage plasticity are limited, though there are PDX and organoid models of AR-negative and neuroendocrine prostate cancer that have been described and characterized (refs. 25–29; Table 1). Dynamic *in vivo* models, such as a PDX model that changes phenotype from an AR-positive adenocarcinoma to an AR-negative NEPC (30), and xenografts that lose AR signaling dependence during enzalutamide resistance (17) have been used to capture the lineage plasticity process. Genetically engineered mouse models such as the TRAMP model and others designed to alter key molecular events, including loss

Table 1. Preclinical models		
Model	Source	Pathologic and molecular features
NCI-H660 cell line	Lymph node metastasis	Small cell carcinoma;
		AR-negative; PSA-negative;
		TMPRSS2-ERG gene fusion-positive;
		synaptophysin, CD56, NSE-positive
LuCAP 49, 93, 145.1, 145.2	Omental metastasis (LuCAP 49), TURP (LuCAP 93),	Neuroendocrine histology;
patient derived xenograft (PDX)	liver (LuCAP 145.1), lymph node (LuCAP 145.2)	AR-negative;
and PDX-organoid models		synaptophysin-positive
MDA PCa 144-4, 144-13, 155-2,	Salvage pelvic exenteration	Small cell and large cell carcinoma;
MDA PCa 177-0, MDA PCa 189-1	(MDA 144, MDA 155-2), prostate	Aggressive variant clinical features;
PDX models	(MDA 177, MDA 189-1)	TMPRSS2-ERG gene fusion positive (MDA 144)
LTL352 and LTL370	Urethral (LTL352) and penile (LTL370) metastasis	Small cell carcinoma;
PDX models		AR-negative; PSA-negative;
		synaptophysin, NSE-positive
LTL331 transdifferentiation	Primary prostate cancer (LTL331) PDX model	Primary high-grade adenocarcinoma (LTR331)
PDX model	that develops castration-resistant NEPC	and neuroendocrine prostate cancer histology (LTL331R);
	in vivo (LTL331R)	TMPRSS2-ERG fusion-positive;
		LTR331: AR-positive:
		LTL331R: AR-negative, PSA-negative,
		Synaptophysin-positive, chromogranin-positive, CD56-positive
Enzalutamide-resistant	Cell lines developed from enzalutamide-resistant	AR-positive: PSA low:
LNCaP (42D, 42F)	LNCaP xenograft tumors	chromogranin, synaptophysin-positive
MSK-PCA4 Patient-Derived	Pleural effusion	Neuroendocrine features;
Organoids		AR low:
5		Synaptophysin-positive
WCM Patient-Derived Organoids	Metastatic lesions liver (155), bone (154), lymph	Small cell carcinoma;
	node (1,078), soft tissue (1,262)	AR-negative; PSA-negative;
		synaptophysin, NSE, chromogranin-positive
TRAMP mouse	C57BL/6 mice expressing the rat probasin driving	Adenocarcinoma to small cell carcinoma; Rb1 and Tp53 loss;
	expression of SV40 large and small T antigens in prostatic epithelial cells	Visceral metastases
p53 ^{PE_/_} Rb ^{PE_/_} mouse	Conditional knockout of p53 and Rb (p53 ^{PE-/-} ; Rb ^{PE-/-})	Small cell carcinoma;
	from the epithelium of all lobes of the mouse prostate	Rb1 and Tp53 loss
N-Myc-myrAKT1 mouse	Human prostate basal cells overexpressing NMYC	Neuroendocrine features;
	and AKT1 implanted subcutaneously in	AR low;
	NOD-SCID-IL2Rynull (NSG) mice	chromogranin, synaptophysin-positive
Pten ^{f/f} ;LSL-MYCN ^{+/+} mouse	GEMM mice carrying MYCN gene integrated into the	Divergent differentiation
	ROSA26 (LSL-MYCN) locus, a Tmprss2-driven	Neuroendocrine features;
	tamoxifen-activated Cre recombinase and a Pten	AR low/AR-negative;
	conditional knockout allele	chromogranin, synaptophysin-positive;
		visceral metastases with castration
PBCre4: <i>Pten^{f/f}:Rb1^{f/f}</i> (DKO),	GEMM mice, PBCre4 transgene is used to delete	Neuroendocrine features with metastases;
PBCre4:Ptenf/f:	floxed alleles specifically in prostate epithelium	AR-positive/AR low;
Rb1f/f:Trp53f/f (TKO)	A 7578	Synaptophysin-positive
NPp53 mice	GEMM mice, inducible Nkx3.1 ^{CreERT2} driver to delete	Abiraterone-resistant;
	PTEN and TP53 genes in adult prostate epithelium	neuroendocrine features- transdifferentiation
		(lineage tracing);
		AR low/AR-negative;
		Synaptophysin-positive
Ptenf/f-Prkcif/f-PbCre4+ mice	GEMM mice, Ptenf/f-PbCre4+ mouse line	Neuroendocrine features;
(DKO)	(PTEN KO) with PTEN specifically deleted in the prostate	
	epithelium, crossed with Prkcif/f mice	AR low/AR-negative;
		chromogranin, synaptophysin-positive

NOTE: Table of preclinical models that display lineage plasticity, small cell /NEPC histologic or molecular features, and/or AR-signaling indifference.

of PTEN, TP53, and RB1, and/or gain of MYCN, are also useful tools to study the cooperation and timing of emerging tumor suppressors and oncogenes (9, 10, 14, 20, 21, 31). Optimizing and sharing protocols for model development and optimization was discussed as an unmet need, especially as fresh tumor biopsies are more commonly performed clinically and may be used for patient-derived model generation.

Open questions

- What are the preclinical models that can be manipulated in such a way to reflect transition from androgen-dependent to -independent states and further transitions that encompass new differentiation programs such as neuroendocrine phenotypes?
- Are the genomics, transcriptomics, epigenetics, and metabolomics of these model systems representative of advanced human prostate cancer? Do they change over time or with conditions?
- Can we develop a series of paired PDX-organoids with morphologic and molecular information of organoids, PDXs, and human tumor of origin representing the complex molecular landscapes of prostate cancer?
- How do we use model systems to assess reversibility and thereby understand the degree of plasticity?
- What are "the human models" that can be utilized to compare and contrast with the animal models (e.g., rapid autopsies, CTCs, cfDNA, etc.)?

Gaps 4 and 5: Identification of Therapeutic **Targets and Novel Trial Designs Dedicated** to the Entity as It Is Defined

Given the relatively high reported frequency of small cell NEPC post AR-directed therapy, the National Comprehensive Cancer Network (NCCN) guidelines now recommend consideration of metastatic biopsy for any CRPC patient to look for small cell transformation. If found, patients could be considered for platinum-based chemotherapy based on extrapolation of clinical data for small cell lung cancer and supported by recent platinumchemotherapy studies in aggressive variant prostate cancer (32). Although these practice guidelines have recently changed, the diagnosis of lineage plasticity remains a clinical challenge due to a lack of standardized or widely accepted clinical or pathologic criteria. Although pure small cell carcinoma defined by morphology is most often congruent between pathologists, those with mixed/hybrid or with varied degrees of neuroendocrine differentiation are often subject to interobserver variability (33).

The diagnosis of other phenotypes may require more detailed studies that involve IHC or other measures of gene expression. There are no standard criteria for when to perform ancillary studies such as IHC for classical neuroendocrine markers (e.g., chromogranin, synaptophysin), AR protein, PSA, or other markers (34, 35). There are also times when AR is expressed in NEPC, but the canonical AR transcriptome (including downstream targets like PSA) is low; identification of downstream genes that may be activated by AR in this setting would be informative and potentially help refine definitions. The incidence of ARnegative or AR-low CRPC without NEPC features or alternative lineage CRPC and the degree of heterogeneity within this spec-

Table 2. Pathology morphology and available ancillary testing

Morphology
%tumor
%glandular
%small cell
Protein studies (bold
Molecular/Cell cy
• Rb (Rb function
• P53 (p53 func

Pro indicates existing CLIA-validated biomarkers) cle

- on: cyclin D1/p16)
- 53 function: p21)
- Ki-67 (discovery for threshold) Lineage markers
 - Chg (Canonical)
 - Syp (Canonical)
 - CD56
 - FOXA2
 - INSM1
 - ASCL
 - Cvtokeratin—Cam5.2
 - Neurofilament
- Androgen signaling
- AR (canonical)
- AR-v7
- PSA

NOTE: Prioritization of pathology assessment when lineage plasticity is suspected. Tissue should be evaluated for morphologic characteristics that may support small cell carcinoma, neuroendocrine differentiation, or other histologies. Possible ancillary protein studies to consider performing by IHC are listed, with markers in **bold** indicating existing Clinical Laboratory Improvement Amendments (CLIA) grade tests.

trum are also not known. The workshop discussed a path toward the standardization of tumor morphology nomenclature and systematic prioritization of ancillary testing in metastatic CRPC (Table 2).

Given the current challenges of performing tumor biopsies and the variability in morphologic features that occur after therapy, platinum-based chemotherapy trials have been conducted for patient with aggressive clinical features even in the absence of tumor biopsy (32). Notably, these patients defined by clinical features suggestive of AR independence often harbor combined somatic tumor alterations involving PTEN, TP53, and/or RB1, similar to what has been observed in small cell NEPC (29).

With a loss of AR expression, tumors may also lose other related proteins including prostate-specific membrane antigen (PSMA). This manifests clinically as PSMA-negative lesions on PSMA PET imaging. Low or heterogeneous PSMA PET-CT combined with FDG positivity identifies patients with poor prognosis (36), therefore representing a potential noninvasive means to identify AR-independent resistance. However, there are still many unknowns regarding PSMA regulation and PSMA imaging characteristics along prostate cancer progression and therapy resistance. Multi-institutional collaborative studies combining PSMA with FDG PET imaging, in combination with tumor biopsies of discordant lesions and liquid/tissue molecular assessment, were designed at the workshop.

There is no known effective next-line therapy for patients with small cell NEPC especially after platinum chemotherapy. Although second-line SCLC regimens may be considered, their data in prostate cancer are scarce. Notably, although loss of AR activity eliminates the AR pathway as a therapeutic target, the acquisition of new characteristics that associate with NEPC and other phenotypes exposes new targets and vulnerabilities. Available drugs targeting the AURKA/MYCN or AURK/RB1 axis, LSD1, EZH2, DLL3, and approaches to target the immune landscape (e.g., vaccine, TGFβi, IL8i, and immune checkpoint inhibitors) are in development for NEPC, as well as drugs targeting FGF/MAPK for double-negative CRPC. The design of rational combination or cotargeting strategies, such as EZH2 inhibition in combination with AR pathway inhibitors or immunotherapy, may also have value. Ultimately, defining the appropriate inclusion criteria and endpoints for trials focused on lineage plasticity will be critical. Trials will require multicenter collaboration and molecularly based biomarker inclusion and careful patient selection. Incorporation of emerging molecular biomarkers in combination with clinical features may help distinguish subcategories of AR-independent CRPC and inform the development of liquid and imaging biomarker approaches for clinical trial design.

Open questions

- What are the clinical and pathologic differences between small cell carcinoma and CRPC with neuroendocrine differentiation? Are IHC markers required and do they capture AR activity?
- Is the increased detection of small cell/NEPC due to increased awareness or is this due to more potent AR-directed therapies? Will the incidence of NEPC increase with recent approvals of potent AR-targeted drugs earlier in the disease (i.e., metastatic castrate-sensitive prostate cancer and nonmetastatic castration-resistant prostate cancer)?
- How well does loss of PSMA or PSMA heterogeneity on imaging in combination with FDG PET-CT noninvasively identify patients developing lineage plasticity? What other radiologic or radiomic (i.e., subvisual tools) may be applied for the early detection of lineage plasticity?
- Platinum sensitivity is also mediated by germline or somatic alterations involving DNA repair genes, which occurs in approximately 20% of CRPC independent of histology. What is the degree of overlap between DNA repair deficiency and lineage plasticity?
- Is reversal of phenotype or tumor kill the primary goal of therapy? What clinical endpoints may be used to assess these outcomes?
- What would a multiarm clinical trial design look like for patients developing lineage plasticity and AR-independent prostate cancer? Which clinical or molecular features are ready to use as inclusion criteria?

Lessons from Other Cancer Types (the Scope of the Problem)

Similar to prostate cancer, malignancies arising from other anatomic sites, tissues, and cell types also develop lineage plasticity as a mechanism of therapy resistance. For instance, 5% to 15% of *EGFR*-mutant lung adenocarcinomas transform to SCLC histology during acquired resistance to EGFR-targeted therapies with retention of the original *EGFR* mutation (37). Cases of small cell transformation in lung cancer have also been reported after immunotherapy (38). *RB1* and *TP53* genomic alterations are universally present in both *de novo* and transformed SCLC and rarely present in unselected lung adenocarcinomas other than those that later develop histologic transdifferentiation (39–41). Whether preexisting *RB1* and *TP53* loss may be used as biomar-

kers to identify high-risk lung adenocarcinoma patients for alternative treatments is yet to be determined. Understanding whether this predisposition for lineage plasticity is also the case for the subset of castration-resistant prostate adenocarcinomas and localized prostate cancers that harbor TP53/RB1 loss has important implications for the early detection and management. In melanoma, phenotypic switching with distinct cellular populations (e.g., invasive vs. proliferative) and developmental cell states (i.e., MITF low or high) frequently coexisting and dynamically regulated plays a central role in metastasis and therapy resistance (42-44). This switching is hypothesized to be largely regulated by epigenetic modifiers, hypoxia, and the tumor microenvironment, but specific factors remain to be fully elucidated. Similar to prostate cancer, much is still to be learned in melanoma plasticity regarding the number and types of phenotypic states that coexist and their interface with the genetics of the tumor (i.e., do some genomic lesions make the cells more or less responsive to plasticity signals?). In pancreatic ductal adenocarcinoma, lineage heterogeneity associates with poor outcomes; lineage tracing studies have pointed to an acinar cell of origin of neuroendocrine cells, and this is regulated by MYC and epigenomic changes in response to environmental signals (45). A subset of breast cancers also develop lineage plasticity, and in some cases, the luminal phenotype and/or estrogen receptor expression are lost with disease progression; this process may be mediated in part by subpopulations of cells with stem-like properties (46). Given these disease parallels, emerging mechanisms underlying plasticity, stemness, and cellular reprogramming during therapy resistance are pointing to shared mechanisms and potential targets across malignancies.

Summary

It is increasingly recognized that a subset of prostate cancers evades AR-targeted therapies through the development of lineage plasticity. This is associated with loss of AR or AR signaling, frequent *RB1/TP53* loss of function, and activation of alternative lineage programs including neuronal, neuroendocrine, stem-like, and developmental pathways. In some instances, lineage plasticity occurs directly through transdifferentiation processes, whereas in other situations, tumor cells dedifferentiate to a stem-like state followed by reprogramming to a new phenotype. Continued tumor evolution under treatment pressures may occur through clonal selection. Although there are many open questions, recent studies have identified newly relevant biological pathways and actionable targets. Addressing the outlined gaps in knowledge will ultimately accelerate the translation of new biologic discoveries into the clinic.

Disclosure of Potential Conflicts of Interest

H. Beltran is a consultant/advisory board member for Janssen, Sanofi Genzyme, and Astellas. H.I. Scher is a consultant/advisory board member for Amgen and Janssen. E.Y. Yu is a consultant/advisory board member for Amgen, Dendreon, Bayer, Merck, AstraZeneca, QED, Incyte, Tolmar, EMD Serono, Pharmacyclics, Seattle Genetics, and Janssen. A. Dicker holds ownership interest (including patents) in Oncohost, is a consultant/advisory board member for Roche, Oncohost, Google, Dreamit Ventures, EMD Serono, Janssen, Cybrexa, and Self Care Catalysts, and reports receiving other remuneration from Wilson Soncini. R. White is a consultant/advisory board member for Inc. E.J. Small holds ownership interest (including patents) in Fortis Therapeutics and Harpoon Therapeutics, Tolero Pharmaceuticals, and Beigene Therapeutics. T. Lotan

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Supplementary Information

Pre-meeting document with Working Group summaries and questions

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Genomic Characterization of Prostatic Ductal Adenocarcinoma Identifies a High Prevalence of DNA Repair Gene Mutations

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Abstract

PURPOSE—Ductal prostate cancer (dPC) is a rare variant of prostatic adenocarcinoma associated with poor outcomes. Although its histopathologic features are well characterized, the underlying molecular hallmarks of this aggressive subtype are not well described. We sought to provide a comprehensive overview of the spectrum of mutations associated with dPC.

METHODS—Three case series across multiple institutions were assembled. All patients had a diagnosis of dPC, and histopathologic classification was confirmed by an expert genitourinary pathologist. Case series 1 included men who were prospectively enrolled in a tumor sequencing study at the University of Washington (n = 22). Case series 2 and 3 included archival samples from men treated at Johns Hopkins Hospital (n = 21) and University of Calgary (n = 8), respectively. Tumor tissue was sequenced on a targeted next-generation sequencing assay, UW-OncoPlex, according to previously published methods. The frequency of pathogenic/likely pathogenic mutations are reported.

RESULTS—Overall, 25 patients (49%) had at least one DNA damage repair gene alteration, including seven (14%) with a mismatch repair gene mutation and 16 (31%) with a homologous repair mutation. Germline autosomal dominant mutations were confirmed or suspected in 10

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patients (20%). Activating mutations in the PI3K pathway (n = 19; 37%), WNT pathway (n = 16; 31%), and MAPK pathway (n = 8; 16%) were common.

CONCLUSION—This study strongly suggests that dPCs are enriched for actionable mutations, with approximately 50% of patients demonstrating DNA damage repair pathway alteration(s). Patients with dPC should be offered next-generation sequencing to guide standard-of-care treatment (eg, immune checkpoint inhibitors) or triaged toward an appropriate clinical trial (eg, poly [ADP-ribose] polymerase inhibitors).

INTRODUCTION

Ductal prostate cancer (dPC) is a rare prostate cancer variant characterized by large glands lined by tall, pseudostratified, columnar, neoplastic epithelial cells, typically arranged over fibrovascular cores or cribriform glands and associated with an aggressive clinical course.^{1–3} Outcomes for dPC generally mirror those of Gleason score 4 + 4 = 8 carcinomas, and tumors with at least 10% ductal morphology have been found to associate with a higher stage and suboptimal response to androgen deprivation.^{2,3} Overall, approximately 3% of all prostate cancers have some component of ductal histology.^{2,4}

Although the histologic features of dPC are well described, there is relatively little information regarding the underlying molecular alterations associated with this prostate cancer subtype. Fluorescence in situ hybridization studies have found that TMPRSS2:ERG fusions are present in 10% to 50% of patients with dPC, and ERG protein expression (consistent with TMPRSS2:ERG fusions) is also present in this range.^{5–8} Limited gene expression profiling studies have found similarities between dPC and patients with acinar tumors, and there is molecular evidence that concurrent ductal and acinar tumors are clonally related.^{4,9,10} More recent immunohistochemical profiling studies have demonstrated that positive phospho-mammalian target of rapamycin staining correlated with risk of biochemical recurrence in patients with ductal carcinoma.¹¹ In a separate study, it was found that loss of PTEN protein expression occurred more frequently in dPC compared with acinar adenocarcinoma, again, potentially implicating mammalian target of rapamycin signaling pathway in the pathobiology of dPC. However, these data remain controversial, because other studies have suggested a lower rate of PTEN protein loss in ductal carcinomas compared with Gleason score 8 acinar carcinomas.⁶ More recently, a study evaluating genomic and transcriptomic differences between foci of ductal and acinar prostatic carcinoma from the same individual found enrichment for mutations in CTNNB1 and PTEN within the ductal foci, with associated WNT- or PI3K- pathway activation.9

Given the rarity of dPC and the relative lack of information regarding the associated molecular features, we compiled a multi-institutional, international cohort of patients with dPC for targeted next-generation sequencing (NGS). We previously reported the NGS results from a small series characterizing patients with dPC at our institution (University of Washington [UW]).¹² In that preliminary study, we observed a high rate of DNA damage repair (DDR) mutations, including loss-of-function mutations in mismatch repair (MMR) genes. Building from our initial case series, we now report sequencing results from an expanded multiinstitutional collaborative cohort of 51 patients with dPC.

METHODS

Study Populations

We assembled three case series comprising 51 patients with dPC from institutions in the United States and Canada (Data Supplement). Histopathologic classification of all tumors was confirmed by an expert genitourinary pathologist at each institution. All tumor tissue was sequenced on the targeted NGS assay UW-OncoPlex according to previously published methods.^{12,13}

Case series 1 consisted of prostate cancer specimens (radical prostatectomies and needle biopsies of prostate and metastatic tumors) from 22 men actively receiving treatment at the University of Washington/Seattle Cancer Care Alliance who were prospectively identified as having a diagnosis of dPC. Tissue used for sequencing was acquired between January 2015 and March 2017. Preliminary sequencing results from this series have been previously published.¹² All men provided informed consent to have their tissue sequenced as part of this study.

Case series 2 included 21 radical prostatectomy samples. A subset was obtained from a tissue microarray composed of primary prostatectomy specimens from men with either dPC (n = 51) or Gleason pattern 4 acinar prostatic adenocarcinoma (n = 75) treated at Johns Hopkins Hospital (JHH) between 1984 and 2004. Details regarding this tissue microarray have been previously published.¹⁴ Additional patients with a ductal carcinoma in the dominant nodule were procured from consecutive radical prostatectomies performed at JHH. Case series 3 included archival tissue from eight men treated by transurethral resection of the prostate at the University of Calgary.

Blinded Morphologic Evaluation

To reevaluate the morphologic classification of all patients in a blinded manner, an expert genitourinary pathologist (J.I.E.) examined scanned digital images of a representative slide from each patient corresponding to the formalin-fixed paraffin-embedded (FFPE) block that was macrodissected for sequencing. Each patient was scored for percentage of the tumor that had ductal morphology overall, as well as the percentage of several described morphologic subtypes of ductal carcinoma: cribriform, papillary, gland-like, prostatic intraepithelial neoplasia–like and solid.

Macrodissection of Tumor Tissue

All tissue was previously FFPE. Hematoxylin and eosin-stained sections served as templates for either macro-dissecting the dPC component from 10-micron sections or obtaining 5.0- \times -0.6-mm punches from regions with the highest percentage of dPC.

Next-Generation Sequencing

For all patients, DNA was extracted from macrodissected FFPE samples and sequenced using the targeted NGS platform UW-OncoPlex, as that which interrogates approximately 1.8 Mb of DNA encompassing 262 genes. Briefly, genomic libraries were made from 500 ng of genomic DNA extracted from prostate tumor FFPE tissue and a custom Agilent (Santa

Clara, CA) SureSelect XT capture set used for target enrichment and sequenced on an Illumina (San Diego, CA) NextSEquation 500 instrument with paired-end 101 bp reads. A custom bioinformatics pipeline detects single nucleotide variants, indels of all sizes, structural rearrangements, *PMS2* pseudogene disambiguation, and copy number changes. Sequencing interpretation was performed by an expert molecular pathologist (C.C.P.). Reported alterations were limited to those deemed pathogenic or likely pathogenic (eg, loss of function mutations in tumor suppressors, activating mutations in genes involved in oncogenic signaling pathways).

All 262 genes in UW-OncoPlex were thoroughly reviewed for potential pathogenic germline mutations by an expert in clinical germline cancer predisposition testing (C.C.P.). All reported confirmed or suspected germline variants were carefully vetted by a team expert in variant classification comprising at least three individuals, per the usual clinical process. Of 18 suspected pathogenic germline mutations, 13 were confirmed in nontumor tissue. Of the five suspected germline mutations that did not have matched nontumor DNA, one additional patient was felt to represent a germline mutation after expert molecular pathologist review through cross-referencing against the ClinVar database and by multivariable analysis of the variant allele fraction in the context of tumor content, ploidy, and loss of heterozygosity status.^{15,16}

RESULTS

Patient Characteristics

Across the three cohorts ($N_{total} = 51$), the median age at the time of diagnosis/tissue acquisition was 67.5 years. The majority of patients with data on tumor stage (23 of 40; 57.5%) had T3 or higher disease. For patients with clinical follow-up (UW and University of Calgary, n = 28), seven (25%) were deceased, and 12 (43%) had developed metastatic disease during long-term follow-up. Additional demographics details are listed in Table 1.

dPC Genomics

Overall, our combined cohort of patients with dPC demonstrated a high number of recurrent genomic alterations (Fig 1; Data Supplement). These included alterations in genes involved in DDR repair (n = 24; 47%), PI3K pathway (n = 19; 37%), WNT-signaling pathway (n = 16; 31%), and MAPK signaling (n = 8; 16%). A large number of patients also had mutations in *FOXA1* (n = 17; 33%), *TP53* (n = 9; 18%), and *SPOP* (n = 6; 12%).

Recurrent DDR alterations.—Twenty-five (49%) of 51 patients had at least one alteration in a DDR pathway gene. Overall, seven of 51 patients (14%) had evidence of MMR alterations, six of whom had evidence of hypermutation (ie, 10 mutation per megabase), consistent with deficient MMR (one patient with monoallelic loss of *MSH2* was not hypermutated). Three patients with MMR alterations also had concurrent secondary mutations in homologous recombination (HR) pathway genes. Sixteen patients (31%) had an HR mutation in the absence of a concurrent MMR mutation. An additional patient with a hotspot *POLD1* mutation was ultramutated (ie, > 100 mutations per megabase).^{17,18} There were 10 patients (20%) with evidence of a pathogenic autosomal dominant germline

alteration in a DDR gene, which is significantly higher than reported by The Cancer Genome Atlas for patients with primary prostate cancer (20% v 5%; P <001) and numerically higher than unselected patients with metastatic prostate cancer (20% v 12%; P= .105).^{19,20} Of note, two individuals in our dPC cohort were carriers of recessive germline alterations in DDR pathway genes—one with an *ERCC2* alteration and the other with an *MUTYH* alteration. Neither had evidence that the second allele was affected in tumor tissue. Compared with published genomic data from men with localized and castration-resistant prostate cancer (CRPC), our combined cohort of men with dPC was significantly enriched for mutations in DDR genes (both MMR and HR genes), as well as other genes of interest (Table 2).^{20,21}

Additional recurrent genomic alterations.—Similar to localized and metastatic CRPC, mutations in *FOXA1* were frequently observed (n = 17; 33%).^{20,21} Interestingly, mutations in genes involved in WNT signaling were also frequent (n = 16; 31%). This includes activating/stabilizing mutations in CTNNB1 (n = 4), as well as inactivating mutations in APC(n = 12), a negative regulator of WNT pathway activation. Similar to a prior report, we found that *PTEN* alterations were generally mutually exclusive of mutations in genes associated with WNT-signaling activation (eg, APC and CTNNB1 mutations), although there was one patient with a pathogenic MSH2 mutation that had secondary alterations in APC, PTEN, and PIK3R1.9 There were three additional patients in whom WNT-pathway alterations co-occurred with PI3K-pathway alterations, including one patient with an APC and PIK3CA mutation, and two patients with CTNNB1 and PIK3CA mutations. Compared with patients with CRPC, there were fewer PTEN alterations and more *PIK3CA* mutations in our dPC cohort, with an overall similar incidence of PI3K-pathway alterations (Table 2). Alterations in AR were infrequent (n = 4; 8%); however, the majority of tissue samples sequenced were primary prostate tissue that had not been exposed to hormonal therapies. ETS fusions were significantly less common in our dPC cohort compared with patients with both localized and CRPC (Table 2).

Pathology correlates.—We have previously reported discordance between expert genitourinary pathologists in diagnosing dPC.²⁴ As such, we performed a secondary pathologic review on available patients. Overall, 46 of the patients (94%) included in this analysis had slides available for central pathologic review (performed by J.I.E. at JHH). Of five ductal histologic subtypes (ie, cribriform, papillary, gland-like, prostatic intraepithelial neoplasia–like, and solid), cribriform (n = 22), and papillary (n = 23) were the most common, and 16 patients showed multiple histologic subtypes present. Although the quantity of dPC in each patient varied, there was no evidence that percentage of ductal involvement correlated with the underlying mutational profile, and a high frequency of DDR mutations was observed regardless of the overall quantity of dPC reported on secondary pathology review (Table 3).

DISCUSSION

To our knowledge, this is the largest cohort of dPC to be examined by NGS. We confirmed that dPCs are enriched for actionable mutations and, remarkably, found that almost half had at least one alteration in a DDR pathway gene. When compared with contemporary prostate

cancer cohorts, we noted significant differences in the mutational profile of dPCs. For instance, in contrast to the Stand Up 2 Cancer-Prostate Cancer Foundation International Prostate Cancer Dream Team discovery set, which reported pathogenic DDR mutations in approximately 25% of unselected patients with metastatic CRPC, we found a significantly higher frequency of DDR alterations in dPCs, including loss-of-function mutations in MMR genes.²¹ In addition, because the vast majority of patients included in this analysis had primary tissue sequenced (48 of 51 patients), it is likely that DDR alterations are early, truncal events, which can be easily identified by sequencing archival tissue, negating the need to obtain fresh metastatic tissue in men with more advanced disease. Although we did not intentionally sequence the acinar carcinoma component in patients with mixed ductalacinar tumors, the fact that concurrent ductal and acinar carcinomas share common ERG rearrangements and other alterations suggests that the DDR alterations are likely shared between these components as well.^{4,9} This study adds to the literature suggesting that aggressive histologic subtypes of localized prostate cancer (eg, primary Gleason pattern 5 acinar carcinomas, small cell carcinomas, and now dPCs) may be enriched for MMR defects.25

It is also notable that in addition to DDR alterations, there were a number of recurrently mutated genes, including those involved in WNT-and PI3K-signaling pathways. Interestingly, and consistent with prior work from our group, we found that PI3K-signaling alterations occurred more commonly in ductal carcinoma via *PIK3CA* mutations than by PTEN gene alterations, which is in contrast to unselected patients with metastatic CRPC.^{6,21} These findings are also consistent with a recent report examining genomic and transcriptomic differences between dPC and acinar prostate cancer foci from the same individual.⁹ However, in that report, it is worth noting that the authors did not observe enrichment for MMR alterations, and DDR alterations were relatively infrequent. Whether this is due to differences between the two series or the fact that their sample size was relatively small (10 patients) is not clear. We also confirmed that ETS gene rearrangements were significantly less common in patients with dPC compared with both primary (The Cancer Genome Atlas) and metastatic (Stand Up 2 Cancer-Prostate Cancer Foundation) patients with prostate cancer.⁴ Importantly, because the NGS panel used in this study (UW-OncoPlex) provides intronic gene coverage for rearrangement hotspot areas in TMPRSS2 and other recurrently rearranged genes, it has a higher degree of sensitivity for detecting ETS fusions and other complex genomic rearrangements that could be missed by panels that only sequence exonic regions.^{13,26} These findings indicate that alternative drivers may underlie dPC biology.

Another interesting observation was the apparent enrichment in patients with dPC for germline DDR gene alterations. A previous study had suggested that men with germline DDR mutations (particularly HR mutations) were more likely to harbor components of ductal or intraductal histology than those with pure acinar histology (48% v 12%; P < .01), although it is recognized that ductal and intraductal features are considered to be histologically distinct.²⁷ In the current analysis, the prevalence of pathogenic or likely pathogenic germline DDR lesions was 20% (10 of 51), significantly higher than that observed in primary prostate cancers (20% v 5%; P < .001) or even in unselected sporadic metastatic prostate cancers (20% v 12%; P = .105).^{19,20} Taken together with the previous

study, these findings suggest that patients with dPC should be preferentially offered germline genetic testing even in the absence of metastatic disease. Indeed, knowledge of germline status in the localized disease setting could afford opportunities for modifying management and improving outcomes before metastases develop.

There were important differences between the cohorts included in this analysis. The JHH and Calgary cohorts were assembled from archival tissue and were highly selected. In contrast, the UW cohort comprised prospectively identified men receiving care for prostate cancer in the clinic, and thus represented a real-world example of selecting patients for sequencing on the basis of histology. Another key difference is that the JHH cohort only included patients who underwent prostatectomy, and no long-term follow-up data were available. Given that all patients in the JHH cohort were considered to be prostatectomy candidates, this raises the possibility that these men had less aggressive disease, especially in light of the fact that 70% of men in the Calgary and UW cohorts either died or developed metastatic disease.

It is also notable that the UW cohort included a number of patients who were disputed in terms of whether dPC was present, and overall, 12 patients (26%) included in this series who underwent secondary pathology review were felt to not contain significant ductal features (n = 11 from UW and n = 1 from JHH). It is important to bear in mind,Ductal Prostate Cancer Genomics however, that all patients included in this analysis were believed to contain a component of ductal histology by at least one expert genitourinary pathologist. In addition, because slides from UW were not scanned before macrodissecting the ductal component, we cannot exclude the possibility that the slides sent for secondary review were not representative of the slides used for sequencing. In addition, the observed interpathologist variance is consistent with prior experience evaluating patients with dPC.²⁸ Importantly, there were no clear differences in mutational profiles for patients felt to not possess a clear ductal component on secondary pathology review or between patients with pure versus mixed ductal histology (Table 3). Larger studies aimed at evaluating differences between ductal and acinar foci from the same patient are warranted but are beyond the scope of this study.

In conclusion, despite the heterogeneity of our cohort, these results indicate that patients with any fraction of dPC should be offered NGS, given that the presence of dPC histology can serve as a rapid means to select patients enriched for actionable mutations, particularly in MMR and HR genes. On the basis of this analysis, nearly half would qualify for treatment with investigational poly (ADP-ribose) polymerase inhibitors, platinum-based chemotherapy, and/or an immune checkpoint inhibitor.^{29–34}

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

Acknowledgments

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CONTEXT

Key Objective

The key objective was to provide an overview of the genomic alterations associated with ductal prostate cancers.

Knowledge Generated

Ductal prostate cancers are associated with a high incidence of mutations in DNA repair genes. Affected genes include those mediating homologous recombination and mismatch repair pathways.

Relevance

Because mutations in genes involved in DNA repair are highly actionable, sequencing all patients with ductal prostate cancer should be considered.



FIG 1.

Landscape of genomic alterations across 51 patients with ductal prostate cancer. Each column represents one patient. Pathogenic mutations were those predicted to either activate oncogenic signaling pathways (eg, WNT-or PI3K-signaling) or inactivate tumor suppressors (eg, DNA damage repair [DDR] genes, *TP53*). HR, homologous recombination; MMR, mismatch repair; VUS, variant of uncertain significance.

TABLE 1.

Demographics and Characteristics

Characteristic	Value
Median age (range), years	67.5 (47–94)
Gleason*	
7	4 (13)
8	7 (23)
9	18 (60)
10	1 (3)
Metastatic disease at presentation †	11 (26)
Source of tissue for sequencing	
TURP	8 (15)
Prostatectomy	29 (56)
Prostate needle biopsy	11 (21)
Metastatic biopsy	3 (6)

NOTE. Data are No. (%) unless otherwise indicated.

Abbreviation: TURP, transurethral resection of the prostate.

 * Gleason score was only provided for patients with mixed ductalacinar histology (n = 30).

 † Disease state at time of initial presentation was only available for Johns Hopkins Hospital and University of Washington (n = 43).

TABLE 2.

Recurrent Genomic Alterations in Patients With Ductal Prostate Cancer Compared With Men With Sporadic Localized and Castration-Resistant Prostate Cancer^{22,23}

	No. of N	Autations (% of men		Ductal Cohort Versus	TCGA	Ductal Cohort Versu	IS SU2C
Gene/Pathway	Ductal Cohort (n = 51)	TCGA $(n = 333)^*$	$SU2C \ (n=150) \mathring{T}$	RR (95% CI)	Р	RR (95% CI)	Р
Any DDR	25 (49)	62 (19)	34 (23)	2.63 (1.84 to 3.77)	< .001	2.16 (1.44 to 3.25)	< .001
MMR alteration	7 (14)	11 (3)	3 (2)	4.16 (1.69 to 10.23)	.002	6.86 (1.84 to 25.55)	.004
MSH2	5 (10)	5 (2)	3 (2)	6.53 (1.96 to 21.77)	.002	4.90 (1.21 to 19.79)	.026
MLH1	1 (2)	1 (0.3)	1 (0.7)	6.53 (0.41 to 102.76)	.182	2.94 (0.18 to 46.17)	.443
MSH6	1 (2)	6 (2)	0	1.09 (0.13 to 8.85)	.937		.254
PMS2	0	4 (1)	0		1.00		
High penetrance HR alterations	15 (29)	44 (13)	29 (19)	2.23 (1.34 to 3.69)	.002	1.52 (0.89 to 2.60)	.125
BRCA1	0	4 (1)	1 (0.7)		1.00		1.00
BRCA2	9 (18)	11 (3)	19 (13)	5.34 (2.33 to 12.25)	< .001	1.39 (0.67 to 2.88)	.371
ATM	5 (10)	24 (7)	7 (7.3)	1.36 (0.54 to 3.40)	.511	1.34 (0.49 to 3.66)	.572
PALB2	1 (2)	5 (2)	0	1.31 (0.16 to 10.95)	.806		.254
WNT pathway	16 (31)	27 (8)	19 (13)	3.87 (2.25 to 6.66)	< .001	2.48 (1.38 to 4.44)	.002
CTNNB1	4 (8)	9 (3)	6 (4)	2.90 (0.93 to 9.08)	.067	1.96 (0.58 to 6.67)	.281
APC	12 (24)	18 (5)	13 (9)	4.35 (2.23 to 8.49)	< .001	2.71 (1.32 to 5.56)	.006
PI3K pathway	19 (38)	103 (31)	73 (49)	1.20 (0.81 to 1.78)	.351	0.77 (0.52 to 1.13)	.182
PTEN	8 (16)	58 (17)	61 (41)	0.90 (0.46 to 1.77)	.762	0.39 (0.20 to 0.75)	.005
PIK3CA	9 (18)	16 (5)	8 (5)	3.67 (1.71 to 7.87)	.001	3.31 (1.35 to 8.12)	600.
PIK3R1	4 (8)	22 (7)	8 (5)	1.19 (0.43 to 3.30)	.743	1.47 (0.46 to 4.68)	.514
AKT1	1 (2)	7 (2)	2 (1)	0.93 (0.12 to 7.43)	.948	1.47 (0.14 to 15.88)	.751
TSC1	1 (2)	5 (2)	2 (1)	1.31 (0.16 to 10.95)	.806	1.47 (0.14 to 15.88)	.751
MAPK pathway	8 (16)	13 (4)	11 (7)	4.02 (1.75 to 9.21)	.001	2.14 (0.91 to 5.02)	.081
BRAF	3 (6)	12 (4)	7 (5)	1.63 (0.48 to 5.59)	.435	1.26 (0.34 to 4.69)	.73
KRAS	3 (6)	1 (0.3)	4 (3)	19.59 (2.08 to 184.72)	600.	2.21 (0.51 to 9.53)	.289
MAP2K1	2 (4)	1 (0.3)	1 (0.7)	13.06 (1.21 to 141.42)	.035	5.88 (0.54 to 63.52)	.144

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	N0. 01	Mutations (% of mer	()	Ductal Cohort Versu	s TCGA	Ductal Cohort Vers	IS SU2C
Gene/Pathway	Ductal Cohort (n = 51)	$TCGA (n = 333)^{*}$	SU2C $(n = 150)^{\dagger}$	RR (95% CI)	Ρ	RR (95% CI)	Ρ
Other							
ETS fusions	4 (8)	199 (60)	84 (56)	0.13 (0.05 to 0.34)	< .001	0.14 (0.05 to 0.36)	< .001
POLD1	1 (2)	2 (1)	0	3.26 (0.30 to 35.36)	.330	I	.254
CHEK2	3 (6)	10 (3)	3(2)	1.96 (0.56 to 6.88)	.294	2.94 (0.61 to 14.12)	.178

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Abbreviations: DDR, DNA damage repair; HR, homologous recombination; MMR, mismatch repair; RR, relative risk; SU2C, Stand Up 2 Cancer; TCGA, The Cancer Genome Atlas.

 $^{*}_{\rm The}$ TCGA data set comprises 333 men with localized prostate cancer.²⁰

 $\dot{\tau}$ SU2C-PCF International Prostate Cancer Dream Team discovery set comprises 150 men with metastatic castration-resistant prostate cancer. The genomic landscape of this population has been previously published.21
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Key Genomic Features Stratified by Ductal Involvement

Ductal Involvement	No.	Any DDR, No. (%)	Ρ	MMR, No. (%)	Ρ	HRD, No. (%)	Ρ	Germline DDR, No. (%)*	Ρ
Ductal features present	12	8 (67)	.314	3 (25)	.173	6 (50)	.37	5 (42)	.265
Ductal features absent	34	15 (44)		3 (9)		12 (35)		7 (23)	1
Pure ductal	10	5 (50)	-	1 (10)	-	5 (50)	.489	1 (13)	.402
Not pure ductal	35	18 (51)		5 (14)		13 (37)		11 (32)	

s and extent of ductal histology were performed. One patient classified as positive for ductal involvement did not provide an estimate on percent involvement.

Abbreviations: DDR, DNA damage repair; HRD, homologous recombination deficiency; MMR, mismatch repair.

 $_{\star}^{*}$ Three patients were indeterminate regarding whether the DDR alteration was germline versus somatic and were therefore excluded from this analysis.

Real-World Outcomes of Sipuleucel-T Treatment in PROCEED, a Prospective Registry of Men With Metastatic Castration-Resistant Prostate Cancer

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BACKGROUND: The large registry, PROVENGE Registry for the Observation, Collection, and Evaluation of Experience Data (PROCEED) (NCT01306890), evaluated sipuleucel-T immunotherapy for asymptomatic/minimally symptomatic metastatic castration-resistant prostate cancer (mCRPC). METHODS: PROCEED enrolled patients with mCRPC receiving 3 biweekly sipuleucel-T infusions. Assessments included overall survival (OS), serious adverse events (SAEs), cerebrovascular events (CVEs), and anticancer interventions (ACIs). Follow-up was for ≥3 years or until death or study withdrawal. RESULTS: In 2011-2017, 1976 patients were followed for 46.6 months (median). The median age was 72 years, and the baseline median prostate-specific antigen level was 15.0 ng/mL; 86.7% were white, and 11.6% were African American. Among the patients, 1902 had 1 or more sipuleucel-T infusions. The median OS was 30.7 months (95% confidence interval [CI], 28.6-32.2 months). Known prognostic factors were independently associated with OS in a multivariable analysis. Among the 1255 patients who died, 964 (76.8%) died of prostate cancer (PC) progression. The median time from the first infusion to PC death was 42.7 months (95% CI, 39.4-46.2 months). The incidence of sipuleuceI-T-related SAEs was 3.9%. The incidence of CVEs was 2.8%, and the rate per 100 person-years was 1.2 (95% CI, 0.9-1.6). The CVE incidence among 11,972 patients with mCRPC from the Surveillance, Epidemiology, and End Results-Medicare database was 2.8%; the rate per 100 person-years was 1.5 (95% CI, 1.4-1.7). One or more ACIs (abiraterone, enzalutamide, docetaxel, cabazitaxel, or radium 223) were received by 77.1% of the patients after siguleucel-T; 32.5% and 17.4% of the patients experienced 1- and 2-year treatment-free intervals, respectively. CONCLUSIONS: PROCEED provides contemporary survival data for sipuleucel-T-treated men in a real-world setting of new life-prolonging agents, which will be useful in discussing treatment options with patients and in powering future trials with sipuleucel-T. The safety and tolerability of sipuleucel-T in PROCEED were consistent with previous findings. Cancer 2019;125: 4172-4180. © 2019 The Authors. Cancer published by Wiley Periodicals, Inc. on behalf of American Cancer Society. This is an open access article under the terms of the Creative Commons Attribution-NonCommercial License, which permits use, distribution and reproduction in any medium, provided the original work is properly cited and is not used for commercial purposes.

KEYWORDS: immunotherapy, overall survival, prostate cancer, safety.

INTRODUCTION

Sipuleucel-T is an autologous cellular immunotherapy for asymptomatic or minimally symptomatic metastatic castration-resistant prostate cancer (mCRPC). In the pivotal phase 3 trial Immunotherapy for Prostate Adenocarcinoma Treatment (IMPACT; NCT00065442), sipuleucel-T significantly reduced the risk of death among patients with mCRPC and improved median overall survival (OS) by 4.1 months versus a placebo.¹ Sipuleucel-T is recommended

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across multiple guidelines²⁻⁷ and as a first-line mCRPC treatment option^{2,3,7} (category 1 recommendation by the National Comprehensive Cancer Network). In patients with low baseline prostate-specific antigen (PSA) levels (\leq 22.1 ng/mL) in IMPACT, retrospective analyses demonstrated a 13-month greater improvement in OS with sipuleucel-T versus a placebo.⁸

Sipuleucel-T was generally well tolerated across sev-eral prostate cancer (PC) trials.^{1,9-14} The most common adverse events (\geq 15%) were chills, fatigue, fever, back pain, nausea, joint ache, and headache of mostly mild to moderate severity. Incidences of grade 3 and 4 adverse events were 23.6% and 4.0%, respectively, with sipuleucel-T and 25.1% and 3.3%, respectively, with a placebo. Serious adverse events (SAEs) included acute infusion reactions and cerebrovascular events (CVEs).¹⁴ Data from 4 randomized, double-blind, placebo-controlled clinical trials (D9901 [NCT00005947],^{12,13} D9902A [NCT01133704],¹³ IMPACT,¹ and PROTECT [NCT00779402]⁹) showed that CVEs, excluding transient ischemic attacks (TIAs), occurred in 3.5% (sipuleucel-T) and 2.6% (placebo) of patients (not statistically significant).¹⁴ The clinical significance and causal relationship are uncertain.

The PROVENGE Registry for the Observation, Collection, and Evaluation of Experience Data (PROCEED; NCT0136890), evaluated real-world safety data and provided an opportunity to analyze efficacy outcomes of mCRPC management involving sipuleucel-T during a time of rapidly evolving management protocols.

MATERIALS AND METHODS

Study Design and Patients

PROCEED was a multicenter, open-label, observational registry conducted at urology and medical oncology clinics in private practice and at academic sites (see the Supporting Methods section in the supporting information). The primary and secondary objectives were to quantify CVE risk and OS, respectively. SAEs were collected. For a protocol-specified, exploratory objective, the proportion of patients receiving subsequent anticancer interventions (ACIs) was assessed. Both the protocol and its single amendment were approved by each center's Institutional Review Board before patient enrollment. Before participation, patients provided written informed consent.

Treatment

No randomization, blinding, or treatment masking was conducted. Patients underwent a 1.5 to $2.0 \times$ blood

volume leukapheresis for antigen-presenting cell (APC) isolation with a sipuleucel-T infusion 3 to 4 days later; this was repeated at approximately 2-week intervals for 3 infusions.

Study Procedures

Safety and survival were assessed during normal clinical practice and were reported every 3 months after the final sipuleucel-T infusion. Use of central venous catheters at the physician's discretion was recorded. PROCEED did not require the recording of all PC-related events after sipuleucel-T treatment. ACI use after the first infusion of sipuleucel-T was recorded. Decisions to use further treatment and the choice and timing of ACI use were at the physician's discretion.

All SAEs (according to MedDRA version 19.1) from the first sipuleucel-T infusion through 60 days after the final infusion were captured. Thereafter, SAEs at least possibly related to sipuleucel-T were recorded. All CVE data were collected, regardless of causality, severity, or outcome, throughout PROCEED. CVEs, adjudicated by an independent neurologist, included all strokes (ischemic and hemorrhagic), intracranial hemorrhage, and TIAs (focal neurologic deficit episodes resolving within 24 hours).¹⁵

Patients were followed for ≥ 3 years or until death or study withdrawal. The cause of death was reported on a case report form. An end-of-study closeout form was completed to ascertain death. For patients lost to follow-up, sites performed a death-sweep search for obituaries.

Statistical Analyses

The sample size was based on an evaluation of the CVE rate. With \geq 1500 patients followed for \geq 3 years (4500 person-years), the 95% confidence interval (CI) for estimating the CVE incidence rate per 100 patient-years would have a width of <1 unit as long as the observed rate was <2.8/100 patient-years.¹⁶ For 1500 patients, the probability of observing 1 or more occurrences of a rare event (1 in 1000) would be 0.78. The sample size was increased from 1500 to allow for 4500 person-years of follow-up.

The predefined analysis population was all patients receiving 1 or more full or partial (>0 mL) sipuleucel-T infusions. Endpoints were summarized descriptively unless otherwise stated. All analyses were performed with SAS (versions 9.2 and 9.4; SAS Institute, Inc, Cary, North Carolina).

OS was measured from the date of the first sipuleucel-T infusion for ≥ 3 years or until the patient had

otherwise gone off the study. If death was not reported, patients were censored from the last study visit. OS data were analyzed with Kaplan-Meier methodology; Cox proportional hazards regression was used to calculate hazard ratios and 95% CIs. These were post hoc analyses with P values that were not adjusted for multiplicity. Univariable, stepwise Cox modeling and multivariable analysis were performed to assess for independent baseline predictors of OS that had both clinical and statistical relevance. Variables were selected in a stepwise process for the final multivariable analysis model at a .1 significance level (see the Supporting Methods for more details). The association of OS with natural logarithm-transformed sipuleucel-T product parameters (APC activation, APC cell count, and total nucleated cell count) was estimated with a Cox proportional hazards regression model; statistical significance was a 2-tailed P value <.05. A post hoc analysis evaluated OS by baseline PSA quartiles; hazard ratios and 95% CIs were calculated by the Cox regression model.

Primary summarization of CVEs excluded TIAs for consistency with how CVE rates had been previously defined.¹⁴ CVEs including TIAs were summarized separately. The PROCEED CVE incidence was compared with a retrospective analysis of the incidence of first-time CVEs in men 65 years old or older with PC, including those with metastatic PC and a castrated state, within the Surveillance, Epidemiology, and End Results (SEER)–Medicare database in 1999-2013 (see the supporting information).

An exploratory analysis described the proportion of patients receiving ACIs after the first sipuleucel-T infusion. The Kaplan-Meier method estimated the proportion of ACI use at 1 and 2 years.

RESULTS

Patients and Treatment

PROCEED was conducted from January 27, 2011 (the first patient registered), to January 17, 2017 (the last patient visit); 1976 consenting patients were enrolled across 192 sites. Overall, 1902 patients received 1 or more sipuleucel-T infusions: 1248 (65.6%) were treated in oncology practices, and 654 (34.4%) were treated in urology practices. Most patients (79.1%) received sipuleucel-T at 140 community clinics; the remainder received it at 52 academic centers (see the Supporting Results in the supporting information for study discontinuation reasons).

Central venous catheters were used in 891 patients (46.8%). Overall, 1813 patients (95.3%) received 3 sipuleucel-T infusions, 57 (3.0%) received 2, and 32 (1.7%) received 1. Reasons for 3 or fewer infusions included an SAE (34 [1.8%]), other (32 [1.7%]), disease progression after the first infusion (22 [1.2%]), patient refusal (16 [0.8%]; including a refusal to transfer location or answer study questions), and venous access problems (4 [0.2%]). Multiple reasons for noninfusion were possible.

Table 1 lists patient characteristics for PROCEED and for IMPACT sipuleucel-T--treated patients for comparison.¹ The median patient age was 72 years; 86.7% were white, and 11.6% were African American. Most patients had an Eastern Cooperative Oncology Group performance status of 0 or 1. The median baseline PSA level was 15.0 ng/mL (interquartile range, 5.2-46.1 ng/mL). Some patients received prior docetaxel, abiraterone, or enzalutamide (commercially or as an investigational agent). Most had bone-dominant metastases with or without lymph node involvement. The metastatic site or status was not reported for 19 patients (1.0%). Supporting Table 1 lists PROCEED baseline CVE risk factors.

Overall Survival

The median OS was 30.7 months (95% CI, 28.6-32.2 months; Fig. 1); the median follow-up was 46.6 months. During follow-up, 1255 patients (66.0%) died. Death or survival could not be ascertained for 45 patients. The main cause of death was PC progression (964 of 1255 [76.8%]); the median time to PC-specific death was 42.7 months (95% CI, 39.4-46.2 months). Other causes of death were unknown (154 [12.3%]), other (136 [10.8%]), a cardiac event (42 [3.3%]), a CVE (17 [1.4%]), and a new primary cancer (8 [0.6%]). More than 1 cause of death could be recorded for a patient.

A post hoc analysis indicated that the median OS was longer for patients in the lowest baseline PSA quartile (\leq 5.27 ng/mL) than patients in the second (>5.27 to \leq 15.08 ng/mL), third (>15.08 to \leq 46 ng/mL), and fourth quartiles (>46 ng/mL): 47.7 months (95% CI, 43.5-50.7 months), 33.2 months (95% CI, 30.9-35.5 months), 27.2 months (95% CI, 24.1-29.8 months), and 18.4 months (95% CI, 15.9-21.2 months), respectively. The hazard ratios for each quartile versus the lowest quartile were 1.6 (95% CI, 1.3-1.9), 2.0 (95% CI, 1.7-2.4), and 3.0 (95% CI, 2.6-3.6), respectively.

Univariable analyses showed that 15 evaluated baseline characteristics were significant predictors of OS (Supporting Table 2). Eleven characteristics were included in the final primary multivariable analysis. Of these, 10 were associated with OS at a significance level

TABLE 1. Demographics, Baseline Disease Characteristics, and Prior Prostate Cancer Treatments in PROCEED and IMPACT¹

Parameter	PROCEED Safety Population (n = 1902)	IMPACT Sipuleucel-T–Treated Arm (n = 341)
Age, median (range, min-max), y	72 (42-97)	72 (49-91)
Race, No. (%)		
White	1649 (86.7)	305 (89.4)
Black or African American	221 (11.6)	23 (6.7)
Asian	22 (1.2)	2 (0.6)
Other	10 (0.5)	11 (3.2)
ECOG performance status, No. (%)		
0	1265 (66.5)	280 (82.1)
1	571 (30.0)	61 (17.9)
≥2	42 (2.2)	0
Unknown	24 (1.3)	0
Gleason sum reported, No. (%)		
≤7	790 (41.5)	257 (75.4)
≥8	963 (50.6)	84 (24.6)
Unknown	149 (7.8)	0
Charlson Comorbidity Index, No. (%)		NA
Low (0-1)	1682 (88.4)	
High (>2)	220 (11.6)	
Bone metastases. No. (%)	n = 1595	
1-10	1117 (70.0)	195 (57.2)
>10	274 (17.2)	146 (42.8)
Unknown	204 (12.8)	0
Disease locations, No. (%)	n = 1883	n = 340
Bone only	1223 (64.3)	173 (50.7)
Bone and lymph nodes	313 (16.5)	143 (41.9)
I ymph nodes only	257 (13.5)	24 (7 0)
Visceral + bone or lymph nodes	90 (4 7)	0
Liver	21 (1 1)	0
	61 (3.2)	0
Brain	2 (0.1)	0
Visceral site(s) not reported	13 (0.7)	0
Laboratory parameters median (IOB 01-03)	13 (0.7)	0
	82 (63-115)	99 (75-146)
	n = 1/99	33 (73 143)
Hemoglobin g/dl	12 8 (11 8-13 7)	12 9 (11 7-13 7)
Hemoglobili, g/dE	n – 1794	12.3 (11.1 10.1)
Lastate debudrogenase 11/1	186 (150, 218)	104 (172 224)
Lactate deliverogenase, 0/L	100(109-210)	194(172-224) n = 340
PSA ng/ml	15 0 (5 2-46 1)	51 7 (22 5-140 3)
T SA, IIg/IIIE	13.0(0.2-40.1)	31.7 (22.3-140.3)
Interval from diagnosis to first sinulousal T	5 0 (2 3 Q 4)	71 (4 4 10 7)
infusion modian (IOP O1 O3) v	5.0(2.5-5.4)	7.1 (4.4-10.7)
Prior local cancer therapy, No. (%)	11 = 1599	
No local thorapy (systemic thorapy only)	420 (22.6)	85 (24 0)
Redical prostatestemy close	429 (22.0)	65 (24.9) 46 (12.5)
	270 (10.3)	40 (13.3)
Radiction therepy alone (external heam/	575 (15.5)	110 (20.9)
hadiation therapy alone (external beam/	504 (29.7)	112 (32.8)
Driacing interapy)		
Androgon torgeting therapy ^a	1001 (00 1)	070 (01 0 ^b
	1001 (90.1)	219 (01.0)
	302 (20.1) 1566 (00.0)	 2.41 (100\ ^C
	157 (0.2)	341 (100)
Enzolutomido	107 (0.3) E4 (0.9)	0
Chemotherapy	34 (2.0)	U
Depetevel	015 (11 0)	
	213(11.3)	əə (15.5)
Dadium 222	32 (1.7) 1 (0.1)	U
naululli 220	i (U.I)	U

Abbreviations: ALP, alkaline phosphatase; ECOG, Eastern Cooperative Oncology Group; IMPACT, Immunotherapy for Prostate Adenocarcinoma Treatment; IQR, interquartile range; LHRH, luteinizing hormone releasing hormone; max, maximum; min, minimum; NA, not applicable; PROCEED, PROVENGE Registry for the Observation, Collection, and Evaluation of Experience Data; PSA, prostate-specific antigen; Q1, first quartile; Q3, third quartile. PROCEED was observational, so calculations were based on values from the number of patients for whom data were available. ^aExcluded enzalutamide.

^bPatients received complete androgen blockade treatment.

^cPatients received an LHRH analogue.



Figure 1. OS in PROCEED as a Kaplan-Meier plot with a 95% Hall-Wellner band. CI indicates confidence interval; OS, overall survival; PROCEED, PROVENGE Registry for the Observation, Collection, and Evaluation of Experience Data.

below .05 (Table 2): age, ethnicity, Eastern Cooperative Oncology Group performance status, time since diagnosis, PSA, alkaline phosphatase, hemoglobin, lymph node only metastases, prior abiraterone/enzalutamide, and prior docetaxel/cabazitaxel.

Cumulative sipuleucel-T product parameters (Supporting Table 3) per unit increase correlated with OS.

Safety

All-grade SAEs, regardless of causality, were reported in 260 patients (13.7%); the most common SAEs were disease progression (28 patients), cerebrovascular accident (16 patients), chills (13 patients), syncope (12 patients), and device-related infection (10 patients; Table 3). Seventy-four patients (3.9%) had 1 or more SAEs considered possibly or probably related to the study drug (all grades); the most common were chills (13 [0.7%]), cerebrovascular accident (9 [0.5%]), deep vein thrombosis (4 [0.2%]), device-related infection (4 [0.2%]), pulmonary embolism (4 [0.2%]), and pyrexia (4 [0.2%]). Grade 3 to 5 SAEs, regardless of causality, occurred in 175 patients (9.2%; Table 3). The incidence of grade 4 SAEs was 1.1% (n = 21). Fifty-two patients (2.7%) had grade 5 SAEs, and 22 deaths were due to disease progression. Central venous catheter-related SAEs were reported in 19 patients

TABLE 2. Final Primary Multivariable Analysis of Overall Survival in PROCEED

Baseline Covariate	HR (95% CI)	P^{a}
Log PSA (ng/mL)	1.22 (1.16-1.27)	<.001
Hemoglobin, per g/dL increase	0.87 (0.83-0.91)	<.001
ECOG performance status, >0 vs 0	1.22 (1.05-1.42)	.009
Log ALP (U/L)	1.60 (1.42-1.81)	<.001
Age (y), >median vs ≤median	1.30 (1.12-1.50)	<.001
Race, white vs all others	1.64 (1.30-2.06)	<.001
Time since diagnosis (y), >median vs ≤median	0.72 (0.62-0.83)	<.001
Lymph node only metastases, yes vs no	0.79 (0.63-0.99)	.044
Visceral metastases, any vs none	1.30 (0.95-1.78)	.098
Prior docetaxel/cabazitaxel, yes vs no	1.54 (1.25-1.90)	<.001
Prior abiraterone/enzalutamide, yes vs no	1.53 (1.16-1.27)	<.001

Abbreviations: ALP, alkaline phosphatase; CI, confidence interval; ECOG, Eastern Cooperative Oncology Group; HR, hazard ratio; PROCEED, PROVENGE Registry for the Observation, Collection, and Evaluation of Experience Data; PSA, prostate-specific antigen.

^aMultivariable Cox modeling.

(1.0%); 13 were grade 3 or 4 with no grade 5 SAEs. Of these 19 patients, 2 and 5 had 1 and 2 sipuleucel-T infusions, respectively.

The overall incidence of adjudicated CVEs (excluding TIAs) in PROCEED was 2.8% (n = 54), and the rate per 100 person-years was 1.2 (95% CI, 0.9-1.6; Supporting Table 4). In the SEER-Medicare data analyses of men with PC at diagnosis who were metastatic at

TABLE 3. Overall Summary of All-Grade SAEs and Grade 3 to 5 SAEs Occurring in 3 (0.2%) or More Patients (in the All-Grade List) Regardless of Causality (n = 1902) in PROCEED

	(%)	
SAE	All Grades	Grades 3-5
Any SAE	260 (13.7)	175 (9.2)
Disease progression	28 (1.5)	25 (1.3)
Cerebrovascular accident	16 (0.8)	11 (0.6)
Chills	13 (0.7)	0 (0)
Syncope	12 (0.6)	7 (0.4)
Device-related infection	10 (0.5)	7 (0.4)
Acute kidney injury	8 (0.4)	7 (0.4)
Deep vein thrombosis	8 (0.4)	2 (0.1)
Pulmonary embolism	8 (0.4)	7 (0.4)
Anemia	7 (0.4)	2 (0.1)
Dyspnea	7 (0.4)	6 (0.3)
Chest pain	6 (0.3)	2 (0.1)
Myocardial infarction	6 (0.3)	5 (0.3)
Pyrexia	6 (0.3)	2 (0.1)
Subdural hematoma	6 (0.3)	6 (0.3)
TIA	6 (0.3)	1 (0.1)
Cerebral hemorrhage	5 (0.3)	5 (0.3)
Pneumonia	5 (0.3)	3 (0.2)
Cerebral infarction	4 (0.2)	4 (0.2)
Congestive cardiac failure	4 (0.2)	3 (0.2)
Dehydration	4 (0.2)	3 (0.2)
Device-related sepsis	4 (0.2)	3 (0.2)
Intracranial hemorrhage	4 (0.2)	2 (0.1)
Nausea	4 (0.2)	1 (0.1)
Spinal cord compression	4 (0.2)	4 (0.2)
Vomiting	4 (0.2)	4 (0.2)
Asthenia	3 (0.2)	1 (0.1)
Atrial fibrillation	3 (0.2)	1 (0.1)
Back pain	3 (0.2)	2 (0.1)
Bacteremia	3 (0.2)	1 (0.1)
Confusional state	3 (0.2)	1 (0.1)
Constipation	3 (0.2)	2 (0.1)
Fall	3 (0.2)	3 (0.2)
Hematuria	3 (0.2)	1 (0.1)
Hypotension	3 (0.2)	2 (0.2)
Infusion-related reaction	3 (0.2)	2 (0.2)
Presyncope	3 (0.2)	1 (0.1)

Abbreviations: PROCEED, PROVENGE Registry for the Observation, Collection, and Evaluation of Experience Data; SAE, serious adverse event; TIA, transient ischemic attack.

follow-up and in a castrated state (n = 11,972), the CVE incidence (excluding TIAs) was 2.8%, and the rate per 100 person-years was 1.5 (95% CI, 1.4-1.7; Supporting Table 5).

Subgroup analyses of CVEs (excluding TIAs) showed higher CVE rates in older patients, African Americans, patients with more advanced PC, and those with preexisting conditions associated with CVEs (Supporting Table 6). Nine patients had a TIA (3 concurrent with another CVE and 6 in isolation). Thus, 60 PROCEED patients (3.2%) had CVEs, including TIAs, and the rate per 100 person-years was 1.3 (95% CI, 1.0-1.7; Supporting Table 4). The observed median time to a CVE (including TIAs) from the last sipuleucel-T infusion was

TABLE 4. Proportion of Patients Receiving an Overall Survival-Prolonging ACI After Sipuleucel-T Treatment

Posttreatment ACI	Safety Population (n = 1902)	Patients Who Died During PROCEED (n = 1255)
No. of posttreatment ACIs,		
No. (%)		
0	419 (22.0)	287 (22.9)
1	565 (29.7)	329 (26.2)
2	462 (24.3)	326 (26.0)
3	319 (16.8)	216 (17.2)
4	126 (6.6)	87 (6.9)
5	11 (0.6)	10 (0.8)
Specific posttreatment ACI,		
No. (%)		
Abiraterone	1036 (54.5)	663 (52.8)
Enzalutamide	831 (43.7)	514 (41.0)
Docetaxel	739 (38.9)	553 (44.1)
Cabazitaxel	309 (16.2)	236 (18.8)
Radium 223	90 (4.7)	61 (4.9)

Abbreviation: ACI, anticancer intervention; PROCEED, PROVENGE Registry for the Observation, Collection, and Evaluation of Experience Data.

321 days (10.5 months; interquartile range, 79-689 days or 2.6-22.6 months). For patients with a CVE (including TIAs), the number and percent of patients with CVE onset within \leq 30, 31-60, 61-180, and >181 days of the most recent sipuleucel-T infusion were 10 (16.7%), 4 (6.7%), 9 (15.0%) and 37 (61.7%), respectively. No appreciable differences in the CVE ± TIA incidence or rate were observed between patients with or without a central venous catheter (Supporting Table 7).

Protocol-Specified, Exploratory Analysis: ACIs

Three hundred thirty-eight patients (17.8%) received an OS-prolonging ACI (abiraterone, enzalutamide, docetaxel, cabazitaxel, or radium 223) before sipuleucel-T. Approximately one-third of the patients (32.5%) did not receive any OS-prolonging ACI at 1 year, and 17.4% did not at 2 years after sipuleucel-T treatment. Of these patients, 9.5% and 7.4% had received an ACI before sipuleucel-T; thus, most of these patients had sipuleucel-T as first-line mCRPC therapy. Among patients in the lowest baseline PSA quartile (\leq 5.27 ng/mL), 44.1% and 25.8% did not receive an ACI at 1 and 2 years, respectively. Of these, 94.3% and 95.0% received sipuleucel-T before any other ACI.

During PROCEED, 1483 of all patients (78.0%) received 1 or more OS-prolonging ACIs, and 48.3% received 2 or more lines of treatment after sipuleucel-T (Table 4). The most commonly used OS-prolonging ACIs after sipuleucel-T treatment were abiraterone (1036 [54.5%]), enzalutamide (831 [43.7%]), and docetaxel

(739 [38.9%]; Table 4). Having sipuleucel-T as the only OS-prolonging treatment in PROCEED was reported in 22.0% of the patients (n = 419).

Similar patterns of ACI use were observed in patients who died during PROCEED (n = 1255), with 968 patients (77.1%) receiving 1 or more OS-prolonging ACIs and 50.9% receiving 2 or more lines of treatment after sipuleucel-T (Table 4). The most common OS-prolonging ACIs reported in those who died were abiraterone (52.8%), docetaxel (44.1%) and enzalutamide (41.0%; Table 4). Sipuleucel-T was the only OSprolonging ACI prescribed in PROCEED for 22.9% of these patients (n = 287).

DISCUSSION

Since the conduct of the phase 3 IMPACT trial¹ with sipuleucel-T (2003-2007), mCRPC treatments¹⁷⁻²² and guidelines²⁻⁷ have rapidly evolved. The PROCEED study (2011-2017), which includes the largest mCRPC patient population treated with sipuleucel-T and prospectively followed in a real-world setting, offers interesting observations about patients with mCRPC, sipuleucel-T use, and the use of other ACIs since IMPACT. The baseline characteristics of PROCEED patients reveal clinical practice changes (Table 1). Although the median age was similar, the median baseline PSA level was much lower in PROCEED versus IMPACT (15.0 vs 51.7 ng/mL); this is noteworthy because a previous analysis of IMPACT showed a much greater OS benefit from sipuleucel-T versus a placebo in patients with lower baseline PSA levels.⁸ Most PROCEED patients had a good performance status, although in comparison with IMPACT, the performance status was somewhat worse (likely because randomized clinical trials have more stringent eligibility criteria). The Gleason score was also higher in PROCEED. PROCEED enrolled a higher proportion of African American patients than IMPACT (11.6% vs 6.7%), and this is notable because this population is often underrepresented in clinical trials. Visceral metastases, an IMPACT exclusion criterion, were reported in 4.7% of PROCEED patients. Furthermore, PROCEED spanned a period of unprecedented progress in mCRPC management as 4 life-extending therapies became available: abiraterone acetate,^{17,18} enzalutamide,^{19,20} cabazi-taxel,²¹ and radium 223.²² Thus, in PROCEED, the median OS (30.7 months) likely, in part, reflects use of these life-prolonging drugs with sipuleucel-T in contrast to the IMPACT (median OS, 25.8 months¹) era, in addition to the use of sipuleucel-T in patients with lower PSA levels.

PROCEED provides further evidence of sipuleucel-T safety and tolerability in a real-world setting. Particularly in an elderly patient population, the safety profile of a treatment deserves careful consideration in decision making. Importantly, the SAE incidence in PROCEED was low and was comparable to that documented during IMPACT.¹ A previous analysis of pooled data from 4 phase 3 trials reported CVE rates (excluding TIAs) of 3.5% (sipuleucel-T) and 2.6% (placebo).¹⁴ The causal relationship of sipuleucel-T with CVEs is unclear. Men with mCRPC are typically elderly with multiple comorbidities that increase the risk of cardiovascular events and CVEs. In PROCEED, a CVE rate of 2.8% was reported. Incidentally, the CVE rate was 2.8% in a SEER-Medicare database analysis with more than 10,000 patients with metastatic PC in a castrated state. Furthermore, subgroup analyses by baseline factors in PROCEED demonstrated that older patients and those with baseline CVE factors had higher rates of CVEs (Supporting Table 6), and this was consistent with published findings.²³⁻²⁵ Moreover, although central venous catheter use (which varied greatly by site) for leukapheresis was high in PROCEED, overall, this practice did not increase CVE risk (Supporting Table 7).

PROCEED also offers confirmation of correlative findings noted in prior phase 3 studies. Patients in the lowest baseline PSA quartile (PSA ≤ 5.27 ng/mL) had significantly longer OS (median survival, 47.7 months) than those in higher PSA quartiles. Similar findings were seen in the post hoc analysis of IMPACT, which demonstrated a greater OS benefit in lower baseline PSA quartiles versus higher baseline PSA quartiles and also suggested that sipuleucel-T was superior to a placebo in each quartile.⁸ Likewise, similar correlations with immune parameters and OS were seen in both PROCEED and IMPACT; in vitro indicators of immune activation and product potency (cumulative APC activation, APC count, and total nucleated cell count in the product) were significantly correlated with OS (Supporting Table 3).^{26,27}

PROCEED also exhibited 10 baseline characteristics that were independent predictors of OS in PROCEED (Table 2). The examined covariates were selected on the basis of those previously observed to be clinically and statistically relevant in this population. Our findings, though broadly consistent with the Halabi model,²⁸ also differ in terms of which significant predictors were identified, potentially because of the treatment being received (chemotherapy in the population used for the Halabi nomogram and sipuleucel-T for the current study), the data coming from a clinical trial versus a registry, the time periods during which the various studies informing these analyses were conducted and the changes in available therapies and PSA levels guiding treatment, and so on. One notable observation is the emergence of race as a statistically significant predictor, and this potentially reflects the relatively high enrollment of African Americans in PROCEED (12%). Further research is warranted to explore these findings.

Another notable finding in PROCEED is that a substantial number of patients experienced a long interval between sipuleucel-T and subsequent therapy with abiraterone, enzalutamide, docetaxel, cabazitaxel, or radium 223. Approximately one-third and one-sixth of the patients had not received any of these agents 1 and 2 years, respectively, after sipuleucel-T. For most of these patients, sipuleucel-T was their first OS-prolonging mCRPC therapy; having a long treatment-free interval after sipuleucel-T may reflect patient selection as well as the clinical benefit of sipuleucel-T. Interestingly, 22% of the overall PROCEED population received sipuleucel-T as their only OS-prolonging treatment for mCRPC. The reasons for this are unclear. However, the long median time to death from PC of 42.7 months observed provides further evidence for the early use of sipuleucel-T for mCRPC followed by other ACIs, as recommended by the National Comprehensive Cancer Network and other guidelines.^{2-4,7}

PROCEED has several limitations. Although OS was prospectively determined, there was no comparator group, so a survival benefit could not be determined. Nonetheless, this observation gives an accurate picture of expected OS with sipuleucel-T plus other life-prolonging drugs that were not available when IMPACT was conducted. Similar reasoning applies to SAE and CVE risk in that there was no placebo arm; hence, the results are descriptive.

PROCEED provides a real-world portrait of the safety profile of sipuleucel-T and defines the expected OS after sipuleucel-T in patients with mCRPC in the modern era of 5 additional life-prolonging agents. This information may be useful in powering future combination trials with sipuleucel-T, and studying the sequencing of therapies in this large population may shed light on optimal treatment approaches.

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CONFLICT OF INTEREST DISCLOSURES

Celestia S. Higano has served in an advisory role for Aptevo, Asana, Astellas, Bayer, Blue Earth Diagnostics, Churchill Pharma, Clovis Oncology, Dendreon, Endocyte, Ferring, Medivation, Orion Corporation, and Pfizer; she has also participated in sponsored research for Aptevo, Bayer, Aragon Pharma, Astellas, AstraZeneca, Dendreon, Genentech, Hoffman-LaRoche, Medivation, Sanofi, and Pfizer, and her spouse was in a leadership role for CTI Biopharma. Andrew J. Armstrong has received grants and personal fees from Dendreon, Pfizer/ Astellas, Janssen, Bayer, and Sanofi-Aventis during this study as well as grants from Novartis, Gilead, Bristol-Myers Squibb, and Genentech/ Roche outside the submitted work. A. Oliver Sartor has served as a consultant for and received personal fees from Advanced Accelerator Applications, Astellas, AstraZeneca, Bavarian-Nordic, Bayer, Bellicum, Blue Earth Diagnostics, Celgene, Constellation, Dendreon, EMD Serono, Endocyte, Johnson & Johnson, Bristol-Myers Squibb, Myovant, Pfizer, Progenics, Sanofi, Teva, and Hinova during this study; he has also received grants from AstraZeneca, Bayer, Constellation, Dendreon, Endocyte, Johnson & Johnson, Bristol-Myers Squibb, Progenics, Sanofi, Innocrin, Invitae, Merck, Roche, and Sotio. Philip W. Kantoff has received personal fees from Astellas, Bayer, Bellicum, BIND Biosciences, Bavarian Nordic Immunotherapies, DRGT, Genentech/Roche, Ipsen Pharmaceuticals, Janssen, Metamark, Merck, Millennium/Prometrika, MTG, Omnitura, OncoCell MDx, OncoGenex, Progenity, Sanofi, Tarveda Pharmaceuticals, Thermo Fisher, GE Healthcare, Context Therapeutics, New England Research Institutes, SEER Biosciences, and Placon; he also has investment interests in DRGT, Tarveda Pharmaceuticals, Context Therapeutics, SEER Biosciences, and Placon. Christopher M. Pieczonka has received personal fees as a consultant for Dendreon, Bayer, Janssen, and Pfizer and as an investigator for Dendreon, Bayer, Janssen, Pfizer, Merck, AstraZeneca, Taiho, Innocrin, and Myovant outside the submitted work. David F. Penson has received personal fees from Dendreon and Janssen as well as a grant from the Vanderbilt University Research Center. Neal D. Shore has served as a consultant for and received personal fees from Ferring, Bayer, Amgen, Janssen, Dendreon, Tolmar, Astellas, Pfizer, AstraZeneca, Genentech/ Roche, Myovant Sciences, Merck, Bristol Meyers Squibb, and Nymox outside the submitted work. Raoul S. Concepcion has served in an advisory role for Dendreon and received personal fees outside the submitted work. David I. Quinn has been involved in payments to the University of Southern California for trial conduct with Dendreon; he has also acted as an advisor for and received personal fees from Dendreon, Bayer, Janssen, Pfizer, Astellas, Genzyme, Clovis, and AstraZeneca. Vahan Kassabian has served as a consultant or speaker for Dendreon, Amgen, Astellas, Pfizer, Janssen, Bayer, UroGPO, Tolmar, and Genomic Health outside the submitted work and is a shareholder of UroGPO. Matt Harmon reports stock ownership in Amgen. Robert C. Tyler has been an employee of Janssen, Dendreon, Medivation, Pfizer, and Innocrin. Nancy N. Chang was a full-time employee of Dendreon at the time of the analyses and drafting of this manuscript. Hong Tang was a full-time employee of Dendreon at the time of the analyses and drafting of the manuscript; is a nonexecutive director of OnQuality Pharmaceuticals; and owns stock in BeiGene, Nektar, Sangamo Therapeutics, Tesaro, Verastem, Editas Medicine, and CVS Health Corporation. Matthew R. Cooperberg has received personal fees from Dendreon in relation to a PROCEED trial steering committee and has served in an advisory or consultancy role for Bayer, MDx Health, and Myriad Genetics; he has also participated in a registry steering committee for Astellas. The other authors made no disclosures.

AUTHOR CONTRIBUTIONS

Celestia S. Higano: Conceptualization, data curation, formal analysis, investigation, methodology, project administration, resources, supervision, visualization, writing-original draft, and writing-review and editing. Andrew J. Armstrong: Conceptualization, investigation, methodology, project administration, resources, supervision, writingoriginal draft, and writing-review and editing. A. Oliver Sartor: Conceptualization, data curation, formal analysis, investigation, methodology, supervision, writing-original draft, and writing-review and editing. Nicholas J. Vogelzang: Investigation, writing-original draft, and writing-review and editing. Philip W. Kantoff: Conceptualization, investigation, and writing-review and editing. David G. McLeod: Writing-original draft and writing-review and editing. Christopher M. Pieczonka: Investigation and writing-review and editing. David F. Penson: Investigation, methodology, and writing-review and editing. Neal D. Shore: Formal analysis, investigation, and writing-review and editing. Jeffrey Vacirca: Data curation, investigation, project administration, resources, software, supervision, validation, and visualization. Raoul S. Concepcion: Investigation and writing-review and editing. Ronald F. Tutrone: Data curation, investigation, and writing-review and editing. Luke T. Nordquist: Investigation and writing-review and editing. David I. Quinn: Investigation and writing-review and editing. Vahan Kassabian: Investigation, validation, visualization, and writingreview and editing. Mark C. Scholz: Investigation, supervision, and writing-review and editing. Matt Harmon: Data curation, methodology, software, visualization, and writing-review and editing. Robert C. Tyler: Conceptualization, data curation, formal analysis, investigation, methodology, project administration, supervision, and writing-review and editing. Nancy N. Chang: Visualization, writing-original draft, and writing-review and editing. Hong Tang: Funding acquisition, resources, supervision, and writing-review and editing. Matthew R. Cooperberg: Conceptualization, methodology, supervision, visualization, and writingreview and editing.

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Phase I Study of DSTP3086S, an Antibody-Drug Conjugate Targeting Six-Transmembrane Epithelial Antigen of Prostate 1, in Metastatic Castration-Resistant Prostate Cancer

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PURPOSE Six-transmembrane epithelial antigen of the prostate 1 (STEAP1) is highly expressed in prostate cancers. DSTP3086S is a humanized immunoglobulin G1 anti-STEAP1 monoclonal antibody linked to the potent antimitotic agent monomethyl auristatin E. This study evaluated the safety and activity of DSTP3086S in patients with metastatic castration-resistant prostate cancer.

METHODS Patients were enrolled in a 3 + 3 dose escalation study to evaluate DSTP3086S (0.3 to 2.8 mg/kg intravenously) given once every 3 weeks followed by cohort expansion at the recommended phase II dose or weekly (0.8 to 1.0 mg/kg).

RESULTS Seventy-seven patients were given DSTP3086S once every 3 weeks, and seven were treated weekly. Two patients in the once-every-3-weeks dose escalation had dose-limiting grade 3 transaminitis. Grade 3 hyperglycemia and grade 4 hypophosphatemia were dose-limiting toxicities in one patient treated at 1.0 mg/kg weekly. Initial cohort expansion evaluated dosing at 2.8 mg/kg once every 3 weeks (n = 10), but frequent dose reductions led to testing of 2.4 mg/kg (n = 39) in the expansion phase. Common related adverse events (> 20%) across doses (once every 3 weeks) were fatigue, peripheral neuropathy, nausea, constipation, anorexia, diarrhea, and vomiting. DSTP3086S pharmacokinetics were linear. Among 62 patients who received > 2 mg/kg DSTP3086S once every 3 weeks, 11 (18%) demonstrated a \ge 50% decline in prostate-specific antigen; two (6%) of 36 with measurable disease at baseline achieved a radiographic partial response; and of 27 patients with informative unfavorable baseline circulating tumor cells \ge 5/7.5 mL of blood, 16 (59%) showed conversions to favorable circulating tumor cells < 5. No prostate-specific antigen or RECIST responses were seen with weekly dosing.

CONCLUSION DSTP3086S has acceptable safety at the recommended phase II dose level of 2.4 mg/kg once every 3 weeks. Antitumor activity at doses between 2.25 and 2.8 mg/kg once every 3 weeks supports the potential benefit of treating STEAP1-expressing metastatic castration-resistant prostate cancer with an STEAP1-targeting antibody-drug conjugate.

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INTRODUCTION

Treatment options with clinical benefit for metastatic castration-resistant prostate cancer (mCRPC) have expanded significantly with the addition of abiraterone,^{1,2} enzalutamide,³ radium-223,⁴ and cabazitaxel.⁵ The long-term benefit for these agents, however, remains limited and is associated with significant toxicity.^{2,3,6,7} Needed are well-tolerated, targeted treatments with improved clinical benefit for patients whose tumors express the therapeutic target.

Six-transmembrane epithelial antigen of the prostate 1 (STEAP1) is a multitransmembrane protein believed to

act as an ion channel or transporter protein.⁸ As a cell surface protein frequently expressed in prostate cancer, with limited expression in nonprostate tissues,⁹⁻¹¹ STEAP1 is an ideal candidate for antibody-derived therapies in patients with mCRPC.

DSTP3086S is an antibody-drug conjugate (ADC) that contains the humanized immunoglobulin G1 anti-STEAP1 monoclonal antibody MSTP2109A linked through a protease labile linker, maleimidocaproylvaline-citrulline *p*-aminobenzyloxycarbonyl, to a potent antimitotic agent, monomethyl auristatin E (MMAE). After antigen-specific binding of the ADC, the complex

ASSOCIATED Content

Data Supplements

Author affiliations and support information (if applicable) appear at the end of this article.

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Downloaded from ascopubs.org by UNIVERSITY WASHINGTON on May 20, 2020 from 128.095.104.109 Copyright © 2020 American Society of Clinical Oncology. All rights reserved. is internalized, and MMAE is released intracellularly, resulting in inhibition of cell division and cell death.¹²⁻¹⁴ Nonclinical efficacy studies in prostate cancer xenografts provided a rationale for investigating DSTP3086S in patients with mCRPC.¹¹

METHODS

Study Design and Patient Selection

This phase I, multicenter, open-label, 3 + 3, doseescalation study was designed to evaluate the safety and identify the recommended phase II dose (RP2D) of DSTP3086S in patients with mCRPC. Secondary and exploratory objectives included assessment of the antitumor activity of DSTP3086S in association with STEAP1 expression and of the predictive value of measuring circulating tumor cell (CTC) counts during treatment. The study protocol was approved by institutional review boards before patient recruitment and conducted in accordance with International Conference on Harmonization E6 Guidelines for Good Clinical Practice. Each patient provided signed informed consent before study enrollment.

Study eligibility criteria, including paraffin-embedded tissue screening for STEAP1 expression, are described in the Data Supplement (online only). In the initial dose-escalation stage, patients received intravenous DSTP3086S (supplied by Genentech, South San Francisco, CA) at 0.3 to 2.8 mg/kg once every 3 weeks, with dosing calculated by weight and eventually capped during the 2.4 mg/kg expansion for patients with a body mass index $> 35 \text{ kg/m}^2$ because of excess toxicity seen in morbidly obese patients at higher dose levels. After completing the once-every-3-weeks dose escalation, a weekly schedule was evaluated at 0.8 and 1 mg/kg.

The RP2D was determined on the basis of cumulative safety data obtained at the time of cohort expansion. Doseexpansion cohorts were enrolled at RP2D to further characterize safety, tolerability, pharmacokinetics (PK) variability, and signals of clinical activity in 49 patients with STEAP1-expressing tumors (immunohistochemistry [IHC] 3+, predominantly strong staining; IHC 2+, predominantly moderate staining; IHC 1+, predominantly weak staining; IHC 0, very weak or no staining in > 90% of tumor cells). Patients enrolled in the expansion phase were required to have an STEAP1 IHC score of 2+ or 3+ in an archival or a pretreatment tissue biopsy specimen. A second expansion cohort enrolled chemotherapy-naïve patients who had progressed on abiraterone and/or enzalutamide and received daily prednisone concurrent with DSTP3086S.

Safety Assessment

Safety was assessed on the basis of reports of adverse events (AEs) and included clinical laboratory testing, vital signs, physical examinations, and ECG. Patients were assessed for AEs at each study visit and as necessary throughout the study. AEs were graded in severity

according to the National Cancer Institute CTCAE (version 4.0). Dose-limiting toxicities (DLTs) were defined as grade \geq 3 nonhematologic or grade \geq 4 hematologic toxicities attributed to treatment that occurred in the first cycle (for exceptions and additional details, see the Data Supplement). Patients with DLTs could continue treatment at a lower dose if toxicities resolved to grade < 2. The maximum tolerated dose was defined as the highest dose at which zero or one of six patients experienced a DLT. PK and immunogenicity assessments are described in the Data Supplement.

Clinical Activity

Preliminary efficacy measures included post-therapy prostate-specific antigen (PSA) changes shown by waterfall plots, disease progression according to Prostate Cancer Clinical Trials Working Group criteria,¹⁵ and radiographic response according to RECIST version 1.0.¹⁶ Per the Prostate Cancer Clinical Trials Working Group, treatment beyond PSA progression in the absence of radiographic or clinically progressive disease was allowed.¹⁵ Exploratory measures of activity included changes in CTC counts from unfavorable \geq 5 cells to favorable \leq 4 cells/7.5 mL of blood per US Food and Drug Administration clearance for Cell-Search (Menarini Silicon Biosystems, Huntingdon Valley, PA).¹⁷⁻²² STEAP1 IHC was performed as described in the Data Supplement.

Statistical Analysis

This study was designed to obtain preliminary safety, PK, and activity information in the treated populations. As such, the sample sizes in the various dose-escalation and dose-expansion cohorts did not reflect explicit, formal power and type I error considerations. Rather, sample sizes were based on an estimation framework either for the ability to identify AEs with various assumed underlying prevalence or for their ability to initially assess antitumor activity and evaluate benefits and risks in this patient population. For safety analysis, all patients who received DSTP3086S were included. Patients were considered for evaluation for response if the baseline PSA was detectable, they had measurable disease as assessed by computed tomography/magnetic resonance imaging by RECIST version 1.0, or they had baseline CTCs \geq 5/7.5 mL of blood.

RESULTS

Patient baseline characteristics for each schedule are listed in Table 1. A total of 84 patients were enrolled, including 77 on the once-every-3-weeks dose schedule of whom 28 were enrolled in the dose escalation (0.3 to 2.8 mg/kg), 10 in an initial expansion at 2.8 mg/kg, and 39 at 2.4 mg/kg in two expansion cohorts. The median number of DSTP3086S dose administrations in the once-every-3-weeks cohort was four (range, one to 25). AEs led to dose delays in 29 patients (38%), dose reductions in 12 (16%), and dose discontinuations in 17 (22%). Peripheral neuropathy was the most

	DSTP3086S Col	10rt, No. (%)
Characteristic	Once Every 3 Weeks	Weekly
No. of patients	77	7
Median age, years (range)	68 (43-88)	67 (47-75)
ECOG performance status		
0	23 (30)	3 (43)
1	53 (69)	3 (43)
2	1 (1)	1 (14)
Sites of metastatic disease		
Bone	69 (90)	5 (71)
Bone only	5 (7)	0 (0)
Soft tissue	50 (65)	6 (86)
Lung	15 (20)	1 (14)
Liver	11 (14)	2 (29)
Lymph node	42 (55)	6 (86)
Prior systemic therapies (selected)		
Docetaxel	43 (56)	3 (43)
Cabazitaxel	8 (10)	1 (14)
Abiraterone	52 (68)	6 (86)
Enzalutamide	35 (45)	3 (43)
Median baseline prognostic factors (range)		
PSA, ng/mL	89 (0.4-8,471)	21 (0.3-274)
Hgb, g/dL	12 (8-15)	11 (10-13)
Alkaline phosphatase, U/L	134 (43-668)	98 (53-277)
LDH, U/L	236 (117-2,023)	212 (192-631)
Albumin, g/dL	4.1 (1.9-4.7)	4.1 (3.2-4.6)
Baseline CTCs/7.5 mL of blood		
Median (range)	6 (0-446)	1 (0-908)
≥ 5	38 (49)	2 (29)

TABLE 1. Patient Demographics and Disease Characteristics

Abbreviations: CTC, circulating tumor cell; ECOG, Eastern Cooperative Oncology Group; Hgb, hemoglobin B, LDH, lactate dehydrogenase; PSA, prostate-specific antigen.

common AE that led to treatment discontinuation. Dose reductions occurred after one to nine cycles of DSTP3086S treatment in the three highest dose cohorts, including 50% of patients at 2.8 mg/kg (Fig 1).

Of the seven patients enrolled in the weekly dose schedule, four were enrolled at 0.8 mg/kg, and three were enrolled at 1.0 mg/kg; no expansions were performed in the weekly schedule. The median number of DSTP3086S dose administrations in the weekly cohort was seven (range, one to 32); one patient (14%) had a dose reduction, three patients (43%) had dose delays, and one patient (14%) discontinued treatment because of AEs.

Safety

In the once-every-3-weeks dose escalation, DLTs included grade 3 transaminitis in one patient each at 2.25 mg/kg and

2.8 mg/kg. The maximum tolerated dose was not reached, and the RP2D for DSTP3086S was determined to be 2.4 mg/kg once-every 3 weeks on the basis of tolerability after an initial expansion at 2.8 mg/kg once every 3 weeks was deemed not tolerable and required frequent dose reductions (Fig 1).

The most common treatment-related AEs, defined as having occurred in > 20% patients (15 of 77) over all once-every-3-week dose levels, were fatigue (56%), peripheral neuropathy (51%), nausea (38%), constipation (35%), decreased appetite (34%), diarrhea (26%), and vomiting (25%). Table 2 lists related AEs that occurred in \ge 10% patients in the once-every-3-weeks dose cohort. AEs reported at a maximum intensity of grade \ge 3 in \ge 5% of patients over all once-every-3-weeks dose levels (regardless of attribution to study drug) were hyperglycemia (eight



FIG 1. Time on treatment by dosing cohort and corresponding best prostatespecific antigen (PSA) changes in the once-every-3-weeks dose cohort. Dose modifications are represented by changes in color.

patients; 10% [includes one event of blood glucose increased]); anemia and fatigue (five patients each; 7%); and back pain, neutropenia, and pulmonary embolism (four patients each; 5%). Treatment-emergent grade \geq 3 AEs reported in at least two patients are listed in the Data Supplement. Grade \geq 3 AEs that the investigator considered to be related to the study drug were reported in 34% of patients (26 of 77) on the once-every-3-weeks dose

TABLE 2. Most Common Related Adverse Events (Any and Grade 3/4) That Occurred in 10% or More Patients in the Once-Every-3-Weeks Dose Cohort

					Grad	e, No. (%)				
					DS	TP3086S				
	≤ 1.5 (n =	mg/kg 15)	2.25 (n :	mg/kg = 7)	2.4 mg/kg	ç (n = 39)	2.8 mg/kg	(n = 16)	Total ((N = 77)
Adverse Event	Any	3/4	Any	3/4	Any	3/4	Any	3/4	Any	3/4
Overall	10 (67)	2 (13)	5 (71)	3 (43)	38 (97)	9 (23)	16 (100)	10 (63)	69 (90)	24 (31)
Fatigue	4 (27)	_	2 (29)	—	25 (64)	—	12 (75)	3 (19)	43 (56)	3 (4)
Peripheral neuropathy*	1 (7)	—	2 (29)	1 (14)	26 (67)	2 (5)	10 (63)	_	39 (51)	3 (4)
Nausea	3 (20)	1 (7)	1 (14)	_	15 (39)	—	10 (63)	_	29 (38)	1(1)
Constipation	3 (20)	—	2 (29)	—	14 (36)	—	8 (50)	1 (6)	27 (35)	1(1)
Appetite decreased	2 (13)	_	1 (14)	_	16 (41)	—	7 (44)	_	26 (34)	—
Diarrhea	2 (13)	—	2 (29)	—	10 (26)	—	6 (38)	_	20 (26)	—
Vomiting	2 (13)	_	_	_	10 (26)	—	7 (44)	_	19 (25)	—
Dyspnea	—	—	1 (14)	—	8 (21)	—	5 (31)	1 (6)	14 (18)	1(1)
ALT increased	1 (7)	_	_	_	9 (23)	2 (5)	1 (6)	_	11 (14)	2 (3)
AST increased	1 (7)		1 (14)	1 (14)	6 (15)		1 (6)	_	9 (12)	1 (1)
Pain in extremity	_	_	2 (29)	_	5 (13)	_	1 (6)	1 (6)	8 (10)	1 (1)

NOTE. None of the most common related adverse events that occurred in $\geq 10\%$ of patients were grade 5. See the Safety section for a description of related grade 5 adverse events and the Data Supplement for a complete list of grade ≥ 3 -related adverse events in the onceevery-3-weeks dose cohort.

*Includes the Medical Dictionary of Regulatory Activities preferred terms peripheral sensory neuropathy, peripheral motor neuropathy, neuropathy peripheral and muscular weakness, hypoesthesia, gait disturbance, and paresthesia and peripheral sensorimotor neuropathy.

schedule (Data Supplement). The most frequently reported grade \geq 3–related AE was neutropenia (four patients; 5%).

Serious AEs are listed in the Data Supplement. Drug-related serious AEs occurred in nine patients at the once-every-3-weeks dose levels, including two fatal events: one as a result of sepsis (at 2.25 mg/kg) and one as a result of sepsis and respiratory failure after initial hospitalization for hyperglycemia (at 2.4 mg/kg). Thirteen patients (17%) had a glucose value consistent with grade \geq 3 hyperglycemia while in the study, with eight (10%) of the 13 reported as grade \geq 3 AEs. Of note, fasting glucose levels, which are used when making the CTCAE determinations, were not required for this study.

In the weekly cohort, one patient treated with 1.0 mg/kg developed grade 3 hyperglycemia and grade 4 hypophosphatemia, which were considered DLTs. AEs commonly experienced by the patients who received weekly treatment are listed in the Data Supplement. Treatment-emergent grade \geq 3 AEs for patients on the weekly dose schedule are listed in the Data Supplement. One of seven patients developed nonfatal serious AEs that included dehydration, hyperglycemia, hypomagnesemia, and hypophosphatemia that led to treatment discontinuation.

Peripheral neuropathy–related AEs, regardless of attribution to study drug (identified using the broad Standardized Medical Dictionary for Regulatory Activities Queries for peripheral neuropathy), were reported in 46 patients (60%) on the once-every-3-weeks dose schedule after a median of 2.8 months of treatment. For patients on the weekly dose schedule, peripheral neuropathy–related AEs were reported in two (29%). Overall, grade 3 peripheral sensory neuropathy was reported in three patients, with one also having grade 3 peripheral motor neuropathy. Overall, nine

TABLE 3. Pharmacokinetic Parameters for DSTP3086S Tab, acMMAE, and

 Unconjugated MMAE Analytes in Cycle 1 at 2.4 mg/kg

	DSTP3086S 2.4 mg/kg Once Every 3 Weeks (n = 36),
Parameter	Mean (% CV)
C _{max}	
Tab, μg/mL	56 (23)
acMMAE, ng/mL	879 (20)
Unconjugated MMAE, ng/mL	5.8 (55)
AUC _{0-∞}	
Tab, day $ imes$ μ g/mL	313 (26)
acMMAE, day $ imes$ ng/mL	2,423 (20)
Unconjugated MMAE, day $ imes$ ng/mL	44 (50)
CL	
Tab, mL/day/kg	8.3 (32)
acMMAE, mL/day/kg	17.5 (23)

Abbreviations: acMMAE, antibody-conjugated monomethyl auristatin E; AUC, area under the curve; CL, clearance; C_{max} , maximum concentration; CV, coefficient of variation; MMAE, monomethyl auristatin E; Tab, total antibody.

patients (12%) on the once-every-3-weeks dose schedule and none of the weekly cohort discontinued DSTP3086S treatment because of a peripheral neuropathy–related AE. The majority of peripheral neuropathy AEs were reported as ongoing at the end of the reporting period for the study, which ended 30 days after a patient's last dose.

PK and Immunogenicity Assessments

Linear PK (0.3 to 2.8 mg/kg) were observed for total antibody (Tab) and antibody-conjugated MMAE (acMMAE [RP2D of 2.4 mg/kg listed in Table 3]). For the once-every-3-weeks regimen, the mean acMMAE maximum concentrations occurred immediately after the infusion, increased with dose, and ranged from 94 to 993 ng/mL. The acMMAE PK showed a multi-exponential decline, with half-life values ranging from 4.6 to 6.4 days. The acMMAE PK was similar to the Tab, with a trend of faster clearance for acMMAE than for the Tab analyte. Unconjugated MMAE levels increased with DSTP3086S dose, and systemic exposure of unconjugated MMAE was consistently low across all time points (approximately 100-fold less than the exposure to acMMAE) and exhibited formation-ratelimited kinetics (Data Supplement). Minimal accumulation was observed for the acMMAE, Tab, and unconjugated MMAE analytes upon repeated dosing on the once-every-3-weeks schedule, and steady state seemed to be reached within the first dose in cycle 1.

For the tested weekly regimen of 0.8 and 1.0 mg/kg, doseproportional maximum concentrations and areas under the curve were observed. On the basis of the limited weekly dosing data, faster clearance was observed for the weekly regimen compared with the once-every-3-weeks regimen. Therefore, no significant accumulation of acMMAE was observed, even when the drug was administrated weekly.

One (1%) of the 75 tested patients who were evaluable for postdose anti-DSTP3086S antibodies was confirmed positive for antidrug antibodies. No differences were observed in the PK profiles, safety features, or efficacy outcomes for this patient (data not shown).

Clinical Activity

For patients on the once-every-3-weeks dosing schedule, a waterfall plot of the best PSA percent change from baseline is shown in Figure 2. In aggregate, 11 (14%; 95% CI, 7% to 24%) of 77 patients met the response criteria of a confirmed PSA reduction of \geq 50%. After restricting to patients treated with DSTP3086S at doses > 2 mg/kg (n = 62), PSA responses were obtained in one (14%; 95% CI, 0% to 58%) of seven at the 2.25 mg/kg, five (13%; 95% CI, 4% to 27%) of 39 at the 2.4 mg/kg, and five (31%; 95% CI, 11% to 59%) of 16 at the 2.8 mg/kg dose levels. PSA changes relative to baseline for patients with PSA responses are shown in the Data Supplement.

Of the 46 patients with evaluable disease per RECIST at baseline, two (4%) had a partial response (one confirmed)



FIG 2. Best response by DSTP3086S once-every-3-weeks dose cohort. Waterfall plot showing best prostate-specific antigen (PSA) change from baseline and corresponding six-transmembrane epithelial antigen of the prostate 1 immunohistochemistry (IHC) and circulating tumor cell (CTC) conversion status. Dashed lines indicate \pm 50% change from baseline.

and 24 (52%) stable disease as best radiographic response. Both patients with partial responses belonged to the subset of 36 evaluable patients per RECIST who received DSTP3086S at doses > 2 mg/kg.

Fourteen patients (18%) remained on study treatment for \geq 6 months (Fig 1), including two patients with a partial response (Fig 3). One was a 72-year-old man with prostatectomy tumor biopsy tissue that demonstrated IHC 2+ STEAP1 expression. This patient had progressive CRPC after successive treatments with bicalutamide, docetaxel, abiraterone, cabozantinib, and palliative radiation therapy. He received DSTP3086S at a starting dose of 2.8 mg/kg and demonstrated a partial response after cycle 4 (confirmed on subsequent imaging), with a maximum PSA decline of 99%. At cycle 10, DSTP3086S dose was reduced to 2.25 mg/kg because of grade 2 peripheral sensory neuropathy, and the patient discontinued study treatment at cycle 13 as a result of disease progression.

The second patient was a 60-year-old man with prostatectomy tumor biopsy tissue that exhibited IHC 3+ STEAP1 expression. This patient had progressive CRPC after bicalutamide, apalutamide, abiraterone, and docetaxel and received DSTP3086S at a starting dose of 2.8 mg/kg, which was reduced to 2.25 mg/kg at cycle 3 because of grade 3 pulmonary embolism. He demonstrated an unconfirmed radiographic partial response after cycle 4 and a maximum PSA decline of 86% from baseline. He continued on study treatment until cycle 8 and discontinued DSTP3086S as a result of disease progression.

In the weekly cohorts, two patients remained on study treatment for \geq 6 months. No patients achieved a PSA or RECIST response.

Biomarker Analysis

Among the 134 patients screened for the study, tumor STEAP1 protein expression by IHC was as follows: IHC 0 in

one (1%), IHC 1+ in 35 (26%), IHC 2+ in 65 (49%), and IHC 3+ in 33 (24%). Given that only patients with IHC 2+ or 3+ tumor were eligible for the expansion cohorts, most had high STEAP1-expressing tumors (Fig 2). Of the 11 patients with PSA declines of \geq 50% from baseline, one (10%) had IHC 1+, five (45%) had IHC 2+, and five (45%) had IHC 3+ tumors. At doses of > 2 mg/kg, one (20%) of five patients with IHC 1+ tumors, five (14%) of 36 with IHC 2+ tumors, and five (24%) of 21 with IHC 3+ tumors had PSA declines of \geq 50% from baseline.

Of the 77 patients who received DSTP3086 once every 3 weeks, 38 (49%; 95% CI, 38% to 61%) had baseline CTCs \geq 5/7.5 mL of blood. CTC conversions from \geq 5 to < 5 cells/7.5 mL of blood after treatment were observed in 19 (50%; 95% CI, 33% to 67%) of 38 patients and in 16 (59%; 95% CI, 39% to 78%) of 27 patients who received DSTP3086S at doses > 2 mg/kg. By dose level, of the CTCinformative patients, CTC conversions were observed in three (27%; 95% CI, 6% to 61%) of 11 patients treated at doses < 1.5 mg/kg, one (20%; 95% Cl, 1% to 72%) of five patients at 2.25 mg/kg, seven (64%; 95% CI, 31% to 89%) of 11 patients at 2.4 mg/kg, and eight (73%; 95% CI, 39% to 94%) of 11 patients at 2.8 mg/kg. Of the 19 CTC converters, the median baseline (pretreatment) CTC count was 31 cells (range, 6 to 304 cells), with 14 (74%) of 19 patients having baseline CTCs > 10/7.5 mL of blood. No patients on the weekly dose schedule demonstrated a CTC conversion.

Among the patients treated once every 3 weeks with DSTP3086S, 53 (69%; 95% Cl, 57% to 79%) of 77 had baseline CTCs \geq 1/7.5 mL of blood, 18 of whom converted to 0 (34%; 95% Cl, 22% to 48%) detectable CTCs on DSTP3086S treatment. This represented 18 (45%; 95% Cl, 29% to 62%) of 40 patients treated with DSTP3086S > 2 mg/kg once every 3 weeks v zero (0%; 95% Cl, 0% to 25%) of 13 patients who received DSTP3086S \leq 1.5 mg/kg once every 3 weeks.¹⁸

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DISCUSSION

ADCs are designed to deliver potent cytotoxic agents directly to tumors that overexpress the target antigen while improving the therapeutic index by reducing normal tissue exposure.²³ DSTP3086S is a novel ADC that targets the STEAP1 antigen frequently expressed in prostate cancer (73% IHC 2+/3+ in patients screened for this trial). In this study, the RP2D of 2.4 mg/kg once every 3 weeks showed preliminary evidence of antitumor activity in patients with progressive mCRPC, including those with prior exposure to microtubule inhibitors. Patients enrolled in the study were enriched for high STEAP1-expressing tumors because they were considered to be the most likely to benefit from DSTP3086S treatment. Antitumor activity was assessed by PSA changes, imaging, and novel CTC-based measurements to broadly investigate potential clinical benefit. Although DSTP3086S would require refinement to optimize its therapeutic index for further clinical development, the phase I data support the feasibility of targeting STEAP1 in mCRPC. As such, the data may be a valuable guide for novel therapeutic modalities, such as improved ADCs, chimeric antigen receptor T cells, and immune cell–recruiting bispecific antibodies that target STEAP1.

Overall, there was a general concordance between measures of antitumor activity (ie, PSA changes, CTC conversions, RECIST changes; Figs 1 to 3). Clinical activity was evident at dose levels > 2 mg/kg as shown by $\ge 50\%$ declines in PSA in 18% of patients, although only two



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patients who received the highest tested dose of DSTP3086S 2.8 mg/kg once every 3 weeks achieved a partial radiographic response. This clinical activity was also noted in heavily pretreated patients.

Half of the patients who received DSTP3086S once every 3 weeks had informative baseline CTCs \geq 5/7.5 mL of blood, where CTC conversion to favorable < 5 cells/7.5 mL of blood after treatment was observed in 50% of patients across all dose levels, with an increasing conversion rate of 64% in the 2.4 mg/kg cohort and 73% in the 2.8 mg/kg cohort. A biomarker panel containing CTC conversions has been shown to be a surrogate for survival at the individual-patient level in trials with novel anti-androgens, such as abiraterone acetate (28% of CTC-informative patients converted) and enzalutamide (24% of CTCinformative patients converted).^{18,21} Although PSA declines and imaging responses with STEAP1-ADC treatment were not common, half of the patients with evaluable CTCs had CTC conversions, some coupled with prolonged disease stability. This suggests activity for STEAP1-ADC that is reflected by CTC conversion rather than by PSA or imaging responses and warrants further investigation. In general, the number of prior treatments (either docetaxel or androgen receptor directed) correlated with worse response to DSTP3086S. A limited number of chemotherapy-naïve patients enrolled in the initial 2.4 mg/kg expansion cohort. Because of an overlapping mechanism of action and toxicity between systemic taxanes and MMAE delivered by DSTP3086S, an additional 17 patients were enrolled to assess DSTP3086S in those who had received abiraterone and/or enzalutamide but were chemotherapy naïve; notably only one PSA response was observed. This suggests that prior chemotherapy exposure is not the only factor that potentially limits DSTP3086S activity.

The PK of DSTP3086S was linear across all doses assessed, driven mainly by the anti-STEAP1 antibody, and is consistent with the behavior observed with other ADCs. Dosing on a weekly schedule did not improve overall drug

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safety, tolerability, or efficacy compared with once every 3 weeks. Fatigue, peripheral neuropathy, and GI symptoms were the most frequent related AEs observed. Dosing at 2.8 mg/kg required more dose reductions compared with 2.4 mg/kg dosing. Therefore, 2.4 mg/kg was selected as the RP2D.

The relationship between exposure and safety events (eg, neuropathy) is unclear given the small number of patients treated at different doses. The development of peripheral neuropathy with repeated dosing, a known AE associated with microtubule inhibition, is likely mediated by the MMAE therapeutic payload.²⁴⁻²⁷ Hyperglycemia was reported as an AE in 13% of patients in the study. The mechanism for a potential association between DSTP3086S and hyper-glycemia remains unclear, although possibly related to MMAE given reports of hyperglycemia with other ADCs conjugated to MMAE.²⁸⁻³⁰

Evaluation of STEAP1 IHC scores suggests a potential association between STEAP1 expression and DSTP3086S clinical activity. However, even with high tumor STEAP1 expression (IHC 3+), the majority of patients did not achieve PSA responses, and the underlying reasons behind intrinsic resistance to DSTP3086S are unknown. It is unknown whether acquired loss of STEAP1 expression after DSTP3086S treatment could explain resistance after an initial response. One effort to better understand STEAP1 expression in patients with CRPC subsequently treated with DSTP3086 was anti-STEAP1-desferrioxamine-⁸⁹Zr-based positron emission tomography imaging.³¹

In summary, DSTP3086S demonstrated an acceptable safety profile, with evidence of antitumor activity confirming that the targeting of STEAP1-expressing mCRPC tumors with an ADC is feasible. Although DSTP3086S would require optimization for further clinical development, these data may inform development of novel ADCs, chimeric antigen receptor T cells, and immune cell–recruiting bispecific antibodies that target STEAP1.

PRIOR PRESENTATION

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AUTHORS' DISCLOSURES OF POTENTIAL CONFLICTS OF INTEREST AND DATA AVAILABILITY STATEMENT

Disclosures provided by the authors and data availability statement (if applicable) are available with this article at DOI https://doi.org/10.1200/JC0.19.00646.

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Help Caregivers Learn About the Importance of Their Role in Cancer Care



Cancer.Net offers a variety of tools and resources for caregivers, including the *ASCO Answers: Caregiving Guide*. Designed to help caregivers learn more about supporting someone with cancer, this guide offers caregivers advice for talking with family and the health care team, convenient symptom and medication trackers, and more. Explore additional resources for caregivers at **cancer.net/caregiving**. Order guides for your practice at **cancer.net/estore**. Free domestic shipping on all patient information resources and ASCO members save 20%.



AUTHORS' DISCLOSURES OF POTENTIAL CONFLICTS OF INTEREST

Phase I Study of DSTP3086S, an Antibody-Drug Conjugate Targeting Six-Transmembrane Epithelial Antigen of Prostate 1, in Metastatic Castration-Resistant Prostate Cancer

The following represents disclosure information provided by authors of this manuscript. All relationships are considered compensated unless otherwise noted. Relationships are self-held unless noted. I = Immediate Family Member, Inst = My Institution. Relationships may not relate to the subject matter of this manuscript. For more information about ASCO's conflict of interest policy, please refer to www.asco.org/rwc or ascopubs.org/jco/site/ifc.

Open Payments is a public database containing information reported by companies about payments made to US-licensed physicians (Open Payments).

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A Phase Ib/IIa Study of the Pan-BET Inhibitor ZEN-3694 in Combination with Enzalutamide in Patients with Metastatic Castration-resistant Prostate Cancer



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ABSTRACT

Purpose: ZEN-3694 is a bromodomain extraterminal inhibitor (BETi) with activity in androgen-signaling inhibitor (ASI)-resistant models. The safety and efficacy of ZEN-3694 plus enzalutamide was evaluated in a phase Ib/IIa study in metastatic castration-resistant prostate cancer (mCRPC).

Patients and Methods: Patients had progressive mCRPC with prior resistance to abiraterone and/or enzalutamide. 3+3 dose escalation was followed by dose expansion in parallel cohorts (ZEN-3694 at 48 and 96 mg orally once daily, respectively).

Results: Seventy-five patients were enrolled (N = 26 and 14 in dose expansion at low- and high-dose ZEN-3694, respectively). Thirty (40.0%) patients were resistant to abiraterone, 34 (45.3%) to enzalutamide, and 11 (14.7%) to both. ZEN-3694 dosing ranged from 36 to 144 mg daily without reaching an MTD. Fourteen patients (18.7%) experienced grade \geq 3 toxicities, including three

Introduction

Prostate cancer is the most common malignancy and second leading cause of death among men in the United States (1). Androgen-signaling blockade with either androgen receptor (AR) antagonism or CYP17 inhibition improves long-term survival in both metastatic castration-resistant prostate cancer (mCRPC) and metastatic castration-sensitive disease (2–5). However, treatment resistance is universal, and cross-resistance between AR antagonists and CYP17 inhibitors limits the clinical utility of these agents when used sequentially (6–10).

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patients with grade 3 thrombocytopenia (4%). An exposuredependent decrease in whole-blood RNA expression of BETi targets was observed (up to fourfold mean difference at 4 hours post–ZEN-3694 dose; $P \le 0.0001$). The median radiographic progression-free survival (rPFS) was 9.0 months [95% confidence interval (CI), 4.6–12.9] and composite median radiographic or clinical progression-free survival (PFS) was 5.5 months (95% CI, 4.0–7.8). Median duration of treatment was 3.5 months (range, 0–34.7+). Lower androgen receptor (AR) transcriptional activity in baseline tumor biopsies was associated with longer rPFS (median rPFS 10.4 vs. 4.3 months).

Conclusions: ZEN-3694 plus enzalutamide demonstrated acceptable tolerability and potential efficacy in patients with ASI-resistant mCRPC. Further prospective study is warranted including in mCRPC harboring low AR transcriptional activity.

Multiple mechanisms of therapeutic resistance to AR pathway inhibitors have been described, including amplification of the *AR* gene and its enhancers, upregulation of intratumoral androgen synthesis, generation of ligand-independent AR splice variants, activation of alternative oncogenic signaling pathways including MYC, transdifferentiation to an AR-independent, neuroendocrine phenotype, and cooption of alternative steroid hormone receptors including the glucocorticoid receptor (GR; refs. 11–16). A broad therapeutic approach capable of affecting expression/signaling of multiple pathways may provide a means to reverse resistance and restore sensitivity to AR-targeting therapy.

Proteins of the bromodomain extraterminal (BET) bromodomain family are epigenetic readers that bind to acetylated histones through their bromodomains to affect gene transcription (17). They preferentially localize at sites of enhancers of various oncogenes to promote tumorigenesis and progression. ZEN-3694 is an orally bioavailable, second-generation, potent pan-BET bromodomain inhibitor (BETi) that leads to downregulation of expression of AR signaling, AR splice variants, MYC, GR, and other oncogenes in multiple CRPC models, and has significant *in vivo* activity as single agents, with evidence of synergy when combined with enzalutamide (18).

We conducted a first-in-human phase Ib/II dose-escalation/ expansion study of ZEN-3694 in combination with enzalutamide in patients with mCRPC and prior progression on one or more androgen-signaling inhibitor (ASI).

Patients and Methods

Patient population

Patients had histologically confirmed mCRPC with progression at study entry by Prostate Cancer Working Group 2 (PCWG2)

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Translational Relevance

Bromodomain extraterminal inhibitors (BETi) demonstrate in vivo activity in enzalutamide-resistant prostate cancer models via downregulation of bypass signaling pathways including MYC. Clinical translation of BETi as a therapeutic strategy in metastatic castration-resistant prostate cancer (mCRPC) has heretofore been limited by significant toxicity including risk of thrombocytopenia. In this phase Ia/IIb study of the pan-BETi, ZEN-3694, in combination with enzalutamide in 75 patients with abirateroneand/or enzalutamide-resistant mCRPC, the combination was well-tolerated without reaching an MTD. Less than 5% of patients experienced a grade ≥3 thrombocytopenia. Robust, dose-dependent, and sustained downregulation of expression of BETi target genes including MYC was observed using a whole-blood RNA assay. Encouraging efficacy was observed including a median radiographic progression-free survival of more than 10 months in those with prior progression on enzalutamide monotherapy. Clinical benefit was particularly pronounced in high-risk subgroups including those with an aggressive variant clinical phenotype as well as those with lower androgen receptor transcriptional activity in baseline tumor biopsies. A randomized study is planned with ZEN-3694 at the recommended phase II dose of 96 mg orally once daily in combination with enzalutamide in mCRPC with prior progression on enzalutamide or abiraterone.

criteria (19). Patients were required to have progression on prior abiraterone and/or enzalutamide treatment prior to study entry, no prior docetaxel for the treatment of mCRPC, serum testosterone <50 ng/dL with maintenance of androgen deprivation therapy during study treatment, Eastern Cooperative Oncology Group (ECOG) performance status of 0 or 1, adequate organ function including absolute neutrophil count >1.5 × 10⁹/L, platelet count >100,000, total bilirubin <1.5 × ULN, and creatinine clearance >60 mL/minute. Patients with uncontrolled hypertension or New York Heart Association class II or higher congestive heart failure were excluded.

Study approval was obtained from the ethics committees at the participating institutions and regulatory authorities. All patients gave written informed consent. The study followed the Declaration of Helsinki and Good Clinical Practice guidelines (NCT02711956).

Study design and treatment schedule

This was a phase Ib/II, multicenter, open-label, combination doseescalation study of ZEN-3694 in combination with the standard dose of enzalutamide, 160 mg daily. Lead-in treatment period with enzalutamide monotherapy (day -14 to day -1) was required in subjects not already receiving enzalutamide at the time of study enrollment. Patients continued treatment until radiographic progression by PCWG2 criteria, unequivocal clinical progression, or unacceptable toxicity. PSA progression alone was not used as a criterion for treatment discontinuation.

The starting dose of ZEN-3694 was 36 mg orally once daily. A 3+3 dose-escalation schema was utilized up to a maximum administered dose of 144 mg daily. Dose expansion was subsequently performed in two cohorts in parallel: (i) low dose, ZEN-3694 at 48 mg daily (N=14), and (ii) high dose, ZEN-3694 96 mg daily (N=26).

A formal interim analysis was not planned; however, interim data were reviewed on an ongoing basis. The final planned analyses were performed after 75 patients were enrolled and the database was locked on February 6, 2020.

The primary study endpoint was safety and the recommended phase II dose of ZEN-3694 in combination with enzalutamide. Secondary endpoints included pharmacokinetics assessment of ZEN-3694 and enzalutamide, PSA50 response (≥50% decline in PSA from baseline confirmed ≥ 4 weeks later) rate, duration of PSA50 response, and radiographic progression-free survival (rPFS). Soft-tissue radiographic progression and responses were assessed according to RECIST v1.1 criteria. Progression of bone metastases was assessed using PCWG2 criteria. Post hoc analyses were performed to assess composite progression-free survival (PFS), defined as first occurrence of radiographic or clinical progression or death, as well as PSA PFS by PCWG2 criteria. Correlative endpoints included pharmacodynamics assessment of ZEN-3694 in combination with enzalutamide and relationship between tumor genomic/transcriptional profile, protein expression, and clinical variables with clinical outcomes on treatment.

Safety and efficacy assessments

Clinical and laboratory assessments were conducted at baseline and weekly during cycles 1 and 2 (28-day cycle length), every 2 weeks in cycle 3, and then every 4 weeks thereafter. Tumor response monitoring was performed using whole-body bone scan and cross-sectional imaging of the chest/abdomen/pelvis at baseline and every 2 cycles thereafter. Adverse events were graded using Common Toxicity Criteria version 4.0.

Pharmacodynamic/exploratory assessments

Whole-blood RNA for assessment of BETi target gene expression (MYC, IL8, CCR1, GPR183, HEXIM1, and IL1RN) was collected predose, 2 hours, 4 hours, 6 hours, and 24 hours post-cycle 1, day 1 dose (20). Baseline and on-treatment metastatic tumor biopsies of bone or soft tissue were obtained whenever feasible, and were evaluated by RNA-sequencing (RNA-seq) and IHC for protein expression of AR. Quality of the FASTQ files was verified by FASTQC2, and reads were aligned on BaseSpace (https://base space.illumina.com) using the RNA-Seq alignment App (version 1.1.1) with the default parameters (STAR aligner version 2.5.0b, UCSC hg19 reference genome). Gene expression levels (FPKM) for baseline biopsies were estimated using Cufflinks (version 2.2.1). For the paired biopsies, aligned reads were used as input for DESeq2 (version 1.1.0) to enable pairwise differential gene expression analysis using the default parameters. Gene set enrichment analysis (GSEA) was performed on transcriptional data when available, and previously validated AR, prostate cancer, and MYC transcriptional signatures were additionally applied to the transcriptional data (21, 22). For the BETi signature, significant genes (P < 0.05) that were >2-fold downregulated upon exposure of 0.5 µmol/L I-BET762 for 24 hours in LNCaP prostate cancer cells were selected (23). Archival tumor tissue was obtained whenever feasible for analysis of whole transcriptome and exome sequencing.

Pharmacokinetics assessments

Plasma levels of ZEN-3694, the bioactive first-order metabolite ZEN-3791, and enzalutamide were measured predose and up to 24 hours postdose on days 1 and 15 of cycle. Plasma concentrations were determined using validated LC/MS-MS analysis.

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BET Inhibitor ZEN-3694 Plus Enzalutamide in mCRPC

Table 1. Baseline characteristics.

	Study cohort (<i>N</i> = 75) ^a
Median age (range), years	70 (47-89)
ECOG score	
0	42 (56%)
1	33 (44%)
Opioid analgesic use	18 (24%)
Visceral metastases at study entry (%)	21 (28%)
Median PSA, ng/mL (range)	26.99 (0.15-1,701.8
Median ALP, U/L (range)	82 (33-487)
Median LDH, U/L (range)	188 (98-543)
Median hemoglobin, g/dL (range)	13.2 (6.4-20.2)
Halabi risk category (ref. 24; %)	
Low	50 (67)
Intermediate	16 (21)
High	8 (11)
Unknown	1 (1)
Prior number of systemic cancer treatments (range)	3 (1-7)
Prior resistance to AR-targeted therapy (%)	
Abiraterone	30 (40)
Enzalutamide	34 (45)
Both	11 (15)
Duration of prior AR-targeted therapy (range),	14.3 (1.0-58.3)
months	
Reason for prior abiraterone or enzalutamide discor	ntinuation
Radiographic progression	8 (11%)
Radiographic and PSA progression	31 (41%)
Clinical and PSA progression	3 (4%)
PSA progression	33 (44%)
Clinical progression	0

Abbreviations: ALP, alkaline phosphatase; LDH, lactate dehydrogenase. ^aFor data recorded in the clinical database as of the data cut-off date of January 7, 2020.

Results

Study population and patient disposition

A total of 75 patients were enrolled from December 2016 to April 2019 across seven investigational sites. Baseline characteristics of the enrolled patients are shown in **Table 1**. At study entry, 30 (40.0%) patients had previously experienced disease progression on abiraterone, 34 (45.3%) on enzalutamide, and 11 (14.7%) on both. Twelve (16%) patients experienced prior primary resistance to first-line AR-targeted therapy, defined in *post hoc* fashion as treatment duration of less than 6 months. Forty-two (56%) patients had evidence of radiographic and/or clinical progression at study entry.

The median duration of treatment was 3.5 months (range, 0-34.7+). As of date of data cutoff, seven patients (9%) remain on treatment without progression, with duration of therapy ranging from 15.0+ to 34.7+ months. Forty-eight patients (64%) discontinued for disease progression; nine patients (12%) discontinued for adverse events, and 11 (16%) withdrew from study.

Safety results

The proportion of patients who experienced grade \geq 3 treatmentrelated adverse event was 18.7% (n = 14). The most common grade \geq 3 adverse events (\geq 2 patients) included nausea (n = 3; 4%), thrombocytopenia (n = 3; 4%), anemia (n = 2; 2.7%), fatigue (n = 2; 2.7%), and hypophosphatemia (n = 2; 2.7%). There were no clinically significant bleeding events observed on treatment. The most commonly reported ZEN-3694–related adverse events (any grade severity, occurring in \geq 10% of patients, in order of incidence) were visual symptoms (described as a transitory perception of brighter lights and/or light flashes, with or without visual color tinges, as well as trouble navigating in dim light; 67%), nausea (45%), fatigue (40%), decreased appetite (25%), dysgeusia (20%), thrombocytopenia (15%), and weight decreased (11%; **Table 2**). Visual symptoms were grade 1 in all cases, resolved 60–90 minutes after dosing, were successfully mitigated with implementation of dosing before bedtime, and resulted in no functional consequences upon repeat eye exams throughout study participation.

Dose reductions and/or treatment discontinuation due to adverse events were required in 24 of 75 (32%) of patients. The percentage of patients requiring dose reduction and/or discontinuation ranged from 10% to 35% for doses from 36 to 96 mg/day, in contrast to 75% and 100% at ZEN-3694 dose levels of 120 and 144 mg/day, respectively (Supplementary Table S1). The class of adverse events leading to dose reduction and/or discontinuation were related to gastrointestinal (GI) toxicities in 83% of occurrences.

Determination of MTD and recommended phase II dose

In the dose escalation, 35 patients were enrolled across dose levels ranging from 36 to 144 mg daily. The MTD was not reached. One patient experienced a dose-limiting toxicity at the 96 mg/day dose level (grade 3 nausea necessitating missing >25% of scheduled doses in cycle 1). On the basis of the aggregate of pharmacodynamics data indicating dose exposure–dependent downregulation of BETi target gene expression with a plateau of effect at doses above 96 mg/day, the high percentage of patients requiring dose interruptions/reductions at doses above 96 mg/day, and a comparable pharmacokinetics/pharmacodynamics effect with preclinical models treated at efficacious doses, 96 mg/day was chosen as the recommended phase II dose of ZEN-3694 for dose expansion (N = 26). An additional dose-expansion cohort of 48 mg/day (N = 14) was also enrolled, to better characterize the exposure–effect relationship.

Pharmacokinetics analyses

The AUC₀₋₂₄ and the C_{max} of combined ZEN-3694 (parent compound) + ZEN-3791 (active metabolite), on day 1 and day 15 of cycle 1, are shown in **Fig. 1A** and **B**, respectively. Less than dose proportional increase in exposure was observed at doses higher than 96 mg daily. The estimated T_{max} and half-life of ZEN-3694 + ZEN-3791 were 2 and 5–6 hours, respectively. The ratio of ZEN-3691 metabolite to parent compound, ZEN-3694, was increased on day 15 compared with day 1, likely related to enzalutamide-mediated induction of CYP3A4 metabolism (**Fig. 1C**). The observed plasma concentrations of ZEN-3694 + ZEN-3791 were similar to ZEN-3694 monotherapy pharmacokinetics reported previously (24). Likewise, there was no significant impact of ZEN-3694 on enzalutamide and desmethyl enzalutamide concentrations (**Fig. 1D**).

Pharmacodynamics analyses

Pre- and up to 24-hour postdose whole-blood RNA analyses were available from 69 patients enrolled on study. There was a dose-dependent two- to fourfold decrease in the whole-blood mRNA levels of the BETi target genes *MYC*, *IL8*, *CCR1*, *GPR183*, and *IL1RN* (**Fig. 2A**) upon treatment with ZEN-3694, which was sustained for at least 8 hours. Decrease in expression of BETi target genes appeared to plateau at ZEN-3694 dose levels \geq 96 mg. There was a direct correlation between cumulative exposure to ZEN-3694 + ZEN-3791 (AUC₀₋₂ for *MYC* and *GPR183*, and AUC₀₋₄ for *CCR1*, *IL1RN*, and

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	36 mg QD <i>n</i> = 4	48 mg QD n = 21	60 mg QD <i>n</i> = 6	72 mg QD <i>n</i> = 6	96 mg QD <i>n</i> = 31	120 mg QD <i>n</i> = 4	144 mg QD <i>n</i> = 3	Total <i>N</i> = 75 (%)
Blood creatinine increased			2		3			5 (6.7)
Constipation		1			3			4 (5.3)
Decreased appetite		2	2	1	10	3	2	20 (26.7)
Diarrhea				1	5			6 (8)
Dizziness				1	3			4 (5.3)
Dysgeusia		2	0	0	10	1	3	16 (21.3)
Dyspepsia		1			2			3 (4)
Fatigue	1	8	1	2	13	3	1	29 (38.7)
Nasal congestion					3			3 (4)
Nausea		7	2	3	17	3	2	34 (45.3)
Photopsia		1			3			4 (5.3)
Photosensitivity		2			3			5 (6.7)
Rash					3			3 (4)
Rash maculopapular		3			1		1	5 (6.7)
Taste disorder			1	1	3			5 (6.7)
Thrombocytopenia		1	1	2	6		1	11 (14.7)
Vision blurred					2	1		3 (4)
Visual symptoms ^a	3	12	4	6	17	4	2	48 (64)
Vomiting		1			3	1		5 (6.7)
Weight loss and abnormal weight loss	1			1	3	1	2	8 (10.7)

Table 2. Summary of all grades treatment-related adverse events by dose level of ZEN-3694.

Abbreviation: QD, every day.

^aVisual symptoms defined as a transitory perception of bright lights and/or light flashes with or without visual color tinges.

IL8) with downregulation of whole-blood mRNA levels of the BETi target genes (R^2 ranging from 0.20 to 0.51; $P \le 0.0001$; **Fig. 2B**).

Four patients had evaluable paired metastatic tumor biopsies obtained at baseline and on-treatment (median duration of treatment 8 weeks prior to on-treatment biopsy). Time after the last ZEN-3694 +

enzalutamide dosing prior to the biopsy ranged from 3.5 to 24 hours. The limited sample size precluded ability to perform statistical analyses of change in expression by dose level. However, on GSEAs, looking at changes between on-treatment versus pretreatment samples, there were strong indications of downregulation of expression of MYC and



Figure 1.

Pharmacokinetics analyses. **A** and **B**, AUC from 0 to 24 hours (AUC₀₋₂₄) and maximum serum concentration, respectively, of ZEN-3694 + ZEN-3791 (first-generation active metabolite) serum concentration on day 1 and day 15 of cycle 1 (red triangles). Overlaid AUC₀₋₂₄ data from the monotherapy (mono) trial of ZEN-3694 (23) are shown for dose levels 48 and 72 mg daily (black circles). **C**, Ratio of ZEN-3791 (first-generation active metabolite) versus ZEN-3694 (parent compound) from the prior monotherapy trial (23) and in combination with enzalutamide (enza) on day 1 and day 15 of cycle 1. **D**, Steady-state serum concentration of enzalutamide and desmethyl enzalutamide following 14 day lead-in of enzalutamide (day -14 to day -1), by ZEN-3694 dose level. QD, every day.

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Figure 2.

Pharmacodynamics assessments. **A**, Fold-change from baseline in whole-blood RNA expression of BETi target genes *CCR1, IL1RN, IL8, MYC*, and *GPR183* by ZEN-3694 dose level. **B**, Correlation between fold change from baseline in whole-blood RNA expression of BETi target genes and AUC₀₋₂₄ of ZEN-3694 + ZEN-3791 indicates strong pharmacokinetics-pharmacodynamics relationship. (*Continued on the following page*.)

AR signaling on-treatment compared with baseline biopsies, as well as downregulation of BET-dependent genes previously identified in LnCaP cells treated with the I-BET762 BETi (**Fig. 2C**; ref. 23).

Efficacy analyses

The median rPFS in the overall cohort was 9.0 months [95% confidence interval (CI), 4.6–12.9], with 7.8 months for patients that had progressed on abiraterone (95% CI, 4.9–10.6) and 10.1 months for patients that had progressed on enzalutamide (95% CI, 4.4–12.9; **Fig. 3A**). Composite median radiographic or clinical PFS was 5.5 months (95% CI, 4.0–7.8) in the overall cohort, and 5.5 months (95% CI, 4.4–7.8) and 5.1 months (95% CI, 3.2–10.1) in those with prior progression on abiraterone and enzalutamide, respectively

(Fig. 3B). Thirteen (17%) and four (5%) patients remained on treatment for greater than 12 and 24 months without progression, respectively (Fig. 3C). In patients with radiographic progression at the time of study entry, the median rPFS was 7.8 months (95% CI, 4.4–10.6; Fig. 3D) and composite PFS was 4.8 months (95% CI, 3.5–7.7). An analysis of the subset of patients with primary resistance to prior first-line AR-targeted therapy (N = 12), defined by progression within 6 months of treatment initiation, demonstrated an on-treatment median rPFS of 10.6 months (95% CI, 7.5–not reached; Fig. 3E). Using a more stringent cutoff of primary resistance of progression within 16 weeks of prior first-line AR-targeted therapy (N = 5), likewise demonstrated prolonged median rPFS (median rPFS, 22.4 months; 95% CI, 7.8–not reached) and composite PFS (median

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Figure 2.

(*Continued.*) **C**, GSEA of change from baseline in gene expression by RNA-seq in paired metastatic tumor biopsies. Downregulation of MYC signaling pathway was observed in on-treatment versus baseline tumor biopsy.

PFS, 10.6 months; 95% CI, 4.0, not reached) in this subset of patients (Supplementary Fig. S1A and S1B).

Of the four exceptional responders who remained on treatment for greater than 24 months duration, three had radiographic progression at study entry, two had progressed on prior enzalutamide, and one of the four patients experienced an objective radiographic response on enzalutamide + ZEN-3694 (Supplementary Table S2).

Six patients (8%) experienced a greater than 50% decline from baseline in serum PSA by PCWG2 criteria (PSA50 response), including two patients with prior progression on enzalutamide monotherapy. All PSA responses were confirmed on repeat measurement. Four patients (5.3%) experienced a greater than 90% decline in serum PSA from baseline on study treatment. PSA50 responses were sustained in the majority of cases with median duration of PSA50 response of 21.1 months (95% CI, 19.0–23.2). The median PSA PFS was 3.2 months (95% CI, 3.2–5.1) in the overall study cohort and 3.2 months (95% CI, 2.8–6.4) in those with PSA-only progression at study entry. There were no substantial differences with respect to rPFS, composite PFS, or PSA PFS noted between 48- and 96-mg dose-expansion cohorts.

In addition, in a subset of patients (n = 21), there was a transient increase of >2 ng/mL and 25% above baseline in serum PSA within the first 12 weeks of treatment with subsequent plateau in serum PSA level (Supplementary Fig. S2A). Patients with transient PSA increase as defined above appeared to derive sustained clinical benefit with median rPFS of 10.1 months (95% CI, 5.6–11.7). In contrast, patients whose serum PSA consistently rose beyond the 12-week timepoint (n = 21) experienced a median rPFS of 7.2 months (95% CI, 3.9–9.0; Supplementary Fig. S2B).

$\label{eq:predictors} \mbox{ prolonged clinical benefit with ZEN-3694} + \mbox{ enzalutamide}$

Exploratory analyses were performed with available genomic and transcriptional data from baseline tumor biopsies to evaluate association with subsequent time to progression (TTP) on treatment.

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Figure 3.

rPFS and duration of treatment. **A**, Kaplan-Meier curve demonstrating rPFS by PCWG2 criteria in all evaluable study participants (black curve), patients with prior enzalutamide (enza) progression (blue curve), or prior abiraterone (abi) progression (green curve). **B**, Kaplan-Meier curve demonstrating composite PFS (time to first clinical or radiographic progression). **C**, Swimmer plot showing duration of treatment, with color labels by ZEN-3694 dose level (hashed line, treatment ongoing). **D** and **E**, Kaplan-Meier curves showing rPFS in subsets of patients with radiographic progression or primary resistance to prior ASI, respectively.

Interestingly, patients whose baseline metastatic tumor biopsies (N = 13) harbored lower canonical AR transcriptional activity, as assessed by 5-gene score (25) as well as the HALLMARK_AN-DROGEN_RESPONSE signature, experienced a longer median TTP (median TTP 19 vs. 45 weeks; **Fig. 4A** and **B**). In support of the notion that tumors with lower canonical AR activity might be more responsive to BET inhibition, we observed a trend toward prolonged TTP among patients meeting clinical criteria for aggressive variant prostate cancer [e.g., low serum PSA <10 ng/mL with concomitant high disease burden (visceral metastases and/or >10 bone metastases); ref. 26]. The median TTP in patients with aggressive variant disease was 11.6 months (95% CI, 7.2–12.8) versus 5.5 months (95% CI, 2.3–10.6, P = 0.24) in those without aggressive variant clinical features at baseline (**Fig. 4C**).

Discussion

Our results demonstrate that the pan-BETi, ZEN-3694, has acceptable tolerability and encouraging preliminary efficacy data in combination with enzalutamide in patients with mCRPC. The median rPFS in the overall cohort was 9 months, and more than 10 months in those with prior progression on enzalutamide monotherapy. ZEN-3694 + enzalutamide treatment led to a two- to fourfold reduction in the expression of BET target genes including *MYC*, which was sustained throughout the 24-hour dosing interval. On the basis of the aggregate of the safety, efficacy, and evidence of robust downregulation of expression of BET-dependent target genes, ZEN-3694 at 96 mg daily has been selected as the recommended phase II dose to move forward in further clinical development in combination with enzalutamide. The clinical and pharmacodynamics data provide clinical evidence that BET inhibition may be able to abrogate resistance mechanisms and resensitize patients to ASIs.

The prolonged PFS observed in this study in relevant subsets, including those with radiographic progression at study entry, primary resistance to prior AR-targeted therapy, as well as those with prior progression on enzalutamide monotherapy, is consistent with an additive or potentially synergistic interaction between enzalutamide and ZEN-3694. The baseline characteristics of the study cohort are representative of other studies in the post-ASI mCRPC setting, including nearly one-third of patients with intermediate- or high-risk disease by Halabi prognostic model (27), and a quarter of whom required opioid analgesics at study entry. These features argue against the possibility of enrichment of better than average-risk group contributing significantly to the prolonged PFS observed on treatment. Taken together, the data support a randomized study to evaluate for the magnitude of benefit of ZEN-3694 in combination with enzalutamide.

With the caveat of cross-trial comparisons, the median PFS observed with ZEN-3694 + enzalutamide in this study compares favorably with outcomes observed with sequential AR targeting in

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Figure 4.

AR signaling score and clinical outcomes. **A**, Lower AR activity level in baseline tumor biopsies is correlated with longer time on study ($R^2 = 0.38$) using either the 5-gene AR score (left) or the HALLMARK_ANDROGEN_RESPONSE (right) signatures. For the hallmark signature, baseline gene expression of biopsies from patients with radiographic progression prior to 24 weeks versus greater than 24 weeks were compared (FDR = 0.04). **B**, Kaplan-Meier curve showing significant increase in time to median rPFS in patients with lower AR signaling compared with patients with higher AR signaling score (median rPFS 10.4 months in tumors with low AR score versus 4.3 months in tumors with high AR activity). **C**, Patients with high tumor burden and lower baseline PSA levels (<10 ng/mL; blue curve) demonstrate longer PFS than patients with higher baseline PSA (>10 ng/mL) levels.

mCRPC with abiraterone followed by enzalutamide, or vice versa, in prior studies. In the prospective SWITCH phase II cross-over study, the median PFSs of second-line enzalutamide and abiraterone were 3.5 and 1.7 months, respectively (6). Similarly, median PFSs with secondline AR-targeting therapy have been less than 8 months in most retrospective series (9). Caution should be applied to overinterpretation of these cross-trial comparisons, and a randomized trial will be necessary to assess the individual contribution of ZEN-3694 added to enzalutamide in mCRPC.

The PSA50 response rate with the combination of ZEN-3694 plus enzalutamide was less than 10% in the study, and median PSA PFS was less than 4 months. Although this may reflect lack of additive benefit of ZEN-3694 in combination with enzalutamide, decline in serum PSA and PSA PFS may not be the best metrics to gauge efficacy of BETis including ZEN-3694. In fact, a subset of patients experienced transient early rises in serum PSA levels by week 8 of treatment, which were associated with longer TTP. In addition, tumors harboring lower AR activity at baseline appeared to derive more clinical benefit from treatment. Finally, those with low serum PSA in relation to metastatic disease burden, a clinical profile consistent with small-cell/neuroendocrine prostate cancer, may also have longer rPFS compared with those with higher baseline serum PSA levels. Although these observations are hypothesis generating and require prospective validation, it raises the intriguing possibility that BETis may restore dependency on AR signaling in tumors that are less reliant on AR prior to BETi or that BETi is blocking important AR-independent survival mechanisms, such as MYC, which have been shown to be critical for BETi effects in CRPC (13, 28, 29). AR-independent mCRPC is becoming more prevalent with the earlier application of ASIs, and is associated with shortened survival and unmet need to develop novel therapeutic approaches (14).

The acceptable toxicity profile of ZEN-3694 in combination with enzalutamide stands in contrast to the results observed with several other recent BETis reported in the literature, which have been limited by thrombocytopenia and GI toxicities (30, 31). In this study, there was substantially less thrombocytopenia observed. GI toxicities were not as prevalent or severe as prior studies and were manageable with early institution of antiemetics and dose reductions, if necessary. The reasons underlying the potentially more favorable toxicity profile observed in this study, as compared with other BETis, may relate to patient factors such as excluding prior chemotherapy for mCRPC. Furthermore, it is possible that a pharmacokinetics interaction between ZEN-3694 and enzalutamide may have accelerated production of the first-generation active metabolite, ZEN-3791, which may have a more favorable toxicity profile. The differential toxicity compared with other BETis does not appear to relate to differences in potency, given the robust downregulation of BETi target genes observed in this study.

There were several limitations of the study, including the limited number of baseline and on-treatment paired biopsies, precluding the ability to identify a consistent predictive biomarker with a high degree of statistical confidence. The nonrandomized nature of the dose expansion portion of the study also limits our ability to draw definitive conclusions regarding the potential additive benefit of ZEN-3694, although evidence of contribution is provided by favorable comparison with contemporary controls from other studies as outlined above. AR-V7 splice variant status in circulating tumor cells, a validated resistance mechanism to AR-targeted therapy that may be downregulated with BETi treatment, was not reliably captured in this study in a sufficient number of patients to permit evaluation. Finally, there did not appear to be a relationship between dose level and efficacy outcomes, potentially related to fairly broad interpatient variability in ZEN-3694 exposure, limited sample size, and limited single-agent activity of ZEN-3694.

With the shift in application of potent AR-targeted therapy in earlier castration-sensitive settings, there is an increasing medical need to develop therapies that reverse therapeutic resistance and restore dependency on AR signaling. The preliminary data provided by the phase Ib/II study of ZEN-3694 plus enzalutamide provides strong justification to further investigate it in a prospective, randomized study.

Disclosure of Potential Conflicts of Interest

R. Aggarwal reports grants from Zenith Epigenetics during the conduct of the study, grants and personal fees from Janssen, Merck, and AstraZeneca, and personal fees from Dendreon and Clovis Oncology outside the submitted work. M.T. Schweizer reports grants from Zenith Epigenetics (research funds to institution) during the conduct of the study, Janssen (research funds to institution), AstraZeneca (research funds to institution), Madison Vaccines (research funds to institution), Pfizer (research funds to institution), and Hoffmann-La Roche (research funds to institution), and personal fees from Resverlogix (consulting fee) outside the submitted work. D.M. Nanus reports personal fees from Genentech Roche (DSMB) outside the submitted work. A. Pantuck reports grants from UCLA (clinical trial contract/grant) during the conduct of the study. E. Campeau reports personal fees and other from Zenith Epigenetics Ltd. (salary paid by Zenith Epigenetics Ltd.) during the conduct of the study and outside the submitted work, as well as has a patent for Combination Therapy for the Treatment of Prostate Cancer pending (all patent rights were transferred to Zenith Epigenetics Ltd.). M. Snyder reports personal fees and other from Zenith Epigenetics (employment) during the conduct of the study and outside the submitted work, as well as reports employment with Zenith Epigenetics. S. Lakhotia reports personal fees and other from Zenith Epigenetics (paid salaried employee of Zenith, lead clinical development for Zenith) during the conduct of the study and outside the submitted work, as well as has a patent on the combination of ZEN-3694 + enzalutamide for the treatment of prostate cancer, owned by Zenith Epigenetics. F.Y. Feng reports personal fees from Janssen Oncology (advisory board), Sanofi (advisory board), and Bayer (consultant), grants and other from Zenith Epigenetics (research funding from Zenith Epigenetics), other from PFS Genomics (founding member, ownership interests), and personal fees from Celgene (advisory board), Blue Earth Diagnostics (advisory board), Genentech (consultant), Myovant Sciences (consultant), Roivant Sciences (consultant), and Astellas Pharma (consultant) outside the submitted work. E.J. Small reports personal fees and other from Fortis Therapeutics (consulting and stock), personal fees from Harpoon Therapeutics (consulting), Janssen (consulting), BeiGene (consulting), Tolero (consulting), and Teon Therapeutics (consulting) outside the submitted work. W. Abida reports grants from Zenith Epigenetics (research funding to institution) during the conduct of the study, grants from Clovis Oncology (research funding to institution) and GlaxoSmithKline (research funding to institution) outside the submitted work, and personal fees from Clovis Oncology, Janssen Biotech, MORE Health, ORIC pharmaceuticals, and Daiichi Sankyo, grants from AstraZeneca (research funding to institution). J. Alumkal reports grants from Zenith Epigenetics (research support to institution), NCI (research support to institution) during the conduct of the study, and Aragon Pharmaceuticals (research support to institution), and Gilead Sciences (research support to institution) outside the submitted work, and grants and personal fees from Astellas (consulting fees and research support to institution) and Janssen Biotech (consulting fees and research support to institution) outside the submitted work. No potential conflicts of interest were disclosed by the other authors.

Authors' Contributions

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A Phase Ib/IIa Study of the Pan-BET Inhibitor ZEN-3694 in Combination with Enzalutamide in Patients with Metastatic Castration-resistant Prostate Cancer

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Implementation of Germline Testing for Prosta Cancer: Philadelphia Prostate Cancer Consensus Conference 2019

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ASSOCIATED CONTENT Appendix

Data Supplement

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PURPOSE Germline testing (GT) is a central feature of prostate cancer (PCA) treatment, management, and hereditary cancer assessment. Critical needs include optimized multigene testing strategies that incorporate evolving genetic data, consistency in GT indications and management, and alternate genetic evaluation models that address the rising demand for genetic services.

METHODS A multidisciplinary consensus conference that included experts, stakeholders, and national organization leaders was convened in response to current practice challenges and to develop a genetic implementation framework. Evidence review informed questions using the modified Delphi model. The final framework included criteria with strong (> 75%) agreement (Recommend) or moderate (50% to 74%) agreement (Consider).

RESULTS Large germline panels and somatic testing were recommended for metastatic PCA. Reflex testing initial testing of priority genes followed by expanded testing—was suggested for multiple scenarios. Metastatic disease or family history suggestive of hereditary PCA was recommended for GT. Additional family history and pathologic criteria garnered moderate consensus. Priority genes to test for metastatic disease treatment included *BRCA2*, *BRCA1*, and mismatch repair genes, with broader testing, such as *ATM*, for clinical trial eligibility. *BRCA2* was recommended for active surveillance discussions. Screening starting at age 40 years or 10 years before the youngest PCA diagnosis in a family was recommended for *BRCA2* carriers, with consideration in *HOXB13*, *BRCA1*, *ATM*, and mismatch repair carriers. Collaborative (point-of-care) evaluation models between health care and genetic providers was endorsed to address the genetic counseling shortage. The genetic evaluation framework included optimal pretest informed consent, post-test discussion, cascade testing, and technology-based approaches.

CONCLUSION This multidisciplinary, consensus-driven PCA genetic implementation framework provides novel guidance to clinicians and patients tailored to the precision era. Multiple research, education, and policy needs remain of importance.

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INTRODUCTION

The role of germline testing (GT) for prostate cancer (PCA) has increased, with growing precision treatment implications and expanded testing options.^{1,2} A primary driver for GT is now precision therapy for

metastatic disease where genetic results inform options and strategies for targeted treatment, therapeutic planning, and clinical trials.¹⁻⁴ Approximately 12% to 17% of men with metastatic PCA harbor germline mutations, primarily in DNA repair genes, such as



BRCA2, CHEK2, BRCA1, ATM, PALB2, and the DNA mismatch repair (MMR) genes,⁵ which are increasingly informing options for poly (ADP-ribose) polymerase (PARP) inhibitors, immune checkpoint inhibitors, platinum chemotherapy, and clinical trials.^{1-4,6} In early-stage disease, emerging data suggest that men with germline BRCA2 mutations, and possibly ATM mutations, have higher rates of upgrading of prostate biopsies while on active surveillance (AS).⁷ GT results are considered increasingly in PCA early detection discussions, particularly for men with BRCA2 mutations for which data support higher rates of PCA detection, younger age at diagnosis, and more clinically significant disease.⁸⁻¹⁰ Many of the genes that are important for PCA therapy, management, and early detection are associated with hereditary cancer syndromes.¹¹ Pathogenic variants in BRCA1 and BRCA2 are associated with hereditary breast and ovarian cancer (HBOC). DNA MMR genes-MLH1, MSH2, PMS2, MSH6, and EPCAM-are associated with Lynch syndrome.¹¹⁻¹⁶ These and other hereditary cancer syndromes confer risks for multiple cancers that must be addressed for men and their kindred.^{8,16}

As PCA GT has increased, new practice and implementation challenges have emerged in three major areas: expanded options for multigene panels, with a resultant lack of clarity regarding optimized panel use and priority genes to test; variability in guidelines regarding GT indications and genetically based management that incorporates emerging data; and a shortage of genetic services.^{1,17-21} Testing options have expanded rapidly, which include focused, guideline-based, comprehensive, and reflex panels.^{17,18} Panels include genes with strong, limited, and unknown risk for PCA and that yet confer risks for multiple cancers.¹⁸ There is a need for clarity on panel choice and priority genes to test in men with metastatic PCA, nonmetastatic PCA, and men at high risk for PCA that balances the benefits of expanded testing (eg, identifying actionable mutations) with considerations (eg, higher rates of variants of uncertain significance [VUS]).^{3,8,10}

Uniform guidance is also needed regarding GT indications and genetically based PCA management that incorporates rapidly emerging, sometimes conflicting, data. Current National Comprehensive Cancer Network (NCCN) guidelines have variability regarding GT on the basis of pathologic—stage and Gleason/Grade Group—and family history (FH) criteria.^{3,8,9} Management guidance is also needed in multiple areas with consideration of gene-specific outcomes, such as treatment of metastatic disease with variable responses by DNA repair mutations^{1-4,6}; AS discussions that consider strong data for *BRCA2*, but limited data for *BRCA1* and *ATM*⁷; and broader consideration of genes for PCA early detection.^{1,2,11} In particular, strategies for PCA early detection need clarification regarding age to begin screening on the basis of genetic status.^{8,9}

Furthermore, the rising need for PCA GT has created a critical shortage of genetic counseling (GC) services.^{1,19}

Health care providers, such as oncologists and urologists, increasingly are ordering PCA GT to expedite testing for management.^{20,21} Concerns include limited guidance on optimal pretest informed consent, optimal panel testing strategies for comprehensive genetic evaluation, inclusion of personal history and FH, and balancing timely GT with appropriate referral to GC to address patient and family needs.^{1,20,21} As referral of all men to GC for PCA GT is not sustainable, health care and genetic providers need implementation strategies that incorporate alternate genetic evaluation models for the timely and responsible delivery of PCA GT for men and their families.^{1,19}

The 2019 Philadelphia Prostate Cancer Consensus Conference was convened to address challenges in PCA germline evaluation and implementation with attention to evolving genetic and precision medicine data. This meeting was a follow-up to the 2017 Philadelphia Consensus Conference, which focused on the role of GT for inherited PCA risk.¹⁸ The 2019 conference had the following 3 goals: to define optimal GT strategies that incorporate expansion of panel testing options and evolving genetic data, to propose consistent PCA GT indications and management, and to propose alternate genetic evaluation models to address the GC shortage. An expert, consensus-driven genetic implementation framework was developed for health care and genetic providers to streamline GT for PCA in the precision medicine era.

METHODS

Overarching Questions Addressing Implementation Gaps

The following questions were primary drivers of the conceptual framework:

- 1. Which men should be considered for germline PCA genetic testing?
- 2. Which panels should be considered and which genes should be prioritized for testing?
- 3. What PCA-specific recommendations should be considered on the basis of genetic results?
- 4. What is optimal informed consent for PCA GT?
- 5. What collaborative strategies may facilitate PCA genetic evaluation between health care and genetic providers?
- 6. What post-test disclosure strategies are most appropriate on the basis of genetic results?
- 7. What barriers must be addressed to enhance PCA GT?

Consensus Conference Participants

The Consensus Conference included 97 participants spanning the fields of urology, medical oncology, radiation oncology, clinical genetics, genetic counseling, primary care, pathology, implementation science, population science, epidemiology, and basic science. Patient stakeholders and advocates were active participants. Members of several national organizations, which included NCCN representatives, also participated. Academic and

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community practices were represented, and panelists were from multiple regions of the United States, as well as Europe and Australia. The final voting panel included 76 participants (Table 1).

Consensus Process

The modified Delphi model was followed that incorporated elements of the Delphi process as previously published.^{18,22,23} Literature was provided to panel members before the meeting. Multiple expert presentations summarizing evidence relevant to genetic implementation were delivered. Evidence review is summarized in the Data Supplement.

Evidence Review

Thematic topics included: genetic contribution to PCA risk/ aggressiveness²⁴⁻⁵⁴; germline mutations by PCA clinical and molecular characteristics^{5,55-66}; PCA clinical multigene testing data^{60,61,67}; germline mutations in diverse populations^{5,24,30,49,61,68-74}; PCA genetic testing capabilities and considerations^{17,75-81} (Fig 1); implementation of GC^{1,3,8,9,17,76,82-93}; NCCN PCA genetic testing guidelines and current variability^{3,8,9}; GT for PCA precision medicine in the metastatic setting^{2,4,6,56,58,94-99}; germline implications for AS of early-stage PCA^{7,35,99,100,101}; and germline implications for PCA early detection.^{8-10,102} Table 2 provides a summary of genetic data for PCA risk and aggressiveness. Full evidence summary is provided in the Data Supplement.

Strength of Consensus

Votes were cast anonymously using a Web-based polling platform. Strength of consensus was \geq 75% agreement for strong consensus, 50% to 74% agreement for moderate consensus, and < 50% agreement for lack of consensus.^{22,23}

Development of PCA Genetic Evaluation and Management Framework

A conceptual framework for PCA genetic evaluation and management was developed (Fig 2). Criteria that achieved strong consensus were designated as "Recommend" and those with moderate consensus were designated as "Consider" in the final framework.

RESULTS

Key premises

The following are guiding principles for clinical genetic evaluation:

Premises based on prior literature and Consensus Conference expert guidance:

- In-person GC is a gold standard of genetics practice.^{2,76,82-84}
- Patients' psychosocial needs or preferences should dictate the mode of counseling.^{1,82-84}
- Full FH is important to collect during the genetic evaluation process:^{1,82-84}



FIG 1. Variability in prostate cancer–specific multigene panels. Genetic testing registry: As of August 2019. Available at: https://www.ncbi.nlm.gov/gtr/. Courtesy of Saud AlDubayan, MD.

Premises based on consensus voting:

- Men should engage in informed decision making for genetic testing (Recommend).
- Building collaborations between health care and genetics providers is important for optimal genetic evaluation (Recommend).

1. Which Men Should Be Considered for Germline PCA Genetic Testing?

Gaps addressed. NCCN guidelines (NCCN Prostate Version 4.2019 and NCCN Breast/Ovary Version 3.2019) at the time of the 2019 Consensus meeting had varying indications for PCA GT.^{3,8} Data regarding clinical, pathologic, and FH features were summarized (Data Supplement).

Criteria for testing. Any one of the following criteria may prompt GT:

- Men with metastatic PCA (castration resistant or castration sensitive; Recommend).
- Men with nonmetastatic PCA—one of the following: • Ashkenazi Jewish ancestry (Consider).
 - Advanced disease (T3a or higher; Consider).
 - Intraductal/ductal pathology (Consider).
 - Grade Group 4 (Gleason sum 8) or above (Consider).
- FH criteria:
 - PCA FH criteria:
 - Men with one brother or father or two or more male relatives with one of the following:
 - Diagnosed with PCA at age < 60 years (Recommend).

- Any of whom died of PCA (Recommend).
- Any of whom had metastatic PCA (Recommend).
- \odot FH of other cancers:
 - Two or more cancers in HBOC or Lynch spectrum in any relatives on the same side of the family (especially if diagnosed at age < 50 years; Consider).

Additional considerations. FH consistent with hereditary PCA achieved a strong recommendation for GT. Additional FH criteria were expanded to consider 2 or more cancers in the HBOC or Lynch spectrum to account for limitations in self-reported FH. Genes corresponding to specific cancers are listed in Table 2. Of note, an unremarkable FH does not necessarily negate consideration of GT, particularly for treatment decisions in the metastatic setting.

All pathologic criteria achieved moderate agreement. Universal screening for Lynch syndrome in PCA is not current practice; however, if immunohistochemistry is performed on a prostate specimen revealing loss of the DNA MMR genes, and particularly MSH2, the recommendation is to proceed with GT to determine if the patient has Lynch syndrome given the significant cancer risks and potential treatment implications. Panelists noted that many centers do not report intraductal/ductal pathology or immunohistochemistry for Lynch syndrome markers, which must be addressed with pathologists. Although multiple unique questions were posed specifically regarding GT for African American men, none met consensus agreement as a result of limited data. Until additional research is completed, testing guidelines as described herein should be applied in under-represented populations.

2. Which Panels Should Be Considered and Which Genes Should Be Prioritized for Testing?

Gaps addressed. Guidance on the use of various gene panels adapted to clinical scenarios is needed given the rapid expansion of panel options and the inclusion of genes with limited association to PCA risk or PCA treatment implications (Fig 1). Furthermore, NCCN guidelines vary regarding genes to test,^{3,8} necessitating consensus prioritization of genes for testing (Data Supplement).

Panels considered. Focused—guidelines-based—panels (approximately 5 to 6 genes), PCA-specific panels (approximately 10 to 15 genes), comprehensive cancer panels (approximately 80 genes), and reflex panels (initial set of genes tested followed by broad gene testing) were considered. Benefits and limitations of various panels were also considered (Data Supplement).

Genes considered. BRCA1, BRCA2, HOXB13, CHEK2, ATM, NBN, MSH2, MSH6, MLH1, PMS2, PALB2, BRIP1, TP53, and Fanconi anemia genes were considered.

Participant Characteristic	No. (%)
Primary area of specialty/work (combination of academic and community settings)	
Urology	29 (38)
Medical oncology	13 (17)
Genetic counseling/implementation science	10 (13)
Radiation oncology	5 (7)
Primary care, pathology, and other	9 (12)
Population science/epidemiology	4 (5)
Patient/patient advocate	6 (8)
Geographic region of practice or work	
Northeast United States	26 (34)
Mid-Atlantic United States	14 (18)
Southeast United States	4 (5)
Midwest United States	15 (20)
Southcentral United States	4 (5)
Northwest United States	6 (8)
Southwest United States	3 (4)
Europe, Australia, and Other	4 (5)
Type of region of work	
Urban	55 (71)
Suburban	15 (19)
Rural	2 (3)
Other	5 (6)

TABLE 1. Characteristics of Voting Consensus Participants
						PCA-Specif Co	ic Clinical Impact of Ge nsensus Conference Su	rmline Testing: mmary	
Gene	Strength of Association for PCA Susceptibility ^a	Risk for Aggressive Disease ^a	Prevalence in Metastatic PCA ^b	Testing for Hereditary Cancer Syndromes and Other Associated Cancers Based on Personal History or FH	Cancer Screening Guidelines for Non- PCAs	Implications for PCA Early Detection/PCA Risk Assessment	Implications for AS Decision Making	Metastatic Treatment Options	Clinical Trial Options
ATM	+	+++++	+++++	Breast, pancreas	×	++/+	+	+++++	+++++++
BRCAI	++++++	-/+	+	HBOC syndrome; breast (male and female), ovarian, pancreas, melanoma	×	++++++		+ + +	+ + +
BRCA2	++++++	+ + +	+ + +	HBOC syndrome; breast (male and female), ovarian, pancreas, melanoma	×	+++++++	++++++	+ + +	+ + +
HOXB13	+++++++++++++++++++++++++++++++++++++++	I	I	Hereditary PCA		++++			
CHEK2	++++	+	+++++	Breast, colon	×				++++++
MSH2/ MSH6	++++	+	+	Lynch syndrome; colorectal, ovarian, uterine, gastric, small bowel, pancreas, upper tract urothelial, kidney, sebaceous carcinoma	×	+++++		+ +	+ + +
MLH1/ PMS2	+	-/+	+	Lynch syndrome; colorectal, ovarian, uterine, gastric, small bowel, pancreas, upper tract urothelial, kidney, sebaceous carcinoma	×	+		+ +	+ + +
NBN	-/+	-/+	+	Breast	×				+
PALB2	I	+	+	Breast, pancreas	×				++++++
<i>RAD51C-L</i> <i>BRIP1</i> , Fancor anemia genes	- -	T	+	ovarian (RAD51C/D, BRIP1)	×				+ +
Abbrev	iations: AS, active survei	llance; FH, fai	mily history; HBO	C, hereditary breast and ovarian cancer; P(CA, prostate cance				

TABLE 2. Genetic Contribution to PCA Risk, Aggressiveness, and Proposed Clinical Implications

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^aEvidence from case-control, familial, cohort, or clinical studies: strong (+++); moderate (++); low (+); conflicting data (+/-); not established (-).

^pHigh prevalence ($\geq 4\%$; +++); moderate prevalence (1% to < 4%; ++); low prevalence (< 1%; +); not reported (-).



FIG 2. Framework for prostate cancer (PCA) genetic evaluation and management. (*) See Table 2 for personal history or family history (FH) of cancers indicating genes to test. GINA, Genetic Information Nondiscrimination Act; HBOC, hereditary breast and ovarian cancer; MMR, mismatch repair; NGS, nextgeneration sequencing; PARP, poly (ADP-ribose) polymerase; PD-1, programmed death 1; VUS, variant of uncertain significance.

Panels and genes prioritized for testing:

Metastatic PCA:

- · Comprehensive (large) panel testing for therapy/ clinical trial eligibility (Recommend).
- Priority germline testing:
 - BRCA2/BRCA1 (Recommend).
 - DNA MMR genes (Recommend).
 - ATM (Consider).
 - Test additional genes on the basis of personal or FH (Recommend).
- Somatic testing:
 - Somatic next-generation sequencing for all men with metastatic PCA (Recommend).
 - Confirmatory germline testing for somatic mutations: • BRCA2 (Recommend).

 - BRCA1, DNA MMR genes, ATM (Consider).
 - Test additional genes on the basis of personal or FH (Table 2; Recommend).
- Nonmetastatic PCA:
 - Reflex testing may be optimal (Consider).
 - Priority genes particularly to inform AS:
 - BRCA2 (Recommend).

- ATM (Consider).
- Test additional genes on the basis of personal or FH (Table 2; Recommend).
- · Men without a diagnosis of PCA meeting FH testing criteria:
 - Reflex testing may be optimal (Consider).
 - Priority genes for risk assessment:
 - BRCA2 (Recommend).
 - HOXB13 (Recommend).
 - BRCA1, ATM, DNA MMR genes (Consider).
 - Test additional genes on the basis of personal or FH (Table 2; Recommend).

Additional considerations. For men with metastatic PCA, broader panel testing may be appropriate, particularly if considering treatment or clinical trial options (Table 2, Fig 2, and Data Supplement). Reflex testing may be considered for all patients, but especially for men with nonmetastatic disease considering AS or men without PCA for early detection, which allows for initial testing of genes that inform management (Data Supplement). Reflex testing also allows for testing of additional genes to account for personal cancer or FH at a later time for comprehensive

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genetic evaluation and may also be more amenable to collaborative genetic evaluation models (see below).

Among MMR genes, *MSH2* has the strongest association to PCA; however, it is recognized that *MLH1*, *PMS2*, *MSH6*, and *EPCAM* also need to be tested to establish the diagnosis of Lynch syndrome. Full MMR testing also may be important for treatment consideration or clinical trials in the metastatic setting; therefore, full Lynch syndrome testing is recommended as indicated.

In addition, confirmatory GT is recommended for men with somatic *BRCA2* mutations and may be beneficial for somatic mutations in *BRCA1*, MMR genes, and *ATM* to identify hereditary cancer predisposition. Additional GT beyond these genes may also be recommended on the basis of personal and FH. Consultation with a genetics professional is advised.

3. What PCA-Specific Recommendations Should Be Considered on the Basis of Genetic Results?

Gaps addressed. There is a need for consensus agreement on genetically informed PCA treatment, management, and early detection^{1,2} (Data Supplement). An additional challenge is inconsistency in NCCN genetically based PCA early detection recommendations regarding which genes to consider and the age at which to begin screening^{8,9} (Data Supplement).

Genetically based recommendations. Genes considered included *BRCA1*, *BRCA2*, *HOXB13*, *CHEK2*, *ATM*, *NBN*, *MSH2*, *MSH6*, *MLH1*, *PMS2*, *PALB2*, *BRIP1*, *TP53*, and Fanconi anemia genes.

- **Metastatic PCA**: GT to inform precision therapy:
 - Enrollment of men with PCA in precision medicine trials is endorsed (Recommend).
 - Mutations in the following genes may inform response to PARP inhibitors:
 - BRCA2 (Recommend).
 - BRCA1 (Consider).
 - Mutations in the following genes may inform response to platinum-based chemotherapy:
 - BRCA2 (Consider).
 - BRCA1 (Consider).
 - Men with DNA repair gene mutations, after progression on abiraterone, may proceed with PARP inhibitor rather than taxane (Consider).
 - Germline mutations in the following genes may inform response to anti–programmed death 1 (PD-1) therapy:
 - DNA MMR genes (Consider).
 - NOTE. The US Food and Drug Administration has granted accelerated approval for anti–PD-1 therapy for microsatellite instability-high/MMRdeficient tumors.
- Nonmetastatic PCA: to inform AS discussions:
 - BRCA2 (Recommend).
 - ATM (Consider).

- Men without a PCA diagnosis to inform PCA early detection:
 - Referral to specialty PCA high-risk clinics and/or early detection trials was endorsed (Recommend).
 - PCA early detection starting at age 40 years or 10 years before the youngest PCA diagnosis in family:
 - BRCA2 (Recommend).
 - BRCA1, HOXB13, ATM, and DNA MMR genes (particularly MSH2; Consider).

Additional considerations. In the metastatic setting, a broad spectrum of genes may be important in determining clinical trial eligibility, and emerging data should continue to refine recommendations. *ATM* garnered consideration for testing, primarily for clinical trial eligibility; however, the panel did not feel that there was sufficient data to endorse *ATM* for informing therapy to PARP inhibitors off study because of the limited independent association to PARP inhibitor response at this time (Data Supplement). *ATM* also garnered moderate consensus for informing AS, but there are limited data at this time (Data Supplement).

For anti–PD-1 therapy, the US Food and Drug Administration has granted accelerated approval for tumors that are microsatellite instability-high or MMR deficient. The panel had moderate consensus regarding a definitive recommendation for anti–PD-1 therapy off study for men with germline MMR mutations, with stronger consideration for clinical trials.

Regarding AS discussions, clinicopathologic criteria, age, and overall health must be considered. *BRCA1* did not achieve consensus for inclusion in AS as a result of limited data for PCA aggressiveness (Data Supplement). Polygenic risk score data were reviewed⁷⁷⁻⁸¹ and did not achieve consensus.

4. What Is Optimal Informed Consent for PCA GT?

Gaps addressed. Current practice guidelines do not provide guidance to health care providers regarding optimal informed consent for PCA GT.

Optimal pretest informed consent elements. Ethical considerations of GC were reviewed (Data Supplement). The following elements garnered strong or moderate consensus to discuss with men before GT (Fig 2 and Table 3):

- Recommend discussing: (1) the purpose of GT; (2) the possibility of uncovering hereditary cancer syndromes;
 (3) potential types of test results; (4) the potential to uncover additional cancer risks; (5) potential out-of-pocket cost; (6) Genetic Information Non-discrimination Act law and other laws that address genetic discrimination; and (7) cascade testing/ additional familial testing.
- Consider discussing: (1) multigene panel options; (2) data sharing/data selling policies of genetic laboratories; and (3) the privacy of genetic tests.

 TABLE 3. Priority Elements of Informed Consent for Prostate Cancer Germline Testing

Elements of Informed Consent	Description
Purpose of germline testing	For precision therapy, early detection strategies, and/or to identify hereditary cancer syndrome/risk
Possibility of uncovering hereditary cancer syndromes	Based on FH, testing may include BRCA1 and BRCA2 (associated with hereditary breast and ovarian cancer) or DNA mismatch repair genes (associated with Lynch syndrome; Table 2). Other hereditary syndromes may also be identified.
Panel options	Various multigene panels may be considered for testing (focused PCA panel v large cancer panel v reflex testing); benefits and risks of each option must be discussed, such as cancer risks uncovered, higher rates of VUS with larger panels, or availability of guidelines for management (Data Supplement).
Potential types of test results	Three main types of results should be discussed, including mutation (pathogenic/likely pathogenic variant), VUS, negative, along with implications of these results on management.
Potential to uncover additional cancer risks	Multiple gene-specific cancer risks may be identified beyond PCA risk that affects men and their families (Table 2).
Potential out-of-pocket cost	Not all insurance plans cover genetic testing for PCA. Some mandate referral to GC. It is important to check with the insurance plan.
Genetic Information Nondiscrimination Act law and other laws that address genetic discrimination	Discuss coverage for health insurance and most employment scenarios. Discuss the lack of coverage for life insurance, long-term care, and disability insurance.
Cascade testing/additional familial testing	Testing blood relatives for pathogenic variants or additional genetic testing on the basis of family history; worry and anxiety that may result from hereditary cancer testing; effect on family relationships
Data-sharing/data-selling policies of genetic laboratories	Each genetic testing laboratory may have unique data-sharing and data-selling policies that patents must be aware of.
Privacy of genetic tests	Protection of genetic data from data breach or access by third parties must be discussed.

Abbreviations: FH, family history; GC, genetic counseling; PCA, prostate cancer; VUS, variant of uncertain significance.

Additional considerations. These elements of pretest informed consent apply to all men who are considering PCA GT^{76,82-84} (Fig 2). Such GC aids as handouts or videos may be useful to deliver this information. However, informed consent is a process during which patients have opportunities to ask questions^{76,82-84}; therefore, a question-and-answer process must be available before testing. Clinicians without specific training/expertise in GC/GT are urged to refer patients to GC before ordering GT. Furthermore, it is important to remain current on the ethics/informed consent process for GT because of the rapidly evolving nature of precision medicine.

5. What Collaborative Strategies May Facilitate PCA Genetic Evaluation Between Health Care and Genetic Providers?

Gaps addressed. Multidisciplinary guidance on the implementation of collaborative models between health care providers and GC is currently lacking.¹⁰³ There is a need to address alternate GC models for timely GT with attention to appropriate pretest informed consent and comprehensive evaluation.

Alternate genetic evaluation delivery strategies. The following strategies were endorsed (Data Supplement and Fig 3):

• Practices should consider multiple models to address patients' needs (Fig 3), including point-of-care models

with limited or full pretest FH collection as well as traditional model with upfront referral to GC (Recommend).

- Videos may be useful to deliver pretest informed consent (Recommend).
- In point-of-care models, reflex genetic testing may be optimal to enable additional testing on the basis of personal/FH (Consider).
- Telehealth/telephone delivery of GC is a suitable alternative to in-person GC (Recommend for men with PCA; Consider for unaffected males).

Additional considerations. If limited pretest FH is collected, practices must proactively address the collection of FH in the post-test setting. Reflex testing enables future testing to account for personal/FH. Telehealth/telephone GC was endorsed to address geographic barriers to GC, although patient outcomes data in males are lacking. Key process questions for practices to consider when implementing point-of-care versus traditional GC models were discussed (Data Supplement).

6. What Post-Test Disclosure Strategies Are Most Appropriate Based on Genetic Results?

Gaps addressed. Joint guidance from oncologists, urologists, and genetic counselors for referral to GC is currently lacking.



FIG 3. Models of collaboration between genetics and health care practices for prostate cancer genetic evaluation. FH, family history; GC, genetic counseling.

Optimal post-test disclosure strategies:

- Referral to a GC for pathogenic/likely pathogenic results (Recommend).
- Patients should receive FH-based recommendations, either in health care or genetic practices (Recommend).
- Cascade/additional familial testing should be conducted in consultation with a genetic professional (Recommend).

Additional considerations. There was no consensus regarding referral of men with VUS or negative results; therefore, providers will need to determine their ability to discuss VUS results and FH-based recommendations. VUS reclassification to "pathogenic/likely pathogenic" and subsequent management are critical for ordering providers to consider and may support the referral of select men with suspicious VUS to GC. Men with FH of cancers may also warrant referral to GC.

7. What Barriers Must Be Addressed to Enhance PCA GT?

Gaps addressed. Multiple practice, research, and policy gaps pose barriers to PCA GT.

Areas in need of additional attention. The following areas achieved strong or moderate consensus to address:

- Genetic education for providers not formally trained in cancer genetics/genetic counseling (Appendix Table A1, online only, and Data Supplement).
- Barriers to implementation of PCA GT (Appendix Table A2, online only).
- Research priorities (Appendix Table A3, online only).

DISCUSSION

As GT for PCA has rapidly increased, responsible implementation of testing and management are of primary concern.^{1,2,19,23} Current practice challenges that pose barriers to operationalizing PCA GT include the variability in testing indications and genetically based management, the need for guidance on panels and priority genes to test, and guidance regarding alternate evaluation models to address GC demand. The 2019 Philadelphia Prostate Cancer Consensus Conference was a focused attempt to address these critical challenges and practice gaps by developing a first-in-field working framework for PCA genetic evaluation, management, and implementation informed by best evidence and expert guidance.

The strength of the consensus framework is the creation of a unified approach regarding GT indications, genetically informed management and treatment, and the integration of GC. Multiple aspects of the framework had strong evidence and strong expert agreement to deem a definitive action of "Recommend". The strongest recommendations encompassed testing all men with metastatic PCA or men with FH suggestive of hereditary PCA. Priority genes for testing included BRCA2, BRCA1, and the DNA MMR genes in metastatic disease to inform treatment or clinical trials; BRCA2 for AS discussions; and BRCA2 and HOXB13 for PCA early detection discussions. This was the first formal, multidisciplinary endorsement for broad panel testing among men with metastatic PCA, recognizing that genetic information may enable men to enroll in clinical trials. Consensus emerged regarding strategies for PCA early detection on the basis of genetic status. For male carriers of BRCA2, a recommendation was made to begin PSA screening at age 40 years or 10 years before the youngest PCA diagnosis in a family and is modeled after colorectal cancer guidelines.¹⁶

An important aspect to the genetic evaluation framework was the integration of care processes and GC to account for the increasing need for GC. Strong recommendations were made for optimal pretest informed consent. Recommended strategies to deliver GC included collaborative GC models, videos, and telehealth to facilitate GT through health care practices and to collaborate with GC. Reflex testing garnered moderate consensus and may be considered, particularly when using collaborative counseling models to enable upfront testing by health care providers, followed by testing additional genes using GC for comprehensive genetic evaluation. In the post-test setting, strong recommendations were made to refer all men with pathogenic mutations to GC, to conduct cascade testing of relatives under the care of genetics professionals, and to determine the delivery of FH-based recommendations.

The panel dealt with many uncertainties in recommendations which garnered moderate consensus. Whereas many genes have a lower level of evidence for PCA risk, aggressiveness, or treatment response, several clinically available multigene panels include lower evidence genes. To indicate these nuances in limited data or moderate consensus, many criteria were designated as "Consider" in the framework. Pathologic criteria for testing, such as disease stage, intraductal/ductal histology, or Grade Group \geq 4, garnered moderate consensus and therefore are included as suggestive criteria for testing.63,65,66 Ashkenazi Jewish ancestry as a standalone criterion achieved moderate consensus, but may be a stronger consideration for testing for men with higher Gleason score per current NCCN guidelines.⁸ Whereas PCA has been linked with HBOC and Lynch syndrome, a working definition of familial features that increase the likelihood of detecting germline mutations is needed. As such, having two or more relatives with cancers in the HBOC or Lynch syndrome spectrum garnered moderate consensus as standalone criteria and may be considered for GT on the basis of patient preference and insurance coverage.

Priority genes to test also presented challenges, particularly regarding ATM, DNA MMR genes, and HOXB13. Initial data have reported that men with ATM mutations experienced clinical response to PARP inhibitors⁹⁴; however, follow-up studies have reported a limited independent effect of ATM.99 Similarly, studies in AS had limited association of ATM mutations alone with upgrading of biopsies.⁷ Until additional data are available, ATM was given a designation of "Consider" for testing, recognizing the potential for clinical trial options for ATM carriers. Additional uncertainties were encountered regarding prioritizing MMR genes for GT. Among MMR genes, MSH2 has the highest reported association to PCA.⁴¹ Although other MMR genes have lower or limited association to PCA, the potential to uncover Lynch syndrome and clinical trial eligibility drove the suggestion to consider full Lynch syndrome testing. MSH2 status may be more informative for PCA early detection discussions.⁴¹ HOXB13 has strong association to PCA risk and early-onset disease, though screening outcomes data are limited. Therefore, the consensus panel recommended testing for HOXB13 and to consider the results in early detection discussions. Overall, BRCA1, HOXB13, and MMR genes were designated as "Consider"

for beginning screening at age 40 years or 10 years before the youngest PCA diagnosis in the family because of the currently limited screening data.⁹ Data from screening studies, such as IMPACT and the National Cancer Institute (ClinicalTrials.gov identifier: NCT03805919), will be important to reconsider strengthening these recommendations.¹⁰ However, this is the first time that screening strategies based on a larger genetic spectrum have been proposed. Additional research in African American males is

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vitally needed. Future consideration of circulating tumor and cell-free DNA is also warranted.

In conclusion, the 2019 Consensus Conference created the first multidisciplinary PCA genetic implementation framework tailored to the precision medicine era. The framework, which importantly had input from NCCN panel leaders, provides guidance to a spectrum of providers to facilitate timely and responsible PCA GT for the benefit of men and their families.

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AUTHORS' DISCLOSURES OF POTENTIAL CONFLICTS OF INTEREST AND DATA AVAILABILITY STATEMENT

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AUTHORS' DISCLOSURES OF POTENTIAL CONFLICTS OF INTEREST

Implementation of Germline Testing for Prostate Cancer: Philadelphia Prostate Cancer Consensus Conference 2019

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No other potential conflicts of interest were reported.

Percent Agreement

TABLE A1. Priority Topics for Provider Education Area of Knowledge

5	
Recommend	
Purpose of genetic testing	100
Understanding types of results (mutation, VUS, negative)	92
Genetic Information Nondiscrimination Act and other laws that address discrimination	89
Hereditary cancer syndromes (HBOC, Lynch syndrome, HPC) that may be uncovered	86
Test options (focused prostate cancer panel v large cancer panel)	86
Additional cancer risks that may be uncovered	84
Potential out-of-pocket costs for genetic testing for patients	84
Privacy considerations of genetic tests	78
Cascade testing/additional familial testing/effect on family relationships	76
Consider	
Choice of laboratory for testing (pros and cons of test accuracy)	68
Data-sharing/data-selling policies of laboratories	62

Data-sharing/data-selling policies of laboratories

NOTE. The Data Supplement provides educational resources for providers or trainees regarding germline testing. Abbreviations: HBOC, hereditary breast and ovarian cancer; HPC, hereditary prostate cancer; VUS, variant of uncertain significance.

TABLE A2. PCA Genetic Testing Implementation Barriers

Barrier Percent Agreement Recommend Increase advocacy and public awareness for PCA genetic testing and 99 impact of genetic results for men and their families 98 Reimburse telehealth and telephone counseling Implement virtual tumor boards, virtual molecular boards, or virtual 79 genetics boards to disseminate genetics and molecular expertise Redefine "actionability" to include familial impact of genetic testing for 75 payer coverage Consider Increase lobbying efforts to enhance payer coverage of PCA genetic 64 testing Engage primary care providers in genetic evaluation for PCA 63

Abbreviation: PCA, prostate cancer.

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 TABLE A3.
 Research Priorities to Advance PCA Genetics Knowledge and Practice

 Priority Area

Percent Agreement

Recommend	
Genetics of PCA in diverse populations of men	93
Clinical outcomes by germline mutation status	93
Precision medicine trials	88
Precision PCA early detection trials	80
Basic science research into metastatic disease biology	76
Consider	
Implementation outcomes research regarding the alternate delivery of genetic counseling	72
Psychosocial outcomes of men undergoing genetic testing through various clinical approaches	63

Abbreviation: PCA, prostate cancer.

Practical Considerations and Challenges for Germline Genetic Testing in Patients With Prostate Cancer: Recommendations From the Germline Genetics Working Group of the PCCTC

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Germline genetic testing is now routinely recommended for patients with prostate cancer (PCa) because of expanded guidelines and options for targeted treatments. However, integrating genetic testing into oncology and urology clinical workflows remains a challenge because of the increased number of patients with PCa requiring testing and the limited access to genetics providers. This suggests a critical unmet need for genetic services outside of historical models. This review addresses current guidelines, considerations, and challenges for PCa genetic testing and offers a practical guide for genetic counseling and testing delivery, with solutions to help address potential barriers and challenges for both providers and patients. As genetic and genomic testing become integral to PCa care, developing standardized systems for implementation in the clinic is essential for delivering precision oncology to patients with PCa and realizing the full scope and impact of genetic testing.

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INTRODUCTION

Genomics is rapidly pushing oncology closer to an actualized version of precision medicine.^{1,2} In the era of poly (ADP-ribose) polymerase inhibition and immunotherapy, genetic testing may yield information that will affect therapeutic choices, in addition to informing the patient about personal and familial risk.³⁻⁵ Multiple guidelines now include germline genetic testing for men with prostate cancer (PCa), although incorporating testing into clinical workflows remains a challenge.^{5,6} This article addresses (1) current guidelines for germline testing, (2) key aspects of testing and counseling, (3) a road map for genetic testing and possible solutions, and (5) benefits and limitations of testing.

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Germline Genetic Counseling for Men With PCa

Since the landmark article by Pritchard et al⁷ that described a relatively high prevalence of germline mutations in DNA repair genes in men with metastatic PCa, other groups have reported the prevalence of germline mutations in PCa ranging between 7.5% and 19%, with *BRCA2* being the highest overall contributor.⁸⁻¹¹ Consequently, several groups issued recommendations for germline testing (Table 1), which place significant

demands on clinical workflows and resources for genetic counseling. Genetic counselors (GCs) are trained to assess family histories for genetic risk, provide pretest and post-test counseling, order appropriate testing, and interpret test results. Unfortunately, access to genetic providers is limited, with the majority of the small workforce usually centered in urban areas and academic institutions.^{12,13} In 2016, the Genetic Counselor Workforce Working Group estimated a growth of 72% in the workforce between 2017 and 2026, with demand not expected to meet population equilibrium until 2024-2030.14 This limited access may necessitate other health care providers, including oncologists, urologists, and primary care physicians, to absorb some responsibility for genetic testing. However, these providers may be insufficiently trained in genetics, resulting in inappropriate testing and misinformation.¹⁵⁻¹⁷

The increased number of men with PCa to be tested and the scarcity of GCs suggest a critical unmet need for expanded genetic services through novel approaches outside of historic delivery models.¹⁸ Evolving service models that incorporate phone and video telemedicine can be particularly useful when geography or public health crises, such as COVID-19, make in-person visits challenging.^{19,20} Hybrid service models



that divide responsibilities between physicians and GCs are also options.²¹ Collaboration between GCs and clinicians is critical to determine which approach best suits a practice, because there is no one-size-fits-all solution.

Delivery of Germline Testing and Counseling

Initiating genetic testing. One of the greatest hurdles is ensuring that appropriate patients are systematically identified for testing. Developing a plan to consistently screen and identify patients based on current guidelines is necessary (Table 1). Assigning screening to a team member or using patient-completed family history questionnaires can facilitate referral and testing processes. Automated electronic medical record (EMR) features can trigger genetic counseling referrals or alert the clinical team based on a diagnosis code for metastatic PCa or family history/pedigree functionality.

After patients are identified, several options for counseling and testing are available:

- Referral to a geneticist or GC for in-person, telephonebased, or telemedicine counseling services in response to manual referral or automated EMR triggers.
- 2. Treating clinicians perform pretest consent and order germline genetic testing directly: If genetic counseling services are unavailable, testing is urgent, or workflow supports providers initiating testing, treating providers can perform pretest education, obtain informed consent, and order genetic testing.²¹ Providers should consider any clinical, psychosocial, and financial issues when determining whether to pursue testing within their practice or refer to a remote/telehealth genetic service if they do not have access within the practice.
- 3. Patient-initiated testing (PIT) platforms: Some commercial genetic testing laboratories, such as Color and Invitae, offer clinical-grade testing that can be initiated by the patient. This process may involve a pretest clinician review and the option for post-test genetic counseling. However, there remain concerns about guidance on test selection, limitations in genetic counseling, lack of follow-up regarding future reclassification of variants, potential for misinterpretation of results, and propagation of misinformation within families. Furthermore, PIT may not include genes important to a patient's personal or family history, potentially creating a false sense of reassurance if testing is negative. Given this, provider-initiated testing is preferred.
- 4. Direct-to-consumer (DTC) testing platforms: DTC genetic testing has become increasingly popular, likely because of easy access and no medical provider oversight. DTC testing is not comprehensive and should not be considered a substitute for clinical-grade testing. Although 23&Me has Food and Drug Administration approval to report on the three known Ashkenazi Jewish BRCA1/2 founder variants, the National Comprehensive Cancer Network (NCCN)

cautions that any results should be confirmed with a clinical-grade test.²² Providers should be skeptical of any raw data findings from secondary companies, such as Promethease, which are prone to false positives and false negatives.²³

Family cancer history intake. Although all patients with high-risk localized or metastatic PCa should undergo germline genetic testing regardless of family history, accurately evaluating a patient's personal and family history is essential to determine whether patients need a broader germline panel. Furthermore, gathering a family history can help inform personal and family screening recommendations in the event of negative testing. Cancer counseling sessions include a three- to four-generation pedigree with information on maternal and paternal relatives with cancer, age of diagnosis, age/cause of death, and any prior genetic testing.^{22,24} For relatives with PCa, the Gleason grade, metastatic status, and/or cause of death can be useful. Information about ancestry (eg, Ashkenazi Jewish) and consanguinity should be noted. Family history questionnaires can be completed in the clinic or electronically.

Complete family histories ensure that the most informative, cost-effective testing is performed. Although the presence of other cancer types in a family history may be explained by a mutation in a PCa predisposition gene, providers should consider expanded testing for genes related to the observed cancers in a family history when necessary. For instance, hereditary pancreatic cancer and PCa typically occur in the setting of a pathogenic *BRCA2* variant. However, it may be reasonable to include other genes associated with pancreatic cancer, such as *CDKN2A* and *CDK4*.

Somatic next-generation sequencing. Somatic next-generation sequencing tumor testing is increasingly used to guide treatment decision making and can be performed in parallel with germline testing. In addition to detecting tumor-specific mutations, it can sometimes identify potential germline mutations. Most somatic testing platforms are not validated to distinguish germline from somatic-only mutations, even if paired testing with a blood or saliva sample is performed. Thus, a referral to genetics is recommended to determine whether confirmatory or more comprehensive testing is warranted. Providers should consider the variant allele frequency, actionability of the gene, classification of the variant, and tumor type when reviewing somatic variants for possible germline origin.²⁵

Pretest education and informed consent. Pretest education and informed consent discussions should review the purpose of testing; general information about included genes; possible test results (Table 2); medical management implications; review of possible benefits, risks, and limitations (Table 3); and the voluntary nature of testing.^{24,26} Several major medical societies have also published detailed guidelines reviewing the components of pretest counseling and informed consent to help clinicians.²⁴ Clinical teams

TABLE 1. Summary of the Current PCa Genetic Testing Guidelines

Organization	Source	Guidelines	Genes
National Comprehensive Cancer Network	Genetic/familial high-risk assessment: breast, ovarian, and pancreatic version 1.2020 ²²	Testing is clinically indicated in the follow scenarios:	ATM BARD1ª BRCA1
	Hereditary cancer testing criteria	1. Individuals with any blood relative with a known pathogenic/likely pathogenic variant in a cancer susceptibility gene	BRCA2 BRIP1
		 Individuals meet the criteria below but with previous limited testing (eg, single gene and/or absent deletion duplication analysis) interested in pursuing multigene testing 	CDH1ª CDKN2Aª CHEK2 MSH2
		3. Personal history of cancer	MLH1
		Metastatic or intraductal PCa at any age	MSH6 PMS2
		• High-grade (Gleason score \geq 7) PCa with:	EPCAM
		o Ashkenazi Jewish ancestry; or	NBN NE 1ª
		$o \ge 1$ close relative with breast cancer at age ≤ 50 years or ovarian, pancreatic, or metastatic or intraductal PCa at any age; or	PALB2 PTEN ^a RAD51C
		$o \ge 2$ close relatives with breast or PCa (any grade) at any age	RAD51D
		 A mutation identified on tumor genomic testing that has clinical implications if also identified in the germline 	TP53
		 To aid in systemic therapy decision making 	
		4. Family history of cancer	
		 An affected or unaffected individual with a first- or second- degree blood relative meeting any of the criteria listed above (except individuals who meet criteria only for systemic therapy decision making) 	
		There is a low probability (< 2.5%) that testing will have findings of documented clinical utility in the following scenarios:	
		 Men diagnosed with localized PCa with Gleason score < 7 and no close relative with breast, ovarian, pancreatic, or PCa 	
National Comprehensive Cancer Network	Prostate cancer, version 1.202044	Germline testing is recommended for patients with PCa and any of the following:	ATM BRCA1
		High-risk, very-high-risk, regional, or metastatic PCa	BRCA2 CHFK2
		Ashkenazi Jewish ancestry	HOXB13
		 Family history of high-risk germline mutations (eg, BRCA1/2, Lynch mutation) 	MLH1 MSH2 - MSH6
		A positive family history of cancer:	PALB2
		o A strong family history of PCa consists of: brother or father or multiple family members who were diagnosed with PCa (but not clinically localized Grade Group 1) at < 60 years of age or who died from PCa; OR	PMS2
		$o \ge 3$ cancers on same side of family, especially diagnoses ≤ 50 years of age: bile duct, breast, colorectal, endometrial, gastric, kidney, melanoma, ovarian, pancreatic, prostate (but not clinically localized Grade Group 1), small bowel, or urothelial cancer	
	(conti	nued on following page)	

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TABLE 1.	Summary	of the Current	PCa Genetic	Testing (Guidelines (continued)
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Organization	Source	Guidelines	Genes
Expert Panel	Philadelphia Consensus meeting publication, 2017 ⁴⁵	Men meeting any one of the following suggested criteria should undergo genetic counseling and genetic testing:	ATM BRCA1
		 All men with PCa from families meeting established testing or syndromic criteria for the following: 	BRCA2 HOXB13
		o HBOC (Consensus: 93%)	MLH1
		o HPC (Consensus: 95%)	PMS2
		o LS (Consensus: 88%)	- 1015110
		 Men with PCa with two or more close blood relatives on the same side of the family with a cancer in the following syndromes: 	-
		 Post-consensus discussion included consideration of age cutoff for this criterion. A specific age cutoff will require additional data, and age at diagnosis is important to inquire about in the genetic counseling session with patients. 	-
		■ HBOC (Consensus: 93%)	-
		■ HPC (Consensus: 86%)	-
		LS (Consensus: 86%)	-
		 All men with metastatic castrate-resistant PCa should consider genetic testing (Consensus: 67%). Post-consensus discussion also included consideration of testing men with metastatic, hormone-sensitive PCa to identify germline mutations to inform potential future treatment options and cascade testing in families. Men with tumor sequencing showing mutations in cancer-risk genes should be recommended for germline testing, particularly after factoring in additional personal and family history (Consensus: 77%). 	
AUA	Clinically localized PCa: AUA/ASTRO/ SUO guideline, 2017 ⁴⁶	The Panel recommends that clinicians take a detailed family history of cancers and give consideration to patient referral for genetic screening and counseling for men with localized high-risk PCa, particularly in the setting of family history of first-degree relatives with cancers of breast, ovary, pancreas, other GI cancers, and lymphoma.	No genes specified for germline testing

Abbreviations: ASTRO, American Society of Therapeutic Radiation and Oncology; AUA, American Urological Association; HBOC, hereditary breast and ovarian cancer syndrome; HPC, hereditary prostate cancer; LS, Lynch syndrome; PCa, prostate cancer; SUO, Society of Urologic Oncology. ^aThese genes are not currently associated with PCa.

should note the requirements for documentation of informed consent, which differ by state and institutional policies.

Test selection and ordering. Many commercial laboratories offer clinical genetic testing for hereditary cancer syndromes. Testing panels range from targeted, guidelinesbased panels to comprehensive, pan-cancer panels that may include preliminary evidence genes. Some major laboratories, such as Ambry Genetics, Invitae, and GeneDx, offer PCa-specific panels that include the following genes: ATM, BRCA1, BRCA2, CHEK2, HOXB13, MLH1, MSH2, MSH6, NBN, PALB2, PMS2, and TP53. Genetic testing panels are subject to change, and decisions regarding specific genetic tests should be individualized based on factors such as laboratory reputation and quality, insurance networks, genes offered and customizability of panels, laboratory billing practices, follow-up testing options for family members, turnaround times, and availability of genetic counseling services.

Clinicians should recognize that larger panels increase the probability of detecting variants of uncertain significance (VUS), incidental/secondary findings (pathogenic variants in genes not related to hereditary PCa), and variants associated with syndromes that may be outside of the scope of clinicians treating PCa (Tables 2 and 3). Clinical workflows must ensure that tasks involved with ordering genetic testing include determination of insurance coverage and submission of orders, standardized collection and shipment of samples, and a clear chain of responsibility.

Insurance coverage for germline testing is in flux. Although the cost of genetic testing has decreased, the possible out-of-pocket (OOP) cost for patients can be difficult to discern because of the varying billing policies of laboratories and insurance coverages.²⁷ Although the NCCN hereditary breast and ovarian cancer guidelines (v3.2019) are often the primary source used by payers, including Medicare, to develop coverage policies, most have their own criteria that

Interpretation	Result	Definition
Positive	Pathogenic	An alteration in the DNA that is associated with increased disease risk.
	Likely pathogenic	An alteration in the DNA that is likely to be associated with increased disease risk. Meets most but not all criteria to be classified as pathogenic.
Uncertain	Variant of uncertain significance	An alteration in the DNA that may or may not be disease causing. Insufficient evidence to classify as either pathogenic or benign.
Negative	Likely benign	An alteration in the DNA that is unlikely to be associated with increased disease risk. Meets most but not all criteria to be classified as benign.
	Benign	An alteration in the DNA that is not associated with increased disease risk.

determine testing coverage. These criteria may not be up to date with current NCCN guidelines, potentially excluding PCa from their criteria completely, and may mandate a consultation with certified GC for approval.

Many, but not all, laboratories work with commercial insurance companies to negotiate coverage into their policies and will provide an estimate of the OOP cost of testing. Not all insurance companies require prior authorization for genetic testing. Laboratory online ordering portals will often indicate whether provider-initiated insurance prior authorization is needed. Typically, all components of the billing process, including submission of insurance prior authorization, are handled by the laboratory. Several commercial laboratories offer a patient-pay or fixed OOP cost, often \$250 or lower, making testing more financially accessible. In addition, patients may qualify for a sponsored testing program at no cost in exchange for de-identified data shared with the sponsoring companies.

Results delivery and follow-up. Methods for delivering test results vary, depending on workflow, availability of genetic counseling services, and provider comfort level and training. Regardless of result type, genetic test reports should be offered to patients for their own records and uploaded into the EMR. Refer to Table 2 for information regarding the following result types. Options for returning results include:

1. Ordering provider refers all patients for post-test counseling, either through referral to a local GC or a telehealth genetic counseling service.

- Ordering provider refers patients with complex results (eg, positive and/or VUS) for post-test counseling. This type of blended approach to genetic testing has been previously discussed and has received strong consensus across multiple disciplines.^{21,26}
 - a) Negative results: Clinical teams can disclose results via telephone, patient portal message, a follow-up appointment, or a letter summarizing the results and providing contact information if there are questions. A templated letter can be generated with GC input. Cancer screening recommendations should be based on the family history and should be reviewed with the patient. For example, men with a first-degree relative with PCa remain at increased risk for PCa and should initiate prostate screening at a younger age per routine guidelines. Patients should be encouraged to discuss updates to personal and family history, which may prompt consideration of additional genetic testing or altered screening recommendations.
- 3. Ordering provider discloses all result types. It is important to note that even in this situation, a referral can be made to genetics for post-test counseling.
 - a) Positive results: Providers should discuss and document the implications of the results in terms of cancer risks associated with the identified gene mutation, additional cancer screening recommendations, appropriate referrals, and possible implications for treatment. Providers should also recommend cascade testing, which entails genetic

 TABLE 3.
 Pretest Talking Points Regarding the Benefits and Risks/Limitations of Genetic Testing^{27,49}

 Benefits
 Risks/Limitations

Delicitis	Kiska Elintations
May help explain personal cancer history	May increase anxiety and guilt regarding hereditary cancer risk
May help inform prognosis	Potential for uncertain results: 1) Variants of uncertain significance, or 2) Positive results in lesser established genes and those with no management guidelines currently available
May help inform risks for additional cancers	Genetic discrimination risks (life insurance or long-term care insurance)
May help guide treatment decisions	Financial barriers
May help inform cancer risks for family members	

counseling and testing in at-risk relatives of individuals identified to carry specific genetic mutations or further testing in the family based on family history. Access to the proband's test report will be essential for family members considering testing.

b) VUS results: It is critical to review the uncertainty of whether the specific gene mutation identified is disease causing or a benign variation. The vast majority of VUS results are later reclassified to negative^{28,29}; thus, they are typically treated as negatives, and screening recommendations are made based on personal and family history. Testing family members for a VUS is typically not recommended unless it is in the context of a variant resolution or research program. When a VUS is reclassified, new reports are customarily issued to the ordering provider, and it is therefore the responsibility of the ordering provider to follow up with patients over the long term concerning any reclassifications. Patients should be encouraged to check in with their providers every few years to see whether there are updates to the classification. It is also important to note the possibility of discrepant variant classifications across laboratories. These discrepancies may cause difficulty determining how to appropriately manage patients and family members. ClinVar is a free, publicly available database that aggregates variant classifications, although a limitation is that entry submissions may not be completely up to date.

Cascade testing. The concept of cascade testing should be introduced as part of pretest counseling. Family letters can facilitate genetic testing for other relatives in the event of a positive result and typically include a short description of the cancer syndrome, the specific mutation identified, information on how to contact a GC in their area, and laboratory/specimen identification for the patient's testing. A number of the genes associated with hereditary PCa, such as BRCA1/2 and the mismatch repair genes, are associated with additional cancers and may have well-defined risk numbers and screening recommendations for males and females. Targeted testing for the known familial variant can clarify the cancer risks for other relatives, allowing for the initiation of appropriate increased cancer screening and risk-reducing therapies, and consideration of reproductive planning options.²⁷ Ultimately, it is the patient's decision and responsibility to inform at-risk relatives about their genetic test results, which underlies the importance of reviewing cascade testing and providing resources to help facilitate this transfer of critical information.

Additional Considerations

Pathogenic mutations identified in DNA-damage repair genes, such as *BRCA1/2* or mismatch repair genes, have implications for management and treatment.^{3,4} Germline mutations are identified in approximately 12% of patients

with metastatic PCa, but because some are not actionable. it is important to manage expectations concerning outcomes for germline testing.⁷⁻¹¹ Many of the genes included on PCa panels are newly associated with PCa and do not yet have well-defined cancer risks. This increases the possibility of a positive result in a gene associated with low-tomoderate increased cancer risk, which may not have clear screening recommendations. Providers need to be clear about the preliminary nature of findings and that there may not be an immediate impact on cancer screening or treatment options. Patients and their families should be encouraged to participate in registries or research studies to better characterize the risk associated with specific variants over time. Providers can refer patients to a GC for further discussion. Finally, as germline mutations continue to be levied for treatment purposes, providers must be aware of the risk of secondary malignancies and treatment-related adverse effects in some mutation carriers.²⁸⁻³²

Some providers may be concerned about the potential for negative consequences from genetic testing. A number of studies have found that most individuals are unlikely to experience significant psychological distress after receiving genetic test results.^{33,34} Notably, the likelihood of psychological distress, family disruption, and nonadherence to surveillance guidelines was greater in settings without adequate patient education, counseling, informed consent, and follow-up.^{33,35} A recent study of men with PCa undergoing genetic testing found genetic counseling to be beneficial.³⁵

Some patients are hesitant about genetic testing because of concerns about discrimination. The Genetic Information Nondiscrimination Act (GINA), a federal law passed in 2008, protects individuals from genetic discrimination from health insurance companies and employers, with specific limitations on the type of employer and size of the company. Importantly, GINA protections do not extend to life, disability, or long-term care insurance. Some states have passed genetic discrimination laws that extend protection beyond GINA. Information regarding GINA is often included in the consent forms for testing laboratories, and summary handouts could be given to patients with additional questions.

Practical Strategies to Overcome Genetic Service Barriers

ASCO and other major health societies strongly encourage and often provide additional education training for nongenetics providers who are interested in responsibly incorporating genetic services into their practice. Courses on genomic cancer risk assessment for physicians, advanced practice providers, nurses, GCs, and other health care professionals are available through organizations such as City of Hope, American Urological Association, and ASCO.

Alternatives to in-person pretest counseling, such as educational handouts, videos, and presentations, are allowing genetic counseling expertise to be shifted to the post-test setting, prioritizing visits for complex counseling patients and/or abnormal results, and facilitating a hybrid service delivery model.^{18,36} Data are still emerging regarding the effectiveness of these models and patient satisfaction. Other practical strategies have focused on increasing GC efficiency and patient volumes, leading to the creation of new support roles, such as GC assistants; incorporation of technologies that reduce appointment time, such as online pedigree collection tools; and group genetic counseling sessions.^{37,38} There are now chatbots, such as Genetic Information Assistance, that can converse with patients about family history and the basics of genetic testing and insurance, and determine who qualifies for genetic testing.

Special attention and strategies to minimize disparities in genetics are essential. It has been well documented that socioeconomically disadvantaged individuals, racial/ethnic minorities, and men are less likely to receive genetic services.^{18,39-43} PCa genetic testing provides a unique opportunity for providers and institutions to address possible disparities and consider offering counseling services within

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a male-friendly environment. It is imperative that health care providers from all specialties work together to provide equal access to genetic services by minimizing biases, improving patient education and understanding, creating culturally sensitive interfacing materials, and expanding services to underprivileged areas.

In conclusion, as genetic testing becomes integral to the care of patients with PCa, coordinated efforts across multiple disciplines are required to deliver optimal care. Developing creative, scalable strategies to deliver high-quality personalized genetics care for patients with PCa will be paramount to realizing the full scope and impact of genetic testing for individual patients and family members. It is clear that expanding education around the need for testing and developing standardized systems for implementation in the clinic are important directions for genetics care delivery and essential for delivering precision oncology to men with PCa.

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AUTHORS' DISCLOSURES OF POTENTIAL CONFLICTS OF INTEREST

Practical Considerations and Challenges for Germline Genetic Testing in Patients With Prostate Cancer: Recommendations From the Germline Genetics Working Group of the PCCTC

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GENITOURINARY CANCERS (DP PETRYLAK AND JW KIM, SECTION EDITORS)

Genetic Testing in Prostate Cancer

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Abstract

Purpose of Review This review summarizes recent advances in prostate cancer (PCa) genetics.

Check for updates

Recent Findings Upwards of 20% of metastatic castration-resistant prostate tumors (mCRPC) carry homologous recombination (HR) repair gene mutations, of which ~ 10% are germline (inherited). Another ~ 5% exhibit microsatellite instability (MSI-H) and/or mismatch repair deficiency (MMRd). Pembrolizumab is approved for tumors with MMRd, thus patients with mCRPC and MMRd are candidates for pembrolizumab. Emerging data indicate that platinum chemotherapy and poly ADP-ribose polymerase inhibitors (PARPi) are effective in PCa exhibiting HR deficiency. NCCN guidelines now recommend germline and somatic tumor testing in specific clinical scenarios due to treatment and family implications.

Summary Genetic testing in PCa patients may inform prognosis, treatment options, and have implications for family counseling. PARPi, platinum chemotherapy, and immune checkpoint inhibitors are promising targeted therapies for PCa with specific molecular features. Therapeutic advances, along with importance to relatives, are driving genetic testing in prostate cancer.

Keywords Prostate cancer · Genetics · BRCA · PARPi · Germline testing

Introduction

Prostate cancer has a significant heritable component. In the past few years, substantial strides have been made in understanding genetic factors influencing prostate cancer susceptibility. Many of the recent discoveries have extended beyond common single-nucleotide polymorphisms (SNPs) to high and moderate penetrance genetic variants, alongside new precision-directed therapeutic implications that are leading to shifts in research and practice.

More than 100 susceptibility loci for prostate cancer have been identified with GWAS (genome-wide association studies), accounting for $\sim 33\%$ of familial prostate cancer risks [1–7]. Many variants identified were high prevalence and

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low-penetrance, and were not clinically used to differentiate risk of aggressive from indolent prostate cancer [7]. The germline *HOXB13 G84E* variant was established in 2012 as a susceptibility loci that significantly increased prostate cancer risk through study of families with multiple cases of prostate cancer [8]. Germline testing of unselected prostate cancer patients showed overall low prevalence of germline pathogenic or likely pathogenic variants (hereafter referred as mutations) in *BRCA2*; 1.2% among men were diagnosed before 65 years old [9, 10]. Prior to 2016, clinical germline testing for prostate cancer risk was not pervasive.

The Molecular Landscape of Metastatic Prostate Cancer

Substantial changes came with a Stand Up To Cancer-Prostate Cancer Foundation Prostate Cancer Dream Team study that sequenced metastatic prostate cancer biopsies and provided molecular characterization of later evolutionary stages of tumorigenesis [11]. A notable finding was that alterations in *BRCA2*, *BRCA1*, and *ATM* were observed in 19.3% (29/150) of metastatic tumors—a much higher frequency compared with localized disease [9, 11]. Eight percent (12/150) of patients with metastatic prostate cancer had pathogenic germline alterations [11].

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Prevalence of Germline Mutations in Metastatic Prostate Cancer

In 2016, Pritchard et al. reported a study of germline sequencing in 692 men with metastatic prostate cancer, unselected for family history or age at diagnosis, and found that 11.8% (82/ 692) had germline DNA repair alterations compared with 4.6% (23/499) among men with localized prostate cancer from the Cancer Genome Atlas (TCGA), and 2.7% (1434/53,105) in persons without a known cancer diagnosis (EXAC) [12...]. A subsequent cross-sectional study by Nicolosi et al. evaluated 3607 men with a personal history of prostate cancer who underwent germline genetic testing between 2013 and 2018. The study found that 4.74% of patients with prostate cancer had gBRCA2 mutations, 2.88% gCHEK2, 2.03% gATM, 1.25% gBRCA1, 1.12% gHOXB13, 0.69% gMSH2, and 0.56% gPALB2 gene mutations [13]. The higher than previously recognized prevalence of DNA repair gene mutations led to changes in clinical testing guidelines.

Emerging data suggest that patients with ductal and intraductal prostate cancer carcinoma have higher risk of having microsatellite instability [14–17] and germline homologous recombination repair mutations [17–20]. Taylor et al. performed whole exome sequencing of prostate cancer tumors from 14 patients with castration-sensitive localized prostate cancer and *gBRCA2* mutations, and showed that these tumors harbor increased genomic instability, and their mutation profiles resemble metastatic tumor [18]. A case study of patients with ductal histology prostate carcinoma showed that 49% (25/51) had DNA repair gene alterations, including 20% (10/ 51) with germline alterations. Somatic tumor sequencing of this patient cohort reported that 14% (7/51) tumors had mismatch repair gene alterations and 31% (16/51) in homologous recombination repair genes [17].

Collectively, these studies suggest that germline DNA repair mutations are present in substantial percentages in specific populations, (1) prostate cancer patients with metastatic disease, (2) those with a family history suggestive of inherited cancer predisposition, (3) ductal and intraductal histologic subtypes. NCCN guidelines for prostate cancer now recommend offering germline genetic testing to men in these groups (Table 1) [21, 22].

Family Impact of Germline Testing

Germline testing in men with prostate cancer can potentially benefit the patient in informing treatment options, and if a mutation is identified, may also guide screening of other cancers and have family implications for cascade genetic testing (testing of close relatives for the same germline mutation). Early cancer detection strategies and preventive measures may be available to relatives identified to have same germline mutations. Cascade family testing can be valuable for family Table 1 Family history for prostate cancer patients

Family history criteria

- Family history of high-risk germline mutations (e.g., *BRCA1/2*, Lynch syndrome)
- Brother or father or multiple family members diagnosed with prostate cancer (but not clinically localized grade group 1) at < 60 years or who died from prostate cancer
- Ashkenazi Jewish ancestry
- \geq 3 cancers on same side of family, especially diagnosed at age \leq 50 years, bile duct, breast, colorectal, endometrial, gastric, kidney, melanoma, ovarian, pancreatic, prostate (but not clinically localized grade group 1), small bowel, or urothelial

members, but unfortunately cascade family testing is currently underperformed, and strategies to overcome barriers, such as lack of knowledge, family communication, lack of access to genetic services, and cost of testing, are needed.

The NCCN guidelines for Genetic/Familial High-Risk Assessment for Breast and Ovarian Cancer [23] recommend breast cancer screening starting at age 25 years for female relatives and age 36 years for male relatives with deleterious *gBRCA1/2* mutations. *gBRCA1/2* female carriers should discuss with their health care provider risk reduction mastectomy and salpingo-oophorectomy, which is typically recommended between 35, 36, 37, 38, 39, 40 years old, and upon completion of childbearing.

Male relatives with gBRCA2 and gBRCA1 mutations may be at increased risk of cancers such as male breast, pancreatic, colon, and prostate. A study of 173 breastovarian cancer families with gBRCA2 mutations showed 4.7- to 8.6-fold increased risks of prostate cancer with cumulative risk of 20–33% in US carriers by the age of 70 years [24]. A study of 913 male gBRCA1 mutation carriers reported that gBRCA1 mutation increases the relative risk of prostate cancer by 3.75-fold and results in an 8.6% cumulative risk by age 65 [25].

The IMPACT study (Identification of Men with a Genetic Predisposition to Prostate Cancer: Targeted screening in gBRCA1/2 mutation carriers and controls) conducted yearly PSA screening in families with known gBRCA1/2 mutations [26, 27]. The study enrolled 2932 men with no personal history of prostate cancer, 919 gBRCA1 carriers, 902 gBRCA2, 497 gBRCA2 noncarriers, and 709 gBRCA1 noncarriers. Preliminary results reported after 3 years of follow-up showed overall 21% positive predictive value (PPV) of PSA > 0.3 ng/ml with 31% PPV in gBRCA2 carriers and 18% in gBRCA2 noncarriers; and 23% in gBRCA1 carriers and 15% in gBRCA1 noncarriers. PPV of prostate biopsy, initiated when PSA > 3.0 ng/ml, was 39% in gBRCA2 carriers and 28% in gBRCA2 noncarriers, but no significant difference was detected between gBRCA1 carriers and gBRCA1 noncarriers. gBRCA2 carriers had higher incidence of prostate cancer diagnosed at younger age and

with more aggressive disease characteristics compared with gBRCA2 noncarriers. The results for gBRCA1 carriers were not definitive, and further investigation is needed. The number needed to screen to detect one clinically significant prostate cancer was 60 for gBRCA2 carriers ages 40–54 years and 13 for carriers ages 55–69 years. Thus, the results from IMPACT suggest annual PSA screening for gBRCA2 mutation carriers between age 40 and 69, using PSA cutoff of 3 ng/ml [27]. Studies evaluating predictive value of lower PSA cutoff and prostate MRI are ongoing (e.g., www.clinicatrials.gov, NCT03805919, NCT01990521).

Prognostic Impact of DNA Repair Gene Mutations

Prostate cancer patients may benefit from germline and/ or somatic genetic testing to inform disease prognosis and treatment decisions, with somatic testing being potentially more relevant for treatment decisions. Several studies showed that germline BRCA1/2 mutations are associated with poor prognosis and worse outcomes in prostate cancer. Castro et al. showed that prostate cancer patients with gBRCA1/2 mutations were more likely to have a Gleason score ≥ 8 , T3/4 stage, nodal involvement, and metastases at the time of diagnosis compared with noncarriers. Moreover, gBRCA1/2 carriers had shorter cancer-specific survival (CSS) compared with noncarriers (15.7 vs 8.6 years) [28]. gBRCA1/2 carriers with localized prostate cancer have worse outcomes after conventional treatment with surgery or radiation compared with noncarriers, 5-year metastasis free survival 72% vs 94%, 5 year CSS 76% vs 97% [29]. A retrospective case study by Na et al. found that proportion of men carrying gBRCA1/2 or gATM mutations was significantly higher in men who died from prostate cancer compared with men with localized disease (6.07% vs 1.44%). This study also showed that among patients with lethal prostate cancer rate of gBRCA1/2 and gATM mutations was higher in patients who died younger, 10% among those who died <60years, 9% for age of death 61-65; 8% 66-70 years, 4% 71-75 years, and 2.97% among those who died >75 years old $[30 \cdot]$. The prospective PROREPAIR-B found that gBRCA2 status is an independent prognostic factor for CSS in metastatic castration-resistant prostate cancer (mCRPC) patients (17.4 vs 33.2 months, p = 0.027) [31...].

Somatic DNA repair gene mutations are present in about 8–10% of localized prostate cancer cases and 20–25% of mCRPC cases, and Marshall et al. reported that presence in localized disease is associated with higher Gleason grade group (\geq 3) and more advance clinical stage (\geq cT3 disease) at the time of diagnoses [32].

Recommendations for Genetic Testing in Prostate Cancer

Based on these and other studies, NCCN guidelines for Prostate Cancer recommend offering germline testing, ideally with genetic counseling access, to the following groups of prostate cancer patients [22]:

- 1. Men with high-risk, very-high risk localized prostate cancer
- 2. Men with metastatic prostate cancer
- 3. Men with intraductal histology
- 4. Men with Ashkenazi Jewish ancestry
- 5. Men meeting family history criteria (see Table 1)

Somatic tumor sequencing should also be considered in prostate cancer patients especially with advanced disease. Sequencing of tumor metastatic biopsies is preferred when available, as tumor clones evolve over time, and primary prostate cancer tissue might miss alterations developed later in the disease course. Men should also be counseled that somatic tumor testing could potentially suggest presence of a germline mutation, and if the case, referral to genetic counseling to discuss dedicated germline testing would be advised. NCCN guidelines for Prostate Cancer recommend that germline and somatic testing panels should include Lynch syndrome associated genes (MLH1, MSH2, MSH6, and PMS2) and homologous recombination genes (BRCA1/2, ATM, PALB2, *CHEK2*) [21, 22]. Other genes might be appropriate for testing in certain scenarios, such as potential enrollment into clinical trials, where significance of newer gene/mutations as biomarkers for new treatments are being explored.

Treatment Implications of Genetic Testing

Advanced Disease

Targeted therapies are being investigated in clinical trials for prostate cancer patients with specific DNA repair gene alterations in tumor and/or germline. At present, the treatment implications of genetic testing are arguably greatest in metastatic disease, as this is the disease space with the majority of therapeutic clinical trials.

Some studies are available in earlier disease states of prostate cancer and more are expected to follow. Patients with homologous DNA repair mutations are candidates for clinical trials using poly ADP-ribose polymerase inhibitors (PARPi) and/or platinum chemotherapy, and novel combinations. There are several ongoing clinical trials evaluating the role of these agents as monotherapy or in various combination therapies in different stages of prostate cancer (e.g., www.clinicatrials.gov, NCT02975934, NCT02952534, NCT02854436, NCT02987543, NCT03413995). Below is a summary of current data on targeted therapy in prostate cancer patients with DNA repair gene mutations, i.e., immunotherapy, PARPi, platinum chemotherapy.

Immunotherapy Pembrolizumab received the first tumor agnostic FDA approval in 2017 for metastatic solid tumors with microsatellite instability (MSI-H) and mismatch repair deficiency (MMRd) [33, 34]. About 5% of mCRPC cases are estimated to be MSI-H/MMRd and would qualify for treatment with pembrolizumab [35•, 36–38]. In a single institution case series of 1033 prostate tumors undergoing next generation sequencing, 3.1% (32/1033) were found to be MSI-H/MMRd, 78% (25/32) tumors had somatic mutations, and 22% (7/32) were found to have germline Lynch-associated mutations [35•]. Somatic and germline testing for MSI-H/MMRd is recommended in certain prostate cancer patient populations (see above) and has direct clinical implications as MSI-H/MMRd patients are eligible for pembrolizumab in second line of mCRPC treatment.

PARPi Patients with DNA repair mutations have higher response rates to PARPi and platinum chemotherapy [39]. The clinical activity of PARPi in prostate cancer was first reported in the TOPARP-A trial (Trial of Olaparib in Patients with Advanced Castrate Resistant Prostate Cancer), which evaluated olaparib in mCRPC patients who failed multiple lines of therapy (98% received prior abiraterone or enzalutamide, 58% cabazitaxel) [40]. TOPARP-A reported that 88% (14/16) of patients with DNA repair mutations had response to olaparib therapy, where response was defined as a reduction in the PSA by 50% (PSA₅₀), a RECIST-defined objective response rate or circulating tumor cell reduction. Only 2 out 32 patients without DNA repair gene alterations responded to olaparib in TOPARP-A trial. As a result of this trial, olaparib received FDA breakthrough therapy designation in January 2016 for patients with BRCA2-, BRCA1-, or ATM-mutated mCRPC who had received prior taxane and either enzalutamide or abiraterone.

The phase 2 TRITON2 (NCT02952534) study evaluated rucaparib in mCRPC patients with homologous recombination gene mutation progressing after 1–2 lines of androgen receptor–directed therapy and 1 prior line of taxane. Preliminary results demonstrated that among *BRCA1/2* carries 44% (11/25) had radiographic response, and 51% (23/45) had PSA₅₀ response [41••]. Based on these results, FDA granted rucaparib breakthrough designation in October 2018 [42].

The phase 2 TOPARP-B is a trial of PARPi in mCRPC patients with DNA damage repair alterations progressing after at least one taxane (n = 98) [43••]. The overall median progression-free survival (mPFS) was 5.4 months. Subgroup analyses per altered gene indicated following response rates (defined as in TOPARP-A study), *BRCA1/2* 83% (25/30; mPFS 8.1 months); *PALB2* 57% (4/7; mPFS 5.3 months);

ATM 37% (7/19; mPFS 6.1 months); *CDK12* 25% (5/20; mPFS 2.9 months); other (*ATRX*, *CHEK1*, *CHEK2*, *FANCA*, *FANCF*, *FANCG*, *FANCI*, *FANCM*, *RAD50*, *WRN*) 20% (4/20; mPFS 2.8 months). The highest PSA₅₀ response rates were observed in the *BRCA1/2* (22/30; 73%) and *PALB2* (4/6; 67%) mutated subgroups.

The first phase 3 randomized clinical trial evaluating PARPi in mCRPC was recently reported [44..]. PROfound enrolled mCRPC patients who progressed on abiraterone or enzalutamide and had mutations in homologous recombination DNA repair genes, identified by tumor sequencing; cohort A, patients with BRCA1/2 and ATM mutations; cohort B, patients with mutations in other homologous recombination repair genes. Patients were randomized to olaparib 300 mg BID or physician's choice of enzalutamide or abiraterone. The results showed improved radiographic PFS (rPFS) in the olaparib arm of cohort A (7.39 vs 3.55 months, homologous recombination (HR) 0.34 p < 0.001), with objective response rate of 33.3% in olaparib and 2.3% in physician's choice arm of cohort A (OR 20.86 p < 0.001). Despite the crossover design, overall survival (OS) was 18.5 months in olaparib arm compared with 15.11 months in abiraterone/ enzalutamide arm of cohort A, although statistical significance was not reached at time of initial reporting. There was also rPFS benefit in combined cohorts A and B, 5.82 months in olaparib arm vs 3.52 months in physician's choice arm (HR 0.49 p < 0.001). We anticipate that the FDA will approve olaparib for subset of mCRPC patients on the basis of the PROfound trial results.

Table 2 summarizes currently available study results reporting response rates to PARPi in prostate cancer.

Platinum chemotherapy Platinum chemotherapy has been proven to be effective in *BRCA1/2* mutated breast and ovarian cancers [49, 50]. Our single institution retrospective case series showed that 3/3 prostate cancer patients with biallelic inactivation of *BRCA2* had exceptional response to platinum chemotherapy after progressing on several therapies [51]. The findings were supported by a retrospective study that showed 75% (6/8) of mCRPC patients with *gBRCA2* mutation had PSA₅₀ response to platinum chemotherapy compared with 17% (23/133) of mCRPC patients without *gBRCA2* mutations [52].

Localized Disease

In an active surveillance cohort, patients with localized prostate cancer and *gBRCA2*, *gBRCA1*, or *gATM* mutations were more likely to experience grade reclassification compared with non-mutation carriers [53]. Further studies are warranted, but these data suggest that this group of patients will be monitored closely, ideally on a clinical trial, or consider a definitive treatment approach. The role of PARPi in localized prostate

Table 2 Response to PARPi in mCRPC patients stratified by HR gene mutations

Study	Agent used	Response measured by	Number of patients responded to PARPi by mutation status				
			BRCA1/2	ATM	CDK12	Other HRD mut	No HRD mut
PROfound, Hussain et al. [44••]	Olaparib vs abiraterone/enzalutamide	Imaging rPFS (months)	84/162 vs 7.39 vs 3.5	42/83 55	~ 3/94 vs	$s \sim 4/48$	N/A
TOPARP-A, Mateo et al. [40]	Olaparib	Imaging PSA ₅₀ CTC	8/8	4/5	N/A	2/3	2/33
TOPARP-B, Mateo et al. [43••]	Olaparib	Imaging PSA50 CTC	24/30	7/19	5/20	8/27	N/A
TRITON2, Abida et al. [41••]	Rucaparib	Imaging	11/25	0/5	0/8	2/8	N/A
		PSA ₅₀	23/45	0/18	1/13	2/9	N/A
NCI study (50) Karzai et al. [45]	Durvalumab + olaparib	Imaging PSA ₅₀	7/11	N/A	N/A	N/A	2/6
GALAHAD, Smith et al. [46]	Niraparib	Imaging PSA50 CTC	18/29	N/A	N/A	5/21	N/A
KEYNOTE-365, Yu et al.	Olaparib + pembrolizumab	Imaging	N/A	N/A	N/A	N/A	8/28
[47] 2019	* *	PSA ₅₀	N/A	N/A	N/A	N/A	5/41
Retrospective analysis, Marshall et al. [48]	Off-label olaparib	PSA ₅₀	13/17	0/6	N/A	N/A	N/A

Mut, mutations; *CTC*, circulating tumor cell DNA; *PSA*₅₀, decline of prostate-specific antigen by 50% from baseline; *Imaging*, radiographic response measured by RECIST criteria; *rPFS*, radiographic progression-free survival

cancer is being evaluated in several ongoing clinical trials (www.clinicaltrials.gov, NCT03570476, NCT02324998 and NCT03432897).

Biochemical Recurrence

Patients historically classified as having biochemically recurrent (BCR) prostate cancer are now moved to the metastatic group with the use of more sensitive treatment modalities such as PSMA-PET and fluciclovine PET. Advances in imaging has changed the BCR patient population. There is currently no standard of care treatment implications of DNA repair mutations in BCR group, but the use of PARPi is currently being studied in phase 2 clinical trial (NCT03047135), evaluated PSA₅₀ response to olaparib in BCR prostate cancer patients. The study is enrolling patients unselected for DNA repair mutation status with an adaptive plan to enrich study population with DNA repair mutation carriers if response is low in first 20 patients.

Conclusions

There has been significant advancement in prostate cancer genetics in the last 5 years. In metastatic castration-resistant prostate cancer, $\sim 20\%$ of tumors harbor homologous recombination repair gene mutations, and 5% harbor mismatch repair gene mutations; alternations in both pathways have clinical implications. The NCCN Prostate Cancer guidelines recommend germline testing for men with high-risk, very high-risk localized prostate cancer, all metastatic prostate cancer

patients, patients with intraductal histology of prostate cancer, and for patients meeting family history criteria. Somatic tumor testing should also be considered for advanced disease as it may inform treatment decisions.

Patients with homologous recombination-deficient prostate cancer appear to respond to PARPi and platinum chemotherapy, although more individual gene-specific data is needed. The PROFound study, a phase 3 randomized clinical trial of olaparib in mCPRC patients with BRCA1/2 and ATM mutations showed improved rPFS. Patients with MSI-H/MMRd are eligible for immune checkpoint inhibitor therapy in second-line treatment for mCRPC. Both germline and somatic tumor genetic testing are recommended for prostate cancer patients in specific clinical scenarios. Clinical trials are ongoing to evaluate treatment implications of alterations in mismatch repair genes and homologous recombination genes, and we expect new indications and combinations of PARPi and immune checkpoint inhibitors to be explored by these trials. Further investigation is needed to identify individual gene contributions to treatment response prediction and germline risk of prostate and other cancers.

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Honing in on PARPi Response in Prostate Cancer: from HR Pathway to Gene-by-Gene Granularity



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SUMMARY

PARP inhibitors (PARPi) are promising in *BRCA2*-altered prostate cancer. Data were presented on PARPi efficacy in prostate cancers with alterations in other DNA damage repair genes which suggest low response rates in ATM-, CHEK2-, CDK12-altered tumors and promising results in PALB2-, RAD51B-, FANCA-, and BRIP1-altered tumors. See related article by Abida et al., p. 2487

In this issue of *Clinical Cancer Research*, Abida and colleagues report response to the PARPi rucaparib in patients with metastatic castration resistant prostate cancer (mCRPC) harboring deleterious alterations in non-*BRCA* DNA damage repair (DDR) genes (1). The data provides early evidence that prostate tumors with *ATM*, *CDK12*, and *CHEK2* alterations may have limited response to rucaparib, while tumors with alterations in *PALB2*, *FANCA*, *BRIP1*, and *RAD51B* may benefit from PARP inhibition (1).

Several studies suggest that PARPis are effective in prostate cancer tumors with *BRCA2* alterations (2). The mechanism of action of PARPi in tumors is typically attributed to impaired double-strand DDR-homologous recombination (HR) repair–deficient tumors, but likely involves additional mechanisms such as (i) trapping of the PARP1–enzyme, which regulates several DNA repair processes; (ii) inhibition of base excision, critical to single-strand DNA repair; (iii) activation of error prone nonhomologous end joining repair, important in double-strand DNA repair; and (iv) inhibition of DNA repair protein recruitment (e.g., *BARD1-BRCA1* complex; ref. 3). Multiple non-*BRCA* genes mediate HR repair (*e.g., ATM, CHEK2*, and others), so many have been included as candidate biomarkers for PARPi sensitivity. However, data to date has been limited by small numbers and technical differences (2).

To begin to address this, Abida and colleagues evaluated response to rucaparib in patients with metastatic castration-resistant prostate cancer and non-*BRCA* DDR gene alterations in the phase II TRITON2 study. Eligibility included patients with disease progression after second-generation androgen receptor-targeted therapy and taxane-based chemotherapy and who were identified to have germline and/or somatic mutations in selected DDR genes (*BRCA1*, *BRCA2*, *ATM*, *BARD1*, *BRIP1*, *CDK12*, *CHEK2*, *FANCA*, *NBN*, *PALB2*, *RAD51*, *RAD51B*, *RAD51C*, *RAD51D*, or *RAD54L*). Whole blood was used for germline testing and somatic sequencing was performed on circulating tumor DNA (ctDNA) or on tumor tissue by central or local laboratory. This *ad hoc* analysis included 78

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These findings are consistent with previously reported data: 1 of 5 patients with *FANCA*-, 4/7 with *PALB2*-, 2/19 with *ATM*-, and 0/20 with *CDK12* -alterations had RECIST or PSA50 response to PARPi in TOPARP-B trial (2). In the PROfound study, patients with *RAD51B* alterations treated with PARPi had a 6-month median radiographic progression-free survival (rPFS) benefit compared with physician choice therapy arm, and similar rPFS was observed between two arms in patients with *ATM* alterations (2). Similarly 0 of 6 patients with *ATM* alterations had PSA50 response in a retrospective study (2). As a field, we must be careful to draw conclusions from small numbers in each analysis, however, in aggregate, patterns are emerging.

The authors of this manuscript acknowledge several limitations (1). First, there was no requirement for central laboratory confirmation of reported alterations. Some, but not all, sequencing results were confirmed by central laboratory, increasing the chance of false positive results for eligibility. Second, clonal hematopoietic (CH) variants may introduce interference in ctDNA studies and mistakenly attributed to tumor-specific alterations (4). Among genes included for eligibility in this study, alterations in *ATM* are more common in CH and thus may contribute to variant origin misclassification (4). Third, loss of heterozygosity (LOH) and tumor sequencing data were not available for several patients, including the patients with *ATM* alterations who had response to rucaparib. It is possible that non-*ATM* tumor alterations contributed to PARPi responses in these patients even though their eligibility was due to an *ATM* alteration.

This study addresses important knowledge gaps by characterizing response to PARPi in tumors with relatively rare alterations in DDR genes. It is especially timely as we anticipate FDA approval of PARPi in prostate cancer based on the positive phase III PROfound study and other eagerly anticipated trials such as TRITON3, GALAHAD and TALAPRO-1 (2). Understanding the efficacy of PARPi in prostate tumors with non-*BRCA* DDR gene alterations is essential before



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Figure 1.

Predictive biomarkers for PARPi efficacy. Currently, alterations in HR repair genes are used to predict loss of HR repair function and to select prostate cancer patients most likely to respond to PARPi, potentially overlooking other causes of HR function loss. HR repair function loss consequences (i.e., genomic footprint) may be a better predictive biomarker for response to PARPi. HRD, homologous recombination deficiency.

widespread clinical use makes the task more challenging. The data presented by Abida and colleagues may help generate hypotheses about mechanisms of response and resistance, and refine predictive biomarkers for PARPi use for patients with prostate cancer, including in subsequent preclinical and clinical trials.

A better understanding of which patients benefit the most from PARPi and which DDR gene mutations could be the best predictors of response to PARPi will help refine precision oncology in prostate cancer therapy. A notable example is that not all BRCA2-mutated tumors respond to PARPi (1, 2) and conversely, in the TOPARP-A study, two patients without evidence of DDR gene mutations achieved response to PARPi, suggesting additional mechanisms of PARPi sensitivity beyond those specifically tested (2). Sensitivity to PARPi is hypothesized to be determined by functional HR deficiency (HRD), such that relying solely on gene mutations to predict PARPi sensitivity may overlook other mechanisms resulting in loss of HR function, for example, DNA hypermethylation. Loss of HR repair function, regardless of the cause, is thought to lead to characteristic genomic changes such as HRD mutational signature and genomic instability. HRD mutational signature is characterized by a more-or-less equal representation of all possible single base substitutions and all 96 mutant nucleotide contexts (5). With the data and specimens from Abida and colleagues and other PARPi studies, examining the downstream consequences of HR loss and the associated genomic footprints with clinical response may facilitate more accurate prediction of response to PARPi in the future (Fig. 1).

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We applaud the authors in reporting their findings of response to PARPi in tumors with non-*BRCA* DDR gene alterations. To further strengthen the available data for patients whose tumors carry these and other rare alterations and the response to PARPi and other treatments, a concerted team approach is needed. Assembling greater numbers of patients with rare mutations will allow more robust investigation of clinical response, mutational signatures of specific gene alterations, mechanisms of resistance such as reversion mutations, and opportunities for model systems to dissect mechanisms. This will further refine predictive biomarkers, stratify appropriate patients to PARPi therapy and improve the precision of our targeted therapies.

Disclosure of Potential Conflicts of Interest

E.Y. Yu is a paid consultant for AstraZeneca, Clovis, Merck, and Janssen, and reports receiving commercial research grants from Merck. H.H. Cheng is a paid consultant for AstraZeneca and reports receiving other commercial research support from Clovis Oncology, Janssen, Medivation, Sanofi, and Color Genomics. No potential conflicts of interest were disclosed by the other author.

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Clinical Cancer Research

Honing in on PARPi Response in Prostate Cancer: from HR Pathway to Gene-by-Gene Granularity

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Two Steps Forward and One Step Back for Precision in Prostate Cancer Treatment

Michael T. Schweizer, MD^{1,2}; Heather H. Cheng, MD, PhD^{1,2}; Peter S. Nelson, MD^{1,2,3}; and R. Bruce Montgomery, MD^{1,2,4}

The recent US Food and Drug Administration approval of two poly (ADP-ribose) polymerase (PARP) inhibitors, rucaparib and olaparib, for men with metastatic castration-resistant prostate cancer (mCRPC) and mutations in homologous recombination (HR) repair genes has finally ushered in the era of precision medicine for advanced prostate cancer.¹⁻⁴ These approvals represent the culmination of years of work and are clearly a major step forward for the field. However, the respective labels for rucaparib and olaparib offer stark contrasts, the former restrictive to only BRCA1- and BRCA2-mutated prostate cancer, and the latter permissive of a larger number of genes directly and indirectly involved in HR repair. The broad approval for olaparib includes several genes that, to date, have not individually been shown to predict for response to PARP inhibition. The unintended consequence of using this permissive biomarker strategy for selecting patients for PARP inhibitor treatment may be that patients who have an unclear chance of benefit are exposed to toxicities and delays in utilizing more effective therapies. In addition, this broad approval could hamper efforts to enroll patients in studies designed to better delineate the ability of relatively rare mutations to predict response to PARP inhibitors.

Rucaparib was granted accelerated approval on the basis of the phase II TRITON2 study.^{1,3} In this trial, patients with mCRPC were eligible if they previously experienced progression on a next-generation androgen receptor-signaling inhibitor (eg, abiraterone, enzalutamide, or apalutamide), received one prior line of taxane-based chemotherapy, and who were identified to have a mutation in at least one gene of a larger panel with roles in HR DNA repair. However, only the group consisting of those with BRCA1 or BRCA2 mutations clearly seemed to be predictive of response.⁵ In total, 115 patients with BRCA-mutated mCRPC enrolled, with 62 having measurable disease. Within this group, a confirmed objective radiographic response was observed in 27 patients (44%), with a duration of response 6 months or longer in 56% of responders (range, 1.7 to \geq 24 months).¹

Whereas the final TRITON2 results are still anticipated, results of a subgroup analysis evaluating clinical

outcomes in those with non-BRCA-mutated mCRPC enrolled has recently been reported.⁵ Overall, responses in those with ATM (n = 49), CDK12 (n = 15), CHEK2 (n = 12), or other HR genes (n = 14) were low. The prostrate-specific antigen (PSA) response rate (ie, 50% or greater decline in PSA) was observed in only 4% of ATM-mutated cases, 7% of CDK12-mutated cases, and 17% of CHEK2-mutated cases. Radiographic responses in the subset with measurable disease were similarly low in non-BRCA HR repair genes. Small numbers of patients with mutations in FANCA (n = 4), NBN (n = 4), BRIP1 (n = 2), PALB2 (n = 2), RAD51 (n = 1), RAD51B (n = 1), and/orRAD54L (n = 1) were also reported. Whereas sample size limitations prevent drawing conclusions about the sensitivity of any given gene, it is notable that responses were observed in those with mutations in genes that directly interact with the BRCA complex (ie, PALB2, FANCA, and BRIP1), which contrasts with the low response rates in genes that either sense DNA damage (eg, ATM, CHEK2) or indirectly regulate BRCA expression (eg, CDK12). Finally, it is worth acknowledging that relatively few men with BRCA1 alterations were included in this study (n = 14), and the true response rate within this population also remains poorly defined.⁶

Olaparib was approved on the basis of the phase III PROfound study, which was a randomized, open-label study evaluating olaparib versus physician's choice of enzalutamide or abiraterone in men with mCRPC and deleterious germline or somatic mutations in HR repair genes.⁴ Similar to TRITON2, the PROfound investigators also focused on the subgroup that previously experienced progression on next-generation and rogen receptor-directed therapy, and, also similar to TRITON2, enrollment was allowed on the basis of a panel of genes involved in the HR repair pathway. Primary end point was progression-free survival (PFS) in the group with BRCA1, BRCA2, and/or ATM mutations (cohort A). A second cohort consisted of patients with mutations in other HR repair-associated genes (cohort B). Secondary end points were analyzed in a hierarchical fashion to control for trial-wide Type 1 error associated with multiple testing, which occurred in the following order: objective response rate (cohort A),

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PFS (combined cohorts A and B), time to pain progression (cohort A), and overall survival (cohort A).

The primary end point was met, with a PFS of 7.4 months versus 3.6 months (P < .001) in the olaparib versus control groups for cohort A. Secondary end points also favored the olaparib group, with an objective response rate in cohort A of 33% versus 2% in control group (P < .001), median PFS of 5.8 months versus 3.5 months for combined cohorts A and B (P < .001), median overall survival of 18.5 months versus 15.1 months for cohort A (P = .02), and median overall survival of 17.5 months versus 14.3 months for combined cohorts A and B (P = .0063). These results led the US Food and Drug Administration to approve olaparib for a broad group of patients with mCRPC with somatic or germline alterations in *BRCA1*, *BRCA2*, or any of 12 additional HR repair pathway genes.

Whereas the magnitude of benefit reported for cohort A in PROfound is apparent, the lack of details provided for cohort B leaves more questions than answers. Examining the data more closely, it seems that the observed benefit was largely driven by *BRCA*-mutated patients, which primarily consisted of men with *BRCA2* mutations (> 90%). There is a clear improvement in PFS for the *BRCA*-mutated group (n = 160), whereas no difference in PFS was observed in either *ATM* (n = 86) or *CDK12*-mutated cases (n = 89; Fig 2B and Supplemental Figure S5). Unfortunately, no detailed analysis of outcomes for cohort B—independent of cohort A—are provided, and the small sample size within any given genomic subgroup limits our ability to determine which of these patients may have benefited from olaparib.

The TOPARP-A and -B studies, which preceded PROfound, tested olaparib in a similar patient population.^{7,8} In TOPARP-B, the authors found low PSA and radiographic response rates for ATM (5.3% and 8.3%, respectively) and CDK12-mutated mCRPC (0% for both).⁸ In addition, the PROfound investigators acknowledged that the benefits of olaparib are most apparent in BRCA-mutated mCRPC. Whereas the design of PROfound was likely informed by the initial TOPARP-A experience, which found that four of five patients with ATM-mutatations responded favorably to olaparib (ie, PSA response and/or favorable changes in circulating tumor cell counts), the biologic and clinical rationale for combining ATM and BRCA1/2 mutations into a single cohort is questionable on the basis of our current knowledge.⁷ Registries capturing clinical and genomics data are ongoing and may provide important insights into the clinical relevance of rare variants⁹; however, additional prospective studies evaluating outcomes for patients with HR repair-associated mutations receiving PARP inhibitors should be conducted on an individual gene basis.

In the case of PROfound, the *BRCA* group seems to have driven the overall effect size observed between the olaparib and control groups. An important concern is that this

experience may motivate the design of future precision medicine trials. The precedent set by the olaparib approval for prostate cancer may incentivize studies that combine molecular subgroups to attain broad indications. This may lead to future study designs that include two groups: one that is expected to benefit (eg, *BRCA2*) and another that is more exploratory and permissive (eg, *ATM/CDK12*). The consequence, intended or not, may be that a *P* value less than .05 could be reached in the combined group as long as the sample size is sufficient to detect a diluted treatment effect. This approach would ultimately run counter to the idea of precision oncology.

As discussed above, the clinical data supporting the use of PARP inhibitors in non-BRCA2-mutated cases remain scant; however, there is a rationale for their routine use in men with mutations in a handful of other HR repair-associated genes. Whereas some data suggest lower response rates in men with BRCA1- compared with BRCA2-mutated prostate cancer (eg, PSA response rate of 29% v 56% per TRITON2) and no clear difference in PFS was observed in men with BRCA1 mutations receiving olaparib versus abiraterone/enzalutamide in PROfound, the small number of patients with BRCA1 mutations included in prospective studies make drawing conclusions regarding differences in activity impossible.^{4,6} Overall, the known biologic role of BRCA1 in HR repair, along with available clinical data, generally supports the use of both olaparib and rucaparib in these patients. Likewise, there is also evidence that PARP inhibitors may afford benefits to those with PALB2 mutations, with responses to olaparib documented in approximately one third of PALB2-mutated prostate cancers.⁸ In addition, because *PALB2* also plays a critical role in HR repair-directly interacting with the BRCA complex-there is a strong biologic rationale for using PARP inhibitors in patients with prostate cancer with inactivating PALB2 mutations.^{5,8,10,11}

The primary advantage of olaparib's broad approval is that providers will have the latitude to use this drug in men with mutations in less common HR repair genes (eg, PALB2) that are likely predictive for response. However, approving olaparib for such a large genomic subgroup could prove detrimental to some patients and the field if not used judiciously. To qualify for olaparib, patients must have already experienced progression on a next-generation hormonal agent (eg, abiraterone or enzalutamide) and owing to the heavily pretreated state of their disease, this population often has rapid disease progression with a short overall survival. On the basis of the published studies, there are limited data to support use of olaparib in the absence of BRCA1/2 mutations, and without other indications of HR repair deficiency, these patients would be better served by participating in clinical trials or receiving a therapy that is beneficial in unselected patients (eg, taxane-based chemotherapy).¹² Using standard-of-care PARP inhibitors in those with uncertain or little chance of benefit could mean missing a window of opportunity for more effective therapy. This may result in decreased survival and hamper clinical trial enrollment to the very studies that could define the predictive utility of individual genes. Cumulative experience should matter, and given our

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understanding of which genes predict response to PARP inhibitors, the use of rucaparib and olaparib should be primarily limited to those with *BRCA1/2* mutations until the development of additional biomarkers that are more predictive of benefit.

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Two Steps Forward and One Step Back for Precision in Prostate Cancer Treatment

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Impact of mutations in homologous recombination repair genes on treatment outcomes for metastatic castration resistant prostate cancer

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Abstract

Introduction

A significant proportion of patients with metastatic castration-resistant prostate cancer (mCRPC) harbor mutations in homologous recombination (HR) repair genes, with some of these mutations associating with increased tumor susceptibility to poly(ADP-ribose) polymerase (PARP) inhibitors and platinum-based chemotherapy. While mutations in some HR repair genes (e.g., *BRCA1/2*) have been associated with a more aggressive clinical course, prior studies correlating HR mutational status with treatment response to androgen receptor (AR) signaling inhibitors (ARSIs) or taxane-based chemotherapy have yielded conflicting results.

Methods

We conducted a single-center retrospective analysis to assess clinical outcomes to conventional, regulatory-approved therapies in mCRPC patients with somatic (monoallelic and biallelic) and/or germline HR repair mutations compared to patients without alterations as determined by clinical-grade next-generation sequencing assays. The primary endpoint was PSA30/PSA50 response, defined as \geq 30%/ \geq 50% prostate-specific antigen (PSA) reduction from baseline. Secondary endpoints of PSA progression-free survival (pPFS) and clinical/radiographic progression-free survival (crPFS) were estimated using Kaplan-Meier methods.

Results

A total of 90 consecutively selected patients were included in this analysis, of which 33 (37%) were identified to have HR repair gene mutations. Age, race, Gleason score, prior

analysis, decision to publish, or preparation of the manuscript.

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surgery, and receipt of prior radiation therapy were comparable between carriers and noncarriers. There was no evidence that PSA30/PSA50 differed by HR gene mutational status. Median pPFS and crPFS ranged 3–14 months across treatment modalities, but there was no evidence either differed by HR gene mutational status (all p>0.05). There was also no difference in outcomes between those with *BRCA2* or *PALB2* mutations (n = 17) compared to those without HR repair mutations.

Conclusion

HR gene mutational status was associated with comparable clinical outcomes following treatment with ARSIs or taxane-based chemotherapy. Additional prospective studies are needed to confirm these findings.

Introduction

DNA damage repair (DDR) pathways play an essential role in maintaining genomic integrity. Individuals harboring germline mutations in DDR genes are more susceptible to cancer development [1]. Germline and somatic DDR mutations are also associated with a more aggressive clinical course in certain cancers: germline *BRCA* mutations have been associated with decreased breast cancer-specific survival [2] and linked to poor outcomes in patients with prostate cancer, including decreased metastasis-free survival in those initially presenting with localized disease [3, 4]. The significance of DDR mutations in prostate cancer has expanded in recent years as studies have demonstrated that their prevalence is higher than previously thought [5, 6].

Importantly, DDR genes specifically involved in homologous recombination (HR) repair may be predictive for response to poly(ADP-ribose) polymerase (PARP) inhibitors in patients with metastatic castration-resistant prostate cancer (mCRPC). Treatment with PARP inhibitors leads to persistent single-strand DNA (ssDNA) breaks through inhibition of base excision repair. These ssDNA breaks then degenerate to double-strand DNA (dsDNA) breaks and, because HR repair deficient cells are unable to efficiently repair dsDNA breaks, PARP inhibitors are synthetically lethal to these cancer cells [7, 8]. Various other mechanisms likely contribute to PARP inhibitor sensitivity in HR repair deficient tumors, including PARP1 trapping and creation of cytotoxic PARP1-DNA complexes at sites of endogenous damage, the promotion of nonhomologous end joining (NHEJ) activity, and inhibition of DNA repair protein recruitment (e.g., *BRCA1, BARD1*) [9, 10].

The two-stage TOPARP trials revealed high response rates to olaparib in mCRPC patients with HR repair gene mutations who were no longer responding to standard therapies [11, 12]. More recently, the phase III PROfound trial demonstrated increased radiographic progression-free survival (PFS) and objective responses in mCRPC patients with HR repair gene mutations receiving olaparib compared to enzalutamide or abiraterone [13], although activity in the patients with mutations in non-*BRCA*-mutated HR repair genes remains uncertain [12, 14, 15]. The phase II TRITON2 study found no clear evidence of response to rucaparib in patients with *ATM*, *CDK12*, and *CHEK2* mutations, whereas patients with mutations in genes that directly interact with the *BRCA* complex (e.g. *PALB2*, *FANCA*, *RAD51*, etc.) showed promising radiographic and prostate-specific antigen (PSA) response [15]. Rupacarib has since gained accelerated FDA approval for mCRPC patients with deleterious *BRCA1/2* mutations who were previously treated with novel androgen receptor (AR) targeted therapy and

taxane chemotherapy [16]. Olaparib has received full approval for mCRPC patients who have at least one line of novel AR targeted therapy and have a suspected or known deleterious HR repair mutation across a broad panel [17].

The presence of HR repair gene mutations in cancers has also been associated with enhanced sensitivity to platinum-based chemotherapy. The likely mechanism behind this sensitivity is through the formation of dsDNA breaks via DNA adducts [18].

Cheng, et al. reported that patients with biallelic *BRCA2* inactivation can achieve excellent clinical response with carboplatin even after progression on first-line therapies for mCRPC [19]. Germline *BRCA2* variants were also found to strongly associate with PSA response \geq 50% in mCRPC patients treated with carboplatin [20].

While significant effort has gone into exploring precision medicine approaches for treating prostate cancer patients with HR repair gene mutations, there are limited reports describing the clinical course of these patients following treatment with standard therapies. Androgen receptor signaling inhibitors (ARSIs), such as abiraterone and enzalutamide, as well as taxane-based chemotherapy, such as docetaxel and cabazitaxel, have been established as standard, regulatory-approved treatment options for patients with mCRPC [21]. Recently, Hussain, et al. reported that somatic HR repair mutations may be associated with improved PSA response and PFS with abiraterone [22]. This contrasted with previous findings of attenuated ARSI response in germline HR gene mutation carriers [23]. Studies examining taxane-based chemotherapy treatment in mCRPC found no significant difference in treatment responses when stratifying by HR gene mutation status [24, 25]. Notably, treatment with cabazitaxel was not evaluated in these reports.

The objective of this paper is to investigate how mutations in genes directly and indirectly involved in the HR repair pathway impact treatment response and long-term outcomes in mCRPC patients treated with abiraterone, enzalutamide, docetaxel, and cabazitaxel. We hypothesized that the presence of HR repair gene mutations will correlate with poor clinical outcomes following treatment with these agents.

Materials and methods

Patients

A retrospective analysis was performed using the institutional Caisis database, which includes prostate cancer patients treated at the University of Washington/Seattle Cancer Care Alliance (UW/SCCA). Prior to data abstraction, this project was reviewed by the Institutional Review Board at the University of Washington and deemed to be minimal risk. As such, the requirement for informed consent was waived. Patient electronic medical records were accessed between 05/2018-02/2020 and were not anonymized to data abstractors. All patient data was de-identified prior to performing statistical analysis.

Our inclusion criteria mandated that patients have pathologically proven prostate cancer and documented mCRPC status, defined as disease progression following surgical/medical castration (i.e. androgen deprivation therapy; ADT) by PSA or radiographic/clinical evidence. Additionally, patients must have previously undergone clinical-grade next-generation sequencing (NGS) of their tumor. An exception was made to include patients with known germline *BRCA2* mutations who did not undergo tumor sequencing, given that these germline cases are most often associated with the loss of the second allele by somatic mutation [6]. The following assays were included: UW-OncoPlex, FoundationOne, Guardant360, GeneTrails, BROCA, Color, BRACAnalysis, and Whole Exome Sequencing (WEC) assay results [5].

We specifically analyzed monotherapy treatments with each of the four agents (abiraterone, enzalutamide, docetaxel, cabazitaxel) that occurred between 2011–2019. Per Prostate Cancer

Working Group 3 (PCWG3) guidelines, we required a minimum 60 days of therapy in order to assess responses and progression endpoints [26]. Patients treated with more than one of the four agents were eligible for analysis in multiple treatment groups if all above inclusion criteria were met. If a patient received multiple courses of the same agent, only the first treatment course was assessed. Confirmation of PSA response/progression was not required since this was not uniformly performed in these non-trial patients. Patients with neuroendocrine or small cell differentiation were excluded unless their treatments occurred prior to pathological confirmation of neuroendocrine/small cell transdifferentiation.

HR repair gene status

Patients were sub-divided into two groups based on the presence or absence of HR repair gene mutations. The HR group contained patients with both somatic and germline mutations in genes involved in HR repair, including those indirectly regulating this pathway [5, 6, 27]. A broad set of genes was included given the recent approval of olaparib across an inclusive set of genes both directly and indirectly involved in HR repair [13, 17]. Monoallelic somatic mutations were considered sufficient for inclusion, given that many assays (e.g., FoundationOne) do not assess for loss of heterozygosity (LOH) or explicitly report germline mutations. Mutations were considered pathogenic if reported as such on the clinical report. Variants of unknown significance or otherwise benign changes were not included in the HR repair mutation cohort.

Data endpoints

The primary objective of this study was to determine the PSA50 and PSA30 response rate for each therapy, which was defined as the proportion of patients achieving \geq 50% and \geq 30% PSA reduction from the baseline PSA, respectively. Nadir PSA was recorded as the lowest PSA after starting treatment and prior to initiating a subsequent therapy.

The secondary objectives included determining PSA PFS (pPFS) and clinical/radiographic PFS (crPFS). PSA progression was defined by a PSA increase that was ≥ 2 ng/mL and $\geq 25\%$ above the nadir on two consecutive lab draws. Clinical/radiographic progression was based on the assessment of the treating physician and was determined through chart review. Response Evaluation Criteria in Solid Tumors (RECIST) criteria were not utilized given that most patients were not treated on a clinical trial.

Statistical analysis

Differences in demographic characteristics and baseline laboratory measurements between the two populations were evaluated using Kruskal-Wallis or Fisher's exact tests. Differences in PSA50 and PSA30 between populations were evaluated using Fisher's exact tests separately for each treatment modality. Kaplan-Meier curves were calculated for pPFS and crPFS for each treatment modality, and differences between populations were evaluated using log-rank tests. A p-value <0.05 was considered statistically significant. All analyses were carried out using R statistical software version 3.6.3.

A secondary analysis estimated probabilities of PSA30/PSA50 using Bayesian logistic regression to adjust for prior receipt of similar therapy. Adjustment for prior similar therapy was examined given numerous studies highlighting varying levels of cross-resistance in these treatment modalities [28–32]. Prior similar therapy was defined as prior receipt of abiraterone or enzalutamide when either ARSI treatment was analyzed and prior receipt of docetaxel or cabazitaxel when either taxane-based chemotherapy was analyzed.

An exploratory analysis compared outcomes specifically for patients with *BRCA2* and *PALB2* mutations to those without HR repair gene mutations. Previous literature has demonstrated that these genes are closely associated with HR repair functional status [33, 34] and appear to be important predictive biomarkers for determining eligibility for DNA damaging agents. PSA30/PSA50 and pPFS/crPFS outcomes were re-evaluated for these comparisons.

Results

Patients

A total of 90 consecutively selected patients were included in this analysis, with HR repair gene mutations identified in 33/90 (37%). Of the 20 patients who underwent dedicated germline testing, 5 (25%) were found to harbor germline HR repair alterations. Mutations were found in 8 unique HR repair genes, with *BRCA2* (n = 16) being the most frequently altered (Table 1, S1 Table). A demographic comparison based on HR status showed similarity in age at diagnosis, Gleason score, prior surgery, and receipt of prior radiation therapy between the two patient populations (Table 2). Over 21% of patients with HR repair mutations were non-white in comparison to 7.1% of patients without HR repair mutations, although this finding did not reach statistical significance (p = 0.07). Laboratory parameters assessed prior to starting each treatment were also similar between the populations (S2–S5 Tables).

Efficacy outcomes

Best PSA response among patients with/without HR repair gene mutations is depicted in Fig 1 using waterfall plots for each treatment modality. Most patients achieved a PSA reduction from baseline in every treatment group except for patients without HR repair mutations treated with cabazitaxel. There was no evidence that PSA30 or PSA50 differed based on HR status for any treatment modality (Table 3). The frequency of patients achieving PSA50 in the population with HR repair gene mutations was 26% higher in the enzalutamide group and 40% higher in the cabazitaxel group compared to patients with no HR repair gene mutations, though neither result was statistically significant (p = 0.09 and p = 0.07, respectively). Regardless of HR repair gene mutation status, the PSA30 response rate was >50% and PSA50 response rate was >40% for all treatment modalities except cabazitaxel. Adjusting for prior similar therapy did not reveal an association between HR repair gene mutation status and PSA30/PSA50 for any of the treatments (S6 Table).

Kaplan-Meier curves of pPFS and crPFS are provided in Fig 2 by treatment modality. Median pPFS ranged between 2.8–6.5 months and median crPFS ranged between 4.2–14.2 months across treatment groups. There was no evidence that pPFS or crPFS differed based on HR repair gene mutation status for any treatment modality (Table 4).

Exploratory analyses comparing patients with mutations in *BRCA2* or *PALB2* to patients without HR repair mutations did not reveal differences in PSA30/PSA50 or pPFS/crPFS for any treatment (<u>S1</u> and <u>S2</u> Figs, <u>S7</u> and <u>S8</u> Tables), although the sample size within any molecular subgroup was small.

Discussion

The principal impetus behind this study was to evaluate whether mCRPC patients harboring mutations both directly and indirectly involved in HR repair achieve comparable outcomes to patients without such mutations following treatment with conventional, regulatory-approved treatment regimens. Given the recent FDA approvals of the PARP inhibitors rucaparib and olaparib, as well as interest in developing platinum-based chemotherapy for patients with HR

Study ID	Sequencing Assay	Affected HR Gene	Germline alteration?	Bi-allelic mutation?	
1	UW-OncoPlex	FANCA	N/A	No	
2	WEC	BRCA2	No	Yes	
4	UW-OncoPlex	BRCA2	N/A	Yes	
9	UW-OncoPlex	MRE11A	N/A	No	
14	UW-OncoPlex	BRCA2	No	Yes	
20	UW-OncoPlex	BRCA2	No	Yes	
24	FoundationOne, Color	BRCA2	Yes	Yes	
25	UW-OncoPlex	CDK12	N/A	Yes	
27	UW-OncoPlex	BRCA2	N/A	No	
28	UW-OncoPlex, WEC	BRCA2	Yes	Yes	
31	UW-OncoPlex	BRCA2	N/A	Yes	
33	UW-OncoPlex	BRCA2	N/A	No	
34	UW-OncoPlex	CDK12	N/A	Yes	
36	FoundationOne	ATM	N/A	Yes	
38	UW-OncoPlex	PALB2	N/A	Yes	
39	UW-OncoPlex	CHD1	N/A	No	
43	UW-OncoPlex	BRCA2	N/A	N/A	
44	Color	BRCA2	Yes	N/A	
48	UW-OncoPlex	CHD1	N/A	Yes	
57	FoundationOne	CDK12	N/A	Yes	
59	UW-OncoPlex	BRCA2	N/A	Yes	
63	BRACAnalysis	BRCA2	Yes	N/A	
69	UW-OncoPlex	CHD1	N/A	Yes	
70	UW-OncoPlex	ATM	N/A	No	
71	UW-OncoPlex	FANCA	N/A	N/A	
72	UW-OncoPlex	CDK12	N/A	N/A	
78	Guardant360, FoundationOne, Color	BRCA2	Yes	N/A	
79	UW-OncoPlex	CHD1	N/A	Yes	
81	FoundationOne	ATM	No	No	
82	GeneTrails	FANCA	N/A	N/A	
84	UW-OncoPlex	BRCA2	N/A	Yes	
86	UW-OncoPlex	MRE11A	N/A	Yes	
90	UW-OncoPlex	BRCA2, CHEK2	N/A	Yes	

Table 1. Complete list of HR mutations.

"WEC" denotes the Whole Exome Sequencing assay.

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repair gene mutations, we felt it was imperative to examine whether current conventional mCRPC treatments retain efficacy in this patient population. Our findings of similar PSA response and PFS in patients with HR repair gene mutations treated with ARSIs and taxanebased chemotherapy suggests that current standard mCRPC treatments are still very reasonable options for this patient population.

Our data largely aligns with the results of the recently published PROREPAIR-B study, which found non-significant differences in PSA50, PFS, and cause-specific survival when comparing germline *ATM/BRCA1/BRCA2/PALB2* carriers to non-carriers [35]. In contrast to the PROREPAIR-B study, which reported decreased survival in men with *BRCA2* mutations in a post hoc analysis, we did not observe survival differences in those with *BRCA2* mutations; although, our small sample size limited our statistical power to detect differences in outcomes.

Measure	No HR (N = 57)	HR (N = 33)	P-value
Age, years, median [IQR]	61.1 [55.2, 66.4]	61.0 [53.0, 67.5]	0.8
Race, N (%)			
• White	53 (93.0)	26 (78.8)	0.07
• Black	1 (1.8)	4 (12.1)	
• Asian/Unknown	3 (5.3)	3 (9.1)	
Gleason Score, N (%)			
• 6	2 (3.5)	0 (0.0)	0.6
• 7	20 (35.1)	10 (30.3)	
• 8-10	31 (54.4)	22 (66.7)	
• Unknown	4 (7.0)	1 (3.0)	
Prior Surgery, N (%)			
• No	31 (54.4)	20 (60.6)	0.4
• Yes	26 (45.6)	12 (36.4)	
• Unknown	0 (0.0)	1 (3.0)	
Prior Radiation Therapy, N (%)			
• No	14 (24.6)	12 (36.4)	0.6
• Yes	29 (50.9)	15 (45.5)	
• Unknown	14 (24.6)	6 (18.2)	

Table 2. Patient characteristics by HR status.

P-value for age from Kruskal-Wallis rank sum test and for other measures from Fisher's exact test.

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It does seem plausible that *BRCA1/2* and other proteins directly interacting with the *BRCA* complex may have distinct clinical and biologic relevance compared to those that indirectly regulate HR repair (e.g., *CDK12, ATM, CHEK2*). Indeed, results from TRITON2, TOPARP-B, and PROfound all suggest that responses to PARP inhibitors are largely observed in those with *BRCA* mutations [12, 13, 15]. These observations support the need to further examine clinical outcomes on an individual gene basis.

The 37% overall HR repair gene mutation rate found within our population is significantly higher than what has been reported in previous studies. It is important to emphasize that our research was not designed to characterize the frequency of HR repair gene mutations within mCRPC patients, but rather to assess clinical response in patients with such mutations. Our population was not cross-sectional and was enriched by our selection criteria. Specifically, our requirement of NGS likely inflated the frequency of HR repair gene mutations found, as NGS was more often performed in patients with significant family history, high-risk tumor histology (e.g., Gleason grade group 4–5 and ductal histology) [5, 36, 37], unique clinical course, or known germline variants.

A major limitation of this study was its small sample size. With 90 total patients and relatively small numbers in each treatment modality, our analyses were underpowered to detect small differences in outcomes. Limited patient numbers also precluded additional sub-analyses, including comparisons of germline versus somatic mutations, monoallelic versus biallelic mutations, and *BRCA1/2*-mutated versus other HR repair gene alterations. We also used a permissive approach for classifying HR repair deficiency. This approach was largely pragmatic in nature and resembles the 'real world' data most practicing oncologists use to make treatment choices given that many NGS platforms do not report LOH events or germline alterations. Until such data becomes more readily reported and operational for providers, our data indicates that standard therapies for mCRPC (i.e. non-DDR-targeted treatments such as ARSIs and taxane chemotherapy) should still be considered for these patients.



Fig 1. Waterfall plot of best PSA response by treatment and HR status. Maximum percent relative change from baseline during treatment or after completing treatment but prior to subsequent treatment. Maximum percent change greater than 100% is truncated at 100%. Dashed horizontal lines show 50% decrease.

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Treatment	Response	No HR, N (%)	HR, N (%)	P-value
Abiraterone	PSA30	19/29 (66%)	14/19 (74%)	0.8
	PSA50	14/29 (48%)	13/19 (68%)	0.2
Enzalutamide	PSA30	17/29 (59%)	17/24 (71%)	0.4
	PSA50	13/29 (45%)	17/24 (71%)	0.09
Docetaxel	PSA30	17/25 (68%)	8/11 (73%)	1.0
	PSA50	13/25 (52%)	7/11 (64%)	0.7
Cabazitaxel	PSA30	3/12 (25%)	2/5 (40%)	0.6
	PSA50	0/12 (0%)	2/5 (40%)	0.07

Table 3. Best PSA response by treatment and HR status.

PSA50 is 50% decrease in PSA relative to baseline. PSA30 is 30% decrease in PSA relative to baseline. P-values from Fisher's exact test.

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The retrospective nature of this study provided its own set of challenges. NGS was performed at variable times during clinical courses, so HR repair gene mutation status may have been unknown at the time of treatment in many patients. While some data suggests that HR repair gene mutations are typically early (i.e. truncal) genomic events, we cannot rule out the possibility that some patient had their HR gene mutational status misclassified [38]. Additionally, when assessing PFS endpoints, we did not require confirmation of PSA or clinical/radiographic progression. No central review was performed, and there were no preset criteria for the evaluation of progression events. PFS outcomes were also dependent on the intervals at which clinical markers for progression were assessed. Whereas a prospective trial could standardize the frequency of clinical evaluations across all patients, ours were entirely provider dependent.

A) PSA progressio	n-free survival (pPFS)				
Treatment HR Status		N	Median pPFS (95% CI)	P-value	
Abiraterone	No HR	29	6.0 (5.4, 10.6)	0.4	
	HR	HR 19 6.1 (3.9, 9.0)			
Enzalutamide	No HR	29	4.4 (3.0, 10.3)	0.15	
	HR	24	6.5 (4.0, 24.0)		
Docetaxel	No HR	25	5.1 (3.7, NA)	0.2	
	HR	11	4.9 (3.2, NA)		
Cabazitaxel	No HR	12	3.2 (2.8, NA)	0.7	
	HR	5	2.8 (2.8, NA)		
(B) Clinical or rad	iographic progression-	free survival (crPl	FS)		
Treatment	HR Status	N	Median crPFS (95% CI)	P-value	
Abiraterone	No HR	28	8.0 (5.8, 13.5)	0.6	

19

29

24

25

11

12

5

14.2 (8.2, NA)

9.3 (6.4, 19.3)

10.2 (6.2, 19.5)

5.7 (4.2, NA)

5.6 (3.9, NA)

4.2 (2.8, NA)

7.2 (2.3, NA)

0.5

0.7

0.6

Table 4. Median (A) PSA progression-free survival and (B) clinical or radiographic progression-free survival by treatment and HR status.

P-values from log-rank tests. NA = not achieved.

HR

HR

HR

HR

No HR

No HR

No HR

Enzalutamide

Docetaxel

Cabazitaxel

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Another potential constraint was our exclusion of treatments lasting less than 60 days. Consistent with PCWG3 guidelines, our intent was to only evaluate patients who had received a sufficient duration of treatment to determine if they would achieve any therapeutic response. In this regard, patients who may have been taken off therapy prematurely for rising PSA values or symptoms consistent with clinical progression would not obscure the remainder of the data set. However, if there happened to be an association between HR repair gene status and frequency of early-onset progression events, it could be indicative of a bias that was manufactured through our inclusion criteria.

Future directions should include an effort to more definitively describe treatment responses in mCRPC patients with HR repair gene mutations using larger, prospective trials with standardized clinical outcomes. In addition, more granular outcomes data for each specific HR repair gene are needed to determine which are predictive and prognostic biomarkers.

Conclusion

In our retrospective analysis of patients with mCRPC, HR repair gene mutational status associated with similar PSA response and PFS following treatment with ARSIs and taxane-based chemotherapy. Available data suggests that standard therapies should still be considered for patients with HR repair gene mutations. Additional prospective and larger studies are needed to confirm these findings.

Supporting information

S1 Fig. Waterfall plot of best PSA response by treatment and HR status (BRCA2 or PALB2 vs no HR). Maximum percent relative change from baseline during treatment or after

completing treatment but prior to subsequent treatment. Maximum percent change greater than 100% is truncated at 100%. Dashed horizontal lines show 50% decrease. (TIF)

S2 Fig. Kaplan-Meier curves of (A) PSA progression-free survival and (B) clinical or radiographic progression-free survival by treatment and HR status (BRCA2 or PALB2 vs no HR). (TIFF)

S1 Table. Specific genetic variants of every patient included in the HR cohort. "WEC" denotes the Whole Exome Sequencing assay. (PDF)

S2 Table. Baseline lab comparisons at start of abiraterone based on HR status. P-values for continuous measures from Kruskal-Wallis rank sum test and for categorical measures from Fisher's exact test.

(PDF)

S3 Table. Baseline lab comparisons at start of enzalutamide based on HR status. P-values for continuous measures from Kruskal-Wallis rank sum test and for categorical measures from Fisher's exact test. (PDF)

S4 Table. Baseline lab comparisons at start of docetaxel based on HR status. P-values for continuous measures from Kruskal-Wallis rank sum test and for categorical measures from Fisher's exact test.

(PDF)

S5 Table. Baseline lab comparisons at start of cabazitaxel based on HR status. P-values for continuous measures from Kruskal-Wallis test rank sum and for categorical measures from Fisher's exact test.

(PDF)

S6 Table. Predicted probabilities of (A) PSA30 and (B) PSA50 adjusted for prior treatment with similar therapy.

(PDF)

S7 Table. Best PSA response by treatment and HR status (BRCA2 or PALB2 vs no HR). PSA50 is 50% decrease in PSA relative to baseline. PSA30 is 30% decrease in PSA relative to baseline. P-values from Fisher's exact test. (PDF)

S8 Table. Median (A) PSA progression-free survival and (B) clinical or radiographic progression-free survival by treatment and HR status (BRCA2 or PALB2 vs no HR). P-values from log-rank tests. NA = not achieved. (PDF)

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A Phase 1b/2a Study of the Pan-BET Bromodomain Inhibitor ZEN-3694 in Combination with Enzalutamide in Patients with Metastatic Castration Resistant Prostate Cancer

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Abstract

Purpose—ZEN-3694 is a bromodomain extra-terminal inhibitor (BETi) with activity in androgen signaling inhibitor (ASI)-resistant models. The safety and efficacy of ZEN-3694 plus enzalutamide (ENZ) was evaluated in a phase 1b/2a study in metastatic castration-resistant prostate cancer (mCRPC).

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RA has received consulting income from Janssen Biotech, Merck, AstraZeneca; research funding to his institution from Zenith Epigenetics; honoraria for speaker's fee from Dendreon and Clovis Oncology

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Experimental Design—Patients had progressive mCRPC with prior resistance to abiraterone (ABI) and/or ENZ. 3+3 dose escalation was followed by dose expansion in parallel cohorts (ZEN-3694 at 48 and 96 mg orally once daily, respectively).

Results—Seventy-five patients were enrolled (N = 26 and 14 in Dose Expansion at low- and high-dose ZEN-3694, respectively). Thirty (40.0%) patients were resistant to ABI, thirty-four (45.3%) to ENZ, and eleven (14.7%) to both. ZEN-3694 dosing ranged from 36 mg to 144 mg daily without reaching an MTD. Fourteen patients (18.7%) experienced grade 3 toxicities, including three patients with Grade 3 thrombocytopenia (4%). An exposure-dependent decrease in whole blood RNA expression of BETi targets was observed (up to 4-fold mean difference at 4 hours post-ZEN-3694 dose; p 0.0001). The median radiographic progression-free survival (rPFS) was 9.0 months (95% CI: 4.6, 12.9) and composite median radiographic or clinical progression-free survival was 5.5 months (95% CI: 4.0, 7.8). Median duration of treatment was 3.5 months (range 0 - 34.7+). Lower AR transcriptional activity in baseline tumor biopsies was associated with longer rPFS (median rPFS 10.4 vs. 4.3 months).

Conclusions—ZEN-3694 plus ENZ demonstrated acceptable tolerability and potential efficacy in patients with ASI-resistant mCRPC. Further prospective study is warranted including in mCRPC harboring low AR transcriptional activity.

Introduction

Prostate cancer is the most common malignancy and second leading cause of death among men in the United States.¹ Androgen signaling blockade with either androgen receptor (AR) antagonism or CYP17 inhibition improves long-term survival in both metastatic castration-resistant prostate cancer (mCRPC) and metastatic castration-sensitive disease.^{2–5} However treatment resistance is universal, and cross resistance between AR antagonists and CYP17 inhibitors limits the clinical utility of these agents when used sequentially.^{6–10}

Multiple mechanisms of therapeutic resistance to AR pathway inhibitors have been described, including amplification of the *AR* gene and its enhancers, up-regulation of intratumoral androgen synthesis, generation of ligand-independent AR splice variants, activation of alternative oncogenic signaling pathways including MYC, trans-differentiation to an ARindependent, neuroendocrine phenotype, and co-option of alternative steroid hormone receptors including the glucocorticoid receptor (GR).^{11–16} A broad therapeutic approach capable of affecting expression/signaling of multiple pathways may provide a means to reverse resistance and restore sensitivity to AR targeting therapy.

Proteins of the BET bromodomain family are epigenetic readers that bind to acetylated histones through their bromodomains to affect gene transcription.¹⁷ They preferentially localize at sites of enhancers of various oncogenes to promote tumorigenesis and progression. ZEN-3694 is an orally bioavailable, second generation, potent pan-BET bromodomain inhibitor that leads to down-regulation of expression of AR-signaling, AR splice variants, MYC, GR, and other oncogenes in multiple CRPC prostate cancer models, and has significant *in vivo* activity as single agents, with evidence of synergy when combined with enzalutamide.¹⁸

We conducted a first-in-human phase 1b/2 dose escalation/expansion study of ZEN-3694 in combination with enzalutamide in patients with mCRPC and prior progression on one or more androgen signaling inhibitor.

METHODS

Patient Population

Patients had histologically confirmed mCRPC with progression at study entry by Prostate Cancer Working Group 2 (PCWG2) criteria.¹⁹ Patients were required to have progression on prior abiraterone and/or enzalutamide prior to study entry, no prior docetaxel for the treatment of mCRPC, serum testosterone < 50 ng/dL with maintenance of androgen deprivation therapy during study treatment, ECOG performance status of 0 or 1, adequate organ function including absolute neutrophil count > 1.5×10^{9} /L, platelet count > 100,000, total bilirubin < $1.5 \times$ ULN, creatinine clearance > 60 ml/min. Patients with uncontrolled hypertension or NYHA class II or higher congestive heart failure were excluded.

Study approval was obtained from the ethics committees at the participating institutions and regulatory authorities. All patients gave written informed consent. The study followed the Declaration of Helsinki and good clinical practice guidelines (NCT02711956).

Study Design and Treatment Schedule

This was a phase 1b/2, multicenter, open-label, combination dose-escalation study of ZEN-3694 in combination with the standard dose of enzalutamide 160 mg daily. Lead-in treatment period with enzalutamide monotherapy (day -14 to day -1) was required in subjects not already receiving enzalutamide at the time of study enrollment. Patients continued treatment until radiographic progression by PCWG2 criteria, unequivocal clinical progression or unacceptable toxicity. PSA progression alone was not used as a criterion for treatment discontinuation.

The starting dose of ZEN-3694 was 36 mg orally once daily. A 3+3 dose-escalation schema was utilized up to a maximum administered dose of 144 mg daily. Dose expansion was subsequently performed in two cohorts in parallel: 1) Low dose: ZEN-3694 at 48 mg daily (N = 14), and 2) High dose ZEN-3694 96 mg daily (N = 26).

A formal interim analysis was not planned, however interim data were reviewed on an ongoing basis. The final planned analyses were performed after 75 patients were enrolled and the database was locked on 06-Feb-2020.

The primary study endpoint was safety and the recommended phase 2 dose of ZEN-3694 in combination with enzalutamide. Secondary endpoints included pharmacokinetic (PK) assessment of ZEN-3694 and enzalutamide, PSA50 response (50% decline in PSA from baseline confirmed 4 weeks later) rate, duration of PSA50 response, and radiographic progression-free survival. Soft tissue radiographic progression and responses were assessed according to RECIST v1.1 criteria. Progression of bone metastases was assessed using PCWG2 criteria. Post-hoc analyses were performed to assess composite progression-free survival, defined as first occurrence of radiographic or clinical progression or death, as well

as PSA progression-free survival by PCWG2 criteria. Correlative endpoints included pharmacodynamic assessment of ZEN-3694 in combination with enzalutamide and relationship between tumor genomic/transcriptional profile, protein expression, and clinical variables with clinical outcomes on treatment.

Safety and Efficacy Assessments

Clinical and laboratory assessments were conducted at baseline and weekly during cycles 1 and 2 (28 day cycle length), every 2 weeks in cycle 3, and then every 4 weeks thereafter. Tumor response monitoring was performed using whole body bone scan and cross-sectional imaging of the chest/abdomen/pelvis at baseline and every 2 cycles thereafter. Adverse events were graded using Common Toxicity Criteria version 4.0.

Pharmacodynamic/Exploratory Assessments

Whole blood RNA for assessment of BET inhibitor target gene expression (MYC, IL-8, CCR1, GPR183, HEXIM1, and IL1RN) was collected pre-dose, 2, 4, 6 and 24 hours post-C1D1 dose.²⁰ Baseline and on-treatment metastatic tumor biopsies of bone or soft tissue were obtained whenever feasible, and were evaluated by RNA-seq and immunohistochemistry (IHC) for protein expression of AR. Quality of the FASTQ files was verified by FASTQC2, and reads were aligned on BaseSpace (https:// basespace.illumina.com) using the RNA-Seq alignment App (version 1.1.1) with the default parameters (STAR aligner version 2.5.0b, UCSC hg19 reference genome). Gene expression levels (FPKM) for baseline biopsies were estimated using Cufflinks (version 2.2.1). For the paired biopsies, aligned reads were used as input for DESeq2 (version 1.1.0) to enable pairwise differential gene expression analysis using the default parameters. Gene set enrichment analysis (GSEA) was performed on transcriptional data when available, and previously validated AR, prostate cancer and MYC transcriptional signatures were additionally applied to the transcriptional data.²¹⁻²² For the BETi signature, significant genes (p-value <0.05) that were >2-fold down-regulated upon exposure of 0.5uM I-BET762 for 24 hours in LNCaP prostate cancer cells were selected.²³ Archival tumor tissue was obtained whenever feasible for analysis of whole transcriptome and exome sequencing.

Pharmacokinetic Assessments

Plasma levels of ZEN-3694, the bioactive first-order metabolite ZEN-3791, and enzalutamide were measured pre-dose and up to 24 hours post-dose on days 1 and 15 of cycle. Plasma concentrations were determined using validated liquid chromatography/ tandem mass spectrometry analysis (LC/MS/MS).

RESULTS

Study Population and Patient Disposition

A total of 75 patients were enrolled from December 2016 to April 2019 across 7 investigational sites. Baseline characteristics of the enrolled patients are shown in Table 1. At study entry, 30 (40.0%) of patients had previously experienced disease progression on abiraterone, 34 (45.3%) on enzalutamide, and 11 (14.7%) on both. Twelve (16%) patients experienced prior primary resistance to first-line AR targeted therapy, defined in post-hoc

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fashion as treatment duration of less than six months. Forty-two (56%) patients had evidence of radiographic and/or clinical progression at study entry.

The median duration of treatment was 3.5 months (range 0 - 34.7+). As of date of data cutoff, 7 patients (9%) remain on treatment without progression, with duration of therapy ranging from 15.0+ - 34.7+ months. Forty-eight patients (64%) discontinued for disease progression; nine patients (12%) discontinued for adverse event, and eleven (16%) withdrew from study.

Safety Results

The proportion of patients who experienced Grade 3 treatment-related adverse event was 18.7% (n = 14). The most common grade 3 adverse events (2 patients) included: nausea (n = 3; 4%), thrombocytopenia (n = 3; 4%), anemia (n = 2; 2.7%), fatigue (n = 2; 2.7%), and hypophosphatemia (n = 2; 2.7%). There were no clinically significant bleeding events observed on treatment.

The most commonly reported ZEN003694-related AEs (any grade severity, occurring in 10% of patients, in order of incidence) were: visual symptoms (described as a transitory perception of brighter lights and/or light flashes, with or without visual color tinges, as well as trouble navigating in dim light) (67%), nausea (45%), fatigue (40%), decreased appetite (25%), dysgeusia (20%), thrombocytopenia (15%), and weight decreased (11%) (Table 2). Visual symptoms were Grade 1 in all cases, resolved 60–90 minutes after dosing, were successfully mitigated with implementation of dosing before bedtime, and resulted in no functional consequences upon repeat eye exams throughout study participation.

Dose reductions and/or treatment discontinuation due to adverse events were required in 24/75 (32%) of patients. The percentage of patients requiring dose reduction and/or discontinuation ranged from 10%–35% for doses from 36 mg – 96 mg/day, in contrast to 75% and 100% at ZEN-3694 dose levels of 120 and 144 mg/day, respectively (Supplementary Table 1). The class of adverse events leading to dose reduction and/or discontinuation were related to GI toxicities in 83% of occurrences.

Determination of Maximum Tolerated Dose and Recommended Phase 2 Dose

In the dose escalation, 35 patients were enrolled across dose levels ranging from 36 to 144 mg daily. The maximal tolerated dose was not reached. One patient experienced a doselimiting toxicity at the 96 mg/day dose level (Grade 3 nausea necessitating missing > 25% of scheduled doses in cycle 1). Based on the aggregate of pharmacodynamic data indicating dose exposure-dependent down-regulation of BETi target gene expression with a plateau of effect at doses above 96 mg/day, the high percentage of patients requiring dose interruptions/ reductions at doses above 96 mg/day, and a comparable PK/PD effect with pre-clinical models treated at efficacious doses, 96 mg/day was chosen as the recommended phase 2 dose of ZEN-3694 for Dose Expansion (N = 26). An additional Dose Expansion cohort of 48 mg/day (N = 14) was also enrolled, to better characterize the exposure-effect relationship.

Pharmacokinetic Analyses

The AUC₀₋₂₄ and the C_{max} of combined ZEN-3694 (parent compound) + ZEN-3791 (active metabolite), on Day 1 and Day 15 of cycle 1, are shown in Figure 1A and Figure 1B, respectively. Less than dose proportional increase in exposure was observed at doses higher than 96 mg daily. The estimated T_{max} and half-life of ZEN-3694+ZEN-3791 were 2h and 5–6h, respectively. The ratio of ZEN-3791 metabolite to parent compound ZEN-3694 was increased on Day 15 compared to Day 1, likely related to enzalutamide-mediated induction of CYP3A4 metabolism (Figure 1C). The observed plasma concentrations of ZEN-3694 + ZEN-3791 were similar to ZEN-3694 monotherapy pharmacokinetics previously reported.²⁴ Likewise, there was no significant impact of ZEN-3694 on enzalutamide and desmethyl enzalutamide concentrations (Figure 1D).

Pharmacodynamic Analyses

Pre- and up to 24 hour post-dose whole blood RNA analyses were available from 69 patients enrolled on study. There was a dose-dependent 2–4 fold decrease in the whole blood mRNA levels of the BET inhibitor target genes *MYC*, *IL-8*, *CCR1*, GPR183, and *IL1RN* (Figure 2A) upon treatment with ZEN-3694, which was sustained for at least 8 hours. Decrease in expression of BET inhibitor target genes appeared to plateau at ZEN-3694 dose levels 96 mg. There was a direct correlation between cumulative exposure to ZEN-3694 + ZEN-3791 (AUC₀₋₂ for *MYC* and *GPR183*, and AUC₀₋₄ for *CCR1*, *IL1RN*, and *IL-8*) with down-regulation of whole blood mRNA levels of the BET inhibitor target genes (R² ranging from 0.20 to 0.51, p values 0.0001) (Figure 2B).

Four patients had evaluable paired metastatic tumor biopsies obtained at baseline and ontreatment (median duration of treatment eight weeks prior to on-treatment biopsy). Time after the last ZEN-3694 + enzalutamide dosing prior to the biopsy ranged from 3.5 to 24 hours. The limited sample size precluded ability to perform statistical analyses of change in expression by dose level. However, on gene set enrichment analyses looking at changes between on-treatment versus pre-treatment samples, there were strong indications of downregulation of expression of MYC and AR-signaling on-treatment compared to baseline biopsies were detected, as well as down-regulation of BET-dependent genes previously identified in LnCaP cells treated with the I-BET762 BET inhibitor²³ (Figure 2C).

Efficacy Analyses

The median radiographic progression-free survival (rPFS) in the overall cohort was 9.0 months (95% CI: 4.6, 12.9), with 7.8 months for patients that had progressed on abiraterone (95% CI: 4.9, 10.6) and 10.1 months for patients that had progressed on enzalutamide (95% CI: 4.4, 12.9) (Figure 3A). Composite median radiographic or clinical progression-free survival was 5.5 months (95% CI: 4.0, 7.8) in the overall cohort, and 5.5 months (95% CI: 4.4, 7.8) and 5.1 months (95% CI: 3.2, 10.1) in those with prior progression on abiraterone and enzalutamide, respectively (Figure 3B). Thirteen (17%) and four (5%) patients remained on treatment for greater than 12 and 24 months without progression, respectively (Figure 3C). In patients with radiographic progression at the time of study entry, the median rPFS was 7.8 months (95% CI: 4.4, 10.6) (Figure 3D) and composite PFS was 4.8 months (95% CI: 3.5, 7.7). An analysis of the subset of patients with primary resistance to prior first-line

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AR targeted therapy (N = 12), defined by progression within 6 months of treatment initiation, demonstrated an on-treatment median rPFS of 10.6 months (95% CI (7.5, not reached) (Figure 3E). Using a more stringent cut-off of primary resistance of progression within 16 weeks of prior first-line AR targeted therapy (N = 5) likewise demonstrated prolonged median rPFS (median rPFS 22.4 months, 95% CI: 7.8, not reached) and composite PFS (median PFS 10.6 months, 95% CI: 4.0, not reached) in this subset of patients (Supplementary Figure 1A and 1B).

Of the four exceptional responders who remained on treatment for greater than 24 months duration, three had radiographic progression at study entry, two had progressed on prior enzalutamide, and one of the four patients experienced an objective radiographic response on enzalutamide + ZEN-3694 (Supplementary Table 2).

Six patients (8%) experienced a greater than fifty percent decline from baseline in serum PSA by PCWG2 criteria (PSA50 response), including two patients with prior progression on enzalutamide monotherapy. All PSA responses were confirmed on repeat measurement. Four patients (5.3%) experienced a greater than ninety percent decline in serum PSA from baseline on study treatment. PSA50 responses were sustained in the majority of cases with median duration of PSA50 response of 21.1 months (95% CI (19.0, 23.2). The median PSA progression-free survival was 3.2 months (95% CI: 3.2, 5.1) in the overall study cohort and 3.2 months (95% CI: 2.8, 6.4) in those with PSA-only progression at study entry. There were no substantial differences with respect to rPFS, composite PFS, or PSA PFS noted between 48- and 96 mg- Dose Expansion cohorts.

Additionally, in a subset of patients (N = 21), there was a transient increase of > 2 ng/mL and 25% above baseline in serum PSA within the first 12 weeks of treatment with subsequent plateau in serum PSA level (Supplementary Figure 2A). Patients with transient PSA increase as defined above appeared to derive sustained clinical benefit with median rPFS of 10.1 months (95% CI: 5.6, 11.7). In contrast, patients whose serum PSA consistently rose beyond the 12 week time point (N = 21) experienced a median rPFS of 7.2 months (95% CI: 3.9, 9.0) (Supplementary Figure 2B).

Predictors of Prolonged Clinical Benefit with ZEN-3694 + Enzalutamide

Exploratory analyses were performed with available genomic and transcriptional data from baseline tumor biopsies to evaluate association with subsequent time to progression on treatment. Interestingly, patients whose baseline metastatic tumor biopsies (N = 13) harbored lower canonical AR transcriptional activity, as assessed by 5-gene score²⁵ as well as the HALLMARK_ANDROGEN_RESPONSE signature, experienced a longer median time to progression (TTP) (median TTP 19 vs. 45 weeks) (Figure 4A and B). In support of the notion that tumors with lower canonical AR activity might be more responsive to BET inhibition, we observed a trend towards prolonged time to progression amongst patients meeting clinical criteria for aggressive variant prostate cancer (e.g. low serum PSA < 10 ng/mL with concomitant high disease burden (visceral metastases and/or > 10 bone metastases)²⁶. The median TTP in patients with aggressive variant disease was 11.6 months (95% CI: 7.2, 12.8) vs. 5.5 months (95% CI: 2.3, 10.6, p = 0.24) in those without aggressive variant clinical features at baseline (Figure 4C).

DISCUSSION

Our results demonstrate that the pan-BET bromodomain inhibitor ZEN-3694 has acceptable tolerability and encouraging preliminary efficacy data in combination with enzalutamide in patients with mCRPC. The median radiographic progression-free survival in the overall cohort was 9 months, and over 10 months in those with prior progression on enzalutamide monotherapy. ZEN-3694 + enzalutamide treatment led to a 2–4 fold reduction in the expression of BET target genes including *MYC*, which was sustained throughout the 24 hour dosing interval. Based on the aggregate of the safety, efficacy, and evidence of robust down-regulation of expression of BET-dependent target genes, ZEN-3694 96 mg daily has been selected as the recommended phase 2 dose to move forward in further clinical development in combination with enzalutamide. The clinical and pharmacodynamic data provide clinical evidence that BET inhibition may be able to abrogate resistance mechanisms and re-sensitize patients to AR-signaling inhibitors.

The prolonged PFS observed in the current study in relevant subsets, including those with radiographic progression at study entry, primary resistance to prior AR targeted therapy, as well as those with prior progression on enzalutamide monotherapy, is consistent with an additive or potentially synergistic interaction between enzalutamide and ZEN-3694. The baseline characteristics of the study cohort are representative of other studies in the post-androgen receptor signaling inhibitor mCRPC setting, including nearly one-third of patients with intermediate or high risk disease by Halabi prognostic model²⁷, and a quarter of which who required opioid analgesics at study entry. These features argue against the possibility of enrichment of better than average risk group contributing significantly to the prolonged PFS observed on treatment. Taken together, the data support a randomized study to evaluate for the magnitude of benefit of ZEN-3694 in combination with enzalutamide.

With the caveat of cross-trial comparisons, the median PFS observed with ZEN-3694 + enzalutamide in the current study compares favorably to outcomes observed with sequential AR targeting in mCRPC with abiraterone followed by enzalutamide, or vice versa, in prior studies. In the prospective SWITCH phase 2 crossover study, the median PFS of second line enzalutamide and abiraterone were 3.5 and 1.7 months, respectively.⁶ Similarly, median progression-free survival with second-line AR targeting therapy have been less than 8 months in most retrospective series.⁹ Caution should be applied to over-interpretation of these cross-trial comparisons, and a randomized trial will be necessary to assess the individual contribution of ZEN-3694 added to enzalutamide in mCRPC.

The PSA50 response rate with the combination of ZEN-3694 plus enzalutamide was less than 10% in the study, and median PSA progression-free survival was less than 4 months. Though this may reflect lack of additive benefit of ZEN-3694 in combination with enzalutamide, decline in serum PSA and PSA progression-free survival may not be the best metrics to gauge efficacy of BET bromodomain inhibitors including ZEN-3694. In fact, a subset of patients experienced transient early rises in serum PSA by week 8 of treatment, which were associated with longer time to progression. In addition, tumors harboring lower AR activity at baseline appeared to derive more clinical benefit from treatment. Finally, those with low serum PSA in relation to metastatic disease burden, a clinical profile

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consistent with small cell/neuroendocrine prostate cancer, may also have longer radiographic progression-free survival compared to those with higher baseline serum PSA levels. Though these observations are hypothesis-generating and require prospective validation, it raises the intriguing possibility that BET bromodomain inhibitors may restore dependency on AR-signaling in tumors that are less reliant on AR prior to BETi or that BETi is blocking important AR-independent survival mechanisms, such as MYC, which has been shown to be critical for BETi effects in CRPC.^{13,28,29} AR-independent mCRPC is becoming more prevalent with the earlier application of AR-signaling inhibitors, and is associated with shortened survival and unmet need to develop novel therapeutic approaches.³⁰

The acceptable toxicity profile of ZEN-3694 in combination with enzalutamide stands in contrast to the results observed with several other recent BET inhibitors reported in the literature which have been limited by thrombocytopenia and GI toxicities.^{31,32} In the current study, there was substantially less thrombocytopenia observed. Gastrointestinal toxicities were not as prevalent or severe as prior studies and were manageable with early institution of anti-emetics and dose reductions, if necessary. The reasons underlying the potentially more favorable toxicity profile observed in current study, as compared with other BET inhibitors, may relate to patient factors such as excluding prior chemotherapy for mCRPC. Further, it is possible that a pharmacokinetic interaction with ZEN-3694 and enzalutamide may have a more favorable toxicity profile. The differential toxicity compared with other BET inhibitors does not appear to relate to differences in potency, given the robust down-regulation of BETi target genes observed in the current study.

There were several limitations of the study, including the limited number of baseline and ontreatment paired biopsies precluding the ability to identify a consistent predictive biomarker with a high degree of statistical confidence. The non-randomized nature of the dose expansion portion of the study also limits our ability to draw definitive conclusions regarding the potential additive benefit of ZEN-3694, though evidence of contribution is provided by favorable comparison to contemporary controls from other studies as outlined above. AR-V7 splice variant status in circulating tumor cells, a validated resistance mechanism to AR targeted therapy that may be down-regulated with BETi treatment, was not reliably captured in this study in a sufficient number of patients to permit evaluation. Finally, there did not appear to be a relationship between dose level and efficacy outcomes, potentially related to fairly broad inter-patient variability in ZEN-3694 exposure, limited sample size, and limited single agent activity of ZEN-3694.

With the shift in application of potent AR targeted therapy in earlier castration-sensitive settings, there is an increasing medical need to develop therapies that reverse therapeutic resistance and restore dependency on AR signaling. The preliminary data provided by the Phase 1b/2 study of ZEN-3694 plus enzalutamide provides strong justification to further investigate in a prospective, randomized study.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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Statement of Translational Relevance

BET bromodomain inhibitors (BETi) demonstrate in vivo activity in enzalutamideresistant prostate cancer models via down-regulation of bypass signaling pathways including MYC. Clinical translation of BETi as a therapeutic strategy in metastatic castration resistant prostate cancer (mCRPC) has heretofore been limited by significant toxicity including risk of thrombocytopenia. In the current phase 1a/2b study of the pan-BETi ZEN-3694 in combination with enzalutamide in 75 patients with abiraterone and/or enzalutamide-resistant mCRPC, the combination was well tolerated without reaching a maximally tolerated dose. Less than 5% of patients experienced a grade 3 thrombocytopenia. Robust, dose-dependent, and sustained down-regulation of expression of BET inhibitor target genes including MYC was observed using a whole blood RNA assay. Encouraging efficacy was observed including a median radiographic progressionfree survival of over 10 months in those with prior progression on enzalutamide monotherapy. Clinical benefit was particularly pronounced in high-risk subgroups including those with an aggressive variant clinical phenotype as well as those with lower androgen receptor (AR) transcriptional activity in baseline tumor biopsies. A randomized study is planned with ZEN-3694 at the recommended phase 2 dose of 96 mg orally once daily in combination with enzalutamide in mCRPC with prior progression on enzalutamide or abiraterone.

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Figure 1. Pharmacokinetic analyses.

A and B. Area-under-the-curve (AUC) from 0 to 24 hours (AUC₀₋₂₄) and maximum serum concentration, respectively, of ZEN-3694 + ZEN-3791 (first generation active metabolite) serum concentration on day 1 and day 15 of cycle 1 (red triangles). Overlaid AUC₀₋₂₄ data from the monotherapy trial of ZEN-3694²³ are shown for dose levels 48 and 72 mg daily (black circles). C. Ratio of ZEN-3791 (first generation active metabolite) vs. ZEN-3694 (parent compound) from the prior monotherapy trial²³ and in combination with enzalutamide on day 1 and day 15 of cycle 1. D. Steady-state serum concentration of enzalutamide (day -14 to day -1), by ZEN-3694 dose level.

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Figure 2. Pharmacodynamic assessments.

A. Fold-change from baseline in whole blood RNA expression of BET inhibitor target genes *CCR1, IL1RN, IL-8, MYC*, and *GPR183* by ZEN-3694 dose level. **B.** Correlation between fold change from baseline in whole blood RNA expression of BET inhibitor target genes with AUC_{0-24} of ZEN-3694 + ZEN-3791 indicates strong PK-PD relationship. **C.** Gene set enrichment analysis of change from baseline in gene expression by RNA-Seq in paired metastatic tumor biopsies. Down-regulation of MYC signaling pathway is observed in ontreatment versus baseline tumor biopsy.

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Figure 3. Radiographic progression-free survival and duration of treatment.

A. Kaplan-Meier curve demonstrating radiographic progression-free survival by PCWG2 criteria in all evaluable study participants (black curve), patients with prior enzalutamide progression (blue curve), or prior abiraterone progression (green curve). **B.** Kaplan-Meier curve demonstrating composite progression-free survival (time to first clinical or radiographic progression) in **C.** Swimmer's plot showing duration of treatment, with color labels by ZEN-3694 dose level (hashed line = treatment ongoing). **D and E.** Kaplan-Meier curves showing radiographic progression-free survival in subsets of patients with radiographic progression or primary resistance to prior androgen signaling inhibitor, respectively.

A.





Figure 4. AR signaling score and clinical outcomes

A. Lower AR activity level in baseline tumor biopsies is correlated with longer time on study (R^2 =0.38) using either the 5-gene AR score (left) or the

HALLMARK_ANDROGEN_RESPONSE (right) signatures. For the hallmark signature, baseline gene expression of biopsies from patients with radiographic progression prior to 24 weeks vs. greater than 24 weeks were compared (FDR = 0.04). **B.** Kaplan-Meier curve showing significant increase in time to median radiographic progression free survival in patients with lower AR signaling compared to patients with higher AR signaling score (median rPFS 10.4 months in tumors with low AR score vs. 4.3 months in tumors with high AR activity). **C.** Patients with high tumor burden and lower baseline PSA levels (< 10 ng/mL) (blue curve) demonstrate longer PFS than patients with higher baseline PSA (> 10 ng/mL) levels.

Table 1:

Baseline Characteristics

	Study Cohort (n=75)
Median age (range), years	70 (47–89)
ECOG score	
0	42 (56%)
1	33 (44%)
Opioid analgesic use	18 (24%)
Visceral metastases at study entry (%)	21 (28%)
Median PSA, ng/mL (range)	26.99 (0.15 – 1701.8)
Median ALP, U/L (range)	82 (33 – 487)
Median LDH, U/L (range)	188 (98 - 543)
Median Hemoglobin, g/dL (range)	13.2 (6.4 – 20.2)
Halabi risk category ²⁴	
Low	50 (67)
Intermediate	16 (21)
High	8 (11)
Unknown	1 (1)
Prior number of systemic cancer treatments (range)	3 (1–7)
Prior resistance to AR targeted therapy (%)	
Abiraterone	30 (40)
Enzalutamide	34 (45)
Both	11 (15)
Duration of prior AR targeted therapy (range), months	14.3 (1.0–58.3)
Reason for prior abiraterone or enzalutamide discontinuation	
Radiographic progression	8 (11%)
Radiographic and PSA progression	31 (41%)
Clinical and PSA progression	3 (4%)
PSA progression	33 (44%)
Clinical progression	0

ALP, alkaline phosphatase; AR, androgen receptor; ECOG, Eastern Cooperative Oncology Group; LDH, lactate dehydrogenase; PSA, prostate-specific antigen.

For data recorded in the clinical database as of the data cutoff date of 07 January 2020.

Table 2.

Summary of All Grades Treatment-related Adverse Events by Dose Level of ZEN-3694

	36mg QD n=4	48 mg QD n=21	6Dmg QD n=6	72mg QD n=6	96mg QD n=31	120mg QD N=4	144mg QD N=3	TOTAL n=75 (%)
Blood creatinine Increased			2		3			5 (6.7)
Constipation		1			3			4 (5.3)
Decreased Appetite		2	2	1	10	3	2	20 (26.7)
Diarrhea				1	5			6(8)
Dizziness				1	3			4 (5.3)
Dysgeusia		2	0	0	10	1	3	16 (21.3)
Dyspepsia		1			2			3(4)
Fatigue	1	8	1	2	13	3	1	29 (38.7)
Nasal congestion					3			3(4)
Nausea		7	2	3	17	3	2	34 (45.3)
Photopsia		1			3			4 (5.3)
Photosensitivity		2			3			5 (6.7)
Rash					3			3(4)
Rash maculopapular		3			1		1	5 (6.7)
Taste disorder			1	1	3			5 (6.7)
Thrombocytopenia		1	1	2	6		1	11 (14.7)
Vision blurred					2	1		3(4)
Visual symptoms	3	12	4	6	17	4	2	48 (64)
Vomiting		1			3	1		5 (6.7)
Weight loss & Abnormal WL	1			1	3	1	2	8(10.7)

 A Visual symptoms defined as a transitory perception of bright lights and/or light flashes with or without visual color tinges
Check for updates

Practical Considerations and Challenges for Germline Genetic Testing in Patients With Prostate Cancer: Recommendations From the Germline Genetics Working Group of the PCCTC

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Germline genetic testing is now routinely recommended for patients with prostate cancer (PCa) because of expanded guidelines and options for targeted treatments. However, integrating genetic testing into oncology and urology clinical workflows remains a challenge because of the increased number of patients with PCa requiring testing and the limited access to genetics providers. This suggests a critical unmet need for genetic services outside of historical models. This review addresses current guidelines, considerations, and challenges for PCa genetic testing and offers a practical guide for genetic counseling and testing delivery, with solutions to help address potential barriers and challenges for both providers and patients. As genetic and genomic testing become integral to PCa care, developing standardized systems for implementation in the clinic is essential for delivering precision oncology to patients with PCa and realizing the full scope and impact of genetic testing.

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INTRODUCTION

Genomics is rapidly pushing oncology closer to an actualized version of precision medicine.^{1,2} In the era of poly (ADP-ribose) polymerase inhibition and immunotherapy, genetic testing may yield information that will affect therapeutic choices, in addition to informing the patient about personal and familial risk.³⁻⁵ Multiple guidelines now include germline genetic testing for men with prostate cancer (PCa), although incorporating testing into clinical workflows remains a challenge.^{5,6} This article addresses (1) current guidelines for germline testing, (2) key aspects of testing and counseling, (3) a road map for genetic testing and possible solutions, and (5) benefits and limitations of testing.

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Germline Genetic Counseling for Men With PCa

Since the landmark article by Pritchard et al⁷ that described a relatively high prevalence of germline mutations in DNA repair genes in men with metastatic PCa, other groups have reported the prevalence of germline mutations in PCa ranging between 7.5% and 19%, with *BRCA2* being the highest overall contributor.⁸⁻¹¹ Consequently, several groups issued recommendations for germline testing (Table 1), which place significant

demands on clinical workflows and resources for genetic counseling. Genetic counselors (GCs) are trained to assess family histories for genetic risk, provide pretest and post-test counseling, order appropriate testing, and interpret test results. Unfortunately, access to genetic providers is limited, with the majority of the small workforce usually centered in urban areas and academic institutions.^{12,13} In 2016, the Genetic Counselor Workforce Working Group estimated a growth of 72% in the workforce between 2017 and 2026, with demand not expected to meet population equilibrium until 2024-2030.14 This limited access may necessitate other health care providers, including oncologists, urologists, and primary care physicians, to absorb some responsibility for genetic testing. However, these providers may be insufficiently trained in genetics, resulting in inappropriate testing and misinformation.¹⁵⁻¹⁷

The increased number of men with PCa to be tested and the scarcity of GCs suggest a critical unmet need for expanded genetic services through novel approaches outside of historic delivery models.¹⁸ Evolving service models that incorporate phone and video telemedicine can be particularly useful when geography or public health crises, such as COVID-19, make in-person visits challenging.^{19,20} Hybrid service models





that divide responsibilities between physicians and GCs are also options.²¹ Collaboration between GCs and clinicians is critical to determine which approach best suits a practice, because there is no one-size-fits-all solution.

Delivery of Germline Testing and Counseling

Initiating genetic testing. One of the greatest hurdles is ensuring that appropriate patients are systematically identified for testing. Developing a plan to consistently screen and identify patients based on current guidelines is necessary (Table 1). Assigning screening to a team member or using patient-completed family history questionnaires can facilitate referral and testing processes. Automated electronic medical record (EMR) features can trigger genetic counseling referrals or alert the clinical team based on a diagnosis code for metastatic PCa or family history/pedigree functionality.

After patients are identified, several options for counseling and testing are available:

- Referral to a geneticist or GC for in-person, telephonebased, or telemedicine counseling services in response to manual referral or automated EMR triggers.
- 2. Treating clinicians perform pretest consent and order germline genetic testing directly: If genetic counseling services are unavailable, testing is urgent, or workflow supports providers initiating testing, treating providers can perform pretest education, obtain informed consent, and order genetic testing.²¹ Providers should consider any clinical, psychosocial, and financial issues when determining whether to pursue testing within their practice or refer to a remote/telehealth genetic service if they do not have access within the practice.
- 3. Patient-initiated testing (PIT) platforms: Some commercial genetic testing laboratories, such as Color and Invitae, offer clinical-grade testing that can be initiated by the patient. This process may involve a pretest clinician review and the option for post-test genetic counseling. However, there remain concerns about guidance on test selection, limitations in genetic counseling, lack of follow-up regarding future reclassification of variants, potential for misinterpretation of results, and propagation of misinformation within families. Furthermore, PIT may not include genes important to a patient's personal or family history, potentially creating a false sense of reassurance if testing is negative. Given this, provider-initiated testing is preferred.
- 4. Direct-to-consumer (DTC) testing platforms: DTC genetic testing has become increasingly popular, likely because of easy access and no medical provider oversight. DTC testing is not comprehensive and should not be considered a substitute for clinical-grade testing. Although 23&Me has Food and Drug Administration approval to report on the three known Ashkenazi Jewish BRCA1/2 founder variants, the National Comprehensive Cancer Network (NCCN)

cautions that any results should be confirmed with a clinical-grade test.²² Providers should be skeptical of any raw data findings from secondary companies, such as Promethease, which are prone to false positives and false negatives.²³

Family cancer history intake. Although all patients with high-risk localized or metastatic PCa should undergo germline genetic testing regardless of family history, accurately evaluating a patient's personal and family history is essential to determine whether patients need a broader germline panel. Furthermore, gathering a family history can help inform personal and family screening recommendations in the event of negative testing. Cancer counseling sessions include a three- to four-generation pedigree with information on maternal and paternal relatives with cancer, age of diagnosis, age/cause of death, and any prior genetic testing.^{22,24} For relatives with PCa, the Gleason grade, metastatic status, and/or cause of death can be useful. Information about ancestry (eg, Ashkenazi Jewish) and consanguinity should be noted. Family history questionnaires can be completed in the clinic or electronically.

Complete family histories ensure that the most informative, cost-effective testing is performed. Although the presence of other cancer types in a family history may be explained by a mutation in a PCa predisposition gene, providers should consider expanded testing for genes related to the observed cancers in a family history when necessary. For instance, hereditary pancreatic cancer and PCa typically occur in the setting of a pathogenic *BRCA2* variant. However, it may be reasonable to include other genes associated with pancreatic cancer, such as *CDKN2A* and *CDK4*.

Somatic next-generation sequencing. Somatic next-generation sequencing tumor testing is increasingly used to guide treatment decision making and can be performed in parallel with germline testing. In addition to detecting tumor-specific mutations, it can sometimes identify potential germline mutations. Most somatic testing platforms are not validated to distinguish germline from somatic-only mutations, even if paired testing with a blood or saliva sample is performed. Thus, a referral to genetics is recommended to determine whether confirmatory or more comprehensive testing is warranted. Providers should consider the variant allele frequency, actionability of the gene, classification of the variant, and tumor type when reviewing somatic variants for possible germline origin.²⁵

Pretest education and informed consent. Pretest education and informed consent discussions should review the purpose of testing; general information about included genes; possible test results (Table 2); medical management implications; review of possible benefits, risks, and limitations (Table 3); and the voluntary nature of testing.^{24,26} Several major medical societies have also published detailed guidelines reviewing the components of pretest counseling and informed consent to help clinicians.²⁴ Clinical teams

TABLE 1. Summary of the Current PCa Genetic Testing Guidelines

Organization	Source	Guidelines	Genes	
National Comprehensive Cancer Network	Genetic/familial high-risk assessment: breast, ovarian, and pancreatic version 1.2020 ²²	Testing is clinically indicated in the follow scenarios:	ATM BARD1ª BRCA1	
	Hereditary cancer testing criteria	 Individuals with any blood relative with a known pathogenic/likely pathogenic variant in a cancer susceptibility gene 	BRCA2 BRIP1	
		 Individuals meet the criteria below but with previous limited testing (eg, single gene and/or absent deletion duplication analysis) interested in pursuing multigene testing 	CDH1 ⁼ CDKN2A ^a CHEK2 MSH2	
		3. Personal history of cancer	MLH1	
		Metastatic or intraductal PCa at any age	MSH6 PMS2	
		• High-grade (Gleason score \geq 7) PCa with:	EPCAM	
		o Ashkenazi Jewish ancestry; or	NBN NE 1ª	
		$o \ge 1$ close relative with breast cancer at age ≤ 50 years or ovarian, pancreatic, or metastatic or intraductal PCa at any age; or	PALB2 PTE№ RAD51C	
		$o \ge 2$ close relatives with breast or PCa (any grade) at any age	RAD51D	
		 A mutation identified on tumor genomic testing that has clinical implications if also identified in the germline 	STK11ª TP53	
		 To aid in systemic therapy decision making 		
		4. Family history of cancer		
		 An affected or unaffected individual with a first- or second- degree blood relative meeting any of the criteria listed above (except individuals who meet criteria only for systemic therapy decision making) 		
		There is a low probability (< 2.5%) that testing will have findings of documented clinical utility in the following scenarios:		
		 Men diagnosed with localized PCa with Gleason score < 7 and no close relative with breast, ovarian, pancreatic, or PCa 		
National Comprehensive Cancer Network	Prostate cancer, version 1.202044	Germline testing is recommended for patients with PCa and any of the following:	ATM BRCA1	
		High-risk, very-high-risk, regional, or metastatic PCa	BRCA2 CHEK2	
		Ashkenazi Jewish ancestry	HOXB13	
		 Family history of high-risk germline mutations (eg, BRCA1/2, Lynch mutation) 	MLH1 MSH2 MSH6	
		A positive family history of cancer:	PALB2	
		o A strong family history of PCa consists of: brother or father or multiple family members who were diagnosed with PCa (but not clinically localized Grade Group 1) at < 60 years of age or who died from PCa; OR	PMS2 _	
		$o \ge 3$ cancers on same side of family, especially diagnoses \le 50 years of age: bile duct, breast, colorectal, endometrial, gastric, kidney, melanoma, ovarian, pancreatic, prostate (but not clinically localized Grade Group 1), small bowel, or urothelial cancer		
	(conti	inued on following page)		

	TABLE 1.	Summary	of the Current	t PCa Genetic	Testing Guidelines	s (continued)
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Organization	Source	Guidelines	Genes
Expert Panel	Philadelphia Consensus meeting publication, 2017 ⁴⁵	Men meeting any one of the following suggested criteria should undergo genetic counseling and genetic testing:	ATM BRCA1
		 All men with PCa from families meeting established testing or syndromic criteria for the following: 	BRCA2 HOXB13 MSH2
		o HBOC (Consensus: 93%)	MLH1
		o HPC (Consensus: 95%)	PMS2
		o LS (Consensus: 88%)	- MSH0
		 Men with PCa with two or more close blood relatives on the same side of the family with a cancer in the following syndromes: 	-
		 Post-consensus discussion included consideration of age cutoff for this criterion. A specific age cutoff will require additional data, and age at diagnosis is important to inquire about in the genetic counseling session with patients. 	-
		■ HBOC (Consensus: 93%)	_
		■ HPC (Consensus: 86%)	_
		■ LS (Consensus: 86%)	-
		 All men with metastatic castrate-resistant PCa should consider genetic testing (Consensus: 67%). Post-consensus discussion also included consideration of testing men with metastatic, hormone-sensitive PCa to identify germline mutations to inform potential future treatment options and cascade testing in families. Men with tumor sequencing showing mutations in cancer-risk genes should be recommended for germline testing, particularly after factoring in additional personal and family history (Consensus: 77%). 	-
AUA	Clinically localized PCa: AUA/ASTRO/ SUO guideline, 2017 ⁴⁶	The Panel recommends that clinicians take a detailed family history of cancers and give consideration to patient referral for genetic screening and counseling for men with localized high-risk PCa, particularly in the setting of family history of first-degree relatives with cancers of breast, ovary, pancreas, other GI cancers, and lymphoma.	No genes specified for germline testing

Abbreviations: ASTRO, American Society of Therapeutic Radiation and Oncology; AUA, American Urological Association; HBOC, hereditary breast and ovarian cancer syndrome; HPC, hereditary prostate cancer; LS, Lynch syndrome; PCa, prostate cancer; SUO, Society of Urologic Oncology. ^aThese genes are not currently associated with PCa.

should note the requirements for documentation of informed consent, which differ by state and institutional policies.

Test selection and ordering. Many commercial laboratories offer clinical genetic testing for hereditary cancer syndromes. Testing panels range from targeted, guidelines-based panels to comprehensive, pan-cancer panels that

may include preliminary evidence genes. Some major laboratories, such as Ambry Genetics, Invitae, and GeneDx, offer PCa-specific panels that include the following genes: *ATM, BRCA1, BRCA2, CHEK2, HOXB13, MLH1, MSH2, MSH6, NBN, PALB2, PMS2,* and *TP53.* Genetic testing panels are subject to change, and decisions regarding specific genetic tests should be individualized based on

Interpretation	Result	Definition	
Positive Pathogenic An alteration in the DNA that is associated with in		An alteration in the DNA that is associated with increased disease risk.	
	Likely pathogenic	An alteration in the DNA that is likely to be associated with increased disease risk. Meets most but not all criteria to be classified as pathogenic.	
Uncertain	Variant of uncertain significance	An alteration in the DNA that may or may not be disease causing. Insufficient evidence to classify as either pathogenic or benign.	
Negative Likely benign An alteration in but not all c		An alteration in the DNA that is unlikely to be associated with increased disease risk. Meets most but not all criteria to be classified as benign.	
	Benign	An alteration in the DNA that is not associated with increased disease risk.	

 TABLE 2. Possible Genetic Test Results^{47,48}

 Interpretation
 Result

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 TABLE 3.
 Pretest Talking Points Regarding the Benefits and Risks/Limitations of Genetic Testing^{27,49}

 Benefits
 Risks/Limitations

Benefits	Risks/Limitations
May help explain personal cancer history	May increase anxiety and guilt regarding hereditary cancer risk
May help inform prognosis	Potential for uncertain results: 1) Variants of uncertain significance, or 2) Positive results in lesser established genes and those with no management guidelines currently available
May help inform risks for additional cancers	Genetic discrimination risks (life insurance or long-term care insurance)
May help guide treatment decisions	Financial barriers
May help inform cancer risks for family members	

factors such as laboratory reputation and quality, insurance networks, genes offered and customizability of panels, laboratory billing practices, follow-up testing options for family members, turnaround times, and availability of genetic counseling services.

Clinicians should recognize that larger panels increase the probability of detecting variants of uncertain significance (VUS), incidental/secondary findings (pathogenic variants in genes not related to hereditary PCa), and variants associated with syndromes that may be outside of the scope of clinicians treating PCa (Tables 2 and 3). Clinical workflows must ensure that tasks involved with ordering genetic testing include determination of insurance coverage and submission of orders, standardized collection and shipment of samples, and a clear chain of responsibility.

Insurance coverage for germline testing is in flux. Although the cost of genetic testing has decreased, the possible out-of-pocket (OOP) cost for patients can be difficult to discern because of the varying billing policies of laboratories and insurance coverages.²⁷ Although the NCCN hereditary breast and ovarian cancer guidelines (v3.2019) are often the primary source used by payers, including Medicare, to develop coverage policies, most have their own criteria that determine testing coverage. These criteria may not be up to date with current NCCN guidelines, potentially excluding PCa from their criteria completely, and may mandate a consultation with certified GC for approval.

Many, but not all, laboratories work with commercial insurance companies to negotiate coverage into their policies and will provide an estimate of the OOP cost of testing. Not all insurance companies require prior authorization for genetic testing. Laboratory online ordering portals will often indicate whether provider-initiated insurance prior authorization is needed. Typically, all components of the billing process, including submission of insurance prior authorization, are handled by the laboratory. Several commercial laboratories offer a patient-pay or fixed OOP cost, often \$250 or lower, making testing more financially accessible. In addition, patients may qualify for a sponsored testing program at no cost in exchange for de-identified data shared with the sponsoring companies. **Results delivery and follow-up.** Methods for delivering test results vary, depending on workflow, availability of genetic counseling services, and provider comfort level and training. Regardless of result type, genetic test reports should be offered to patients for their own records and uploaded into the EMR. Refer to Table 2 for information regarding the following result types. Options for returning results include:

- 1. Ordering provider refers all patients for post-test counseling, either through referral to a local GC or a telehealth genetic counseling service.
- Ordering provider refers patients with complex results (eg, positive and/or VUS) for post-test counseling. This type of blended approach to genetic testing has been previously discussed and has received strong consensus across multiple disciplines.^{21,26}
 - a) Negative results: Clinical teams can disclose results via telephone, patient portal message, a follow-up appointment, or a letter summarizing the results and providing contact information if there are questions. A templated letter can be generated with GC input. Cancer screening recommendations should be based on the family history and should be reviewed with the patient. For example, men with a first-degree relative with PCa remain at increased risk for PCa and should initiate prostate screening at a younger age per routine guidelines. Patients should be encouraged to discuss updates to personal and family history, which may prompt consideration of additional genetic testing or altered screening recommendations.
- 3. Ordering provider discloses all result types. It is important to note that even in this situation, a referral can be made to genetics for post-test counseling.
 - a) Positive results: Providers should discuss and document the implications of the results in terms of cancer risks associated with the identified gene mutation, additional cancer screening recommendations, appropriate referrals, and possible implications for treatment. Providers should also recommend cascade testing, which entails genetic counseling and testing in at-risk relatives of

individuals identified to carry specific genetic mutations or further testing in the family based on family history. Access to the proband's test report will be essential for family members considering testing.

b) VUS results: It is critical to review the uncertainty of whether the specific gene mutation identified is disease causing or a benign variation. The vast majority of VUS results are later reclassified to negative^{28,29}; thus, they are typically treated as negatives, and screening recommendations are made based on personal and family history. Testing family members for a VUS is typically not recommended unless it is in the context of a variant resolution or research program. When a VUS is reclassified, new reports are customarily issued to the ordering provider, and it is therefore the responsibility of the ordering provider to follow up with patients over the long term concerning any reclassifications. Patients should be encouraged to check in with their providers every few years to see whether there are updates to the classification. It is also important to note the possibility of discrepant variant classifications across laboratories. These discrepancies may cause difficulty determining how to appropriately manage patients and family members. ClinVar is a free, publicly available database that aggregates variant classifications, although a limitation is that entry submissions may not be completely up to date.

Cascade testing. The concept of cascade testing should be introduced as part of pretest counseling. Family letters can facilitate genetic testing for other relatives in the event of a positive result and typically include a short description of the cancer syndrome, the specific mutation identified, information on how to contact a GC in their area, and laboratory/specimen identification for the patient's testing. A number of the genes associated with hereditary PCa, such as BRCA1/2 and the mismatch repair genes, are associated with additional cancers and may have well-defined risk numbers and screening recommendations for males and females. Targeted testing for the known familial variant can clarify the cancer risks for other relatives, allowing for the initiation of appropriate increased cancer screening and risk-reducing therapies, and consideration of reproductive planning options.²⁷ Ultimately, it is the patient's decision and responsibility to inform at-risk relatives about their genetic test results, which underlies the importance of reviewing cascade testing and providing resources to help facilitate this transfer of critical information.

Additional Considerations

Pathogenic mutations identified in DNA-damage repair genes, such as *BRCA1/2* or mismatch repair genes, have implications for management and treatment.^{3,4} Germline mutations are identified in approximately 12% of patients with metastatic PCa, but because some are not actionable,

it is important to manage expectations concerning outcomes for germline testing.⁷⁻¹¹ Many of the genes included on PCa panels are newly associated with PCa and do not yet have well-defined cancer risks. This increases the possibility of a positive result in a gene associated with low-tomoderate increased cancer risk, which may not have clear screening recommendations. Providers need to be clear about the preliminary nature of findings and that there may not be an immediate impact on cancer screening or treatment options. Patients and their families should be encouraged to participate in registries or research studies to better characterize the risk associated with specific variants over time. Providers can refer patients to a GC for further discussion. Finally, as germline mutations continue to be levied for treatment purposes, providers must be aware of the risk of secondary malignancies and treatment-related adverse effects in some mutation carriers.²⁸⁻³²

Some providers may be concerned about the potential for negative consequences from genetic testing. A number of studies have found that most individuals are unlikely to experience significant psychological distress after receiving genetic test results.^{33,34} Notably, the likelihood of psychological distress, family disruption, and nonadherence to surveillance guidelines was greater in settings without adequate patient education, counseling, informed consent, and follow-up.^{33,35} A recent study of men with PCa undergoing genetic testing found genetic counseling to be beneficial.³⁵

Some patients are hesitant about genetic testing because of concerns about discrimination. The Genetic Information Nondiscrimination Act (GINA), a federal law passed in 2008, protects individuals from genetic discrimination from health insurance companies and employers, with specific limitations on the type of employer and size of the company. Importantly, GINA protections do not extend to life, disability, or long-term care insurance. Some states have passed genetic discrimination laws that extend protection beyond GINA. Information regarding GINA is often included in the consent forms for testing laboratories, and summary handouts could be given to patients with additional questions.

Practical Strategies to Overcome Genetic Service Barriers

ASCO and other major health societies strongly encourage and often provide additional education training for nongenetics providers who are interested in responsibly incorporating genetic services into their practice. Courses on genomic cancer risk assessment for physicians, advanced practice providers, nurses, GCs, and other health care professionals are available through organizations such as City of Hope, American Urological Association, and ASCO.

Alternatives to in-person pretest counseling, such as educational handouts, videos, and presentations, are allowing genetic counseling expertise to be shifted to the post-test setting, prioritizing visits for complex counseling patients and/or abnormal results, and facilitating a hybrid service delivery model.^{18,36} Data are still emerging regarding the effectiveness of these models and patient satisfaction. Other practical strategies have focused on increasing GC efficiency and patient volumes, leading to the creation of new support roles, such as GC assistants; incorporation of technologies that reduce appointment time, such as online pedigree collection tools; and group genetic counseling sessions.^{37,38} There are now chatbots, such as Genetic Information Assistance, that can converse with patients about family history and the basics of genetic testing and insurance, and determine who qualifies for genetic testing.

Special attention and strategies to minimize disparities in genetics are essential. It has been well documented that socioeconomically disadvantaged individuals, racial/ethnic minorities, and men are less likely to receive genetic services.^{18,39-43} PCa genetic testing provides a unique opportunity for providers and institutions to address possible disparities and consider offering counseling services within

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a male-friendly environment. It is imperative that health care providers from all specialties work together to provide equal access to genetic services by minimizing biases, improving patient education and understanding, creating culturally sensitive interfacing materials, and expanding services to underprivileged areas.

In conclusion, as genetic testing becomes integral to the care of patients with PCa, coordinated efforts across multiple disciplines are required to deliver optimal care. Developing creative, scalable strategies to deliver high-quality personalized genetics care for patients with PCa will be paramount to realizing the full scope and impact of genetic testing for individual patients and family members. It is clear that expanding education around the need for testing and developing standardized systems for implementation in the clinic are important directions for genetics care delivery and essential for delivering precision oncology to men with PCa.

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Disclosures provided by the authors and data availability statement (if applicable) are available with this article at DOI https://doi.org/10.1200/ OP.20.00431.

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AUTHORS' DISCLOSURES OF POTENTIAL CONFLICTS OF INTEREST

Practical Considerations and Challenges for Germline Genetic Testing in Patients With Prostate Cancer: Recommendations From the Germline Genetics Working Group of the PCCTC

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Open Payments is a public database containing information reported by companies about payments made to US-licensed physicians (Open Payments).

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Association of Clonal Hematopoiesis in DNA Repair Genes With Prostate Cancer Plasma Cell-free DNA Testing Interference

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Key Points

Question

How often are cell-free DNA (cfDNA) studies in prostate cancer confounded by clonal hematopoiesis (CHIP) variants in genes used for poly(ADP) ribose polymerase inhibitor (PARPi) eligibility?

Findings

In this case series study of 69 men with advanced prostate cancer, 7 (10%) had CHIP variants in genes used for US Food and Drug Administration-approved indications of PARPi treatment, most frequently in ATM.

Meaning

Men with prostate cancer are at high risk of being misdiagnosed as being eligible for PARPi therapy using current cfDNA tests; assays should use a whole-blood control sample to distinguish CHIP variants from prostate cancer.

Abstract

Importance

Cell-free DNA (cfDNA) testing is increasingly used in the treatment of patients with advanced prostate cancer. Clonal hematopoiesis of indeterminate potential (CHIP) can interfere with cfDNA testing and cause incorrect interpretation of results. There is an urgent need to better understand this problem

following recent US Food and Drug Administration approval of poly(ADP) ribose polymerase inhibitors (PARPi) for metastatic prostate cancer based on variants in DNA repair genes that can be affected by CHIP.

Objective

To determine the prevalence of clinically relevant CHIP interference in prostate cancer cfDNA testing.

Design, Setting, and Participants

We report a case series of 69 patients with advanced prostate cancer (metastatic disease or with rising PSA following localized therapy) who had cfDNA variant testing with a large panel cancer next generation sequencing assay (UW-OncoPlexCT). To determine the source of variants in plasma, we tested paired cfDNA and whole blood control samples. The study was carried out in an academic medical center system reference laboratory.

Main Outcomes and Measures

Prevalence and gene spectrum of CHIP interference in patients with prostate cancer undergoing cfDNA testing.

Results

We detected CHIP variants at 2% or more variant fraction in cfDNA from 13 of 69 men with prostate cancer (19%; 95% CI, 10%-30%). Seven men (10%; 95% CI, 4%-20%) had CHIP variants in DNA repair genes used to determine PARPi candidacy, including *ATM* (n = 5), *BRCA2* (n = 1), and *CHEK2* (n = 1). Overall, CHIP variants accounted for almost half of the somatic DNA repair gene variants detected. Participant CHIP variants were exponentially correlated with older age ($R^2 = 0.82$). CHIP interference variants could be distinguished from prostate cancer variants using a paired whole-blood control.

Conclusions and Relevance

In this case series, approximately 10% of men with advanced prostate cancer had CHIP interference in plasma cfDNA in DNA repair genes that are used for eligibility of PARPi therapy, most frequently in *ATM*. Clinical cfDNA testing should include a paired whole-blood control to exclude CHIP variants and avoid misdiagnosis.

Introduction

Cell-free DNA (cfDNA) variant analysis is used to guide treatment decisions for men with metastatic prostate cancer (mPC) and to enroll patients on clinical trials.¹ Two poly(ADP) ribose polymerase inhibitors (PARPi) were recently granted US Food and Drug Administration (FDA) approval for use in selected patients with mPC based on DNA repair gene status: rucaparib for patients with *BRCA1* or *BRCA2* variants and olaparib for patients with *ATM*, *BRCA1*, *BRCA2*, *BARD1*, *BRIP1*, *CDK12*, *CHEK1*, *CHEK2*, *FANCL*, *PALB2*, *RAD51B*, *RAD51C*, *RAD51D* or *RAD51L* variants.² Following these biomarker-guided approvals we expect cfDNA testing will sharply increase for patients with mPC because it offers the convenience and simplicity of testing on a blood sample in the advanced disease setting.^{1,3,4} Thus, there is an urgent need to understand cfDNA testing performance and sources of test interferences.

Clonal hematopoiesis of indeterminate potential (CHIP) is a known confounder of cfDNA testing. $\frac{5.6}{6}$ Clonal hematopoiesis of indeterminate potential variants are detected in both plasma and whole blood, whereas prostate cancer variants are detected in plasma only. Yet most commercial labs perform cfDNA testing using a plasma-only approach that cannot reliably distinguish variants derived from prostate cancer

vs those arising from CHIP. To improve cfDNA assay performance, we developed an approach (UW-OncoPlexCT) that simultaneously analyzes plasma and paired whole-blood control samples.⁴ Using this paired testing approach we sought to determine to what degree CHIP interferes with the results of prostate cancer cfDNA testing.

Methods

We retrospectively reviewed cfDNA study results from 69 patients with advanced prostate cancer (metastatic disease or with rising PSA following localized therapy) sequenced by our Clinical Laboratory Improvement Amendments (CLIA)-certified and College of American Pathologists (CAP)-accredited clinical UW-OncoPlexCT protocol. Plasma cfDNA and a paired whole-blood control sample were tested in every patient.^{4,7} We defined CHIP interference as a pathogenic variant with variant allele fractions (VAFs) of at least 2% in both the whole blood and plasma. Germline variants were distinguished from CHIP clones by tumor sequencing. Sequencing data analysis and variant interpretation were performed by an expert molecular pathologist (C.C.P.). All data were manually reviewed in the integrated genomics viewer (IGV) to exclude sequencing artifacts. Data were generated and preprocessed by the University of Washington NGS Laboratory and Analytics group. This study was performed in accordance with the Declaration of Helsinki guidelines and approved by the University of Washington/Fred Hutchinson Cancer Consortium institutional review board and all patients provided written informed consent.

Results

We detected CHIP interference clones at least 2% variant fraction in 13 of 69 patients (19%; 95% CI, 10%-30%). Seven patients (10%; 95% CI, 4%-20%) had CHIP variants in DNA repair genes that are used for PARPi selection (*ATM* n = 5, *BRCA2*, n = 1 and *CHEK2*, n = 1) (Figure) (Table). The 6 remaining patients had CHIP interference in genes frequently impacted by CHIP: *ASXL1*, *DNMT3A*, *PTEN*, *TET2*, and *TP53* (Figure) (eFigure in the Supplement).^{8,9}

We observed that CHIP interference correlated exponentially with increasing age ($R^2 = 0.82$). We detected CHIP in 0% (0/6) of men aged 40 to 50 years, 12.5% (2/16) of men aged 51 to 60 years, 6.3% (1/16) of men aged 61 to 70 years, 20.8% (5/24) of men aged 71 to 80 years, and 71% (5/7) of men aged 81 to 90 years (Figure, A).

In 20 patients with advanced prostate cancer, we detected a total of 23 pathogenic variants in DNA repair gene variants used for selection of PARPi therapy, from the following source(s): CHIP interference somatic (n = 8, 1 patient had 2), non-CHIP somatic (n = 9), germline (n = 6) (Figure, B). We considered germline variants and non-CHIP somatic variants as true positives (n = 15) and CHIP interference as false positives (n = 8). Restricting the assay to a plasma-only analysis, only 65% of DNA repair gene variants detected were true positives (15/23). When incorporating a paired whole-blood control to remove CHIP interference, all DNA repair gene variants were true positives (15/15, 100%).

The patient with *BRCA2* CHIP interference had cfDNA testing done in parallel by an outside commercial laboratory using a plasma-only assay, which was unknown to our laboratory at the time of testing. The *BRCA2* CHIP clone was clinically reported by the commercial lab with the recommendation to use PARPi therapy.

Discussion

We found that a strikingly high proportion of DNA repair gene variants in the plasma of patients with advanced prostate cancer are attributable to CHIP. The CHIP variants were strongly correlated with increased age, and even higher than expected by age group. The high rate of CHIP may also be influenced by prior exposure to chemotherapy.^{10,11} We are concerned that CHIP interference is causing false-positive cfDNA biomarker assessments that may result in patient harm from inappropriate treatment, and delays in https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7645740/?report=printable

delivering alternative effective treatment options. Without performing a whole-blood control, 7 of 69 patients (10%) would have been misdiagnosed and incorrectly deemed eligible for PARP-inhibitor therapy based on CHIP interference in plasma. In fact, 1 patient in this series had a *BRCA2* CHIP clone that had been previously reported by a commercial lab with the recommendation to use a PARPi. To mitigate these risks, cfDNA results should be compared to results from whole-blood control or tumor tissue.¹²

Challenges of accurate cfDNA testing are beginning to be described. A recent report¹³ highlighted inaccuracies of commercial laboratory cfDNA testing in patients with prostate cancer. In that report, cfDNA samples from 40 patients were sent to 2 separate CLIA-certified laboratories and only 9 of 40 (23%) demonstrated congruence (complete or partial) of positive findings.¹³ The consistent findings included *ATM* and *TP53* variants in patients with low PSA at the time of blood draw, raising suspicion that these may be CHIP clones. The CHIP interference in cfDNA testing has also been reported in other cancer types. In renal-cell carcinoma (RCC), for example, CHIP was found to affect cfDNA results in 43% of patients.¹⁴

Overall, *ATM* accounted for the majority of clinically relevant CHIP interference in our series. The *ATM* gene has been described as a frequent CHIP clone in clinical cancer predisposition testing, along with *CHEK2* and *TP53*.¹⁰ We speculate that CHIP interference in cfDNA testing could be affecting results of PARPi clinical studies of patients with metastatic prostate cancer. Trials allowing plasma-only cfDNA testing for enrollment may have included patients with false-positive results associated with CHIP in DNA repair genes, particularly in *ATM*.¹⁵ We speculate that this could be contributing to low PARPi response rates reported in patients with *ATM* variants, such as recently reported from the TRITON2 study.¹⁵

Limitations

This study has several limitations including relatively small sample size, the retrospective nature of the study, and heterogeneity in patient populations and prior therapies.

Conclusions

Findings of this study suggest that CHIP substantially interferes with plasma cfDNA testing in patients with advanced prostate cancer. There is a risk for widespread misdiagnosis and overtreatment of men with PARPi using currently available commercial cfDNA assays. We recommend that all cfDNA testing in patients with prostate cancer include a whole-blood control to distinguish CHIP from prostate cancer variants.

Notes

Supplement.

eFigure. All Variants Detected in Plasma Cell-Free DNA From 69 Men With Advanced Prostate Cancer. Each column represents 1 unique patient sorted by age.

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Figures and Tables



Source of Variants Detected in Prostate Cancer cfDNA Studies

A, The prevalence of CHIP variants increased with age. CHIP was particularly prevalent (71%) in the 81 to 90 year age range. B, Consecutive series of 69 cfDNA studies. The DNA repair genes associated with PARPi eligibility are depicted along with other genes in which CHIP was detected. Each column represents 1 unique patient sorted by age. Variants detected in plasma are color coded by source, red indicates CHIP interference, somatic; green indicates non-CHIP, somatic (prostate cancer); yellow indicates germline. cfDNA indicates cell-free DNA; CHIP, clonal hematopoiesis of indeterminate potential; PARPi, poly(ADP) ribose polymerase inhibitor.

Table.

CHIP Clones Detected in DNA Repair Genes Used for PARPi Eligibility

Age,	Gene ^a	CHIP Variant(s)	VAF	VAF blood	Notes
У			cfDNA	control	
81	ATM	p.R3008C,	16%; 5%	16%; 5%	CHIP hotspot, reported by outside lab in bone
		p.E3007D			marrow
54	ATM	p.S305*	2%	3%	
82	ATM	p.G2891D	12%	13%	Kinase domain
81	ATM	c.2921+1G>A	78%	65%	Not germline based on tumor testing
87	ATM	p.L2492R	7%	9%	CHIP hotspot
76	BRCA2	p.T3310Nfs*17	3%	3%	Reported by outside lab, recommending
					PARPi
74	CHEK2	p.P426H	19%	18%	Kinase domain

Abbreviations: CHIP, clonal hematopoiesis of indeterminate potential; VAF, variant allele fraction; PARPi, poly(ADP) ribose polymerase inhibitor.

^a*ATM* reference sequence: <u>NM_000051.3</u>, *BRCA2* reference sequence <u>NM_000059.3</u>; *CHEK2* reference sequence: <u>NM_007194.3</u>.



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Regulation of CEACAM5 and therapeutic efficacy of an anti-CEACAM5-SN38 antibody-drug conjugate in neuroendocrine prostate cancer

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Abstract

Purpose: Neuroendocrine prostate cancer (NEPC) is an aggressive form of castration-resistant prostate cancer (CRPC) for which effective therapies are lacking. We previously identified carcinoembryonic antigen-related cell adhesion molecule 5 (CEACAM5) as a promising NEPC cell surface antigen. Here we investigated the scope of CEACAM5 expression in end-stage prostate cancer, the basis for CEACAM5 enrichment in NEPC, and the therapeutic potential of the CEACAM5 antibody-drug conjugate labetuzumab govitecan in prostate cancer.

Experimental design: The expression of CEACAM5 and other clinically relevant antigens was characterized by multiplex immunofluorescence of a tissue microarray comprising metastatic tumors from 34 lethal mCRPC cases. A genetically defined neuroendocrine transdifferentiation assay of prostate cancer was developed to evaluate mechanisms of CEACAM5 regulation in NEPC. The specificity and efficacy of labetuzumab govitecan was determined in CEACAM5⁺ prostate cancer cell lines and patient-derived xenografts models.

^{*}Corresponding author: John K. Lee, 1100 Fairview Ave N., E2-112, Seattle, WA 98109, 206-667-6819, jklee5@fredhutch.org. **Author contributions:** D.C.D., T.M.C., M.T.S., and J.K.L. conceived and designed experiments. D.C.D, M.P.L., A.Z., L.A., and J.K.L. performed experiments. D.C.D., M.P.L., A.Z., J.E.H., N.D.S, I.C, R.M.G., L.D.T., and M.H., performed data analysis. E.C., C.M., and P.S.N. provided biological samples. D.C.D. and J.K.L. wrote the paper.

Conflict of interest statement: D.C.D. and J.K.L. received research funding from Immunomedics, Inc. T.M.C. was employed by Immunomedics, Inc., and holds stock or stock options in Immunomedics. Inc.

Data and material availability: Raw and analyzed RNA-seq and ATAC-seq data are available at GEO accession number GSE154576. All other materials will be available upon request and completion of a Material Transfer Agreement.

Results: CEACAM5 expression was enriched in NEPC compared to other mCRPC subtypes and minimally overlapped with PSMA, PSCA, and Trop2 expression. We focused on a correlation between the expression of the pioneer transcription factor *ASCL1* and *CEACAM5* to determine that ASCL1 can drive neuroendocrine reprogramming of prostate cancer which is associated with increased chromatin accessibility of the *CEACAM5* core promoter and CEACAM5 expression. Labetuzumab govitecan induced DNA damage in CEACAM5⁺ prostate cancer cell lines and marked antitumor responses in CEACAM5⁺ CRPC xenograft models including chemotherapy-resistant NEPC.

Conclusions: Our findings provide insights into the scope and regulation of CEACAM5 expression in prostate cancer and strong support for clinical studies of labetuzumab govitecan for NEPC.

Keywords

labetuzumab govitecan; CEACAM5; ASCL1; pioneer transcription factor; neuroendocrine prostate cancer

Introduction:

While androgen deprivation therapy (ADT) is initially effective for the treatment of hormone-sensitive prostate adenocarcinoma (PRAD), resistance is inevitable and leads to a state known as castration-resistant prostate cancer (CRPC). CRPC is heterogeneous and comprises multiple molecular phenotypes that diverge from conventional PRAD and include neuroendocrine prostate cancer (NEPC) which is a high-grade, poorly differentiated, and lethal neuroendocrine carcinoma with no effective treatments. NEPC accounts for up to 20% of lethal metastatic CRPC (mCRPC) and exhibits rapid metastatic dissemination, loss of androgen receptor (AR) signaling, and expression of neuroendocrine differentiation markers. NEPC rarely arises *de novo* and primarily emerges from PRAD through a process of neuroendocrine transdifferentiation as an adaptive response to the selective pressure of ADT (1).

While an understanding of the determinants of neuroendocrine transdifferentiation of prostate cancer remains incomplete, several genetic alterations have been associated with progression to NEPC. These include loss of the tumor suppressor genes *RB1* and *TP53*, amplification or overexpression of *MYCN* and *AURKA*, and activation of the PI3K/AKT pathway (2,3). These genetic derangements are also common to poorly differentiated neuroendocrine cancers arising from other epithelial tissues including the lung. In genetically engineered mouse models, combined loss of *Rb1*, *Trp53*, and *Pten* in the prostate promotes the development of tumors displaying castration resistance, lineage plasticity, and a neuroendocrine cancer phenotype (4,5). Human prostate epithelial transformation models have also underscored the importance of these genetic perturbations in the initiation of NEPC (6,7). Yet neuroendocrine transdifferentiation does not appear to be an obligate outcome of these genetic events in human prostate cancer (8), indicating that other factors may be involved.

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In general, NEPC represents an epigenetic cancer state distinct from PRAD with unique patterns of DNA methylation, chromatin accessibility, and epigenetic regulator expression (6,9,10). However, NEPC can vary in histologic appearance and neuroendocrine marker expression, likely due to molecular heterogeneity. Small-cell lung cancer (SCLC) shares many phenotypic characteristics with NEPC. Recently, four molecular subtypes of SCLC have been identified, of which two are marked by differential expression and activity of the pioneer neural basic helix-loop-helix transcription factors achaete-scute homologue 1 (ASCL1) and neurogenic differentiation factor 1 (NeuroD1) (11). In a mouse model of SCLC driven by *Rb1* and *Trp53* loss, *Ascl1* but not *Neurod1* was required for the initiation of SCLC (12). NeuroD1^{high} SCLC appears to progress from an ASCL1^{high} SCLC state through a process mediated by enhanced *MYC* expression (13). Given the biological parallels between SCLC and NEPC, these lineage-defining transcription factors may also be operative in NEPC.

The expression of cell surface proteins reflects specific cellular lineage programs in normal development and in cancer. The development of targeted therapies directed against prostate cancer cell surface antigens is an active area of research that must account for the heterogeneity of CRPC phenotypes reflecting diverse cancer differentiation states. Using a systematic approach, we previously identified expression of the human carcinoembryonic antigen-related cell adhesion molecule 5 (CEACAM5, also known as CEA) in a large subset of NEPC (14). CEACAM5 is a cell surface protein that is upregulated in a variety of other human epithelial malignancies including colorectal cancer (15) and has been functionally associated with tumor differentiation, invasion, and metastasis (16,17). Multiple therapeutic approaches to target CEACAM5 in cancer are in development including vaccines, bispecific T cell engagers, chimeric antigen receptor T cell therapies, and antibody-drug conjugates (ADC). Labetuzumab govitecan (IMMU-130) is a CEACAM5 ADC composed of a humanized CEACAM5 monoclonal antibody named labetuzumab conjugated to the potent topoisomerase I inhibitor 7-ethyl-10-hydroxycamptothecin (SN-38) via a unique hydrolysable linker (CL2A) (18). SN-38 is the active metabolite of irinotecan which is commonly used as chemotherapy for colorectal and pancreatic cancer (19). Labetuzumab govitecan has demonstrated activity in preclinical models of colorectal cancer (18,20) as well as safety and potential efficacy in a phase I/II clinical trial in patients with treatmentrefractory metastatic colorectal cancer (21). However, labetuzumab govitecan has yet to be evaluated in the treatment of prostate cancer.

Here we characterize CEACAM5 expression in end-stage mCRPC relative to other cell surface antigens that are the active clinical focus of diagnostic and therapeutic development. We investigate the molecular basis for CEACAM5 expression in NEPC and uncover insights into the cancer differentiation-specific regulation of CEACAM5. Lastly, we evaluate the antitumor activity of labetuzumab govitecan in preclinical models of CEACAM5⁺ CRPC, including NEPC, to justify the clinical investigation of this therapeutic agent in prostate cancer.

Materials and Methods:

Cell lines.

DU145 (Cat# DU-145, RRID:CVCL_0105), 22Rv1 (Cat# CRL-2505, RRID:CVCL_1045), C4–2B (Cat# CRL-3315, RRID:CVCL_4784), and NCI-H660 (Cat# CRL-5813, RRID:CVCL_1576) cell lines were purchased from the American Tissue Culture collection (ATCC; Manassas, VA) and LNCaP95 were a gift from Dr. Stephen R. Plymate (University of Washington). All cell lines were validated by short tandem repeat analysis after receipt. DU145, 22Rv1, C4–2B, and MSKCC EF1 (derived from the organoid line MSKCC-CaP4) were maintained in RPMI medium supplemented with 10% fetal bovine serum (FBS), 100 U/ml penicillin and 100 ug/ml streptomycin, and 4 mM GlutaMAXTM. NCI-H660 cells were maintained in Advanced DMEM/F12 medium supplemented with B27, 4 mM GlutaMAXTM, and 10 ng/ml recombinant human bFGF and EGF. Cell lines were cultured no more than three weeks after thawing prior to use in described experiments.

mIF of TMAs.

UW mCRPC TAN TMA (Prostate Cancer Biorepository Network) and FDA normal organ TMA (US Biomax Inc.) were used for mIF studies (Tables S1, S2, and S3). Slides were stained on a Leica BOND Rx stainer (Leica, Buffalo Grove, IL) using Leica Bond reagents for antigen retrieval, antibody stripping (Epitope Retrieval Solution 2), and rinsing after each step (Bond Wash Solution). A high stringency wash was performed after the secondary and tertiary applications using high-salt TBST solution (0.05 M Tris, 0.3 M NaCl, and 0.1% Tween-20, pH 7.2–7.6). Opal Polymer HRP Mouse plus Rabbit (PerkinElmer, Hopkington, MA) was used for all secondary applications.

H-scoring of CEACAM5 expression.

H-scores were generated from the CEACAM5 mIF data using the CytoNuclear LC v2.0.6 module and HALO software. Briefly, individual cells were classified as having negative, weak, moderate, or strong CEACAM5 staining and assigned intensity scores of 0, 1, 2, and 3, respectively. The intensity score ranges were defined based on CEACAM5 fluorescent intensity values as follows: 0 = 0 - positive CEACAM5 threshold value, 1 = threshold value -25^{th} quartile median, $2 = 25^{th}$ quartile median -75^{th} quartile median, and $3 = 75^{th}$ quartile median – maximum value reported. Intensity scores were then multiplied by the percentage of stained cells for a range of 0–300.

Serum CEA quantification.

Cryopreserved serum samples obtained at rapid autopsy or a patient visit prior to rapid autopsy were obtained from the UW TAN repository. CEA quantification was performed using a CLIA-licensed Carcinoembryonic Antigen ELISA test (University of Washington Research Testing Services).

Exome sequencing analysis.

Paired-end exome sequencing (NGS) was performed using Illumina HiSeq or Illumina NovaSeq on genomic DNA isolated from rapid autopsy tissue samples. Sequence reads were

aligned to the human reference genome hg19 using the BWA aligner (RRID:SCR_010910). GATK (RRID:SCR_001876) best practice was adopted to process all aligned BAM files. Germline and somatic mutation analyses were performed using HaplotypeCaller and Mutect2. All detected mutations were annotated using ANNOVAR hg19 (RRID:SCR_012821) and manual curation was performed before determination of pathogenicity. Copy number was derived following the standardized Sequenza pipeline (RRID:SCR_016662). All copy number calls were manually curated for potentially missed mid-sized structural aberrations (15–50 nt indels).

C4–2B neuroendocrine transdifferentiation assay.

C4–2B cells were seeded in 6-well tissue culture plates at a density of 10⁵ cells per ml in 3 ml of RPMI medium supplemented with 10% fetal bovine serum (FBS), 100 U/ml penicillin and 100 ug/ml streptomycin, and 4 mM GlutaMAXTM. Cells were transduced approximately 4–6 hours after seeding at a defined multiplicity-of-infection of 4 for each lentivirus. Seventy-two hours after transduction, cells were trypsinized, washed, and transferred to 100 mm tissue culture plates in 15 ml of Advanced DMEM/F12 medium supplemented with B27, 4 mM GlutaMAXTM, and 10 ng/ml recombinant human bFGF and EGF. Media was replenished every 3–4 days. Cells were collected 11 days post-transduction for analysis.

ATAC sequencing.

Briefly, 50,000 cells were lysed in buffer containing NP-40, Tween-20, and digitonin. Nuclei were collected after centrifugation and transposed with Tn5 transposase for 30 minutes at 37°C. DNA was purified by MinElute Reaction Cleanup Kit (Qiagen) followed by PCR amplification to append indices/adapters, library purification, and quality control by Agilent TapeStation and library quantitation by qPCR. ATAC-seq libraries underwent paired-end 50 bp sequencing on an Illumina NovaSeq 6000. Raw reads were processed with the ENCODE ATAC-seq pipeline (22) for quality control, alignment by Bowtie 2 (RRID:SCR_005476), and peak calling by MACS2 (RRID:SCR_013291). Inferred transcription factor activity was determined by HINT-ATAC (23) using HOCOMOCO (RRID:SCR_005409) and JASPAR (RRID:SCR_00300) binding motifs.

ATAC quantitative PCR.

ATAC-qPCR targeting the *CEACAM5* core promoter peak was performed using ATAC libraries on the QuantStudio5 System (Thermo Fisher Scientific) with Applied Biosystems PowerUp SYBR Green Master Mix (Thermo Fisher Scientific). The mean cycle threshold (Ct) obtained for each promoter region was normalized to the *AK5* control primers (24).

Immunoblots.

Whole cell extracts were fractionated by SDS-PAGE and transferred to a nitrocellulose membrane using a transfer apparatus according to the manufacturer's instructions (Invitrogen). Membranes were blocked with 5% nonfat milk in PBST (DPBS + 0.5% Tween 20) for 30 minutes while shaking, then incubated with primary antibodies at 4°C for 16 hours. Membranes were washed three times for 5 minutes with PBST and incubated with horseradish peroxidase-conjugated anti-mouse or anti-rabbit secondary antibody for 1 hour

at room temperature. Blots were washed three times for 5 minutes each with PBST and developed with ImmobilonTM Western Chemiluminescent HRP Substrate (MilliporeSigma) for three minutes at room temperature. Blot images were acquired with a ChemiDoc^{MP} Imaging System (Bio-Rad) or autoradiography film.

CEACAM5 surface protein detection by flow cytometry.

DU145, 22Rv1, and MSKCC EF1 cells were dissociated with Versene-EDTA (Thermo Fisher Scientific) into single cell suspensions. Cells were washed once with monoclonal antibody wash buffer (MW; PBS + 0.1% FBS + 0.1% sodium azide) then resuspended in 100 μ l MW and 5 μ l of anti-CEACAM5-APC or IgG isotype-APC per 10⁶ cells and incubated at room temperature in the dark for 30 minutes. Cells were washed once with MW, resuspended in MW, acquired on a BD FACSCanto II (BD Biosciences), and analyzed with FlowJo (v10) (RRID:SCR_008520).

Labetuzumab cell surface binding.

DU145, 22Rv1, and MSKCC EF1 cell lines expressing empty vector or CEACAM5 vector were dissociated non-enzymatically with Versene-EDTA into single cell suspensions. Cells were washed once with PBS and resuspended in 100 ul of 1 ug/ml of h679 or labetuzumab (Immunomedics, Inc.) and incubated at 4°C on ice for 1 hour. Cells were then washed twice with PBS, incubated with an anti-human IgG- PE-Cy5 secondary antibody (Thermo Fisher Scientific) at 4°C on ice for 30 minutes, washed with PBS, acquired on a SH800 (Sony), and analyzed with FlowJo (v10).

γH2AX detection of dsDNA breaks.

DU145, 22Rv1, and MSKCC EF1 cells were dissociated non-enzymatically with Versene-EDTA (Thermo Fisher Scientific), washed with PBS, resuspended in PBS and prechilled on ice at 4°C for 20 minutes, followed by incubation with labetuzumab govitecan or h679-SN-38 (Immunomedics, Inc.), or SN-38 (Sigma) for 30 minutes on ice at 4°C. Cells were then washed six times with cold PBS, and cultured for 16 hours in culture media at 37°C. For extended SN-38 treated conditions, cells were cultured at 37°C in media containing SN-38 for 16 hours. Cells were then dissociated with trypsin 0.25%, washed with MW, fixed with BD Cytofixation Buffer (BD Biosciences), permeabilized with BD Phosflow Perm Buffer II (BD Biosciences), and stained with anti- γ H2AX-BV421 or IgG isotype control, as per manufacturer's instructions. Cells were washed twice with MW, resuspended in MW, acquired on a BD FACSCanto II (BD Biosciences), and analyzed with FlowJo (v10).

SN-38 dose responses in prostate cancer cell lines.

DU145, 22Rv1, MSKCC EF1, and NCI-H660 cells were seeded at 5×10^3 cells (50 µl) per well in 96-well flat bottom, tissue culture treated, white plates (Corning). Cells were treated with serial dilutions of SN-38 (50 µl) in replicates of 8, diluted in appropriate culture media, at 37°C for 96 hours. Cell viability was determined using the CellTiter-Glo 2.0 Assay (Promega).

Immunohistochemistry of LuCaP PDX tumors.

Formalin-fixed, paraffin-embedded tissue sections were baked at 65°C for 1–2 hours, deparaffinized in xyline, and rehydrated in 100%, 95%, and 70% ethanol. Tissue sections were heated in antigen retrieval buffer (0.2 M citric acid and 0.2 M sodium citrate) within a pressure cooker followed by PBS wash. Tissue slices were blocked with 2.5% horse serum for 30 minutes and then incubated with primary antibody diluted in 2.5% horse serum overnight at 4°C. HRP was detected with ImmPRESS-HRP anti-mouse or anti-rabbit IgG peroxidase detection kits (Vector Laboratories) and staining was visualized with DAB peroxidase substrate (Dako). Tissue sections were counterstained with hematoxylin and dehydrated for mounting.

Mouse xenograft studies.

All animal care and studies were performed in accordance with an approved Fred Hutchinson Cancer Research Center Institutional Animal Care and Use Committee protocol and Comparative Medicine regulations. Six-week old, male NSG (NOD-SCID-IL2R γ -null, RRID:BCBC_4142) mice were obtained from the Jackson Laboratory. 5×10^6 cells from each prostate cancer cell line were suspended in 100 µl of cold Matrigel (Corning) and implanted by injection subcutaneously into NSG mice. For LuCaP PDXs, a 1 mm³ piece of prostate tumor tissue was surgically implanted subcutaneously into NSG mice. Mice were enrolled into a treatment arm when tumors reached 150 mm³ and treated by intraperitoneal injection at the frequency and with the doses described. Labetuzumab govitecan and h679-SN-38 doses were prepared fresh through reconstitution with 0.9% preservative-free sodium chloride (McKesson Medical-Surgical). Cisplatin and etoposide (NIH Developmental Therapeutics Program, RRID:SCR_003057) were prepared and stored at room temperature and 4°C, respectively. Mice were monitored biweekly for tumor growth, weight, and body condition score. A complete response is defined as an undetectable tumor.

Complete blood counts and serum chemistries.

Retro-orbital bleeds yielding \sim 200 µl of blood were performed on mice prior to receiving the first dose at enrollment on day 0, as well as on days 14 and 28 of the study. Blood was collected into green top lithium heparin microcontainers (Becton Dickinson) and tested within 24 hours (Phoenix Labs, Seattle, WA).

Statistical methods.

All data are shown as mean \pm SD. For sample sizes less than 40, normality testing was performed with the D'Agostino-Pearson test. For single comparisons, statistical analyses were performed using a two-sided Student's t-test. For multiple comparisons, statistical analyses were performed using ANOVA with Tukey's post hoc correction. Data not normally distributed were alternatively analyzed using a two-sided Kruskal-Wallis nonparametric test or Brown-Forsythe and Welch ANOVA with Games-Howell nonparametric post hoc correction. For correlation analysis, Pearson correlations or Spearman rank correlations were performed for normal and not normal data, respectively. Best fit curves were generated with linear regression modeling. Significance was defined as p 0.05.

All studies were conducted in accordance with the ethical guidelines expressed in the World Medical Association Declaration of Helsinki.

Results:

Enrichment of CEACAM5 protein expression in NEPC

To examine CEACAM5 expression across phenotypic subtypes of advanced prostate cancer, we performed immunofluorescence (IF) staining on a clinically and histologically annotated tissue microarray (TMA) of lethal mCRPC tissues from 34 patients collected at rapid autopsy through the University of Washington Tissue Acquisition Necropsy (UW TAN) program (25). Two of 34 patient samples were excluded due to poor quality cores, allowing for the complete analysis of 32 patient tissues. Tissues were classified into four tumor subtypes based on immunohistochemical staining for androgen receptor (AR), prostatespecific antigen (PSA), chromogranin A (ChrA), and synaptophysin (SYP): 1) androgen receptor positive prostate cancer (ARPC: AR⁺ or PSA⁺, ChrA⁻, and SYP⁻); 2) neuroendocrine prostate cancer (NEPC: AR- and PSA-, ChrA+ or SYP+); 3) doublenegative prostate cancer (DNPC: AR⁻, PSA⁻, ChrA⁻, and SYP⁻); or 4) amphicrine prostate cancer (AMPC: AR⁺ or PSA⁺ and ChrA⁺ or SYP⁺). Stromal regions of tissue cores were classified based on morphology (Figure 1A) and excluded from all analyses to focus on tumor parenchyma. Image analysis revealed that the overall level of CEACAM5 expression was heightened in NEPC based on fluorescence intensity (Figure 1 B) and that NEPC cores contained significantly more CEACAM5⁺ cells ($44\% \pm 39.6\%$) (Figure 1C). Integrated CEACAM5 H-scores (% cells stained x staining intensity) were substantially higher in NEPC (81 ± 87.5) (Figure 1D) compared to other prostate cancer subtypes.

CEACAM5 expressed on the surface of cells is often shed into the bloodstream and can be measured as serum CEA. Serum CEA is a common clinical cancer biomarker but has had a relatively limited role in the clinical management of prostate cancer. Elevation of serum CEA combined with neuroendocrine tumor marker expression has previously been reported as a clinical criterion for aggressive variant prostate cancer, a spectrum of prostate cancers including NEPC that are molecularly characterized by combined defects in TP53, RB1, and PTEN and respond poorly to AR-directed therapies (26). To explore the relationship between serum CEA levels and tumor CEACAM5 expression in lethal mCRPC subtypes, we assayed banked serum samples collected concurrently with tumor tissue from 18 of the 34 patients represented in the UW mCRPC TAN TMA. We found a significant correlation between serum CEA levels and tumor CEACAM5 expression (r=0.40) based on H-score (Figure 1E). The correlation appeared to be driven primarily by patients with NEPC compared to other mCRPC subsets (Figure S1, A and B) but subgroup analysis was not statistically significant potentially due to limited sample size. These data suggest that serum CEA could be a valuable adjunct clinical biomarker of NEPC and should be investigated further as a part of prospective clinical trials.

Genomic profiling of prostate cancer by next-generation sequencing has identified distinct molecular disease subtypes (27). We performed a limited exploratory analysis of whole exome sequencing of 38 prostate cancer tissues (17 CEACAM5⁺ and 21 CEACAM5⁻) from 28 of 34 patients represented on the UW mCRPC TAN TMA. Our analysis focused on a

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subset of genes commonly altered in mCRPC including *RB1* and *TP53* and genes in the PI3K/AKT signaling pathway (Table S). Monoallelic or biallelic copy loss of *RB1*, *TP53*, and *PTEN* appeared to be equally common in CEACAM5⁺ and CEACAM5⁻ mCRPC tissues, at frequencies consistent with prior reports (8,28). Predicted functional mutations were observed in *RB1* and *TP53*, and the mutational frequency was similar in CEACAM5⁺ and CEACAM5⁻ tissues. Monoallelic or biallelic copy loss of *FOXO3*, *MAP3K7*, and *RRAGD* was enriched in CEACAM5⁺ samples compared to CEACAM5⁻ samples by a factor of two. *MAP3K7* loss has specifically been reported to promote the development of clinically aggressive prostate cancer, and is associated with AR loss and neuroendocrine differentiation (29).

As tissues were collected from multiple metastatic sites (Tables S1 and S2) and variable CEACAM5 expression was identified within tissues, we next characterized the intra-patient phenotypic heterogeneity of mCRPC in the NEPC samples from the UW mCRPC TAN cohort. Four of eight (50%) patients with NEPC had mixed disease based on the presence of additional histologic phenotypes at other tumor sites (Figure 1F). To evaluate CEACAM5 expression in the context of this intra-patient heterogeneity, we examined all cores from each of these eight NEPC patients. Five of eight patients (62.5%) were found to have CEACAM5⁺ NEPC (Patients 2, 5, 6, 7, and 8). In these five cases, CEACAM5 expression was present at all NEPC tissue sites, albeit with variability in the frequency of CEACAM5⁺ cells between sites (Figure 1F). Additionally, the metastatic samples within these five patients that lacked CEACAM5 expression exhibited non-NEPC phenotypes (Figure 1F). These data further demonstrate enhanced CEACAM5 expression in NEPC, not only across a diverse series of patients, but also within patients harboring phenotypically heterogeneous mCRPC.

We also profiled CEACAM5 expression by IF in a normal human organ TMA (Tables S1 and S3). Consistent with prior reports, CEACAM5 expression was detectable at low levels in multiple healthy tissues including the lung, stomach, small intestine, and colon (Figure S2, A–C) (14,30,31). However, the intensity of CEACAM5 staining in normal organs was significantly lower than in NEPC samples represented in the UW mCRPC TAN TMA (Figure 1D). This difference in expression could signify a therapeutic window for agents directed at CEACAM5 when applied to NEPC. Collectively, these results provide a comprehensive assessment of CEACAM5 expression in patients with lethal mCRPC, including NEPC, and in healthy human tissues.

CEACAM5 expression relative to other targetable cell surface antigens in prostate cancer

Multiple clinically relevant prostate cancer antigens including trophoblast cell surface antigen 2 (Trop2), prostate-specific membrane antigen (PSMA), and prostate stem cell antigen (PSCA) are the focus of intense clinical development for mCRPC. The Trop2directed ADC sacituzumab govitecan (IMMU-132) is currently being evaluated in a phase II study for mCRPC (32). PSMA bispecific T cell engagers, PSMA radioligand therapies, and PSMA and PSCA chimeric antigen receptor T cell therapies are also under clinical investigation for mCRPC. We focused on characterizing the co-expression of CEACAM5 and these prostate cancer antigens in lethal mCRPC using a multiplex IF (mIF) staining

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panel on the UW mCRPC TAN TMA (Figure S3). mIF image analysis demonstrated inverse patterns of 1) CEACAM5 and 2) Trop2, PSMA, and PSCA staining frequencies and intensities in NEPC and ARPC tissue cores (Figure 2, A and B). Specifically, CEACAM5 expression was enriched in NEPC while Trop2, PSMA, and PSCA expression was heightened in ARPC. Further, PSMA and PSCA were frequently expressed in Trop2⁺ cores in ARPC but not in NEPC, DNPC, or AMPC (Figure 2C). These results are consistent with the prior characterization of Trop2 as an epithelial marker and the established androgenregulated nature of PSMA and PSCA expression (33,34). In contrast, Trop2, PSMA, and PSCA were much less frequently expressed in CEACAM5⁺ cores in NEPC (Figure 2D).

We evaluated mIF data at a single-cell level across all ARPC and NEPC tissue cores to investigate more granular, digital relationships between 1) Trop2, PSMA, and PSCA coexpression in ARPC and 2) CEACAM5, Trop2, PSMA, and PSCA co-expression in NEPC. Trop2 and PSMA (r=0.42) but not PSCA (r=0.01) expression were correlated in ARPC cells (Figure 2E). On the other hand, CEACAM5 did not correlate with Trop2 (r=0) or PSMA (r=0.13) and weakly correlated with PSCA (r=0.27) expression in NEPC cells (Figure 2F). The variable co-expression of Trop2, PSMA, and/or PSCA indicate the presence of highly heterogeneous ARPC cell populations in lethal mCRPC. Further, these findings suggest that diagnostic and therapeutic modalities under investigation to target Trop2, PSMA, and PSCA in prostate cancer may not effectively localize and treat CEACAM5⁺ NEPC.

Association between ASCL1 and CEACAM5 expression in NEPC

CEACAM5 is highly expressed in colorectal cancer where prior studies have implicated transforming growth factor beta (TGF-β) and retinoic acid signaling in *CEACAM5* transcriptional regulation (35,36). However, little is known about the regulation of *CEACAM5* expression in other cancer types including NEPC. Based on published literature, we discovered that CEACAM5 is expressed in some neuroendocrine carcinomas such as medullary thyroid carcinoma (MTC) and SCLC but not others like Merkel cell carcinoma (37,38). MTC arises from parafollicular cells which represent calcitonin-secreting neuroendocrine cells of the thyroid that require ASCL1 for their development (39). In SCLC, *CEACAM*5 expression is specifically enriched in the ASCL1^{high} subtype over other subtypes including NeuroD1^{high} SCLC (Figure S4, A and B). In contrast, Merkel cell carcinoma does not express ASCL1 and instead uniformly expresses NeuroD1 (37,40).

Based on these associations in other neuroendocrine carcinomas, we postulated that ASCL1 may regulate CEACAM5 expression in NEPC. To explore this possibility, we first examined the two available cell line models of NEPC, NCI-H660 and MSKCC EF1. Previously, we have shown that NCI-H660 cells express CEACAM5 and MSKCC EF1 cells do not (14). Transcriptome profiling revealed differential enrichment of *ASCL1* in NCI-H660 and *NEUROD1* in MSKCC EF1 cells (Figure 3A), consistent with our hypothesis. We further examined gene expression data from Stand Up To Cancer (SU2C) mCRPC biopsies (41), UW mCRPC TAN rapid autopsies (42), and the LuCaP patient-derived xenograft (PDX) series (42) to scrutinize *CEACAM5*, *ASCL1*, and *NEUROD1* expression in NEPC. Across these three datasets, *CEACAM5* expression generally associated with *ASCL1* expression but not *NEUROD1* expression in NEPC samples (Figure 3B). In the SU2C dataset, *CEACAM5*

expression was strongly correlated with *ASCL1* (r=0.95), but not *NEUROD1* (r=0.12) across mCRPC samples demonstrating a neuroendocrine score of >0.4 consistent with NEPC (Figure 3, C and E). The Beltran 2016 NEPC cohort (9) also showed a positive correlation for *CEACAM5* and *ASCL1* (r=0.75) and interestingly *NEUROD1* to a lesser extent (r=0.44) (Figure 3, D and F). The correlation between *ASCL1* and *NEUROD1* expression was negative (r=-0.27) in the SU2C dataset while the same comparison showed a positive correlation (r=0.39) in the Beltran dataset (Figure 3, G and H). These findings may reflect increased representation of mixed ASCL1^{high} and NeuroD1^{high} NEPC tumors in the Beltran dataset. Of note, Delta-like 3 (DLL3) is a Notch ligand enriched in NEPC (43) that is the target of multiple therapeutics in clinical development for SCLC and is known to be regulated by ASCL1 (44). *CEACAM5* expression correlated with *DLL3* expression in the SU2C (r=0.54) and Beltran 2016 NEPC (r=0.46) datasets (Figure S5, A and B), suggesting that both genes might be regulated by similar programs.

Regulation of CEACAM5 expression during neuroendocrine transdifferentiation of prostate cancer

To uncover possible cis-regulatory elements involved in the transcriptional regulation of CEACAM5 in prostate cancer, we examined chromatin accessibility of the CEACAM5 gene locus using Assay for Transposase-Accessible Chromatin using sequencing (ATAC-seq) in multiple prostate cancer cell lines, including the NEPC cell lines NCI-H660 and MSKCC EF1 and the AR⁺ cell lines 22Rv1 and LNCaP95. We identified a differential chromatin accessibility peak located at -191 to -92 upstream of the CEACAM5 transcriptional start site encompassing FANTOM5 Cap Analysis of Gene Expression (CAGE) tags of promoter elements in the CEACAM5⁺ NCI-H660 cell line but not in the CEACAM5⁻ MSKCC EF1. 22Rv1, or LNCaP95 cell lines (Figure 4A). This peak overlaps with the previously described core promoter region spanning -403 to -124 of the CEACAM5 gene locus (45) and was also prominent in pan-cancer The Cancer Genome Atlas (TCGA) ATAC-seq data (46) in tumor types where CEACAM5 is expressed including colorectal (COAD), esophageal (ESCA), gastric (STAD), and breast cancer (BRCA) (Figure 4A). Consistent with these findings, a coinciding DNase I hypersensitivity site was observed in CEACAM5⁺ normal colon tissues but not in CEACAM5⁻ normal breast tissues analyzed by the Encyclopedia of DNA Elements (ENCODE) Project (Figure S6). In addition, the peak heights of the DNase I hypersensitivity site corresponded to reported levels of CEACAM5 expression in colorectal and breast cancer cell lines (Figure S6).

Inferred transcription factor binding from ATAC-seq indicated enhanced activity of ASCL1 in NCI-H660 cells and NeuroD1 in MSKCC EF1 cells (Figure 4B) which is in concert with their differential expression in these cell lines. However, functional validation studies with short hairpin RNA (shRNA)-mediated knockdown of ASCL1 in NCI-H660 cells and ectopic expression of ASCL1 in MSKCC EF1 cells had no discernable effect on CEACAM5 expression (Figure 4C). ASCL1 and NeuroD1 knockdown in the respective NCI-H660 and MSKCC EF1 cells lines was detrimental to cell viability compared to controls (Figure S7, A–C), indicating perhaps that these lines are genetically hardwired and intolerant of perturbations to these transcription factors. The data could also imply that ASCL1 may not regulate CEACAM5 expression through direct transactivation. To corroborate this idea, we

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examined published ASCL1 chromatin immunoprecipitation followed by sequencing (ChIPseq) data across multiple studies from ASCL1^{high} SCLC cell lines (12,47,48), including the NCI-H889 and NCI-H1755 cell lines which express outlier levels of CEACAM5 (Figure S8A). These analyses indicate the absence of ASCL1 binding peaks near the *CEACAM5* gene locus (Figure S8B) but the presence of previously characterized peaks associated with genes bound by ASCL1 such as *DLL3* and *BCL2 (12,44)* (Figure S8, C and D). We therefore hypothesized that ASCL1, as a pioneer neural transcription factor, may epigenetically regulate *CEACAM5* by chromatin remodeling. We also reasoned that genetic studies in the hardwired NCI-H660 and MSKCC EF1 NEPC cell lines may not recapitulate dynamic epigenetic regulation of *CEACAM5* expression that occurs during the progression of human prostate cancer.

As an alternative approach, we developed a genetically defined system to induce neuroendocrine transdifferentiation of prostate cancer. We introduced ASCL1 and other factors causally associated with neuroendocrine transdifferentiation of prostate cancer including dominant-negative TP53 R175H, shRNA targeting RB1 (shRb1), and MYCN either alone or in combination into the androgen-independent ARPC cell line C4-2B. While C4–2B cells do not express CEACAM5 at baseline, we discovered that all conditions in which ASCL1 was introduced stimulated expression of CEACAM5 and the neuroendocrine markers synaptophysin (SYP) and insulinoma-associated protein 1 (INSM1) (Figure 4D). In contrast, all other C4-2B conditions in which ASCL1 was omitted did not exhibit neuroendocrine differentiation (Figure 4D). We discovered that ectopic expression of NeuroD1 within this system also induced CEACAM5, SYP, and INSM1 expression (Figure 4E). Notably, expression of ASCL1 and/or NeuroD1 downregulated AR and AR-dependent NK3 homeobox 1 (NKX3–1) expression (Figure 4E), indicating that these factors may be critical in orchestrating lineage reprogramming from ARPC to NEPC. We also observed that overexpression of NeuroD1 induced ASCL1 expression and the introduction of both ASCL1 and NeuroD1 further enhanced CEACAM5 expression (Figure 4E).

We evaluated a second ASCL family member, ASCL2, in the C4–2B cell line to determine whether these effects may be specific to ASCL1. ASCL2 is also a pioneer transcription factor involved in the specification of multiple lineages including trophectoderm (49), T-helper cells (50), and intestinal stem cells (51). Further, ASCL2 expression is associated with the non-neuroendocrine POU2F3^{high} variant subtype of SCLC (52) and is enriched in multiple cancer types where CEACAM5 is commonly expressed (Figure S9, A–C). Enforced expression of *ASCL2*, in combination with *TP53* R175H, shRB1, and *MYCN*, in C4–2B cells suppressed AR and NKX3–1 expression, but did not upregulate CEACAM5, SYP, or INSM1 expression (Figure 4F). These data emphasize the differential competence of pioneer transcription factors to effect neuroendocrine transdifferentiation of prostate cancer and induce CEACAM5 expression within this system.

To investigate the epigenetic regulation of the core promoter of *CEACAM5* in our C4–2B functional studies, we developed ATAC-quantitative polymerase chain reaction (qPCR) assays incorporating universal normalization control primers targeting *AK5* and three unique primer pairs targeting the differential chromatin accessible and DNase I hypersensitive site we identified in the core promoter of *CEACAM5*. The assays were validated using ATAC

libraries generated from the NCI-H660 and MSKCC EF1 cell lines (Figure 4G). C4–2B cells reprogrammed with ASCL1 revealed a five-fold enhancement in chromatin accessibility at the core promoter of *CEACAM5* relative to control conditions (Figure 4H). In contrast, no increase in chromatin accessibility was associated with ASCL2 and only a minor, non-significant increase was associated with NeuroD1 (Figure 4H). These results point to one mechanism by which neuroendocrine transdifferentiation driven by ASCL1 may be epigenetically linked to CEACAM5 expression in prostate cancer.

In vitro specificity and cytotoxicity of labetuzumab govitecan in NEPC

We previously reported that a CEACAM5 chimeric antigen receptor T cell therapy demonstrates antitumor activity in NEPC cell line models (14). However, we recognized the lengthy time horizon and numerous hurdles to advancing this type of cancer treatment to the clinic. We therefore concentrated on studies to target CEACAM5 in prostate cancer by redirecting the established CEACAM5 ADC labetuzumab govitecan with the anticipation that compelling results could lead to an accelerated path to clinical translation. We first characterized the specific binding of labetuzumab, the humanized antibody component of labetuzumab govitecan, to prostate cancer cell lines with native and engineered expression of CEACAM5. CEACAM5 was stably expressed in three CEACAM5⁻ prostate cancer cell lines: the AR⁺ line 22Rv1, the AR⁻ line DU145, and the NEPC line MSKCC EF1 (Figure 5A). We detected labetuzumab binding in all four cell lines expressing CEACAM5 as well as the natively CEACAM5⁺ NCI-H660 cell line, but not in isogenic negative control cell lines (Figure 5B).

We then investigated the genotoxic effects of labetuzumab govitecan on the prostate cancer cell line panel by measuring γ H2AX, a marker of double-stranded DNA (dsDNA) breaks. Cells were incubated with labetuzumab govitecan for 30 minutes, extensively washed to remove unbound drug, and propagated in cell culture for 16 hours prior to staining and analysis. Labetuzumab govitecan provoked greater γ H2AX signal in the CEACAM5⁺ 22Rv1 cell line relative to the control 22Rv1 cell line and compared to incubation with the non-specific ADC, h679-SN-38 (Figure 5C). In contrast, SN-38 alone induced yH2AX in an antigen-independent manner in both the CEACAM5⁺ and CEACAM5⁻ 22Rv1 cell lines (Figure 5C). H679-SN-38, labetuzumab govitecan, and SN-38 did not generate substantial yH2AX signal in the DU145 and MSKCC EF1 cell lines, irrespective of CEACAM5 expression status (Figure 5, D and E). To determine the overall susceptibility of the cell lines to SN-38, we assessed γ H2AX levels following a longer exposure to SN-38 in culture. After a 16 hour incubation, SN-38 induced yH2AX in all three cell lines (Figure S10, A-C), albeit to different extents consistent with drug sensitivity based on IC₅₀ calculations from doseresponse curves in each of the cell lines with the exception of DU145 (Figure S10D). These data confirm the specificity of labetuzumab binding and the genotoxicity of labetuzumab govitecan in CEACAM5⁺ prostate cancer cell lines which generally correlates with the relative sensitivities of the lines to SN-38.

In vivo antitumor activity of labetuzumab govitecan in NEPC

We first examined the antitumor activity of labetuzumab govitecan *in vivo* using CEACAM5⁺ NCI-H660 NEPC cell line xenograft tumors established in NOD-*scid IL2ry*^{null}

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(NSG) mice. Mice were treated with labetuzumab govitecan, h679-SN-38, or vehicle by intraperitoneal injections weekly for a total of four treatments over 28 days. By day 17 and day 24, 100% of tumors in the labetuzumab govitecan treatment arm (n=10) and the h679-SN-38 arm (n=9) were undetectable, respectively (Figure S11A). In contrast, tumors in the vehicle treatment arm demonstrated uncontrolled growth (Figure S11A). No significant changes in mouse weight (Figure S11B) or body condition score (Figure S11C) were observed throughout the study at the 25 mg/kg dose. Four of nine (45%) vehicle-treated mice were sacrificed prior to completion of the study as they exceeded institutional tumor size restrictions (Figure S11D).

We next tested labetuzumab govitecan treatment in multiple LuCaP PDXs established from lethal mCRPC tissues (53) that express varying levels of CEACAM5. The LuCaP 49 and LuCaP 145.1 NEPC PDXs were classified as CEACAM5^{low/moderate} and CEACAM5^{high} expression models, respectively, based on intensity of immunohistochemical staining (Figure S12). Mice were treated with labetuzumab govitecan or h679-SN-38 at 25 mg/kg or vehicle by intraperitoneal injection every four days. Complete responses were observed in 100% of labetuzumab govitecan (n=10) and h679-SN-38-treated mice (n=8) bearing LuCaP 49 PDX tumors by day 14 (Figure 6A). Complete responses were also observed in 100% of labetuzumab govitecan-treated mice (n=8) with LuCaP 145.1 PDX tumors by day 14, while h679-SN-38 treatment suppressed tumor growth but did not eradicate tumors in any mice (Figure 6B). Importantly, the LuCaP 49 and LuCaP 145.1 tumor models were relatively resistant to cisplatin and etoposide chemotherapy (Figure 6, A and B) which is considered the standard-of-care frontline treatment for extensive stage NEPC.

In the LuCaP 49 study, the average weight loss in the labetuzumab govitecan group comparing treatment pre-enrollment to day 28 was 10%. However, this weight loss occurred within the first week of treatment and weights otherwise remained stable in all groups for the remainder of the study (Figure S13A). Additionally, no significant changes in body condition scores were observed (Figure S13A). No significant changes in weight or body condition score were observed in mice in the LuCaP 145.1 study (Figure S13B). Adverse effects on liver and kidney function are often reported in association with irinotecan chemotherapy. We performed serum chemistries on days 0, 14, and 28 to assess for these and other toxicities (Figure S14A). Across both studies, three of 18 (17%) labetuzumab govitecan-treated mice exhibited elevated aspartate aminotransferase (AST) levels at day 28 that were less than twice the upper limit of the reference range (Figure S14, B and C), indicating mild hepatotoxicity in these animals. Complete blood counts were also performed (Figure S14D). Across both studies, six of 18 (33%) labetuzumab govitecan-treated mice exhibited leukocytosis at day 28 (Figure S14E) with an increase in the neutrophil fraction (Figure S14F). Similar results were observed in the h679-SN-38 and cisplatin and etoposidetreated mice compared to vehicle-treated mice (Figure S14D).

Given the striking antitumor effects but mild toxicities associated with labetuzumab govitecan at the 25 mg/kg dose, we tested labetuzumab govitecan at a reduced dose with less frequent dosing. NSG mice bearing CEACAM5^{low/moderate} LuCaP 49 NEPC PDX tumors or CEACAM5^{high} LuCaP 176 AR^{low}/NE⁻ PDX tumors were treated with labetuzumab govitecan or h679-SN-38 at 25 mg/kg or 12.5 mg/kg by intraperitoneal injection weekly. In

the LuCaP 49 model, both dose levels of labetuzumab govitecan led to complete responses in 100% of mice (n=7) by day 21. While both dose levels of h679-SN-38 inhibited tumor growth, only the 25 mg/kg dose led to tumor eradication (Figure 6C). The LuCaP 176 model displayed more of a dose-dependent treatment response compared to LuCaP 49. The 25 mg/kg dose of labetuzumab govitecan led to complete responses in 100% of mice (n=6) by day 17. In contrast, tumor eradication was observed in three of six (50%) of mice treated with 12.5 mg/kg of labetuzumab govitecan (Figure 6D). Both dose levels of h679-SN-38 slowed tumor growth but did not diminish tumor volume. No significant changes in weight or body condition score were detected for either study (Figure S13, C and D). These studies highlight the potency and efficacy of labetuzumab govitecan in CEACAM5⁺ prostate cancer PDX models by demonstrating that a reduced dose and administration schedule are also capable of achieving complete responses.

Discussion:

The development and translation of safe and effective new therapies for NEPC are necessary to alter the course of this highly aggressive and deadly disease. The identification of tumorrestricted cell surface antigens and their targeting with antibodies, ADCs, or adoptive cell therapies has yet to make a clinical impact on the management of NEPC. Recent, substantial efforts have focused on targeting the ASCL1-regulated Notch ligand DLL3, but advanced clinical development of the promising DLL3-targeting ADC rovalpituzumab tesirine was discontinued due to excessive toxicity likely related to the pyrrolobenzodiazepine dimer payload (54). Our work indicates that CEACAM5 is a compelling cell surface antigen for therapeutic targeting in NEPC as it is expressed in over 60% of NEPC across multiple cohorts of patients, including those with end-stage disease, and demonstrates limited systemic expression. To accelerate therapeutic development, we redirected the existing CEACAM5-targeted ADC, labetuzumab govitecan, currently being evaluated for metastatic colorectal cancer, to NEPC. In multiple preclinical studies, labetuzumab govitecan treatment of patient-derived CEACAM5-expressing tumors resulted in complete responses. Labetuzumab govitecan is similar in design to the ADC sacituzumab govitecan, which was recently approved for the treatment of metastatic triple-negative breast cancer and has received fast-track designation for metastatic urothelial carcinoma and non-small cell lung cancer. Labetuzumab govitecan and sacituzumab govitecan share the same unique hydrolyzable linker, as well as SN-38 as the cytotoxic payload, and have collectively demonstrated manageable toxicities in patients across several clinical studies (21,55,56).

Our studies examining the expression of CEACAM5 and other relevant cell surface antigens in a large cohort of lethal mCRPC samples provide significant biological insights and have important clinical implications. We identified a correlation between serum CEA levels and CEACAM5 expression in tumor tissues across a small series of end-stage mCRPC patients, which appears most prominent in cases of NEPC. The measurement of serum CEA in the appropriate prostate cancer context (e.g. disease progression with a low prostate-specific antigen) might have value for diagnostic and/or therapeutic purposes in the identification, treatment selection, and disease monitoring of patients with CEACAM5⁺ NEPC. Further investigation of serum CEA as a biomarker in clinical trials for NEPC will be necessary to determine its utility. While expression of Trop2, PSMA, and PSCA has been reported to be

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relatively homogeneous in early stages of prostate cancer, our results indicate that there is significant heterogeneity in their expression in end-stage mCRPC. Our results show that CEACAM5 expression marks a biologically distinct subset of prostate cancer that has relatively minor overlap with Trop2, PSMA, or PSCA expression. The clinical implication is that CEACAM5⁺ NEPC will not be detected by emerging imaging modalities and may be impervious to treatment approaches directed at Trop2, PSMA, or PSCA.

We also established the functional relevance of ASCL1 and NeuroD1 expression in driving neuroendocrine lineage reprogramming of prostate cancer. These transcription factors appear to induce a simultaneous reduction in AR expression, AR-dependent NKX3–1 expression, and the acquisition of neuroendocrine differentiation markers. Global epigenetic reprogramming of prostate cancer induced by these pioneer transcription factors may coordinately silence the AR-enforced epithelial cancer program and engender neuroendocrine cancer programs. Studies are underway to characterize the contributions of ASCL1 and NeuroD1 to the process of neuroendocrine transdifferentiation of prostate cancer through the integration of genetic, transcriptomic, and epigenetic approaches. Our findings indicate that the biology of NEPC may parallel that of SCLC in that they share ASCL1^{high} and NeuroD1^{high} disease subtypes. However, whether the tuft cell variant POU2F3^{high} or YAP1^{high} subtypes found in SCLC (11) also exist in NEPC has yet to be determined. A recent publication suggests potential biological divergence of NEPC from SCLC in that YAP1 expression is de-enriched in NEPC compared to other subsets of mCRPC (57).

A mechanistic understanding of the regulation of CEACAM5 expression and its specificity to certain cancers has generally been lacking. Previous studies have shown that the wide-ranging modulation of cancer cell differentiation states by retinoic acid or sodium butyrate treatment impacts CEACAM5 expression (36). Our work demonstrates that ASCL1 promotes neuroendocrine transdifferentiation of prostate cancer which results in increased chromatin accessibility of the core promoter of *CEACAM5*. We suspect that this mechanism of *CEACAM5* regulation by ASCL1 may be conserved in other neuroendocrine carcinomas including SCLC, but additional functional studies will be necessary for confirmation. An interesting question arising from our findings is whether additional pioneer transcription factors may similarly modulate the epigenomes of other tumor types to permit CEACAM5 expression in non-neuroendocrine cancer cell contexts.

The diversity of prostate cancer phenotypes that emerge with castration-resistance and their coexistence in late-stage patients indicate that single-targeted therapies may be ineffective. The existence of multiple subtypes of NEPC that may impact expression of target antigens like CEACAM5 and DLL3 in NEPC further compound this issue. Targeted prostate cancer therapies with multiple mechanisms of action or combinations of treatments may be necessary to conquer such diversity. Our *in vivo* studies demonstrate strong antitumor activity of labetuzumab govitecan and, to a lesser extent, the non-specific h679-SN-38 ADC which is likely a consequence of linker hydrolysis and systemic release of SN-38. Labetuzumab govitecan therefore represents a monotherapy that delivers both regional, antigen-specific and systemic, non-specific tumor killing. The benefit of a moderately stable ADC linker may be increased efficacy in patients with inter- and intra-tumoral heterogeneity.
such as that observed in cases of mixed NEPC which occurs in up to 50% of cases. This bystander effect has also been demonstrated in a number of other tumor types for the sister molecule sacituzumab govitecan (58,59).

The results of these studies have led to planning for a forthcoming phase I/II clinical trial of labetuzumab govitecan for patients with CEACAM5⁺ NEPC. CEACAM5 is also expressed in other neuroendocrine carcinomas including SCLC and MTC. More than half of SCLC are ASCL1^{high} (11) with the majority expressing CEACAM5, while advanced MTC are almost uniformly ASCL1^{high} and express CEACAM5 (38). Investigation of whether labetuzumab govitecan is effective in these and other CEACAM5⁺ neuroendocrine carcinomas may also be warranted.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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Statement of Translational Relevance:

Neuroendocrine prostate cancer (NEPC) is an aggressive subtype of castration-resistant prostate cancer without effective treatments. Here we examined the expression of CEACAM5 compared to other relevant prostate cancer antigens in a series of lethal, metastatic prostate cancers. CEACAM5 is preferentially expressed in NEPC and tumor expression appears to correlate with serum CEA levels in NEPC cases. Through functional genomics studies, we illustrate the potential role of the pioneer transcription factor ASCL1 in the epigenetic regulation of CEACAM5 expression and neuroendocrine transdifferentiation of prostate cancer. Lastly, we redirect the anti-CEACAM5-SN38 antibody-drug conjugate, labetuzumab govitecan, for preclinical studies in prostate cancer and demonstrate tumor eradication in multiple xenograft models of CEACAM5⁺ prostate cancer including NEPC. Overall, we describe the scope of CEACAM5 gene regulation by ASCL1, and provide evidence to support imminent clinical investigation of labetuzumab govitecan in men with CEACAM5⁺ NEPC.



Figure 1. CEACAM5 expression is enriched in the NEPC subtype of mCRPC.

(A) Representative TMA images of individual cores with tumor and stroma annotation as well as fluorescent CEACAM5 (red) and nuclear DAPI (blue) staining (scale bars, 200 µm; original magnification, 20X). (B) Intensity of CEACAM5 staining, (C) percentage of cells with CEACAM5 expression, and (D) H-scores of neuroendocrine (NEPC, n=20), androgen receptor positive (ARPC, n=70), double-negative (DNPC, n=14), and amphicrine (AMPC, n=3) prostate cancers tissue samples. (E) CEA levels in mCRPC patient serum correlated to relative CEACAM5 protein expression (mIF H-score) in corresponding NEPC (n=5) and

non-NEPC (ARPC or DNPC) (n=13) patient tumor samples. CEA normal range: 0–5.0 ng/ml. (F) CEACAM5⁺ cell percentage within the tumor region of cores from all UW mCRPC TAN TMA patient donors with at least one NEPC classified biopsy core. Histograms depict mean + SD. ** p<0.01; *** p<0.001; **** p<0.0001. Red Dash = CEACAM5 staining intensity positive threshold. r=correlation coefficient. Kruskal-Wallis p values are shown for plots C and D. Spearman rank correlation coefficient (r) and p value is shown for plot E.

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Figure 2. CEACAM5 expression relative to other targetable prostate cancer cell surface antigens. (A) Percentage of cells expressing CEACAM5, Trop2, PSMA, and PSCA, and (B) staining intensity from mIF of ARPC (n=70), NEPC (n=20), DNPC (n=14), and AMPC (n=3) tissue cores. (C) Co-expression of PSMA and PSCA in Trop2⁺ cells per core. (D) Co-expression of Trop2, PSMA, and PSCA in CEACAM5⁺ cells per core. (E) Quantitative single-cell mIF signal intensities of proteins (rows) in cells from ARPC (n=655,676) and (F) NEPC cores (n=113,509). Error bars represent \pm SD. * p<0.05; ** p<0.01; *** p<0.001; **** p<0.001.

Kruskal-Wallis p values are shown for plots A-D. Pearson correlation coefficient (r) and P values for each measured protein is shown numerically next to heatmap rows.



Figure 3. Association of ASCL1 and CEACAM5 expression in NEPC.

(A) RNA-seq gene expression heatmap of *ASCL1* and *NEUROD1* in NCI-H660, MSKCC EF1, 22Rv1, and LNCaP95 cell lines. (B) RNA-seq gene expression heatmap of NEPC samples (columns) from the Stand Up To Cancer (SU2C) mCRPC cohort, the University of Washington Tissue Acquisition Necropsy (UW TAN) lethal mCRPC cohort, and LuCaP patient-derived xenograft lines. (C-D) Correlation dot plots of CEACAM5 and ASCL1, (E-F) CEACAM5 and NEUROD1, and (G-H) ASCL1 and NEUROD1 gene expression in NEPC samples defined by a neuroendocrine gene signature score >0.4 in the SU2C dataset

(n=10) and the Beltran 2016 NEPC dataset (n=15). Pearson correlation coefficients (r) are shown for correlative gene expression analyses.

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Figure 4. Regulation of CEACAM5 expression during neuroendocrine transdifferentiation. (A) Integrative Genomics Viewer tracks showing an ATAC-seq peak at the promoter (orange arrow) upstream of the transcriptional start site of *CEACAM5*. (B) Lineplots demonstrating inferred ASCL1 and NeuroD1 activity in the NCI-H660 and MSKCC EF1 cell lines using differential transcription factor binding motif footprinting of ATAC-seq data. (C) Immunoblots demonstrating CEACAM5 protein expression in NCI-H660 cells with ASCL1 knockdown by shRNA and in MSKCC EF1 cells with ectopic ASCL1 expression. (D) Immunoblots showing CEACAM5 and neuroendocrine differentiation marker expression in

C4–2B cells overexpressing ASCL1, (E) NeuroD1, or (F) ASCL2 in the context of p53 R175H, Rb1 knockdown, and/or overexpression of N-Myc. Chromatin accessibility of the *CEACAM5* promotor determined by ATAC-qPCR in (G) NCI-H660 cells relative to MSKCC EF1 cells and (H) C4–2B control cells and cells reprogrammed with ASCL1, ASCL2, or NeuroD1. P=p53 R175H; R=shRB1; N=N-Myc; A=ASCL1. Histograms depict means + SD for biological replicates each with two technical replicates. * p<0.05. Student's T test p values are shown for panel G and Kruskal-Wallis p values are shown for panel H.

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Figure 5. Labetuzumab govitecan induces dsDNA damage in a CEACAM5-specific manner. (A) CEACAM5 surface protein expression determined by flow cytometry in prostate cancer cell lines transduced with lentiviral expression constructs. (B) Labetuzumab binding to CEACAM5 in prostate cancer cell lines. Measurement of intracellular γ H2AX staining of (C) 22Rv1, (D) DU145, and (E) MSKCC EF1 cells 16 hours after treatment with h679-SN-38, labetuzumab govitecan, or SN-38 for 30 minutes on ice. MFI = Mean fluorescence intensity. Histograms depict means + SD for experimental duplicates.

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Tumor volumes monitored bi-weekly are shown for (A-B) single dose trials and (C-D) two dose trials. (A-B) Mice received eight treatments (red arrows) over 28 days with vehicle, h679-SN-38 (25 mg/kg), or labetuzumab govitecan (25 mg/kg). Cisplatin (5 mg/kg) was administered on day 0 and etoposide (8 mg/kg) was administered on days 0 and 2 (orange arrows). (C-D) Mice received four treatments (red arrows) over 28 days with vehicle, h679-SN-38, or labetuzumab govitecan at the doses indicated. Line graphs depict means ± SD. *

p<0.05; ** p<0.01; *** p<0.001; **** p<0.0001. Day 28 ANOVA p values are shown for all panels.



TRANSFORMER: A Randomized Phase II Study Comparing Bipolar Androgen Therapy Versus Enzalutamide in Asymptomatic Men With Castration-Resistant Metastatic Prostate Cancer

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PURPOSE Prostate cancer (PCa) becomes resistant to androgen ablation through adaptive upregulation of the androgen receptor in response to the low-testosterone microenvironment. Bipolar androgen therapy (BAT), defined as rapid cycling between high and low serum testosterone, disrupts this adaptive regulation in castration-resistant PCa (CRPC).

METHODS The TRANSFORMER (Testosterone Revival Abolishes Negative Symptoms, Fosters Objective Response and Modulates Enzalutamide Resistance) study is a randomized study comparing monthly BAT (n = 94) with enzalutamide (n = 101). The primary end point was clinical or radiographic progression-free survival (PFS); crossover was permitted at progression. Secondary end points included overall survival (OS), prostate-specific antigen (PSA) and objective response rates, PFS from randomization through crossover (PFS2), safety, and quality of life (QoL).

RESULTS The PFS was 5.7 months for both arms (hazard ratio [HR], 1.14; 95% CI, 0.83 to 1.55; P = .42). For BAT, 50% decline in PSA (PSA50) was 28.2% of patients versus 25.3% for enzalutamide. At crossover, PSA50 response occurred in 77.8% of patients crossing to enzalutamide and 23.4% to BAT. The PSA-PFS for enzalutamide increased from 3.8 months after abiraterone to 10.9 months after BAT. The PFS2 for BAT→enzalutamide was 28.2 versus 19.6 months for enzalutamide→BAT (HR, 0.44; 95% CI, 0.22 to 0.88; P = .02). OS was 32.9 months for BAT versus 29.0 months for enzalutamide (HR, 0.95; 95% CI, 0.66 to 1.39; P = .80). OS was 37.1 months for patients crossing from BAT to enzalutamide versus 30.2 months for the opposite sequence (HR, 0.68; 95% CI, 0.36 to 1.28; P = .225). BAT adverse events were primarily grade 1-2. Patient-reported QoL consistently favored BAT.

CONCLUSION This randomized trial establishes meaningful clinical activity and safety of BAT and supports additional study to determine its optimal clinical integration. BAT can sensitize CRPC to subsequent antiandrogen therapy. Further study is required to confirm whether sequential therapy with BAT and enzalutamide can improve survival in men with CRPC.

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INTRODUCTION

Since the discovery by Charles Huggins of remarkable palliative benefit from castration in men with symptomatic prostate cancer (PCa), the mainstay of treatment has been inhibition of androgen receptor (AR) function through primary androgen deprivation (ADT).¹ Although highly effective, therapeutic resistance is almost universal. Second-generation therapies that potently inhibit AR have become standard therapy based on modest improvements in survival

versus placebo,^{2,3} but resistance increases with each subsequent line of AR-directed therapy.⁴⁻⁶ Importantly, PCa cells can develop resistance to androgen ablation through an adaptive marked upregulation of AR over time in response to low-androgen conditions (Data Supplement, online only).⁷⁻⁹ Preclinical studies document that adaptive AR upregulation produces therapeutic vulnerability allowing PCa cells to be killed by exposure to supraphysiologic testosterone.⁹⁻¹² Episodic exposure to supraphysiologic testosterone can

ASSOCIATED CONTENT Data Supplement

Protocol

Author affiliations and support information (if applicable) appear at the end of this article.

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CONTEXT

Key Objective

Is bipolar androgen therapy (BAT) superior to enzalutamide and does BAT overcome antiandrogen resistance in patients with metastatic prostate cancer progressing on abiraterone?

Knowledge Generated

BAT was not superior to enzalutamide but demonstrated similar time to progression and prostate-specific antigen response following treatment with abiraterone. BAT is safe, has meaningful clinical activity, can enhance quality of life, and markedly improve the magnitude and duration of response to enzalutamide.

Relevance

Sequential BAT→enzalutamide could be a safe and effective single third-line therapy for men with metastatic castrationresistant prostate cancer progressing on abiraterone. Further study is warranted to define the potential for this sequential treatment to produce significant survival improvement in men with castration-resistant prostate cancer.

produce downregulation of AR levels leading to potential resensitization to androgen-ablative therapies (Data Supplement).¹³ Initial clinical studies documented the safety of rapid cycling between polar extremes of supraphysiologic and near-castrate serum testosterone, a concept termed bipolar androgen therapy (BAT), in asymptomatic men with metastatic castration-resistant PCa (CRPC).^{14,15} The key findings have been that BAT was safe, did not accelerate disease progression, produced sustained prostate-specific antigen (PSA) and objective responses (ORs), and resensitized response to subsequent antiandrogens.^{14,15}

Here, we hypothesized that BAT would have superior efficacy against PCa made resistant as a result of chronic exposure to low androgen and adaptively sensitize these cells to antiandrogens. We conducted the TRANSFORMER (Testosterone Revival Abolishes Negative Symptoms, Fosters Objective Response and Modulates Enzalutamide Resistance) trial to compare the effects of BAT versus the antiandrogen enzalutamide in asymptomatic men with CRPC progressing on abiraterone. Additionally, we explored the effect of sequential exposure to AR agonists or antagonists by allowing crossover to the opposite treatment upon progression.

METHODS

Trial Design

TRANSFORMER (ClinicalTrials.gov identifier: NCT02286921) was a multicenter, open-label, randomized, phase II trial whose objective was to determine the effectiveness of BAT versus enzalutamide on clinical or radiographic progression-free survival (PFS) in men with metastatic CRPC (mCRPC) progressing on abiraterone. Secondary objectives were to determine the effects on overall survival (OS), PSA-PFS, adverse events (AEs), and quality of life (QoL). Although crossover was not mandated, patients with radiographic progression on either arm who continued to meet eligibility requirements had the option to cross over to the opposite

treatment. The objectives for this crossover were to evaluate time to PSA progression and time to second PSA progression from randomization through crossover treatment (termed PFS2). PSA50 response was an end point for both study phases.

Patients and Treatment

Eligible patients were asymptomatic with mCRPC documented by computed tomography (CT), technetium-99 bone scan, or both and Eastern Cooperative Oncology Group (ECOG) performance status (PS) score of ≤ 2 . Patients had evidence of PSA or radiographic progression after treatment with abiraterone acetate and prednisone. Patients were ineligible if they had pain because of mCRPC requiring treatment intervention or opioids or prior treatment with docetaxel or cabazitaxel for mCRPC. The Clinical Protocol and Data Supplement are available with the full text of this article (online only).

Patients were randomly assigned (1:1) to receive testosterone cypionate (at US Food and Drug Administration [FDA]-approved dose of 400 mg intramuscularly once every 28 days) or enzalutamide (160 mg by mouth daily) until clinical or radiographic progression or prohibitive toxicity. Patients were concurrently maintained on continuous testosterone suppression via surgical castration or luteinizing hormone-releasing hormone agonists or antagonists. At progression, asymptomatic patients who continued to meet eligibility requirements were allowed to cross over to alternate therapy. Clinical status and PSA were assessed each cycle during initial phase and crossover. CT and bone scan were obtained every 12 weeks during initial phase but not at crossover. Patients on either study arm with clinical progression because of pain from PCa were not permitted to cross over. QoL was assessed at baseline and 1, 3, 6, and 12 months postrandomization using RAND-SF36 Quality of Life Survey, FACIT-F Version 4, I-PANAS-SF, International Index of Erectile Function (IIEF), and the Brief Pain Inventory, respectively.



FIG 1. TRANSFORMER CONSORT diagram. BAT, bipolar androgen therapy.

Randomization was performed centrally using a minimization approach, with stratification by length of prior abiraterone exposure (< or \geq 6 months) and clinical center.

Trial Oversight

The trial was designed and led by the principal investigator (S.R.D.) and co-investigators at Johns Hopkins (M.A.E. and E.S.A.). The trial was conducted at 17 US academic centers. The authors were solely responsible for writing the manuscript.

A Transformative Impact Award from the Department of Defense (DoD) provided financial support for trial conduct. DoD representatives reviewed and approved the protocol and consent documents at each participating site but were not otherwise involved in any study aspect. ADT, enzalutamide, testosterone cypionate, and all subsequent treatments were accessed and administered according to local standard practice. The authors vouch for the accuracy and completeness of the reported data and for fidelity to the protocol.

An independent data and safety monitoring committee reviewed the progress and results of the trial. The trial was conducted in accordance with the principles of Good

Clinical Practice guidelines and Declaration of Helsinki. The protocol was independently reviewed and approved as required at each participating institution. All patients provided written informed consent.

End Points

The primary end point of clinical or radiographic PFS was measured as the interval from randomization to the earliest sign of radiographic progression according to the criteria of the PCa Working Group 2 (PCWG2) for bone lesions and the RECIST version 1.1 for soft-tissue lesions, the development of symptoms or complications attributable to cancer progression, or the initiation of another anticancer treatment for PCa¹⁶ and censored at the date of last scan or clinical visit for those who did not have the event at the time of data cutoff. The secondary end point of OS was the interval from randomization to death and censored at the date of last known alive. PSA-PFS was measured as the interval from randomization to the time of PSA progression according to the PCWG2 criteria (a confirmed relative increase in the PSA level from the nadir value by $\geq 25\%$ and by ≥ 2 ng/mL) or censored at the last date of PSA assessment for patients without PSA progression. The secondary end point PFS2 was defined as the interval from randomization to second

TABLE 1. Characteristics of the Patients at Baseline

Characteristic	BAT $(n = 94)$	Enzalutamide (n = 101)
Median age (range), years	71.0 (45.0-87.0)	71.0 (49.0-91.0)
Race, n (%)		
American Indian	1 (1.1)	0
Asian	2 (2.1)	3 (3.0)
Black or African American	7 (7.4)	7 (6.9)
White	82 (87.2)	88 (87.1)
Other	2 (2.1)	3 (3.0)
Ethnic group, n (%)		
Hispanic or Latino	4 (4.3)	2 (2.0)
Not Hispanic or Latino	86 (91.5)	97 (96.0)
Unknown	4 (4.3)	2 (2.0)
ECOG PS, n (%)		
0	53 (56.4)	73 (72.3)
1	40 (42.6)	25 (24.8)
2	1 (1.1)	1 (1.0)
Missing	0	2 (2.0)
Gleason sum, n (%)		
≤ 5	4 (4.3)	1 (1)
6	4 (4.3)	13 (12.9)
7	22 (23.4)	27 (26.7)
8	21 (22.3)	10 (9.9)
9-10	39 (41.5)	44 (43.6)
Missing	4 (4.3)	6 (5.9)
Baseline PSA, mean (range)	44.3 (1.1-323.3)	50.6 (1.1-559.2)
Baseline alkaline phosphatase, mean (range)	113.3 (41-992)	94.1 (34-284)
Duration of prior abiraterone, months (%)		
\leq 6 months	18 (19.1)	19 (18.8)
> 6 months	76 (80.9)	82 (81.2)
Prior therapy type, n (%)		
Radiation (primary)	50 (53.2)	48 (47.5)
Surgery (prostatectomy)	40 (42.6)	47 (46.5)
Secondary hormonal therapy	91 (96.8)	97 (96.0)
Docetaxel chemotherapy	13 (13.8)	11 (10.9)
Investigational	21 (22.3)	20 (19.8)
Total number of metastases, median (range)	2 (1-10)	2 (1-8)
Patients with visceral metastases, n (%)	52 (55.3)	62 (61.4)

Abbreviations: BAT, bipolar androgen therapy; ECOG, Eastern Cooperative Oncology Group; PS, performance status; PSA, prostate-specific antigen.

PSA progression following crossover therapy. For patients who did not cross over, PFS2 was censored at the time of PFS or last follow-up with no progression on initial treatment. OR was defined as complete response or partial response per RECIST and PCWG2 among those with measurable baseline disease. AEs were graded according to the National Cancer Institute Common Terminology Criteria for Adverse Events, version 4.02. AE data were collected during the

treatment period, with a final safety assessment performed 30-42 days after the cessation of the trial regimen.

Statistical Analysis

Assuming a median PFS of 6 months in the enzalutamide group on the basis of two previous studies of enzalutamide in patients with mCRPC progressing on abiraterone, we determined that enrollment of 194 patients (with 156 PFS



FIG 2. Kaplan-Meier estimates of (A) PFS and (B) OS, (C) waterfall plot of PSA response to initial therapy, (D) subgroup analysis of OS. BAT, bipolar androgen therapy; ECOG, Eastern Cooperative Oncology Group; HR, hazard ratio; INF, infinity; OS, overall survival; PFS, progression-free survival; PSA, prostate-specific antigen.

events) would provide a power of 80% to detect a hazard ratio (HR) of 0.667 in the BAT group versus the enzalutamide group, with a one-sided type I error of 0.05. Two interim analyses of efficacy and futility for PFS were conducted as planned, the first after approximately 45% of the information and the second after 70% of the information. An independent data and safety monitoring committee reviewed interim data and recommended to continue to full accrual.

The primary efficacy end point PFS and the secondary efficacy end points PSA-PFS, OS, and PFS2 were based on

the intention-to-treat principle and included all patients who had undergone randomization. Patients who had undergone randomization and received a dose of any trial drug were included in safety analyses.

PFS and other time-to-event end points were estimated using Kaplan-Meier method, and each was compared between the arms using a stratified log-rank test, with stratification factor of duration of prior abiraterone treatment (< or \geq 6 months). The Cox regression model, stratified for the same baseline stratification factor, was used to estimate HRs between the two arms and

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TABLE 2. Prespecified Secondary Efficacy End Points (ITT Population)

End Point	n	BAT	95% CI	n	Enzalutamide	95% CI	HR	Р
Initial treatment								
Time to PSA progression, months	91	2.79	1.81 to 4.50	98	3.81	2.8 to 6.4	1.53 (1.08-2.19)	.0181
Unverified PSA50 response, n (%)	85	24 (28.2)		94	24 (25.5)			.7908
OR, n (%)	33	8 (24.2)		24	1 (4.2)			.072
Radiographic PFS, months	94	6.05	5.56 to 8.42	101	8.29	5.69 to 11.09	1.24 (0.87-1.77)	.2332
OS, months	94	32.9	28.2 to 37.3	101	29	26.2 to 35.5	0.95 (0.66-1.39)	.8015
OS, all patients	195	30.1	27 to 34.3					
Duration of abiraterone treatment								
< 6 months, %	18	19.1		19	18.8		0.60 (0.29-1.25)	.1742
\geq 6 months, %	76	80.9		82	81.2		1.31 (0.93-1.84)	.1252
Crossover treatment		BAT to enzal	lutamide		Enzalutamide	to BAT		
Time to PSA progression, months	36	10.9	6.1 to NA	47	1.1	0.9 to 7.6		.0001
Unverified PSA50 response, n (%)	36	28 (77.8)		47	10 (21.3)			
OR, n (%)	35	10 (28.6)	0.15 to 0.46	41	3 (7.3)	0.02 to 0.20		.03
PFS2, months	94	28.2	23.6 to NA	101	19.6	12.9 to 29.7	0.44 (0.22-0.88)	.0152
OS (BAT-enzalutamide v enzalutamide-BAT), months	37	37.1	30.5 to NA	46	30.2	25.9 to NA	0.68 (0.36-1.28)	.2252
OS (BAT-enzalutamide v enzalutamide only), months	37	37.1	30.5 to NA	53	28.6	24.3 to 35.5	0.52 (0.29-0.96)	.031
OS (BAT-enzalutamide v BAT only), months	37	37.1	30.5 to NA	57	25	20 to 34	0.46 (0.25-0.84)	.0092

Abbreviations: BAT, bipolar androgen therapy; HR, hazard ratio; ITT, intention-to-treat; NA, not available; OR, objective response; OS, overall survival; PFS, progression-free survival; PSA, prostate-specific antigen.

corresponding 95% Cls. For each QoL module, summary statistics of scores was reported at baseline and 1, 3, 6, and 12 months postrandomization. Scores at each follow-up time, as well as change pre- and post-treatment, were compared between the arms using Mann-Whitney tests.

RESULTS

From April 2015 to April 2018, we randomly assigned 195 men to receive either BAT (94 patients) or enzalutamide (101 patients) across 17 sites in the United States (Fig 1). The data cutoff date for this report was November 2019; median follow-up time among patients who are alive is 31.9 months. Baseline characteristics of all the patients are summarized in Table 1.

Primary End Point

The primary analysis of PFS was performed in November 2018, after progression had occurred in 156 patients. The median PFS was 5.6 months in the BAT arm versus 5.7 months in the enzalutamide arm (HR, 1.13; 95% Cl, 0.82 to 1.57; P = .45) (Fig 2A). With additional follow-up at data cutoff in November 2019, results remained unchanged (5.7 months for both arms; HR, 1.14; 95% Cl, 0.83 to 1.55; P = .42). In a prespecified analysis, PFS in men with short prior response to abiraterone (< 6 months) favored BAT (HR, 0.60; 95% Cl, 0.29 to 1.25), whereas PFS in those with longer prior response to abiraterone (\geq

6 months) favored enzalutamide (HR, 1.31; 95% Cl, 0.93 to 1.84; $P_{\text{interaction}} = .10$) (Table 2 and Data Supplement).

Secondary End Points

Median OS was not statistically different, but hypothesisgenerating, for the BAT arm compared with the enzalutamide arm (32.9 v 29.0 months; HR, 0.95; 95% CI, 0.66 to 1.39; P = .80) (Fig 2B and Table 2). In a subset analysis, OS in men with short prior response to abiraterone (< 6 months) favored BAT (HR, 0.55; 95% CI, 0.24 to 1.26), whereas OS in those with longer prior response to abiraterone (\geq 6 months) favored enzalutamide (HR, 1.08; 95% CI, 0.71 to 1.64; $P_{\text{interaction}} = .14$) (Fig 2D). The percentage of patients who achieved a PSA50 response during the initial phase of treatment was similar between the two groups (28.2% [24/ 85] for BAT versus 25.5% [24/94] for enzalutamide) (Fig 2C and Table 2). Time to first PSA progression was short for both the groups but favored the enzalutamide arm (2.8 months for BAT v 3.8 months for enzalutamide; HR, 1.51; 95% CI, 1.06 to 2.16; P = .02) (Table 2). Conversely, the OR rate favored the BAT group over enzalutamide (24.2% [8/33] v 4.2% [1/ 24], respectively; P = .07) (Table 2).

Crossover Treatment

Patients who remained asymptomatic and continued to meet eligibility requirements were provided the opportunity



FIG 3. Kaplan-Meier estimates of OS in the crossover population. (A) Comparison of OS in the subset of patients receiving BAT→enzalutamide versus enzalutamide→BAT, after eliminating those who came off study without crossing over. (B) Comparison of OS in the subset of patients receiving BAT→enzalutamide (after eliminating patients who did not cross over) versus enzalutamide-only patients who did not cross over to receive BAT. BAT, bipolar androgen therapy; HR, hazard ratio; NA, not accessible; OS, overall survival.

to cross over, after a 28-day washout period, to the alternate treatment at time of progression. Crossover was not permitted in patients in either arm with clinical progression because of pain from PCa. Overall, 37 (39.3%) patients initially on BAT crossed over to receive enzalutamide, whereas 48 (47.6%) patients crossed from enzalutamide to BAT (Table 1). For patients who did not cross over, approximately equal numbers (14% on BAT and 18% on enzalutamide) had clinical progression. Overall, 37% of patients receiving BAT and 43% receiving enzalutamide crossed over as a result of radiographic progression (Data Supplement).

The majority of the patients who crossed over did so as a result of radiographic progression (95% of the BAT group and 90% of the enzalutamide group) (Data Supplement). There was no significant difference in characteristics (age, ECOG PS, race, ethnicity, target lesions, nontarget lesions, and duration of prior abiraterone therapy) of the crossover population compared with the noncrossover population (Data Supplement). Characteristics of each crossover arm were similar (Data Supplement). Crossover to enzalutamide following BAT was associated with greater benefits than crossover to BAT following enzalutamide, for all secondary end points (Table 2). Median OS for those crossing over to enzalutamide post-BAT was 37.1 months versus 30.2 months for those crossing to BAT postenzalutamide (HR, 0.68; 95% CI, 0.36 to 1.28; P = .23) (Fig 3A and Table 1) versus 28.6 months for those who received enzalutamide-only without crossover (HR, 0.52; 95% Cl,

0.29 to 0.96; P = .03) versus 25 months (HR, 0.46; 95% CI, 0.25 to 0.84; P = .009) for those who received BAT-only without crossover (Fig 3B and Table 1). The OR of 28.6% (10/35) for enzalutamide post-BAT was higher than the response of 7.3% (3/41) with BAT postenzalutamide (Table 2). The PSA50 response was 77.8% (28/36) for those who crossed to enzalutamide compared with 21.3% (10/47) for those who crossed to BAT (Fig 4A and Table 1). Patients receiving enzalutamide immediately after abiraterone had significantly shorter median PSA-PFS with enzalutamide (3.8 months) compared with those who received enzalutamide following BAT (10.9 months) (HR, 0.45; 95% CI, 0.24 to 0.86; P = .008) (Table 2).

Considering the sequencing of BAT and enzalutamide, patients who received the treatment sequence of BAT→enzalutamide had significantly longer PFS2 compared with the opposite sequence (28.2 v 19.6 months; HR, 0.44; 95% CI, 0.22 to 0.88; P = .02) (Fig 4B and Data Supplement). Subgroup analysis of PFS2 favored the BAT→enzalutamide sequence (arm A) across all subgroups (Fig 4C).

Androgen Receptor Expression

Baseline blood samples (n = 187) were analyzed for transcript expression of full-length AR (AR-FL) and the truncated ligand-independent AR variant (AR-V7) in circulating tumor cells (CTCs), according to previously published methods.¹⁷ Overall, 41% of patients on BAT and 37%



FIG 4. (A) Waterfall plot of PSA response to crossover therapy, (B) Kaplan-Meier estimates of PFS2, (C) subgroup analysis of PFS2. BAT, bipolar androgen therapy; ECOG, Eastern Cooperative Oncology Group; PFS, progression-free survival; PSA, prostate-specific antigen.

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TABLE 3. Effect of AR-FL and AR-V7 Expression on PFS and OS

	ВАТ				Enzalutamide					
AR Isotype	Positive	Negative	HR	Р	Positive	Negative	HR	Р		
AR-FL										
n (%)	37 (41.1)	53 (58.9)			36 (37.1)	61 (62.9)				
PFS, months	4.6	5.8	1.70 (1.05-2.76)	.0321	3	8.3	1.99 (1.25-3.15)	.0044		
OS, months	29.6	32.9	1.48 (0.82-2.68)	.1909	28	30.3	1.55 (0.9-2.66)	.1225		
AR-V7										
n (%)	11 (12.2)	79 (87.8)			7 (7.2)	90 (92.8)				
PFS, months	4	5.8	2.07 (1.0-4.16)	.0719	2.5	5.7	3.0 (1.30-6.93)	.022		
OS, months	13.8	34	6.08 (2.95-12.54)	< .001	17.3	30.2	3.08 (1.17-8.15)	.0451		

Abbreviations: AR, androgen receptor; BAT, bipolar androgen therapy; HR, hazard ratio; OS, overall survival; PFS, progression-free survival.

on enzalutamide tested positive for AR-FL, consistent with increased AR expression in CTCs following abiraterone pretreatment (Table 3). AR-V7 transcript was detected at baseline in 12% of patients on BAT and 7% on enzalutamide (Table 3). Detection of AR-FL and AR-V7 transcripts were both generally associated with shorter PFS and OS on BAT and enzalutamide (although not all differences were statistically significant), consistent with the broad negative prognostic impact in patients with mCRPC (Table 3 and Data Supplement).¹⁷ However, neither AR-FL nor AR-V7 status was predictive of better or worse clinical outcomes using BAT or enzalutamide, suggesting that neither factor can be used as a treatment selection biomarker in this context.

Safety and QoL

The majority of AEs were grade 1-2 (BAT, 68.5%; enzalutamide, 62.8%); grade 3-4 AEs occurred in 28.1% of patients on BAT and 35.1% on enzalutamide (Table 4). Only one grade 5 AE of death not otherwise specified was observed in a patient on enzalutamide. Serious AEs occurred in 19.1% of patients on BAT and 20.6% on enzalutamide. The percentage discontinuing therapy as a result of AEs was slightly higher for BAT (9.0%) than enzalutamide (5.2%) (Table 4).

The incidence of AEs was generally similar in the two groups. Notable exceptions included fatigue with 48.5% of patients on enzalutamide experiencing grade 1-2 and 7.2% of patients grade 3-4 fatigue, compared with 31.5% of BAT patients experiencing only grade 1-2 fatigue. Enzalutamide was associated with a higher percentage of constitutional symptoms such as anorexia, depression, anxiety, insomnia, headache, and generalized muscle weakness as well as GI complaints (diarrhea, constipation, abdominal pain, and flatulence). BAT was associated with increased sexual side effects (hot flashes, breast tenderness, and gynecomastia) and musculoskeletal complaints (peripheral edema and generalized musculoskeletal pain).

Patient-reported QoL consistently favored BAT at 1, 3, and 6 months after initiation of treatment (Data Supplement).

DISCUSSION

The TRANSFORMER trial is unique in that it compares two treatments with diametrically opposite effects on the AR therapeutic target. In this trial, BAT was not superior to enzalutamide with respect to the primary end point clinical or radiographic PFS in asymptomatic men with mCRPC progressing on abiraterone. Although not powered to show equivalency, the treatments were similar in terms of median PFS (5.7 months in both the arms), time to PSA progression (2.8 v 3.8 months), and PSA50 responses (28.2% v 25.5%). The similarity of response, despite the opposing nature of the treatments, may relate to PCa cells' ability to adaptively regulate AR levels in response to androgen levels. Interestingly, the greatest benefit from BAT was in patients experiencing progression on prior abiraterone within 6 months, suggesting that BAT may partially reverse lineage plasticity in PCa cells losing AR addiction.¹⁸ Unfortunately, neither baseline AR-FL nor AR-V7 expression was identified as a potential treatment selection biomarker. However, consistent with the hypothesis that increased AR-FL can make PCa resistant to androgen ablation but vulnerable to high-dose testosterone,⁹ PFS was significantly increased for BAT and decreased for enzalutamide in AR-FL-positive patients (Table 3).

BAT also maintained or improved QoL, particularly in domains of fatigue and physical and sexual function compared with enzalutamide. The incidence of AEs was similar between treatments and primarily low-grade. BAT was associated with less fatigue and GI and constitutional symptoms but increased edema, generalized pain, and sexual side effects compared with enzalutamide.

Approximately 40% of patients crossed over to the opposite treatment at progression. There were no significant differences between noncrossover versus crossover patient characteristics. Patients who crossed to enzalutamide post-BAT showed significantly enhanced response compared with those who received enzalutamide immediately after progression on abiraterone. Median time to PSA progression increased to 10.9 months compared with 3.8 months,

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TABLE 4. Summary of AEs During Initial Treatment (Safety Analysis Population)

	BAT (n	= 89)	Enzalutamide (n = 97)		
AE	Any Grade, n (%)	Grade 3 or 4, n (%)	Any Grade, n (%)	Grade 3 or 4, n (%)	
Any AE	86 (96.6)	25 (28.1)	95 (97.9)	34 (35.1)	
Serious AE	17 (19.1)		20 (20.6)		
Grade 5 AE	0		1 (1.0)		
AE leading to discontinuation of the trial	8 (9.0)		5 (5.2)		
AE that occurred in \geq 5% of patients in either group	Grade 1 or 2, n (%)	Grade 3 or 4, n (%)	Grade 1 or 2, n (%)	Grade 3 or 4, n (%)	
Fatigue	28 (31.5)	0	47 (48.5)	7 (7.2)	
Generalized pain	28 (31.5)	3 (3.4)	16 (16.5)	1 (1.0)	
Edema limbs	21 (23.6)	1 (1.1)	11 (11.3)	0	
Localized edema	8 (9.0)		6 (6.2)		
Back pain	18 (20.2)	3 (3.4)	12 (12.4)	7 (7.2)	
Pain in extremity	13 (14.6)	1 (1.1)	14 (14.4)	2 (2.1)	
Bone pain	10 (11.2)	0	6 (6.2)	1 (1.0)	
Arthralgia	4 (4.5)	1 (1.1)	9 (9.3)	0	
Myalgia	4 (4.5)	0	7 (7.2)	1 (1.0)	
Generalized muscle weakness	2 (2.2)		7 (7.2)		
Diarrhea	10 (11.2)		23 (23.7)		
Nausea	12 (13.5)	1 (1.0)	21 (21.6)	1 (1.0)	
Constipation	14 (15.7)		13 (13.4)		
Vomiting	4 (4.5)		7 (7.2)		
Abdominal pain	1 (1.1)		5 (5.2)		
Flatulence	1 (1.1)		6 (6.2)		
GERD	0		5 (5.2)		
Anorexia	11 (12.4)	0	27 (27.8)	2 (2.1)	
Hypertriglyceridemia	5 (5.6)	0	5 (5.2)	1 (1.0)	
Hyperglycemia	2 (2.2)		5 (5.2)		
Headache	5 (5.6)		14 (14.4)		
Dizziness	7 (7.9)		9 (9.3)		
Paresthesia	3 (3.4)		7 (7.2)		
Weight loss	6 (6.7)		13 (13.4)		
Alkaline phosphatase increased	3 (3.4)		9 (9.3)		
Creatinine increased	8 (9.0)		4 (4.1)		
Insomnia	5 (5.6)	0	13 (13.4)	1 (1.0)	
Depression	1 (1.1)		13 (13.4)		
Anxiety	2 (2.2)		9 (9.3)		
Cough	12 (13.5)		11 (11.3)		
Dyspnea	9 (10.1)				
AEs of interest					
Hematuria	6 (6.7)	1 (1.1)	6 (6.2)	0	
Urinary frequency	6 (6.7)		4 (4.1)		
Urinary retention	2 (2.2)		5 (5.2)		
Urinary urgency	3 (3.4)		1 (1.0)		
Hemoglobin increased	3 (3.4)		0		
	(continued on follow	wing page)			

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TABLE 4.	Summary	of AEs	During Initial	Treatment (S	Safety Ana	alysis F	Population)	(continued)
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	BAT (n = 89)	Enzalutamide (n = 97)		
AE	Any Grade, n (%)	Grade 3 or 4, n (%)	Any Grade, n (%)	Grade 3 or 4, n (%)	
Mood swings	1 (1.1)		0		
Increased temper or anger	1 (1.1)		0		
Personality change	1 (1.1)		0		
Hypertension	2 (2.2)	0	3 (3.1)	4 (4.1)	
Seizures	0		0		
Stroke	1 (1.1)		0		
Thrombolic event	1 (1.1)	0	0	2 (2.1)	
Chest pain	1 (1.1)		1 (1.0)		
Palpitations	1 (1.1)		1 (1.0)		
Testicular pain	4 (4.5)		1 (1.0)		
Breast pain or tenderness	5 (5.6)		0		
Gynecomastia	4 (4.5)		0		
Hot flashes	7 (7.9)		10 (10.3)		

Abbreviations: AE, adverse event; BAT, bipolar androgen therapy; GERD, gastroesophageal reflux disease.

PSA50 response improved to 78% versus 25%, and OR improved to 29% versus 4%. Overall, our results support our hypothesis that BAT may reverse antiandrogen resistance via adaptive downregulation of AR expression (Data Supplement).

The use of PSA progression is nuanced because PSA expression is directly stimulated by testosterone, which could likely shorten time to PSA progression on BAT. However, as an exploratory end point we measured PFS2, which was significantly increased for patients treated with BAT→enzalutamide compared with the opposite sequence (28.2 v 19.6 months, respectively). Although our PFS2 results do not include the duration of treatment with prior abiraterone, they compare favorably with Khalaf et al¹⁹ who reported median PFS2 of 19.3 months in 73 patients treated with abiraterone followed by enzalutamide. Median survival of 25-28 months has been reported in small studies of patients with mCRPC

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receiving abiraterone followed by enzalutamide.¹⁹⁻²¹ In

contrast, in our study, median postabiraterone survival for

In conclusion, TRANSFORMER establishes meaningful

clinical activity of BAT and supports additional study to determine its optimal clinical integration. Although the trial

failed to demonstrate superior PFS with BAT over enzalu-

tamide in postabiraterone CRPC, it demonstrated that BAT is

safe, enhances QoL, and has efficacy comparable to

enzalutamide in this patient population. However, the most

important finding is that postabiraterone, BAT can markedly

improve the magnitude and duration of response to enza-

lutamide when used as an intervening therapy. These results

support further evaluation of sequential BAT→enzalutamide

as a single therapy. Further study is warranted to define the

potential for sequential treatment to produce significant

BAT→enzalutamide was 37.1 months.

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TRANSFORMER: A Randomized Phase II Study Comparing Bipolar Androgen Therapy Versus Enzalutamide in Asymptomatic Men With Castration-Resistant Metastatic Prostate Cancer

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ORIGINAL ARTICLE

The Prostate WILEY

Comparison of germline mutations in African American and Caucasian men with metastatic prostate cancer

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Abstract

Background: The goal of this study is to evaluate germline genetic variants in African American men with metastatic prostate cancer as compared to those in Caucasian men with metastatic prostate cancer in an effort to understand the role of genetic factors in these populations.

Methods: African American and Caucasian men with metastatic prostate cancer who had germline testing using multigene panels were used to generate comparisons. Germline genetic results, clinical parameters, and family histories between the two populations were analyzed.

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Results: A total of 867 patients were included in this retrospective study, including 188 African American and 669 Caucasian patients. There was no significant difference in the likelihood of a pathogenic or likely-pathogenic variants (PV/LPVs) between African American and Caucasian patients (p = .09). African American patients were more likely to have a variant of unknown significance than Caucasians (odds ratio [OR] = 1.95; p < .0001). BRCA1 PV/LPVs were higher in African Americans (OR = 4.86; p = .04). African American patients were less likely to have a PV/LPV in non-BRCA DNA repair genes (OR = 0.30; p = .008). Family history of breast (OR = 2.09; p = .002) or ovarian cancer (OR = 2.33; p = .04) predicted PV/LPVs in Caucasians but not African-Americans. This underscores the limitations of family history in AA men and the importance of personal history to guide germline testing in AA men.

Conclusions: In metastatic prostate cancer patients, PV/LPVs of tested genes did not vary by race, BRCA1 PV/LPVs were more common in the African American subset. However, PV/LPVs in non-BRCA DNA repair genes were less likely to be encountered in African Americans. Family history associated with genetic testing results in Caucasians only.

KEYWORDS

African American, genetics, germline, metastatic prostate cancer, pathogenic variants, racial disparity

1 | INTRODUCTION

Racial disparity has been a persistent and challenging problem in prostate cancer research despite ongoing efforts. African American men are at higher risk of prostate cancer and approximately twofold higher risk of dying from prostate cancer compared to other racial or ethnic groups (1, 2). For African Americans there are significant differences in screening and treatment patterns, enrollment in clinical trials, outcomes, limited understanding of tumor biology and biomarker utility specific to African American patients.^{1–8} Similar to race, family history is also a potent risk factor for prostate cancer. The inherited risk of prostate cancer is estimated to be as high as 60% and men with a first degree relative (FDR) with prostate cancer have been reported to be twice as likely to develop this disease.⁹ While risk factors such as family history and race have been well characterized, much remains unknown about how genetic factors influence risk in African Americans with prostate cancer. To date, African American men have been underrepresented in germline genetic studies of prostate cancer.^{8,10}

Studies in advanced prostate cancer have been conducted primarily on Caucasian/European cohorts, and these studies have highlighted the prevalence and clinical significance of germline alterations. For example, Pritchard, et al.¹¹ showed that pathogenic/likely pathogenic germline variants (PV/LPV) in DNA repair genes were present in 11.8% of patients with metastatic prostate cancer. Patients with selected DNA repair germline PV/LPV not only have an increased risk of developing cancer, but a number of mutations are associated with a poor prognosis. Importantly, patients with germline *BRCA1* and *BRCA2* pathogenic mutations and metastatic prostate cancer may respond better to PARP inhibitors and platinum-based chemotherapy.¹²⁻¹⁴ Specifically, patients with mCRPC and *BRCA1* or *BRCA2* alterations had significantly longer progression free and overall survival with olaparib, compared to those treated with abiraterone or enzalutamide. The benefit of PARP inhibitors may be extended to patients with selected alterations detected in other homologous recombination repair genes.¹⁵ Both olaparib and rucaparib are now Food and Drug Administration (FDA) approved for treatment of mCRPC and both approvals specifically note germline *BRCA1/2* mutations. Studies have shown that mismatch repair gene status in tumors predicts for a positive therapeutic response to PD-1 inhibitors¹⁶ and pembrolizumab was FDA-approved in 2018.

In a cross-sectional study of 3607 men with prostate cancer, 17.2% (*n* = 620) were found to have pathogenic or likely pathogenic germline variants. Age, race, and family history did not correlate with positive test results though these clinical data were quite limited. Only 227 (~6%) of the men tested were African American. African Americans had lower rates of positive variants compared to other ethnic groups (odds ratio [OR] = 0.527; *p* = .006).¹⁷ In a study focusing on a subset of well characterized genes, African American patients with prostate cancer had significantly fewer germline alterations compared to Caucasians (7.5% vs. 13.9%, respectively).¹⁸ This study was problematic because clinical data were limited. Kwon et al.¹⁹ had a variety of ethnic groups in a large analysis but only 41 patients were of African American men remain suboptimal.

ELAC/HPC2,²⁰ *MSR1*,²¹ *CHEK2*²², and *EPHB2*²³ have been reported in association with prostate cancer risk in African American men but await confirmatory studies. Multiple linkage and GWAS studies have linked the 8q24 region with prostate cancer; these risk SNPs are

relatively small in magnitude of effect and the underlying etiology of noncoding changes remains under study.^{24–26} Though these associations have been identified in African American patients with prostate cancer, reproducible causal or risk genes have not been identified and current gene panels used for germline genetic testing are primarily derived from variants identified in other ethnicities. Given the underrepresentation in clinical genetic testing and research, and the clinical importance, for patients and their families, it is especially critical to better understand racial disparity with respect to germline PV/LPV data.

Given the notable paucity of germline data on African American men, especially those with advanced prostate cancer, the goal of the present study is to evaluate germline alterations in African American men, all of whom had documented metastatic prostate cancer. Ultimately, understanding the landscape of germline variants in African Americans, with concomitant clinical cofactors and family history, is critical for understanding and reducing health care disparities.

2 | MATERIALS AND METHODS

2.1 | Patient cohort

African American and Caucasian men with metastatic prostate cancer were recruited from seven sites including Tulane University Cancer Center, Levine Cancer Institute/Carolinas Medical Center, The Sidney Kimmel Comprehensive Cancer Center at Johns Hopkins University, University of Washington, Mayo Clinic, and Atlantic Urology Clinics. All patients in this cohort had distant metastatic disease, confirmed by radiographic imaging, and all had germline genetic testing. In addition to germline testing results, clinical data including self-reported race, Gleason score, age at diagnosis, clinical staging, and self-reported cancer family history were retrospectively compiled from medical records. All clinical data were deidentified before analyses under Tulane University IRB protocol number 2019-329 which waived the requirement to obtain written patient informed consent.

2.2 | Germline panel composition and testing

Patients in this cohort had prior germline testing with a commercially available clinical panel between 2015 and 2020. Institutions used a variety of germline panels evaluating germline alterations in 12–86 cancer-associated genes. The panels utilized included: Invitae Multi-Cancer panel (N = 645) (Invitae), Color Hereditary Cancer panel (N = 183) (Color Genomics), Myriad MyRisk panel (N = 7) (Myriad Genetics), BROCA panel (N = 6) (UW Medical Center), and other commercial panels (N = 16). Variants were evaluated and subjected to clinical interpretation using American College of Medical Genetics and Genomics criteria.²⁷ According to the results reported by each commercial panel, variants interpreted as pathogenic (PV) or likely-pathogenic (LPV) were considered positive and have previously been established to have pathogenic consequences. Variants of unknown significance (VUS) were also identified using standard classification procedures.

	African American	Caucasian
Median age of diagnosis	60 (40-82)	63 (42-93)
Median age at time of germline testing	68 (40-89)	69 (43-93)
Gleason score		
<7	6% (n = 9)	6% (n = 26)
=7	34% (n = 50)	28% (n = 125)
>7	58% (n = 87)	67% (n = 301)
Metastatic at diagnosis	44% (n = 65)	37% (n = 136)

2.3 | Statistical analysis

The χ^2 test and confidence intervals were calculated using SAS 9.7 (SAS). To compare proportions between groups when the number of occurrences in a cell were fewer than 5, the Fisher exact test was used. The *p* values less than .05 were considered significant. These tests were used to assess associations between genetic alterations and clinical variables including race and family history. To accommodate the diversity of genetic panels and institutions, for individual gene analyses, patients were excluded if the panel used for germline testing did not include the given gene of interest.

3 | RESULTS

3.1 | Study population

A total of 867 patients were included in this retrospective study. This included 188 African American patients and 669 Caucasian patients (see Table 1 and Table S1); all patients had radiographic positive metastatic prostate cancer. The median age at diagnosis was 60 years (range = 40-82) for African Americans and 63 years (range = 42-93) for Caucasians. At the time of germline testing, the median age for African Americans was 68 years (range = 40-89) and 69 years (range = 43-93) for Caucasians. In African Americans, 6% (n = 9) had a Gleason score of less than 7, 34% (n = 50) had a Gleason score of 7, and 58% (n = 87) had a Gleason score more than 7. In Caucasians, 6% (n = 26) had a Gleason score of less than 7, 28% (n = 125) had a Gleason score of 7, and 67% (n = 301) had a Gleason score of more than 7. 44% of African Americans (n = 65) were metastatic at diagnosis compared to 37% of Caucasians (n = 136). No statistically significant differences between the African American and Caucasian groups were seen in terms of age at diagnosis, age at testing, Gleason scores, or metastatic disease at diagnosis.

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	Negative	PV/LPV	PV/LPV + VUS	VUS	Tota
African American	35.1% (n = 66)	5.3% (n = 10)	4.3% (n = 8)	55.3% (n = 104)	188
Caucasian	48.9% (n = 327)	8.1% (n = 54)	6.4% (n = 43)	36.6% (n = 245)	669
Unknown	50% (n = 5)	30% (n = 3)	0% (<i>n</i> = 0)	20% (n = 20)	10
Grand total	44.4% (n = 385)	9.2% (n = 80)	5.8% (n = 51)	40.5% (n = 351)	867

TABLE 2 Germline variants detected

Abbreviations: LPV, likely-pathogenic variants; PV, pathogenic variants.

3.2 | Pathogenic, likely-pathogenic, and VUS

In the African American patients, 6% of patients (n = 11) had a PV/ LPV, 55% of patients (n = 104) had a VUS, 4% of patients (n = 8) had both a PV/LPV and VUS, and 35% of patients had no PV/LPV or VUS reported (n = 65) (Table 2). For Caucasians, 10% of patients (n = 66) had a PV/LPV germline alteration, 37% of patients (n = 245) had a VUS, 6% of patients (n = 43) had both a PV/LPV and VUS, and 47% of patients had no germline alterations (n = 315). Overall, there was no significant difference in the likelihood of a PV/LPV between African American and Caucasian patients (p = .09). African American patients were more likely to have a VUS than Caucasians (OR = 1.95; 95% confidence interval [CI [1.40, 2.71]; p < .0001).

Each gene represented on a germline panel was compared between African American and Caucasian patients with metastatic prostate cancer (Table S2). Of the genes evaluated, African Americans were more likely to have a *BRCA1* PV/LPV (OR = 4.86; 95% CI [1.08, 21.93]; p = .04), however, we note the small number of cases as a limitation. There were no other PV/LPVs detected which were significantly different between African American and Caucasian patients. Among VUSs, VUS in *BRCA2* (p = .04), *PALB2* (p = .0007), and *PTCH1* (p = .03) were more frequent in African Americans compared to Caucasians. There were no other gene specific VUSs which were significantly different between African Americans and Caucasians (Table S3).

Next, functionally related genes were evaluated as a group (Tables 3–5). African American patients were substantially less likely to have a PV/LPV in any non-*BRCA* gene (OR = 0.27; 95% CI [0.12, 0.64]; p = .0008). Additionally, African American patients were less likely to have a PV/LPV in a non-BRCA DNA repair gene (*MSH2*, *MSH6*, *PMS2*, *MLH1*, *ATM*, *RAD50*, *RAD51D*, *NBN*, *CHEK2*, *BRIP1*, *PALB2*, *RAD51C*, *ATM*, *BLM*, and *TP53*) (OR = 0.30; 95% CI [0.11, 0.85]; p = .008). Among all DNA repair genes analyzed herein (including *BRCA1* and *BRCA2*) there was no

significant difference between African American and Caucasian patients (p = .29).

3.3 | Family history

Cancer family history was collected from patient charts (see Tables S4, S5, S6, and S7). Among these prostate cancer patients, PV/ LPV findings were more likely in Caucasians with at least one FDR with ovarian cancer (OR = 2.33; 95% CI [1.05, 5.17]; p = .04). However, there was no significant difference in the frequency of PV/LPV alterations in African Americans with FDR with ovarian cancer (OR = 6.33; 95% CI [0.98, 40.76]; p = .08). There was no significant difference in the frequency of PV/LPVs in African Americans (p = .12) or Caucasians (p = .33) with at least one FDR with prostate cancer. In Caucasians, PV/LPV germline alterations were more likely with at least one FDR with breast cancer (OR = 2.09: 95% CI [1.31, 3.32]: p = .002). However, there were no significant difference in the frequency of PV/LPV alterations in African Americans with at least one FDR with breast cancer (OR = 2.15: 95% CI [0.75, 6.19]; p = .21). There was no significant difference in the frequency of PV/LPV alterations in Caucasians (p = .80) with at least one FDR with pancreatic cancer. None of the African American patients reported a family history of pancreatic cancer.

4 | DISCUSSION

These findings highlight the importance of testing and expanding access to testing especially for African American patients with metastatic prostate cancer. We did not find any overall differences in the frequency of PV/LPVs between African Americans and Caucasians in this population of men with metastatic prostate cancer. However, African American patients were less likely to have a PV/

PV/LPV non- BRCA gene	African American	Caucasian	OR	p Value	95% CI
Yes	3% (<i>n</i> = 6)	11% (n = 72)	0.2749	.0008	0.1176, 0.6426
No	97% (n = 181)	89% (n = 597)			

TABLE 3PV/LPV in any non-BRCA gene

Abbreviations: CI, confidence interval; LPV, likely-pathogenic variants; OR, odds ratio; PV, pathogenic variants.

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TABLE 4 PV/LPV in DNA-repairgenes (BRCA1, BRCA2, MSH2, MSH6,PMS2, MLH1, ATM, RAD50, RAD51D, NBN,CHEK2, BRIP1, PALB2, RAD51C, ATM,BLM, and TP53)	PV/LPV DNA repair genes	African American	Caucasian	OR	p Value	95% CI
	Yes	9% (n = 16)	12% (n = 77)	0.7152	.2887	0.4066, 1.2579
	No	91% (n = 172)	88% (n = 592)			
	Abbreviations: CI, confider	nce interval; LPV, lik	ely-pathogenic v	ariants; O	R, odds rat	tio; PV, pathogenic

TABLE 5PV/LPV in non-BRCA DNArepair genes (MSH2, MSH6, PMS2, MLH1,ATM, RAD50, RAD51D, NBN, CHEK2,BRIP1, PALB2, RAD51C, ATM,BLM, and TP53)

PV/LPV non-BRCA DNA repair gene	African American	Caucasian	OR	p Value	95% CI
Yes	2% (n = 4)	7% (n = 45)	0.3014	.00836	0.107, 0.8493
No	98% (n = 184)	93% (n = 624)			

Abbreviations: CI, confidence interval; LPV, likely-pathogenic variants; OR, odds ratio; PV, pathogenic variants.

LPV in any non-*BRCA* genes and in non-*BRCA* DNA repair genes. African Americans were more likely to have a PV/LPV *BRCA1* compared to their Caucasian counterparts.

African Americans in this study had a significantly higher overall incidence of germline VUSs. In a gene specific analysis, VUS alterations in BRCA2, PALB2, and PTCH1 were more frequently detected in African Americans compared to Caucasians. Unlike PV/LPV, for any given VUS, by definition, there is insufficient evidence to determine whether or not a mutation is detrimental or contributes to cancer risk. In African Americans, the significantly increased detection of VUSs likely reflects a bias in variant classification of genes, which relies on patient data primarily assembled and validated from Caucasian cohorts. Importantly, this bias may also extend to PV/LPVs and may account for the overall lower frequency of pathogenic variants in this African American cohort. Regardless of the pathogenicity of individual VUSs, the higher frequency of VUSs in African Americans indicates that this population may be underrepresented in population data utilized in identifying variants. This underrepresentation may be especially critical for germline variants in prostate cancer given the high significantly higher incidence of prostate cancer in African Americans. More data are necessary to further classify these VUS into pathogenic or non-pathogenic categories.

The higher frequency of *BRCA1* in African Americans with metastatic prostate cancer is notable given the recent FDA approvals of olaparib and rucaparib for patients with germline *BRCA1* or *BRCA2*. These data emphasize the importance of improving access to genetic counseling and germline genetic testing for inherited cancer risk for African American men with advanced prostate cancer. Similarly, when comparing somatic tumor DNA from metastatic prostate cancer in African Americans and Caucasians, there were more tumoral *BRCA1* mutations in African Americans (4%) compared to Caucasians (1%).²⁸ We are cautious to note that conclusions need replication in larger data sets before they can be considered definitive.

Guidelines reliant on family history have a number of shortcomings and current National Comprehensive Cancer Network guidelines are not reliant on family history alone. It is well known that family history is incomplete for many, and even important genes have incomplete penetrance. Herein, however, family history was associated with PV/LPV in several selected Caucasian populations but not in African Americans. Caucasians but not African Americans with a FDR with breast or ovarian cancer (but not prostate cancer) were more likely to have a PV/LPV. This may or may not reflect differences in recall, family structure, health communication, and genetic dependency, as well a smaller sample sizes resulting in a relatively under-powered assessment in the African American dataset.

While this study included a large number of metastatic prostate cancer patients there were significant limitations. A larger sample size is needed to optimally assess the germline landscape in this population. Additionally, it is possible that the current gene panels are incomplete when it comes to important genes associated with prostate cancer, especially in African Americans. This was a retrospective study of metastatic prostate cancer patients and testing biases are possible. We have not tracked how many patients refused to undergo testing. Clinical practices at different institutions may have varied in unknown manners. Though most of the genes tested, especially DNArepair genes, were the same across panels, there were clear variations in other cancer related genes in accordance with what panel was used. This is a limitation of the study. Similarly, the number of genes included on the panels varied. While this was taken in to account for the present analyses for individual genes, optimally all patients should have been tested with a standardized gene panel. This study was also limited to self-reported data for both race and family history. Similarly, since this is a multi-institutional study, genetic variability attributable to geographic factors may also be a limitation.

More access to clinical genetic testing and more research opportunities are needed to address disparities and underrepresentation of African American prostate cancer patients. Further studies are critical for understanding the germline genetic components contributing to disparities in prostate cancer risk and prostate cancer outcomes.
CONFLICT OF INTERESTS

Dr. Sartor has research funding to his institution from AAA, AstraZeneca, Bayer, Merck, Endocyte, Progenics, Novartis, and Janssen. Dr. Sartor has received consulting fees from Astellas, Blue Earth Diagnostics, EMD Serono, Pfizer, Constellation, Dendreon, Bristol-Myers Squibb, Invitae, Merck, Innocrin, Sotio, AAA, AstraZeneca, Bayer, Endocyte, Progenics, Novartis, Janssen, Astellas, Blue Earth Diagnostics, EMD Serono, Pfizer, Constellation, Noria Therapeutics, Clovis, Myriad, Noxopharm, Point Biopharm, Tenebio, Theragnostics, Telix, Clarity Pharmaceuticals, and Fusion. Dr. Shore has research support and consulting fees for AbbVie, Amgen, Astellas, Astra Zeneca, Bayer, BMS, Dendreon, Exact Sciences, Fergene, Foundation Medicine, Invitae, Janssen, Merck, Myriad, Pfizer, and Sanofi, Tolmar. Dr. Cheng receives funding from PNW SPORE CA097186, DOD W81XWH-17-2-0043, NIH CA015704, Prostate Cancer Foundation; research funding to her institution from Clovis, Janssen, Sanofi, Medivation/Astellas, Color Foundation, and consulting fees from AstraZeneca. Dr. Antonarakis has served as a paid consultant/ advisor for Invitae, Janssen, Pfizer, Sanofi, Dendreon, Merck, Bristol-Myers Squibb, AstraZeneca, Clovis, Bayer, Constellation, Eli Lilly and Amgen; and has received research funding to his institution from Janssen, Johnson & Johnson, Sanofi, Dendreon, Genentech, Novartis, Bayer, Merck, Bristol-Myers Squibb, AstraZeneca, ESSA and Constellation. Additionally, Dr. Antonarakis is partially supported by the Patrick Walsh Prostate Cancer Research Fund, the Prostate Cancer Foundation. the NCI Cancer Center Support Grant 5P30 CA006973-52, the NIH grant R01 CA238384, and the DOD Clinical Consortium award W81XWH-16-PCRP-CCRSA. Dr. Bryce received honoraria from Foundation Medicine, Novartis, Astellas, and Merck. Dr. McKay has served as a paid consultant for Janssen, Novartis, Tempus, Exelixis, Pfizer, Bristol-Mvers Squibb. Astellas Medivation. Dendreon. Vividion Therapeutics. Bayer and has research funding to her institution from Pfizer and Bayer. Dr. Burgess has received consulting fees from Johnson and Johnson, honoraria from Exelixis and Bayer, and research funding to his institution from Pfizer and Astellas Pharma. Dr. Zhu has served as a paid consultant for NGM Biopharmaceuticals and Bayer. All other authors have no conflict of interests to disclose.

DATA AVAILABILITY STATEMENT

The data that support the findings of this study are available on request from the corresponding author. The data are not publicly available due to privacy or ethical restrictions.

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SUPPORTING INFORMATION

Additional Supporting Information may be found online in the supporting information tab for this article.

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Platinum Priority – Editorial Referring to the article published on pp. 295–303 of this issue

Molecular Subtyping in the Neoadjuvant Setting in Prostate Cancer: Envisioning the Possibilities

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A persistent clinical challenge is that approximately half of men diagnosed with high-risk localized prostate cancer experience recurrence. In other solid tumor cancers, neoadjuvant therapy for localized disease reduces the risk of recurrence and is the standard of care. Despite studies investigating intensive androgen deprivation therapy (ADT) and ADT in combination with docetaxel [1–3], this approach has not been standard for prostate cancer. Molecular subtyping, which has seen major advances in metastatic prostate cancer, may add value to stratification and better treatment selection in the high-risk localized disease setting.

It has been 5 yr since the discoveries that DNA damage repair (DDR) genes are altered in up to a guarter of metastatic castration-resistant prostate cancers [4] and that inherited (germline) DDR (gDDR) gene alterations occur in 11.8% of men with metastatic prostate cancer, higher than the rate in localized disease and among men without cancer [5]. Men who carry germline BRCA1/2 mutations and develop prostate cancer have more aggressive disease and worse outcomes than men without these mutations [6]. Thus, men with gDDR alterations, including in BRCA1/2, may be at the highest risk of disease recurrence and may benefit most from neoadjuvant treatment approaches. In addition, the PARP inhibitors rucaparib and olaparib have been approved by the US Food and Drug Administration for metastatic castration-resistant prostate cancer associated with germline and/or somatic BRCA1/2 mutations, and in the case of olaparib, a longer list of DDR gene alterations for treatment candidacy.

We have needed more data informing prevalence of gDDR alterations in men with unfavorable intermediate-

risk or high-risk localized disease. There are other key questions regarding prostate cancers arising in the context of gDDR alterations. What is the response to inhibition of androgen receptor (AR) signaling in localized disease? What is the response to DNA-damaging agents (PARP inhibition, platinum chemotherapy)? Would sequential or combination approaches be more effective?

Some key answers are reported in this issue of European Urology by Berchuck et al [7] in their manuscript on the impact of pathogenic gDDR alterations on response to intense neoadjuvant androgen deprivation therapy (ADT). The study was a retrospective analysis of 201 patients pooled from five completed, prospective neoadjuvant trials of intensive neoadjuvant ADT in the setting of high-risk localized prostate cancer. The authors report 9.5% (19/201) of the men had pathogenic gDDR variants, with BRCA2 (n = 6) and ATM (n = 4) being the most common; others included BRCA1, CHEK2, RAD50, RAD51D, MSH6, and PMS2. Patients with and without gDDR alterations achieved similar rates of exceptional pathologic complete response (defined as pathologic complete response of cancer or minimal residual disease) of 26% versus 22%. The 3-yr biochemical recurrence-free survival was 45% (95% confidence interval [CI] 7.9-78%) among men with gDDR alterations compared to 55% (95% CI 44-64%) for men not found to have gDDR alterations. While the absolute numbers are small, the findings are impactful.

A strength of this study is its freedom from skewing due to ascertainment biases; simply put, the five studies were largely conducted in an era before our current knowledge of gDDR mutations in prostate cancer. As awareness of germline variants increases, so will self-selection and proportional

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skewing in prospective studies, particularly between studies that are selected versus unselected for specific alterations. Thus, these findings serve as important supportive evidence for NCCN prostate cancer guideline recommendation to offer germline testing and genetic counseling to men with a personal history of high-risk localized prostate cancer [8] and as a foundation for planning future studies.

An acknowledged and important limitation is the absence of tumors for somatic evaluation; this is the result of a lack of available pretreatment biopsies and the fact that pathologic responses may leave insufficient residual tumor for nextgeneration sequencing and other studies (an ironic consequence of success). The makes it impossible to identify somatic-only alterations in DDR genes among the non-gDDR comparator group, so there may be a subset of DDR-deficient tumors (without germline association) within the non-gDDR comparator group that could . The absence of tumor also precludes a deeper examination of the non-BRCA2 genes, that is, the rarer and/or moderate-penetrance genes (eg, ATM, CHEK2, BRCA1, RAD50). For these genes, evaluation of second allele inactivation, functional studies, and newer molecular profiling techniques may provide evidence about whether a given germline variant is more central or peripheral to the tumor biology. Future neoadjuvant studies will hopefully incorporate systematic collection of diagnostic biopsies in addition to surgical specimens.

Importantly, for patients with gDDR alterations and intermediate- or high-risk localized disease, there was not an obvious was not an inferior response to neoadjuvant intensive ADT, although the results were shy of statistical signifiance.more nu. More studies are needed to follow up on this observation, which mirrors those in the metastatic setting, in which AR-targeting agents in aggregate do to demonstrate in total inferior responses for patients with gDDR alterations [9,10]. Thus, there remains a strong rationale to pursue neoadjuvant approaches in men with gDDR alterations who have localized prostate cancer, whether with intensive ADT or ADT in combination with DNA-damaging agents such as platinum chemotherapy or PARP inhibitors. Indeed, there are trials ongoing and in development, such as the PROTEUS study (NCT03767244), a niraparib study (NCT04030559), the GUNS study (NCT04812366), and others. Dedicated De genetic registries such as PROMISE (www.prostatecancerpromise.org) will help facilitate identification of carriers of gDDR alterations for trial efforts, and together with long term follow-up, will foster collaborative learning about biology and treatment outcomes in prostate cancers arising in the context of the rare and ultra-rare germline mutations and variants.

In summary, Berchuck, Taplin, and their colleagues report a 9.5% prevalence of gDDR alterations in a pooled, unselected cohort of men with intermediate- and high-risk prostate cancer, justifying the NCCN prostate guideline recommendation to offer men with high-risk localized disease germline genetic testing and the additional studies investigating neoadjuvant ADT-based approaches for this patient population. Finally, the view for the future is more widespread identification of men who carry gDDR alterations earlier in the disease course, ideally soon after or even before a prostate cancer diagnosis. This could facilitate options for molecularly informed definitive treatment perhaps with effective neoadjuvant approaches—and hopefully an overall reduction in the number and proportion of men who carry gDDR alterations who develop metastatic prostate cancer. That would be the kind of skewing we could all get behind.

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ORIGINAL ARTICLE

The Prostate WILEY

Efficacy of systemic therapies in men with metastatic castration resistant prostate cancer harboring germline ATM versus BRCA2 mutations

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Abstract

Background: Among men with metastatic prostate cancer, about 10% have germline alterations in DNA damage response genes. Most studies have examined *BRCA2* alone or an aggregate of *BRCA1/2* and *ATM*. Emerging data suggest that *ATM* mutations may have distinct biology and warrant individual evaluation. The objective of this study is to determine whether response to prostate cancer systemic therapies differs between men with germline mutations in *ATM* (g*ATM*) and *BRCA2* (g*BRCA2*). **Methods:** This is an international multicenter retrospective matched cohort study of men with prostate cancer harboring g*ATM* or g*BRCA2*. PSA₅₀ response (\geq 50% decline in prostate-specific antigen) was compared using Fisher's exact test.

Results and Limitations: The study included 45 gATM and 45 gBRCA2 patients, matched on stage and year of germline testing. Patients with gATM and gBRCA2 had similar age, Gleason grade, and PSA at diagnosis. We did not observe differences in PSA₅₀ responses to abiraterone, enzalutamide, or docetaxel in metastatic castration resistant prostate cancer between the two groups; however, 0/7 with gATM and 12/14 with gBRCA2 achieved PSA₅₀ response to PARPi (p < .001). Median (95% confidence interval) overall survival from diagnosis to death was 10.9 years (9.5-not reached) versus 9.9 years (7.1not reached, p = .07) for the gATM and gBRCA2 cohorts, respectively. Limitations include the retrospective design and lack of mutation zygosity data.

Conclusions: Conventional therapies can be effective in gATM carriers and should be considered before PARPi, which shows limited efficacy in this group. Men with gATM mutations warrant prioritization for novel treatment strategies.

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KEYWORDS

abiraterone, ATM, BRCA2, docetaxel, enzalutamide, germline, homologous recombination deficiency, PARPi, platinum

1 | INTRODUCTION

Approximately 10% of men with metastatic prostate cancer have germline (inherited) DNA damage response (gDDR) gene alterations. *BRCA2* is a homologous recombination (HR) gene and is the most frequent pathogenic germline alteration in advanced prostate cancer (3%–5%), followed by *ATM* (1.6%–2%) and *BRCA1* (0.8%–1.3%).^{1–3} Several studies have shown that germline *BRCA2* mutations (*gBRCA2*) are associated with poor prognosis and worse prostate cancer outcomes and/or increased genomic instability.^{3–8}

Castro et al.,⁶ reported that at diagnosis, patients with prostate cancer and gBRCA1/2 mutations are more likely to have Gleason Grade Group \geq 4 disease, T3/4 stage, nodal involvement, metastases, and shorter cancer-specific survival compared to noncarriers. The IMPACT study showed that gBRCA2 mutation carriers have a higher incidence of prostate cancer and are more likely to be diagnosed at a younger age and have clinically significant disease compared to noncarriers, whereas no difference in age or tumor characteristics was detected between gBRCA1- and noncarriers.⁵ Na et al.,⁹ reported that the combined gBRCA1/2 and germline ATM (gATM) mutation rate was higher in lethal prostate cancer compared to localized disease. However, features of tumors and treatment responses linked to gATM mutations as a separate cohort are not characterized.

gATM mutation carriers have not been well-characterized despite ATM being the second most frequently observed DNA damage response gene alteration in metastatic prostate cancer. Several retrospective and prospective studies have reported that ATM-deficient prostate tumors may have attenuated response to poly-ADP-ribose polymerase inhibitors (PARPi) and platinum chemotherapy.^{7,10-15} Preliminary results of the phase II TRITON2 study demonstrated radiographic response to PARPi rucaparib in 51% (50/98) of men with BRCA1/2 and only 4% (2/49) of men with ATM mutations.^{11,16} The US Food and Drug Administration (FDA) granted rucaparib an accelerated approval for men with metastatic castration resistant prostate cancer (mCRPC) and BRCA1/2 mutations who were previously treated with docetaxel. In the phase III randomized PROfound study of the PARPi olaparib vs AR targeting agent, the primary endpoint of radiographic progression-free survival (rPFS) in men with mCRPC harboring mutations in BRCA1/2 and/or ATM (cohort A) was met, and olaparib also received FDA approval. While the primary endpoint was met for cohort A, in a post hoc subgroup analysis of men whose prostate cancer harbored ATM alterations, olaparib did

not significantly improve rPFS (median 5.4 months vs. 4.7 months for controls).¹² One potential explanation for the observed differences in clinical activity of PARPi in men with *BRCA2* versus *ATM* mutations may relate to the distinctive roles these proteins play in HR repair, with *ATM* acting as a sensor of DNA double strand break and *BRCA2* being a core effector of HR DNA repair.

Conventional systemic prostate cancer therapies, such as androgen receptor (AR) targeted or taxane agents, are not currently selected by biomarkers. These therapies have been reported to be effective in gBRCA1/2 carriers with prostate cancer.^{3,17} PROREPAIR-B, a prospective cohort study, compared response outcomes for mCRPC treatments among gBRCA2 carriers and non-carriers and showed similar response rates.³ Efficacy in patients with gATM, as a distinct cohort, has not been evaluated. Given the uncertain response to HR-deficiency targeted treatments in these men, we sought to investigate whether these patients respond to conventional biomarker-agnostic therapies. We hypothesized that, compared to men carrying gBRCA2, those carrying gATM would have a similar response to AR-targeted agents and docetaxel yet attenuated responses to platinum and PARPi therapies.

2 | METHODS

This is an international, retrospective, matched cohort study of Consecutive patients with prostate cancer who underwent clinical germline genetic testing between 2014 and 2019 at the University of Washington (UW), Johns Hopkins (JH) Hospital, CNIO-IBIMA Genitourinary Cancer Unit, or Tulane University Cancer Center. We selected patients who had gATM or gBRCA2 mutations identified with germline genetic testing panels (Ambry Color, Invitae, Myriad, or inhouse germline genetic testing at CNIO, JH, and UW). Only alterations designated as pathogenic or likely pathogenic by the American College of Medical Genetics were included.¹⁸ The gBRCA2 cohort was chosen as a comparison group because it has the most characterized HR-deficient prostate cancer phenotype and established management guidelines. To facilitate comparisons, the gBRCA2 cohort was individually matched (1:1) to the gATM group by stage at diagnosis (metastatic vs. nonmetastatic), year of germline testing and by center at which patients were treated.

A total of 45 patients with gATM and 45 matched gBRCA2 cases were included. Two patients included in the current study were also reported in the analysis by Marshall et al.¹⁰: one gATM and one gBRCA2 mutation carrier. Medical records review was performed after local institutional review board approvals at participating centers.

2.1 | Statistical analysis

Baseline characteristics for gATM and gBRCA2 cohorts were compared using the Mann-Whitney test for continuous variables and Fisher's exact test for categorical variables. The primary efficacy endpoint was the percentage of men achieving at least one prostate-specific antigen value that was ≥50% below baseline (PSA₅₀ response). Treatment-specific PSA₅₀ responses were compared using Fisher's exact tests. Follow-up was calculated using reverse Kaplan-Meier estimation. Metastasis-free survival (MFS) was defined as time from diagnosis to death, last clinical evaluation, or evidence of metastasis on conventional imaging. determined at the local radiologists' discretion and broadly consistent with the Prostate Cancer Clinical Trials Working Group 3 guidelines.¹⁹ Overall survival (OS) was defined as time from prostate cancer diagnosis to death or last clinical evaluation. Time on therapy was defined as time from initiation to termination of therapy or last clinical evaluation, and time to next treatment was defined as time from the start of treatment to the initiation of the next regimen or last clinical evaluation. OS, MFS, median time on therapy, and median time to next treatment were estimated using

Kaplan–Meier methods. Differences between gATM and gBRCA2 cohorts were estimated using the log-rank test. All tests were two-sided and p < .05 was considered statistically significant. R, version 3.6.3, was used for statistical analysis.

3 | RESULTS

3.1 | Cohort characteristics

The study included 90 men with prostate cancer: 45 with gATM mutations and 45 with gBRCA2 mutations. Specific mutations in gATM and gBRCA2 genes are documented in Figure 1. Baseline characteristics, including age, PSA, Gleason Grade Group, were similar in the gATM and gBRCA2 cohorts (Table 1). A similar number of patients had a family history of cancer, meeting Prostate Cancer NCCN Guidelines²⁰ for germline testing. Distribution of pathology patterns (e.g., cribriform, neuroendocrine), definitive treatment. and anatomical sites of metastases were also similar between the two cohorts. The median follow-up time since diagnosis was 11.8 years in the gATM cohort and 8.0 years in the gBRCA2 cohort. Metastases developed in 23/28 gATM and 20/28 gBRCA2 patients after a median follow-up of 15.7 and 15.0 years, respectively, for the subgroup of men diagnosed with localized prostate cancer. Of the 12 men in the gATM cohort and 14 men in the gBRCA2 cohort for whom tumor sequencing results were available, none were reported to have somatic alterations in other HR genes.



FIGURE 1 Distribution of ATM and BRCA2 mutations [Color figure can be viewed at wileyonlinelibrary.com]

3.2 | PSA₅₀ response rates

Responses to systemic therapies in the mCRPC setting, as measured by PSA₅₀, are summarized in Table 2. Comparing patients with gATM versus gBRCA2 mutations, there was no evident difference in PSA₅₀ response to abiraterone: 9/16 (56%) versus 11/19 (58%); to enzalutamide: 9/16 (56%) versus 8/12 (67%); or to docetaxel: 9/13 (69%) versus 9/16 (60%). Only 1 of 3 patients with gATM versus 5 of 7 patients with gBRCA2 responded to platinum, numbers are too small to draw conclusions. In contrast, there appeared to be a difference in responses to PARPi–0/7 (0%) patients with gATM mutations responded versus 12/14 (86%) patients with gBRCA2 mutations (p < .001).

TABLE 1 Patient characteristics

Characteristics	gATM	gBRCA2	р
Number of patients	45	45	
Stage M1 at diagnosis (%)	17 (38)	17 (38)	
Age (median [IQR])	58 [54, 66]	62 [55, 67]	.2
PSA (median [IQR])	24 [9, 76]	11 [6, 46]	.13
Grade (%)			
2	6 (17)	4 (11)	
3	7 (20)	5 (14)	
4	5 (14)	8 (22)	
5	17 (49)	20 (54)	
Family history of cancer meeting Prostate Cancer NCCN Guidelines for germline testing ²⁰ (%)	25 (60)	29 (71)	.4
Known other primary cancers (%)	5 (11)	4 (9)	>.9
Pathology (%)			
acinar	24 (80)	22 (76)	
ductal	3 (10)	3 (10)	
intraductal	0 (0)	1 (3)	
cribriform	1 (3)	1 (3)	
neuroendocrine	2 (7)	2 (7)	
Prostatectomy (%)	20 (44)	22 (50)	.7
Radiotherapy (%)	22 (51)	24 (56)	.8
Bone metastasis at the time of diagnosis (%)	14 (31)	15 (33)	>.9
Nodal metastasis at the time of diagnosis (%)	13 (29)	11 (24)	.8
Visceral metastasis at the time of diagnosis (%)	1 (2)	3 (7)	.6

3.3 | Time on treatment

Median time on mCRPC treatment for the gATM and gBRCA2 cohorts is shown in Table 3. Overall, for abiraterone, enzalutamide, and docetaxel, there was no evidence of different duration from the start to the end of treatment between the cohorts. In the mCRPC setting, median (95% confidence interval [CI]) time on AR-targeted therapies in gATM compared to gBRCA2 cohort was 9.7 (6.5-23) versus 6.4 (5.4-15.5) months for abiraterone (p = .5); 6.5 (4.6-not reached) vs 9 (4.9-not reached) months for enzalutamide (p > .9); and 5.1 (3.7-not reached) versus 4 (3-6) months for docetaxel-based chemotherapy (p = .06). Median time on platinum-based chemotherapy in the mCRPC setting was 3 (1-not reached) months in the gATM cohort compared to 6 (4-not reached) months in the gBRCA2 cohort (p = .11). We observed a difference in treatment duration on PARPi: 3 (2-not reached) months in the gATM cohort compared to 12 (6.9-not reached) months in the gBRCA2 cohort (p = .004). Time on treatment for each therapy is shown in Figures 5SA-SE.

3.4 | Overall survival

During the study follow-up period, 15/45 (33.3%) gATM and 18/45 (40%) gBRCA2 patients died. Median (95% CI) OS from diagnosis to death was 10.9 years (9.5-not reached) versus 9.9 years (7.1-not reached, p = .07) for the gATM and gBRCA2 cohorts, respectively (Figure 2). There was no evidence of OS difference between gATM and gBRCA2 cohorts when analyzing subgroups of patients initially diagnosed with localized (not reached vs 9.9 years, respectively, p = .07) or metastatic disease (8.7 vs. 3.6 years, respectively, p = .4; Figure S3).

TABLE 2 PSA₅₀ response

Therapy	Prior	gATM	gBRCA2	р
Abiraterone	Overall	9/16 (56%)	11/19 (58%)	>.9
	Pre-enza	9/14 (64%)	10/17 (59%)	
	Post-enza	0/2 (0%)	1/2 (50%)	
Enzalutamide	Overall	9/16 (56%)	8/12 (67%)	.7
	Pre-abi	7/10 (70%)	5/7 (71%)	
	Post-abi	2/6 (33%)	3/5 (60%)	
Docetaxel	Overall	9/13 (69%)	9/16 (56%)	.7
	Pre-abi/enza	7/9 (78%)	4/7 (57%)	
	Post-abi/enza	2/4 (50%)	5/9 (56%)	
PARPi	Overall	0/7 (0%)	12/14 (86%)	<.001
	Pre-plat	0/3 (0%)	10/11 (91%)	
	Post-plat	0/4 (0%)	2/3 (67%)	

TABLE 3 Time on treatment

		gATM	gATM		gBRCA2			
Therapy	Setting	Number of pts	Median time on therapy (95% CI)	Number of pts	Median time on therapy (95% CI)	Р		
Abiraterone	Overall	19	9.71 (6.5-23)	24	6.44 (5-15.5)	.6		
	HSPC	2	3 (3-N/A)	5	6 (5-N/A)	>.9		
	CRPC	17	9.71 (6.5–23)	19	6.44 (5.38-15.5)	.5		
Enzalutamide	CRPC	16	6.5 (4.62-N/A)	12	9 (4.92-N/A)	>.9		
PARPi	CRPC	7	3 (2-N/A)	15	12 (6.9-N/A)	.004		
Platinum	CRPC	3	3 (1-N/A)	7	6 (4-N/A)	.11		
Docetaxel	Overall	18	4.13 (4-7)	21	4 (3-6)	.12		
	HSPC	5	4 (N/A-N/A)	4	4.5 (3-N/A)	.4		
CRPC		13	5.12 (3.7-N/A)	17	4 (3-6)	.06		
			Median time to next therapy (Cl 95%)		Median time to next therapy (Cl 95%)			
	CRPC	13	10.47 (6.47-N/A)	15	7 (4.16–12.82)	.15		

Abbreviations: CRPC, castration resistant prostate cancer; HSPC, hormone sensitive prostate cancer; Pts, patients.



FIGURE 2 Overall survival [Color figure can be viewed at wileyonlinelibrary.com]

Among the 28 patients in each cohort diagnosed with localized prostate cancer, median (95% Cl) MFS was 5.7 years (5.1–11.1) versus 5.0 years (4.1–7.0, p = .13) for the gATM and gBRCA2 cohorts, respectively (Figure S4).

4 | DISCUSSION

Prostate tumors with alterations in DDR genes, particularly those in the HR repair pathway, represent a group of interest particularly in light of recent FDA approvals of the PARP inhibitors rucaparib and olaparib. While broadly grouped with gBRCA1/2 carriers, patients with prostate cancer in the setting of gATM mutations have not been characterized as an independent cohort. This study focuses on patients with prostate cancer and gATM mutations and describes responses to conventional and emerging systemic therapies with the aim of improving our understanding of therapeutic approaches for these patients.

Among men diagnosed with prostate cancer, those carrying *gBRCA2* mutations are recognized to have a more aggressive phenotype (Table S3).⁶ Another retrospective study, albeit with limited numbers of *gATM* carriers, found that *gBRCA1/2* and *gATM* are associated with earlier age of death and shorter cancer-specific survival.⁹ Dedicated attention is warranted for *gATM* mutation carriers to further define specific prostate cancer risks and response to treatment.

Our data support the concept that while ATM-deficient prostate cancer may share features with BRCA2-deficient tumors, such as enrichment in the metastatic setting and response to nontargeted agents, they have distinct clinical characteristics. For example, we observed an attenuated response to PARPi in the gATM cohort compared to the gBRCA2 cohort, consistent with a retrospective study by Marshall et al.,¹⁰ in which 0/8 patients with germline or somatic ATM mutations responded to PARPi. This difference in sensitivity to PARPi may partially be explained by different roles for ATM and BRCA2 in the HR repair pathway. ATM's primary role is to recognize double-strand break and to activate downstream HR repair proteins, such as Chk2.²¹⁻²³ Once activated, Chk2 has an overlapping function with ATM and phosphorylates the core HR repair pathway effectors, for example, BRCA1, BRCA2.²¹ Chk2 can be activated by proteins other than ATM, such as DNA-dependent protein kinase, suggesting that HR repair pathway can be activated even in cells with loss of ATM function.²² These mechanistic differences in ATM and BRCA2 may account for observed differences in sensitivity to HR-targeted therapies between the two cohorts of our study. In addition, Neeb et al.,⁷ have recently reported that ATM protein

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expression as measured by ATM IHC is not perfectly overlapping with ATM mutations identified by NGS and suggest that protein expression may be another factor for treatment selection, potentially more predictive than DNA sequencing.

Abiraterone, enzalutamide, and docetaxel have mechanisms of action largely independent of *BRCA2* and *ATM*. A previous study reported that these therapies are similarly effective in *gBRCA2* mutation carriers compared to noncarriers and *gBRCA2* mutation carriers might benefit from upfront androgen-directed therapy rather than taxanes.³ We observed comparable PSA₅₀ response rates in the two cohorts in our study. Thus, our data suggest that abiraterone, enzalutamide, and docetaxel should be offered to patients with mCRPC who carry *gATM* mutations.

Recent data suggest that platinum chemotherapy is effective in patients with *BRCA2* mutations.^{24–26} In our study, patients with gATM mutations appeared to have a reduced response to platinum chemotherapy compared to the *gBRCA2* cohort, but this comparison was not statistically significant owing to the small numbers. However, our observations are consistent with other studies reporting disappointing responses to platinum chemotherapy among *ATM* mutation carriers with prostate cancer.^{15,26} To date, reported numbers of patients with mCRPC and *ATM* alterations treated with platinum chemotherapy remain small and further studies are needed.

Our data highlight the need to explore new targeted therapies in patients with mCRPC and ATM alterations. Preclinical data suggest that ATM-deficient prostate tumors may be sensitive to ATR inhibitors, which, when combined with PARPi, result in apoptosis in PARPi-resistant prostate cancer cell lines.^{7,27} Several ongoing clinical trials are evaluating ATR inhibitors in prostate cancer (e.g., NCT04267939, NCT03787680).

We did not observe a significant difference in OS between the two cohorts, although this could be attributable to the limited numbers of patients and deaths and to different proportions of men receiving PARPi in the two groups. More men in gBRCA2 cohort received PARPi, which has a proven OS benefit for these patients.^{12,28}

There are a number of important limitations to our study. First, this is a non-randomized retrospective study with a relatively small sample size. Second, the indications for germline testing in prostate cancer have been and remain evolving, so there are likely differences in practice from 2014 to 2019, as well as ascertainment biases. We attempted to minimize confounding effect by matching cases by year of testing; we acknowledge that men undergoing germline testing 2014–2019 will have been largely those with a strong family history of cancer and/or aggressive phenotype, although both gATM and gBRCA2 cohorts are likely to have been similarly affected. Third, the two cohorts are matched only for the year of testing, stage at diagnosis and treatment center; other patient characteristics were not matched. Fourth, the study does not include a control group of men without gATM and gBRCA2 mutations, which limits broader implications for treatment response. Fifth, the study does not include radiographic response assessment or confirmed PSA₅₀ responses, limiting treatment response assessments. Clinical practices at

different institutions may vary. For example, imaging was performed at clinician discretion without predefined standard intervals, which may have affected the time on treatment and MFS assessments. Finally, somatic alterations in other genes, mutation zygosity and protein expression were not fully addressed, but interference from clonal hematopoiesis of indeterminant potential would be less of an issue.²⁹ Nevertheless, given the greater prevalence of gATM mutations^{30,31} in general population, compared to gBRCA2 mutations,^{32,33} we believe that specific examination of gATM remains important to this patient population.

5 | CONCLUSIONS

Our data provide evidence that standard therapies may be similarly effective in gATM- and gBRCA2-associated prostate cancer, whereas PARPi appear less effective in gATM-associated prostate cancer. We did not find that abiraterone, enzalutamide, and docetaxel were less effective in patients with prostate cancer with gATM mutations and thus these agents should remain standard of care options for patients. This important subgroup of patients should continue to be studied and incorporated into clinical trials—especially those incorporating novel agents and combination strategies, for example, ATR inhibitors.

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CONFLICT OF INTERESTS

Catherine H. Marshall: Consulting from Dendreon, Bayer, McGraw-Hill Publishing Company. Travel from Dava Oncology.

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ETHICS STATEMENT

This study was approved by IRB board at each participating site.

DATA AVAILABILITY STATEMENT

Data available on request due to privacy/ethical restrictions.

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SUPPORTING INFORMATION

Additional Supporting Information may be found online in the supporting information tab for this article.

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ORIGINAL ARTICLE

The Prostate WILEY

Efficacy of systemic therapies in men with metastatic castration resistant prostate cancer harboring germline ATM versus BRCA2 mutations

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Abstract

Background: Among men with metastatic prostate cancer, about 10% have germline alterations in DNA damage response genes. Most studies have examined *BRCA2* alone or an aggregate of *BRCA1/2* and *ATM*. Emerging data suggest that *ATM* mutations may have distinct biology and warrant individual evaluation. The objective of this study is to determine whether response to prostate cancer systemic therapies differs between men with germline mutations in *ATM* (g*ATM*) and *BRCA2* (g*BRCA2*). **Methods:** This is an international multicenter retrospective matched cohort study of men with prostate cancer harboring g*ATM* or g*BRCA2*. PSA₅₀ response (\geq 50% decline in prostate-specific antigen) was compared using Fisher's exact test.

Results and Limitations: The study included 45 gATM and 45 gBRCA2 patients, matched on stage and year of germline testing. Patients with gATM and gBRCA2 had similar age, Gleason grade, and PSA at diagnosis. We did not observe differences in PSA₅₀ responses to abiraterone, enzalutamide, or docetaxel in metastatic castration resistant prostate cancer between the two groups; however, 0/7 with gATM and 12/14 with gBRCA2 achieved PSA₅₀ response to PARPi (p < .001). Median (95% confidence interval) overall survival from diagnosis to death was 10.9 years (9.5-not reached) versus 9.9 years (7.1not reached, p = .07) for the gATM and gBRCA2 cohorts, respectively. Limitations include the retrospective design and lack of mutation zygosity data.

Conclusions: Conventional therapies can be effective in gATM carriers and should be considered before PARPi, which shows limited efficacy in this group. Men with gATM mutations warrant prioritization for novel treatment strategies.

Center for Strategic Scientific Initiatives, National Cancer Institute; Prostate Cancer Foundation; Institute for Prostate Cancer Research; Washington State Medical Oncology Society; Advancing Cancer Treatment; Patrick Walsh Prostate Cancer Research Fund; NCI; DoD

KEYWORDS

abiraterone, ATM, BRCA2, docetaxel, enzalutamide, germline, homologous recombination deficiency, PARPi, platinum

1 | INTRODUCTION

Approximately 10% of men with metastatic prostate cancer have germline (inherited) DNA damage response (gDDR) gene alterations. *BRCA2* is a homologous recombination (HR) gene and is the most frequent pathogenic germline alteration in advanced prostate cancer (3%–5%), followed by *ATM* (1.6%–2%) and *BRCA1* (0.8%–1.3%).^{1–3} Several studies have shown that germline *BRCA2* mutations (*gBRCA2*) are associated with poor prognosis and worse prostate cancer outcomes and/or increased genomic instability.^{3–8}

Castro et al.,⁶ reported that at diagnosis, patients with prostate cancer and gBRCA1/2 mutations are more likely to have Gleason Grade Group \geq 4 disease, T3/4 stage, nodal involvement, metastases, and shorter cancer-specific survival compared to noncarriers. The IMPACT study showed that gBRCA2 mutation carriers have a higher incidence of prostate cancer and are more likely to be diagnosed at a younger age and have clinically significant disease compared to noncarriers, whereas no difference in age or tumor characteristics was detected between gBRCA1- and noncarriers.⁵ Na et al.,⁹ reported that the combined gBRCA1/2 and germline ATM (gATM) mutation rate was higher in lethal prostate cancer compared to localized disease. However, features of tumors and treatment responses linked to gATM mutations as a separate cohort are not characterized.

gATM mutation carriers have not been well-characterized despite ATM being the second most frequently observed DNA damage response gene alteration in metastatic prostate cancer. Several retrospective and prospective studies have reported that ATM-deficient prostate tumors may have attenuated response to poly-ADP-ribose polymerase inhibitors (PARPi) and platinum chemotherapy.^{7,10-15} Preliminary results of the phase II TRITON2 study demonstrated radiographic response to PARPi rucaparib in 51% (50/98) of men with BRCA1/2 and only 4% (2/49) of men with ATM mutations.^{11,16} The US Food and Drug Administration (FDA) granted rucaparib an accelerated approval for men with metastatic castration resistant prostate cancer (mCRPC) and BRCA1/2 mutations who were previously treated with docetaxel. In the phase III randomized PROfound study of the PARPi olaparib vs AR targeting agent, the primary endpoint of radiographic progression-free survival (rPFS) in men with mCRPC harboring mutations in BRCA1/2 and/or ATM (cohort A) was met, and olaparib also received FDA approval. While the primary endpoint was met for cohort A, in a post hoc subgroup analysis of men whose prostate cancer harbored ATM alterations, olaparib did

not significantly improve rPFS (median 5.4 months vs. 4.7 months for controls).¹² One potential explanation for the observed differences in clinical activity of PARPi in men with *BRCA2* versus *ATM* mutations may relate to the distinctive roles these proteins play in HR repair, with *ATM* acting as a sensor of DNA double strand break and *BRCA2* being a core effector of HR DNA repair.

Conventional systemic prostate cancer therapies, such as androgen receptor (AR) targeted or taxane agents, are not currently selected by biomarkers. These therapies have been reported to be effective in *gBRCA1/2* carriers with prostate cancer.^{3,17} PROREPAIR-B, a prospective cohort study, compared response outcomes for mCRPC treatments among *gBRCA2* carriers and non-carriers and showed similar response rates.³ Efficacy in patients with *gATM*, as a distinct cohort, has not been evaluated. Given the uncertain response to HR-deficiency targeted treatments in these men, we sought to investigate whether these patients respond to conventional biomarker-agnostic therapies. We hypothesized that, compared to men carrying *gBRCA2*, those carrying *gATM* would have a similar response to AR-targeted agents and docetaxel yet attenuated responses to platinum and PARPi therapies.

2 | METHODS

This is an international, retrospective, matched cohort study of Consecutive patients with prostate cancer who underwent clinical germline genetic testing between 2014 and 2019 at the University of Washington (UW), Johns Hopkins (JH) Hospital, CNIO-IBIMA Genitourinary Cancer Unit, or Tulane University Cancer Center. We selected patients who had gATM or gBRCA2 mutations identified with germline genetic testing panels (Ambry Color, Invitae, Myriad, or inhouse germline genetic testing at CNIO, JH, and UW). Only alterations designated as pathogenic or likely pathogenic by the American College of Medical Genetics were included.¹⁸ The gBRCA2 cohort was chosen as a comparison group because it has the most characterized HR-deficient prostate cancer phenotype and established management guidelines. To facilitate comparisons, the gBRCA2 cohort was individually matched (1:1) to the gATM group by stage at diagnosis (metastatic vs. nonmetastatic), year of germline testing and by center at which patients were treated.

A total of 45 patients with gATM and 45 matched gBRCA2 cases were included. Two patients included in the current study were also WILEY-The Prostate

reported in the analysis by Marshall et al.¹⁰: one gATM and one gBRCA2 mutation carrier. Medical records review was performed after local institutional review board approvals at participating centers.

2.1 Statistical analysis

Baseline characteristics for gATM and gBRCA2 cohorts were compared using the Mann-Whitney test for continuous variables and Fisher's exact test for categorical variables. The primary efficacy endpoint was the percentage of men achieving at least one prostate-specific antigen value that was ≥50% below baseline (PSA₅₀ response). Treatment-specific PSA₅₀ responses were compared using Fisher's exact tests. Follow-up was calculated using reverse Kaplan-Meier estimation. Metastasis-free survival (MFS) was defined as time from diagnosis to death, last clinical evaluation, or evidence of metastasis on conventional imaging. determined at the local radiologists' discretion and broadly consistent with the Prostate Cancer Clinical Trials Working Group 3 guidelines.¹⁹ Overall survival (OS) was defined as time from prostate cancer diagnosis to death or last clinical evaluation. Time on therapy was defined as time from initiation to termination of therapy or last clinical evaluation, and time to next treatment was defined as time from the start of treatment to the initiation of the next regimen or last clinical evaluation. OS, MFS, median time on therapy, and median time to next treatment were estimated using

Kaplan-Meier methods. Differences between gATM and gBRCA2 cohorts were estimated using the log-rank test. All tests were two-sided and p < .05 was considered statistically significant. R, version 3.6.3, was used for statistical analysis.

3 | RESULTS

3.1 | Cohort characteristics

The study included 90 men with prostate cancer: 45 with gATM mutations and 45 with gBRCA2 mutations. Specific mutations in gATM and gBRCA2 genes are documented in Figure 1. Baseline characteristics, including age, PSA, Gleason Grade Group, were similar in the gATM and gBRCA2 cohorts (Table 1). A similar number of patients had a family history of cancer, meeting Prostate Cancer NCCN Guidelines²⁰ for germline testing. Distribution of pathology patterns (e.g., cribriform, neuroendocrine), definitive treatment. and anatomical sites of metastases were also similar between the two cohorts. The median follow-up time since diagnosis was 11.8 years in the gATM cohort and 8.0 years in the gBRCA2 cohort. Metastases developed in 23/28 gATM and 20/28 gBRCA2 patients after a median follow-up of 15.7 and 15.0 years, respectively, for the subgroup of men diagnosed with localized prostate cancer. Of the 12 men in the gATM cohort and 14 men in the gBRCA2 cohort for whom tumor sequencing results were available, none were reported to have somatic alterations in other HR genes.



FIGURE 1 Distribution of ATM and BRCA2 mutations [Color figure can be viewed at wileyonlinelibrary.com]

3.2 | PSA₅₀ response rates

Responses to systemic therapies in the mCRPC setting, as measured by PSA₅₀, are summarized in Table 2. Comparing patients with gATM versus gBRCA2 mutations, there was no evident difference in PSA₅₀ response to abiraterone: 9/16 (56%) versus 11/19 (58%); to enzalutamide: 9/16 (56%) versus 8/12 (67%); or to docetaxel: 9/13 (69%) versus 9/16 (60%). Only 1 of 3 patients with gATM versus 5 of 7 patients with gBRCA2 responded to platinum, numbers are too small to draw conclusions. In contrast, there appeared to be a difference in responses to PARPi–0/7 (0%) patients with gATM mutations responded versus 12/14 (86%) patients with gBRCA2 mutations (p < .001).

TABLE 1 Patient characteristics

Characteristics	gATM	gBRCA2	р
Number of patients	45	45	
Stage M1 at diagnosis (%)	17 (38)	17 (38)	
Age (median [IQR])	58 [54, 66]	62 [55, 67]	.2
PSA (median [IQR])	24 [9, 76]	11 [6, 46]	.13
Grade (%)			
2	6 (17)	4 (11)	
3	7 (20)	5 (14)	
4	5 (14)	8 (22)	
5	17 (49)	20 (54)	
Family history of cancer meeting Prostate Cancer NCCN Guidelines for germline testing ²⁰ (%)	25 (60)	29 (71)	.4
Known other primary cancers (%)	5 (11)	4 (9)	>.9
Pathology (%)			
acinar	24 (80)	22 (76)	
ductal	3 (10)	3 (10)	
intraductal	0 (0)	1 (3)	
cribriform	1 (3)	1 (3)	
neuroendocrine	2 (7)	2 (7)	
Prostatectomy (%)	20 (44)	22 (50)	.7
Radiotherapy (%)	22 (51)	24 (56)	.8
Bone metastasis at the time of diagnosis (%)	14 (31)	15 (33)	>.9
Nodal metastasis at the time of diagnosis (%)	13 (29)	11 (24)	.8
Visceral metastasis at the time of diagnosis (%)	1 (2)	3 (7)	.6

3.3 | Time on treatment

Median time on mCRPC treatment for the gATM and gBRCA2 cohorts is shown in Table 3. Overall, for abiraterone, enzalutamide, and docetaxel, there was no evidence of different duration from the start to the end of treatment between the cohorts. In the mCRPC setting, median (95% confidence interval [CI]) time on AR-targeted therapies in gATM compared to gBRCA2 cohort was 9.7 (6.5-23) versus 6.4 (5.4-15.5) months for abiraterone (p = .5); 6.5 (4.6-not reached) vs 9 (4.9-not reached) months for enzalutamide (p > .9); and 5.1 (3.7-not reached) versus 4 (3-6) months for docetaxel-based chemotherapy (p = .06). Median time on platinum-based chemotherapy in the mCRPC setting was 3 (1-not reached) months in the gATM cohort compared to 6 (4-not reached) months in the gBRCA2 cohort (p = .11). We observed a difference in treatment duration on PARPi: 3 (2-not reached) months in the gATM cohort compared to 12 (6.9-not reached) months in the gBRCA2 cohort (p = .004). Time on treatment for each therapy is shown in Figures 5SA-SE.

3.4 | Overall survival

During the study follow-up period, 15/45 (33.3%) gATM and 18/45 (40%) gBRCA2 patients died. Median (95% CI) OS from diagnosis to death was 10.9 years (9.5-not reached) versus 9.9 years (7.1-not reached, p = .07) for the gATM and gBRCA2 cohorts, respectively (Figure 2). There was no evidence of OS difference between gATM and gBRCA2 cohorts when analyzing subgroups of patients initially diagnosed with localized (not reached vs 9.9 years, respectively, p = .07) or metastatic disease (8.7 vs. 3.6 years, respectively, p = .4; Figure S3).

TABLE 2 PSA₅₀ response

Therapy	Prior	gATM	gBRCA2	p
Abiraterone	Overall	9/16 (56%)	11/19 (58%)	>.9
	Pre-enza	9/14 (64%)	10/17 (59%)	
	Post-enza	0/2 (0%)	1/2 (50%)	
Enzalutamide	Overall	9/16 (56%)	8/12 (67%)	.7
	Pre-abi	7/10 (70%)	5/7 (71%)	
	Post-abi	2/6 (33%)	3/5 (60%)	
Docetaxel	Overall	9/13 (69%)	9/16 (56%)	.7
	Pre-abi/enza	7/9 (78%)	4/7 (57%)	
	Post-abi/enza	2/4 (50%)	5/9 (56%)	
PARPi	Overall	0/7 (0%)	12/14 (86%)	<.001
	Pre-plat	0/3 (0%)	10/11 (91%)	
	Post-plat	0/4 (0%)	2/3 (67%)	

		gATM		gBRCA2		
Therapy	Setting	Number of pts	Median time on therapy (95% Cl)	Number of pts	Median time on therapy (95% CI)	Ρ
Abiraterone	Overall	19	9.71 (6.5–23)	24	6.44 (5-15.5)	.6
	HSPC	2	3 (3-N/A)	5	6 (5-N/A)	>.9
	CRPC	17	9.71 (6.5-23)	19	6.44 (5.38–15.5)	.5
Enzalutamide	CRPC	16	6.5 (4.62-N/A)	12	9 (4.92-N/A)	>.9
PARPi	CRPC	7	3 (2-N/A)	15	12 (6.9-N/A)	.004
Platinum	CRPC	3	3 (1-N/A)	7	6 (4-N/A)	.11
Docetaxel	Overall	18	4.13 (4-7)	21	4 (3-6)	.12
	HSPC	5	4 (N/A-N/A)	4	4.5 (3-N/A)	.4
	CRPC	13	5.12 (3.7-N/A)	17	4 (3-6)	.06
			Median time to next therapy (Cl 95%)		Median time to next therapy (Cl 95%)	
	CRPC	13	10.47 (6.47-N/A)	15	7 (4.16-12.82)	.15

TABLE 3 Time on treatment

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Abbreviations: CRPC, castration resistant prostate cancer; HSPC, hormone sensitive prostate cancer; Pts, patients.



FIGURE 2 Overall survival [Color figure can be viewed at wileyonlinelibrary.com]

Among the 28 patients in each cohort diagnosed with localized prostate cancer, median (95% Cl) MFS was 5.7 years (5.1–11.1) versus 5.0 years (4.1–7.0, p = .13) for the gATM and gBRCA2 cohorts, respectively (Figure S4).

4 | DISCUSSION

Prostate tumors with alterations in DDR genes, particularly those in the HR repair pathway, represent a group of interest particularly in light of recent FDA approvals of the PARP inhibitors rucaparib and olaparib. While broadly grouped with gBRCA1/2 carriers, patients with prostate cancer in the setting of gATM mutations have not been characterized as an independent cohort. This study focuses on patients with prostate cancer and gATM mutations and describes responses to conventional and emerging systemic therapies with the aim of improving our understanding of therapeutic approaches for these patients.

Among men diagnosed with prostate cancer, those carrying *gBRCA2* mutations are recognized to have a more aggressive phenotype (Table S3).⁶ Another retrospective study, albeit with limited numbers of gATM carriers, found that *gBRCA1/2* and gATM are associated with earlier age of death and shorter cancer-specific survival.⁹ Dedicated attention is warranted for gATM mutation carriers to further define specific prostate cancer risks and response to treatment.

Our data support the concept that while ATM-deficient prostate cancer may share features with BRCA2-deficient tumors, such as enrichment in the metastatic setting and response to nontargeted agents, they have distinct clinical characteristics. For example, we observed an attenuated response to PARPi in the gATM cohort compared to the gBRCA2 cohort, consistent with a retrospective study by Marshall et al.,¹⁰ in which 0/8 patients with germline or somatic ATM mutations responded to PARPi. This difference in sensitivity to PARPi may partially be explained by different roles for ATM and BRCA2 in the HR repair pathway. ATM's primary role is to recognize double-strand break and to activate downstream HR repair proteins, such as Chk2.²¹⁻²³ Once activated, Chk2 has an overlapping function with ATM and phosphorylates the core HR repair pathway effectors, for example, BRCA1, BRCA2.²¹ Chk2 can be activated by proteins other than ATM, such as DNA-dependent protein kinase, suggesting that HR repair pathway can be activated even in cells with loss of ATM function.²² These mechanistic differences in ATM and BRCA2 may account for observed differences in sensitivity to HR-targeted therapies between the two cohorts of our study. In addition, Neeb et al.,⁷ have recently reported that ATM protein

Abiraterone, enzalutamide, and docetaxel have mechanisms of action largely independent of *BRCA2* and *ATM*. A previous study reported that these therapies are similarly effective in *gBRCA2* mutation carriers compared to noncarriers and *gBRCA2* mutation carriers might benefit from upfront androgen-directed therapy rather than taxanes.³ We observed comparable PSA₅₀ response rates in the two cohorts in our study. Thus, our data suggest that abiraterone, enzalutamide, and docetaxel should be offered to patients with mCRPC who carry *gATM* mutations.

Recent data suggest that platinum chemotherapy is effective in patients with *BRCA2* mutations.^{24–26} In our study, patients with *gATM* mutations appeared to have a reduced response to platinum chemotherapy compared to the *gBRCA2* cohort, but this comparison was not statistically significant owing to the small numbers. However, our observations are consistent with other studies reporting disappointing responses to platinum chemotherapy among *ATM* mutation carriers with prostate cancer.^{15,26} To date, reported numbers of patients with mCRPC and *ATM* alterations treated with platinum chemotherapy remain small and further studies are needed.

Our data highlight the need to explore new targeted therapies in patients with mCRPC and ATM alterations. Preclinical data suggest that ATM-deficient prostate tumors may be sensitive to ATR inhibitors, which, when combined with PARPi, result in apoptosis in PARPi-resistant prostate cancer cell lines.^{7,27} Several ongoing clinical trials are evaluating ATR inhibitors in prostate cancer (e.g., NCT04267939, NCT03787680).

We did not observe a significant difference in OS between the two cohorts, although this could be attributable to the limited numbers of patients and deaths and to different proportions of men receiving PARPi in the two groups. More men in gBRCA2 cohort received PARPi, which has a proven OS benefit for these patients.^{12,28}

There are a number of important limitations to our study. First, this is a non-randomized retrospective study with a relatively small sample size. Second, the indications for germline testing in prostate cancer have been and remain evolving, so there are likely differences in practice from 2014 to 2019, as well as ascertainment biases. We attempted to minimize confounding effect by matching cases by year of testing; we acknowledge that men undergoing germline testing 2014–2019 will have been largely those with a strong family history of cancer and/or aggressive phenotype, although both gATM and gBRCA2 cohorts are likely to have been similarly affected. Third, the two cohorts are matched only for the year of testing, stage at diagnosis and treatment center; other patient characteristics were not matched. Fourth, the study does not include a control group of men without gATM and gBRCA2 mutations, which limits broader implications for treatment response. Fifth, the study does not include radiographic response assessment or confirmed PSA₅₀ responses, limiting treatment response assessments. Clinical practices at

different institutions may vary. For example, imaging was performed at clinician discretion without predefined standard intervals, which may have affected the time on treatment and MFS assessments. Finally, somatic alterations in other genes, mutation zygosity and protein expression were not fully addressed, but interference from clonal hematopoiesis of indeterminant potential would be less of an issue.²⁹ Nevertheless, given the greater prevalence of gATM mutations^{30,31} in general population, compared to gBRCA2 mutations,^{32,33} we believe that specific examination of gATM remains important to this patient population.

5 | CONCLUSIONS

Our data provide evidence that standard therapies may be similarly effective in gATM- and gBRCA2-associated prostate cancer, whereas PARPi appear less effective in gATM-associated prostate cancer. We did not find that abiraterone, enzalutamide, and docetaxel were less effective in patients with prostate cancer with gATM mutations and thus these agents should remain standard of care options for patients. This important subgroup of patients should continue to be studied and incorporated into clinical trials—especially those incorporating novel agents and combination strategies, for example, ATR inhibitors.

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CONFLICT OF INTERESTS

Catherine H. Marshall: Consulting from Dendreon, Bayer, McGraw-Hill Publishing Company. Travel from Dava Oncology.

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ETHICS STATEMENT

This study was approved by IRB board at each participating site.

DATA AVAILABILITY STATEMENT

Data available on request due to privacy/ethical restrictions.

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SUPPORTING INFORMATION

Additional Supporting Information may be found online in the supporting information tab for this article.

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PRECISION MEDICINE

abstract

Differential Activity of PARP Inhibitors in BRCA1- Versus BRCA2-Altered Metastatic Castration-Resistant Prostate Cancer

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PURPOSE Two poly (ADP-ribose) polymerase (PARP) inhibitors (olaparib and rucaparib) are US Food and Drug Administration–approved for patients with metastatic castration-resistant prostate cancer (mCRPC) harboring *BRCA1/2* mutations, but the relative efficacy of PARP inhibition in *BRCA1-* versus *BRCA2-*altered mCRPC is understudied.

METHODS We conducted a multicenter retrospective analysis involving 12 sites. We collected genomic and clinical data from 123 patients with *BRCA1/2*-altered mCRPC who were treated with PARP inhibitors. The primary efficacy end point was the prostate-specific antigen (PSA) response (\geq 50% PSA decline) rate. Secondary end points were PSA progression-free survival (PSA-PFS), clinical or radiographic PFS, and overall survival. We compared clinical outcomes, and other genomic characteristics, among *BRCA1*- versus *BRCA2*-altered mCRPC.

RESULTS A total of 123 patients (13 *BRCA1* and 110 *BRCA2*) were included. PARP inhibitors used were olaparib (n = 116), rucaparib (n = 3), talazoparib (n = 2), and veliparib (n = 2). At diagnosis, 72% of patients had Gleason 8-10 disease. *BRCA1* patients were more likely to have metastatic disease at presentation (69% v37%; P = .04). Age, baseline PSA, metastatic distribution, and types of previous systemic therapies were similar between groups. There were equal proportions of germline mutations (51% v 46%; P = .78) in both groups. *BRCA1* patients had more monoallelic (56% v 41%; P = .49) and concurrent *TP53* (55% v 36%; P = .32) mutations. PSA₅₀ responses in *BRCA1*- versus *BRCA2*-altered patients were 23% versus 63%, respectively (P = .01). *BRCA2* patients achieved longer PSA-PFS (HR, 1.94; 95% CI, 0.92 to 4.09; P = .08), PFS (HR, 2.08; 95% CI, 0.99 to 4.40; P = .05), and overall survival (HR, 3.01; 95% CI, 1.32 to 6.83; P = .008). Biallelic (compared with monoallelic) mutations, truncating (compared with missense) mutations, and absence of a concurrent *TP53* mutation were associated with PARP inhibitor sensitivity.

CONCLUSION PARP inhibitor efficacy is diminished in *BRCA1*- versus *BRCA2*-altered mCRPC. This is not due to an imbalance in germline mutations but might be related to more monoallelic mutations and/or concurrent *TP53* alterations in the *BRCA1* group.

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INTRODUCTION

Metastatic castration-resistant prostate cancer (mCRPC) remains a lethal disease with a poor prognosis.¹ Germline or somatic mutations in DNA damage repair genes have been described in approximately 20%-25% of these patients, which include BRCA1 and BRCA2.^{2,3} Although patients with these mutations generally have more aggressive disease and higher mortality than those with proficient homologous recombination repair (HRR),^{4,5} they also present as a novel therapeutic opportunity. Poly (ADP-ribose) polymerase (PARP) inhibitors efficiently kill tumor cells by synthetic lethality in cancers with damaged BRCA1 or BRCA2 genes, with PARP-mediated repair pathway inhibition resulting in DNA disruption and, therefore, genomic instability causing cancer cell death.^{6,7}

In May 2020, the US Food and Drug Administration approved two PARP inhibitors (olaparib and rucaparib) for men with mCRPC harboring a germline or somatic mutation in a gene associated with HRR.⁸ The approval of olaparib was based on the PROfound study in which men with previously treated mCRPC and HRR deficiency (mutation in one of the 14 HRR genes) who received olaparib had improved progression-free survival and overall survival relative to next-generation hormone therapy (enzalutamide and abiraterone).^{9,10} The approval of rucaparib was based on the TRITON2 trial, which reported prostate-specific antigen (PSA) and objective response rates of 63 and 44 percent in men with previously treated mCRPC and somatic or germline BRCA1 and BRCA2 mutations, respectively.¹¹ One of the most interesting post hoc findings from

ASSOCIATED Content

CONTENT Appendix

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CONTEXT

Key Objective

We conducted a multicenter retrospective study to determine whether the efficacy of poly (ADP-ribose) polymerase (PARP) inhibitors differs between cancers with *BRCA1* and *BRCA2* mutations and to examine differences in other genomic alterations that coexist with *BRCA1/2* mutations.

Knowledge Generated

We show that PARP inhibitor efficacy is diminished in *BRCA1*- versus *BRCA2*-altered metastatic castration-resistant prostate cancer. This is not due to an imbalance in germline mutations but might be related to more monoallelic mutations and/or concurrent *TP53* alterations in the *BRCA1* group.

Relevance

Additional therapeutic approaches are needed for patients with *BRCA1*-altered prostate cancer. These findings may have broad implications for other *BRCA1/2*-associated malignancies (breast, ovarian, and pancreatic cancers) where PARP inhibitors are used.

TRITON2 study was the possible disparity in the effectiveness of rucaparib in men with *BRCA1* relative to *BRCA2* mutations. More precisely, the therapeutic activity of rucaparib appeared to be generally higher in *BRCA2*-altered compared with *BRCA1*-altered mCRPC tumors, although formal statistical analyses comparing outcomes by gene mutation were not conducted. Similar trends were observed in the PROfound study, which also suggested dampened activity of olaparib in the *BRCA1* population.¹⁰

The activity of rucaparib was also previously explored in patients with mCRPC harboring non-*BRCA1/2* HRR gene mutations and was not sufficient to merit regulatory approval for that molecular subset of patients¹²; similar observations have been made with olaparib in the gene-bygene post hoc analyses from the PROfound study.^{9,10} However, differences in PARP inhibitor sensitivity between patients with *BRCA1*- and *BRCA2*-mutated mCRPC have not been formally examined to date. We hypothesized that patients with *BRCA1* mutations would not exhibit the same responses to PARP inhibition as patients with *BRCA2* mutations. Here, we describe the differential sensitivity to treatment with PARP inhibitors among men with *BRCA1* versus *BRCA2* mutations.

METHODS

Study Population and Design

This was a multicenter retrospective analysis of 123 consecutive patients from 12 academic sites with mCRPC who received single-agent PARP inhibitor treatment between December 2014 and July 2020. All PARP inhibitors were permitted in this analysis. Only patients harboring deleterious (somatic or germline) mutations in *BRCA1* or *BRCA2* were included in the study; other HRR genes were excluded. All centers participating in the study obtained local institutional review board approval before data abstraction.

Deleterious mutations in *BRCA1/2* were defined as any alterations resulting in protein truncation (frameshift or

nonsense mutations, canonical splice-site mutations, and truncating rearrangements) or homozygous genomic deletions. Selected missense mutations in *BRCA1/2* were also classified as deleterious, but only if they were designated as pathogenic or likely pathogenic in the ClinVar and/or COSMIC databases. All other alterations were considered variants of unknown significance and were excluded. Mutation origin (germline or somatic) and zygosity status (monoallelic or biallelic) were also recorded.

Study Outcomes

Demographic, clinical, and genomic characteristics were collected for all patients. This included age, Gleason score, PSA level, stage at diagnosis, metastatic distribution, and the type and number of previous systemic therapies received. We also captured information on concurrent genomic alterations in key prostate cancer genes (namely, *TP53, PTEN, RB1, SPOP, AR,* and *TMPRSS2-ERG*).

The primary efficacy end point was the percentage of men achieving a confirmed \geq 50% decline in PSA level from baseline at the initiation of PARP inhibitor treatment (PSA₅₀ response). Secondary end points were PSA progressionfree survival (PSA-PFS, defined as the time until a \geq 25% increase in PSA from baseline or nadir), progression-free survival (PFS, defined as the time to investigator-assessed clinical or radiographic progression, excluding PSA progression), and overall survival (OS, defined as the time to death from any cause). These definitions are broadly consistent with the Prostate Cancer Working Group 3 guidelines.¹³

Statistical Analysis

The desired sample size was prospectively defined, on the basis of the primary end point. In the published literature, the prevalence of *BRCA2* mutations relative to *BRCA1* mutations in prostate cancer is approximately $9:1.^{14,15}$ We hypothesized that the PSA₅₀ response rate to PARP inhibition would be 60% in *BRCA2*-mutated prostate cancers

and 20% in *BRCA1*-mutated prostate cancers. To achieve 80% power to detect this difference using Fisher's exact test with a one-sided alpha of .05, we would need to collect at least a total of 120 patients (108 with a *BRCA2* mutation and 12 with a *BRCA1* mutation).

PSA₅₀ response rates were compared between BRCA1and BRCA2-altered patients using logistics regression. Time-to-event outcomes of PSA-PFS, PFS, and OS were estimated using Kaplan-Meier method, and comparisons between groups were carried out using Cox proportionalhazards model. Multivariable logistic regression and Cox models were used to estimate odds ratio (OR) for PSA response and hazard ratios (HRs) for time-to-event outcomes and corresponding 95% CIs and to test for the association between BRCA mutation and patient outcomes, after adjusting for important clinical variables of age, Gleason sum, M stage, baseline PSA, and previous taxane treatment. Separate multivariable models were used to estimate the association between BRCA1/2 mutations and clinical outcomes adjusting for TP53 and PTEN mutations. The database was locked on August 30, 2020. Patients not meeting one or more of the time-to-event end points at the time of database lock were censored for that end point at the time of the last contact with the health system. R 4.0.1 was used for statistical analyses. All tests were two-sided, and P values of \leq .05 were considered statistically significant: adjustments were not made for multiple statistical comparisons.

RESULTS

Cohort Characteristics

One hundred twenty-three consecutive mCRPC patients with deleterious mutations in BRCA1 (n = 13) or BRCA2 (n = 110) were included in this analysis. Most mutations were frameshift alterations (58%), followed by homozygous deletions (13%); missense alterations were found in 8.1% of cases. PARP inhibitors used were olaparib (n = 116), rucaparib (n = 3), talazoparib (n = 2), and veliparib (n = 2). Table 1 displays the baseline demographic, clinical, and genomic characteristics of these patients. Men with BRCA1 mutations did not significantly differ from those with BRCA2 mutations, except that more patients in the *BRCA1* group had metastatic disease at initial diagnosis (69% v 37% P = .04). In the overall cohort, 72% of patients had Gleason 8-10 disease, the median age at the time of PARP inhibitor initiation was 67 years (interguartile range 61-71), and the median baseline PSA level was 44.3 ng/mL (interquartile range 8.7-140). Germline (compared with somatic) BRCA1/2 mutations were equally distributed in the two groups. There were numerically more monoallelic mutations (56% v41%; P = .49) and more concurrent *TP53* mutations (55% v 36%; P = .32) in the BRCA1 group, but broadly similar numbers of mutations in other key genes (PTEN, RB1, SPOP, TMPRSS2-ERG, and AR) across groups (Fig 1). Differences in the mechanisms of biallelic inactivation among the *BRCA1*- versus *BRCA2*-altered cancers are summarized in Appendix Table A1 and Figure A1.

Relationship Between BRCA1/2 and TP53 Mutations

To further explore the potential relationship between BRCA1/2 mutations and concurrent TP53 mutations, we interrogated the cBioPortal for Cancer Genomics database¹⁶ that contains DNA sequencing analysis on 6,875 patients with prostate cancer. Of those, 49 (0.7%) had deleterious BRCA1 mutations or deletions and 323 (4.7%) had deleterious BRCA2 alterations. With respect to TP53, 39% of BRCA1-altered (19 of 49) and 22% of BRCA2-altered (71 of 323) prostate cancers also harbored a deleterious TP53 mutation (P for difference, .019). There were no differences with respect to concurrent PTEN alterations; 20% of BRCA1-altered (10 of 49) and 17% of BRCA2-altered (55 of 323) prostate cancers also harbored a PTEN alteration (P for difference, .548). Conversely, RB1 mutations or deletions were enriched in BRCA2-altered cases; 12% of BRCA1-altered (6 of 49) and 30% of BRCA2-altered (97 of 323) prostate cancers also harbored an RB1 alteration (P for difference, .001).

We then examined the association between BRCA1/2 mutations and concurrent TP53 mutations in the other BRCA-associated cancers, again using cBioPortal.¹⁶ Among 9,134 patients with breast cancer, 50% of BRCA1-altered (144 of 288) and 41% of BRCA2-altered (143 of 350) breast cancers also harbored deleterious TP53 mutations (P for difference, .025). Similarly, among 1,206 patients with pancreatic cancer, 56% of BRCA1altered (14 of 25) and 44% of BRCA2-altered (7 of 16) pancreatic cancers also harbored deleterious TP53 mutations, although this did not reach significance (P for difference, .328). Conversely, among 1,668 patients with ovarian cancer, the prevalence of concurrent TP53 mutations was very high in both BRCA1-altered (94%; 77 of 82) and BRCA2-altered (94%; 80 of 85) ovarian cancers (P for difference, .604).

PSA Response Rate

The best PSA response for each patient (at any time) is depicted in Figure 2A. Overall, 72 of 123 patients (59%) achieved a PSA₅₀ response to PARP inhibitor treatment. There were significantly fewer PSA₅₀ responses in patients with BRCA1-altered versus BRCA2-altered mCRPC (23% v 63% respectively; OR, 0.18; 95% CI, 0.04 to 0.62; P = .01). This difference persisted after adjusting for age, Gleason sum, stage, baseline PSA, and previous taxane treatment (adjusted OR, 0.20; 95% CI, 0.04 to 0.76; P = .03) and after adjusting for concurrent TP53 and PTEN mutations (adjusted OR, 0.22; 95% CI, 0.05 to 0.86; P = .04; Table 2). Paradoxically, the median time to best PSA response (in those who achieved a response) was shorter in the BRCA1 than the BRCA2 group (6 v 17 weeks; P < .01). A forest plot showing other clinical and molecular factors that influenced PSA₅₀ responses is depicted in Figure 3A. PSA₅₀

 TABLE 1. Baseline Demographic, Clinical, and Genomic Data Overall and by Mutation Type

Characteristic	Overall Patients, No. (%)	BRCA1 Patients, No. (%)	BRCA2 Patients, No. (%)	Р
Gleason sum at diagnosis	123	13	110	.01
8-10	89 (72.4)	10 (76.9)	79 (71.8)	
6-7	25 (20.3)	0 (0)	25 (22.7)	
Unknown	9 (7.3)	3 (23.1)	6 (5.5)	
Age at start of therapy, years	123	13	110	.07
Median/mean	67/66.1	71/69.9	66.5/65.6	
Min-max	46-91	57-86	46-91	
Q1-Q3	61-71	67-73	60.2-71	
Baseline PSA, ng/mL	123	13	110	.3
Median/mean	44.3/281.3	47.2/172.3	43.8/294.1	
Min-max	0-6,394.9	0-1,459	0-6,394.9	
Q1-Q3	8.7-140.4	4.3-137.7	9.1-179.8	
T stage at diagnosis	85	8	77	1
T1-T2	31 (36.5)	3 (37.5)	28 (36.4)	
T3-T4	54 (63.5)	5 (62.5)	49 (63.6)	
N stage at diagnosis	123	13	110	.7
NO	100 (81.3)	10 (76.9)	90 (81.8)	
N1	23 (18.7)	3 (23.1)	20 (18.2)	
M stage at diagnosis	123	13	110	.03
MO	73 (59.3)	4 (30.8)	69 (62.7)	
M1	50 (40.7)	9 (69.2)	41 (37.3)	
Prior docetaxel or cabazitaxel	123	13	110	.2
No	49 (39.8)	3 (23.1)	46 (41.8)	
Yes	74 (60.2)	10 (76.9)	64 (58.2)	
Prior enzalutamide or abiraterone	123	13	110	1
No	14 (11.4)	1 (7.7)	13 (11.8)	
Yes	109 (88.6)	12 (92.3)	97 (88.2)	
Presence of bone metastases	119	13	106	1
No	16 (13.4)	1 (7.7)	15 (14.2)	
Yes	103 (86.6)	12 (92.3)	91 (85.8)	
Presence of visceral metastases	119	13	106	.3
No	91 (76.5)	12 (92.3)	79 (74.5)	
Yes	28 (23.5)	1 (7.7)	27 (25.5)	
Presence of nodal metastases	119	13	119	1
No	54 (45.4)	6 (46.2)	48 (45.3)	
Yes	65 (54.6)	7 (53.8)	58 (54.7)	
Origin of mutation	123	13	110	.7
Germline	62 (50.4)	6 (46.2)	56 (50.9)	
Somatic	61 (49.6)	7 (53.8)	54 (49.1)	
Allelic status of mutation	89	9	80	.49
Monoallelic	38 (42.7)	5 (55.6)	33 (41.2)	
Biallelic	51 (57.3)	4 (44.4)	47 (58.8)	

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Characteristic	Overall Patients, No. (%)	BRCA1 Patients, No. (%)	BRCA2 Patients, No. (%)
Mutation mechanism	123	13	110
Frameshift	71 (57.7)	3 (23.1)	68 (61.8)
Homozygous deletion	16 (13)	0 (0)	16 (14.5)
Missense	10 (8.1)	4 (30.8)	6 (5.5)
Nonsense	12 (9.8)	3 (23.1)	9 (8.2)
Rearrangement	11 (8.9)	2 (15.4)	9 (8.2)
Splicing	3 (2.4)	1 (7.7)	2 (1.8)
Concurrent TP53 mutation	103	11	92
No	64 (62.1)	5 (45.5)	59 (64.1)
Yes	39 (37.9)	6 (54.5)	33 (35.9)
Concurrent PTEN mutation	110	11	99
No	87 (79.1)	10 (90.9)	77 (77.8)
Yes	23 (20.9)	1 (9.1)	22 (22.2)
Concurrent RB1 mutation	110	11	99
No	91 (82.7)	11 (100)	80 (80.8)
Yes	19 (17.3)	0 (0)	19 (19.2)
Concurrent SPOP mutation	110	11	99
No	106 (96.4)	11 (100)	95 (96)
Yes	4 (3.6)	0 (0)	4 (4)
Concurrent AR mutation	109	11	98
No	89 (81.7)	10 (90.9)	79 (80.6)
Yes	20 (18.3)	1 (9.1)	19 (19.4)

Т

Abbreviations: M, metastasis; N, node; PSA, prostate-specific antigen; T, tumor.

Concurrent TMPRSS2-ERG fusion

No

Yes

responses were numerically lower in patients with somatic (compared with germline) mutations, monoallelic (compared with biallelic) mutations, missense (compared with truncating) mutations, and concurrent TP53 mutations.

110

95 (86.4)

15 (13.6)

Time-to-Event Outcomes

11

10 (90.9)

1 (9.1)

The median PSA-PFS with PARP inhibitor treatment was 40.7 weeks (95% CI, 29.3 to 53.0) in the entire cohort. PSA-PFS was shorter in BRCA1-mutated compared with

99

85 (85.9)

14 (14.1)

Р .001

.32

.4

.2

1

.68

1

Zygosity Germline (*) mutation <i>BRCA2</i>	89%	
BRCA1	11%	
PTEN	21%	
TP53	38%	
AR	18%	
RB1	17%	
TMPRSS2-ERG	13%	
SPOP	3%	
Genetic alteration		Frameshift mutation Missense mutation Pathogenic mutation, not otherwise specified Rearrangement mutation
		Homozygous deletion mutation Splice site mutation No alterations
Zygosity		Biallelic Monoallelic Unknown

FIG 1. Summary of key genetic alterations identified among patients in the overall cohort (N = 123).

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FIG 2. Efficacy outcomes, according to type of *BRCA* mutation. (A) Waterfall plot of best PSA response, comparing *BRCA1*- and *BRCA2*-altered patients. (B) Kaplan-Meier analysis of PSA-PFS, (C) PFS, and (D) OS, comparing *BRCA1*- and *BRCA2*-altered patients. HR, hazard ratio; NR, not reached; OS, overall survival; PARPi, poly (ADP-ribose) polymerase inhibitor; PFS, progression-free survival; PSA, prostate-specific antigen.

BRCA2-mutated patients (median 27.1 v 43.9 weeks; HR, 1.94; 95% CI, 0.92 to 4.09; P = .08; Fig 2B). This difference weakened after adjusting for age, Gleason sum, stage, baseline PSA, and previous taxane treatment (adjusted HR, 1.63; 95% CI, 0.73 to 3.63; P = .23) and after adjusting for concurrent *TP53* and *PTEN* mutations (adjusted HR, 1.40; 95% CI, 0.59 to 3.31; P = .44; Table 2). PSA-PFS was numerically shorter in patients with monoallelic (compared with biallelic) mutations, missense (compared with truncating) mutations, and concurrent *TP53* mutations (Fig 3B).

The median PFS was 43.4 weeks (95% CI, 36.0 to 53.0) in the overall cohort. Again, PFS was shorter in *BRCA1*-compared with *BRCA2*-mutated patients (median 43.4 v 45.4 weeks; HR, 2.08; 95% CI, 0.99 to 4.40; P = .05; Fig

2C). This difference persisted after adjusting for age, Gleason sum, stage, baseline PSA, and previous taxane treatment (adjusted HR, 2.20; 95% CI, 0.96 to 5.04; P = .06) and after adjusting for concurrent *TP53* and *PTEN* mutations (adjusted HR, 2.20; 95% CI, 0.97 to 4.96; P = .06; Table 2). PFS was numerically shorter in patients with monoallelic mutations, missense mutations, and concurrent *TP53* alterations (Fig 3C).

We also explored PSA-PFS and PFS in the responding patients only, examining *BRCA1* and *BRCA2* patients separately. Overall, 72 of 123 patients achieved a PSA₅₀ response: three patients with *BRCA1* and 69 patients with *BRCA2* mutations. Differences in baseline characteristics between the responding and nonresponding patients are

TABLE 2. Multivariable Analyses for PSA₅₀ Response, PSA-PFS, PFS, and OS

					Multivariable Analysis of PSA ₅₀ Response			Multivariable Analysis of PSA-PFS			Multivariable Analysis of PFS				Multivariable Analysis of OS			
Name	Levels	Reference	OR	Lower 95% Cl	Upper 95% CI	Р	HR	Lower 95% Cl	Upper 95% Cl	Р	HR	Lower 95% Cl	Upper 95% Cl	Р	HR	Lower 95% Cl	Upper 95% Cl	Р
Clinical																		
BRCA mutation	BRCA1	BRCA2	0.20	0.04	0.76	.0271	1.63	0.73	3.63	.2298	2.20	0.96	5.04	.0627	3.50	1.36	9.02	.0094
Gleason sum at diagnosis	6-7	8-10	1.14	0.43	3.13	.7915	0.93	0.51	1.68	.8137	1.08	0.60	1.94	.7981	0.97	0.48	1.96	.9238
Age at start of therapy, years	Continuous		1.00	0.95	1.05	.8882	1.02	0.99	1.05	.2966	1.00	0.97	1.03	.8457	0.99	0.95	1.02	.4644
Baseline PSA, ng/mL	Continuous		1.00	1.00	1.00	.4079	1.00	1.00	1.00	.5325	1.00	1.00	1.00	.5434	1.00	1.00	1.00	.0959
T stage at diagnosis	T3-T4	T1-T2	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
N stage at diagnosis	N1	NO	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
M stage at diagnosis	M1	MO	1.53	0.65	3.71	.3358	1.03	0.61	1.73	.9213	0.74	0.44	1.27	.2739	0.77	0.41	1.43	.4024
Prior enzalutamide or abiraterone	Yes	No	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Prior docetaxel or cabazitaxel	Yes	No	0.67	0.30	1.47	.3220	1.48	0.90	2.43	.1188	1.66	1.02	2.71	.0432	2.53	1.34	4.79	.0042
Presence of bone metastases	Yes	No	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Presence of visceral metastases	Yes	No	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Presence of nodal metastases	Yes	No	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Molecular																		
BRCA mutation	BRCA1	BRCA2	0.22	0.05	0.86	.0389	1.40	0.59	3.31	.4416	2.20	0.97	4.96	.0586	2.61	1.07	6.39	.0356
Origin of mutation	Somatic	Germline	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Allelic status of mutation	Biallelic	Monoallelic	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Homozygous deletion <i>v</i> rest	Homozygous deletion	Rest	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Frameshift mutation v rest	Frameshift mutation	Rest	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Missense mutation v rest	Missense mutation	Rest	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

(Continued on following page)

TABLE 2. Multivariable Analyses for PSA₅₀ Response, PSA-PFS, PFS, and OS (Continued) Multivariable Analysis of PSA

	Levels	Reference	Response				Multivariable Analysis of PSA-PFS				Multivariable Analysis of PFS				Multivariable Analysis of OS			
Name			OR	Lower 95% Cl	Upper 95% Cl	Р	HR	Lower 95% Cl	Upper 95% Cl	Р	HR	Lower 95% Cl	Upper 95% Cl	Р	HR	Lower 95% Cl	Upper 95% Cl	Р
Concurrent <i>TP53</i> mutation	Yes	No	0.51	0.22	1.19	.1204	2.82	1.70	4.68	.0001	1.79	1.11	2.89	.0167	2.26	1.27	4.05	.0058
Concurrent PTEN mutation	Yes	No	0.85	0.31	2.43	.7609	1.17	0.68	2.01	.5669	1.17	0.68	2.01	.5712	1.44	0.77	2.70	.2588
Concurrent <i>RB1</i> mutation	Yes	No	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Concurrent SPOP mutation	Yes	No	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Concurrent AR mutation	Yes	No	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Concurrent TMPRSS2-ERG fusion	Yes	No	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

Abbreviations: HR, hazard ratio; M, metastasis; N, node; NA, not available; OR, odds ratio; OS, overall survival; PFS, progression-free survival; PSA, prostate-specific antigen; T, tumor.

PSA Response Rate

Subgroup

Α

Subgroup		Event No./Total No. (%) [95% Cl]
Overall	├──● ──┤	72/123 (58.5) [49.3 to 67.3]
Mutation		
BRCA1		3/13 (23.1) [5 to 53.8]
BRCA2		69/110 (62.7) [53 to 71.8]
Gleason sum at diagnosis		
6-7	├─── ●───┤	16/25 (64) [42.5 to 82]
8-10	· · · · · ·	53/89 (59.6) [48.6 to 69.8]
Age at start of therapy, years		
< 70	├──● ──┤	47/78 (60.3) [48.5 to 71.2]
≥ 70	⊢	25/45 (55.6) [40 to 70.4]
Baseline PSA, ng/mL		
≥ 44.31	├── ┥	33/62 (53.2) [40.1 to 66]
< 44.31	· · · · · · · · · · · · · · · · · · ·	39/61 (63.9) [50.6 to 75.8]
M stage at diagnosis		
M1	├ ── ● ──┤	29/50 (58) [43.2 to 71.8]
MO	·	43/73 (58.9) [46.8 to 70.3]
Prior docetaxel or cabazitaxel		
Yes	├──● ──┤	40/74 (54.1) [42.1 to 65.7]
No	·	32/49 (65.3) [50.4 to 78.3]
Origin of mutation		
Somatic	├──● ──┤	29/61 (47.5) [34.6 to 60.7]
Germline	└── ┥	43/62 (69.4) [56.3 to 80.4]
Allelic status of mutation		
Biallelic	├ ───┥	30/51 (58.8) [44.2 to 72.4]
Monoallelic	├ ───┥	19/38 (50) [33.4 to 66.6]
Homozygous deletion v rest		
Homozygous deletion	├───	9/16 (56.2) [29.9 to 80.2]
Rest		63/107 (58.9) [49 to 68.3]
Missense mutation v rest		
Missense mutation		3/10 (30) [6.7 to 65.2]
Rest	⊢ ⊸–⊣	69/113 (61.1) [51.4 to 70.1]
Concurrent TP53 mutation		
Yes	⊢	19/39 (48.7) [32.4 to 65.2]
No	· · · ·	43/64 (67.2) [54.3 to 78.4]
Concurrent PTEN mutation	1 1	
Yes		13/23 (56.5) [34.5 to 76.8]
No	' ⊢⊸ '	54/87 (62.1) [51 to 72.3]
Concurrent SPOP mutation	1 1	
Yes	<u> </u>	
No	' ⊨_●]	63/106 (59.4) [49.5 to 68.9]
Concurrent AB mutation	1 1	
Voc		9/20 (40) [10 1 to 62 0]
No		58/89 (65 2) [54 3 to 75]
Concurrent TMPRSS2_ERG fusion		30/03 (03.2/ [34.3 (0 / 3]
Voc		7/15 (46 7) [21 2 to 72 4]
No		60/95 (63 2) [52 6 to 72 9]
0 10	0 20 30 40 50 60 70 80 90	100
	PSA Response Rate (95% CI)	

FIG 3. Forest plot analysis of clinical and molecular factors influencing efficacy outcomes. (A) Variables influencing PSA (> 50%) response rates. (B) Variables influencing PSA-PFS. (C) Variables influencing PFS. (D) Variables influencing OS. M, metastasis; N, node, NR, not reached; OS, overall survival; PFS, progression-free survival; PSA, prostate-specific antigen; T, tumor.

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FIG 3. (Continued).

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С							
Subgroup	PFS, Weeks Event No./Total No. (median time to event) [95% CI]						
Overall -	85/123 (43.4) [36 to 53]						
Mutation							
BRCA1	► 8/13 (43.4) [13.4 to NR]						
BRCA2	77/110 (45.4) [36.4 to 56.9]						
Gleason sum at diagnosis							
6-7	18/25 (49) [29 to 104.3]						
8-10	62/89 (43.4) [36.4 to 55.4]						
Age at start of therapy, years							
< 70	55/78 (40) [29 to 57.3]						
≥ 70	30/45 (46) [42.1 to 58.4]						
Baseline PSA, ng/mL							
≥ 44.31	44/62 (40) [24 to 53]						
< 44.31	41/61 (49) [37.3 to 72]						
M stage at diagnosis							
M1	33/50 (43.4) [32 to 58.4]						
M0	52/73 (42.7) [29 to 57.3]						
Prior docetaxel or cabazitaxel							
Yes	59/74 (40) [29 to 51.4]						
No H	> 26/49 (56.9) [45.4 to NR]						
Origin of mutation							
Somatic	40/61 (45.9) [29.3 to 61.4]						
Germline	45/62 (43.4) [36.4 to 54.9]						
Allelic status of mutation							
Biallelic	33/51 (45.4) [33.6 to 58.4]						
Monoallelic	30/38 (32) [20 to 57.3]						
Homozygous deletion v rest							
Homozygous deletion	• 10/16 (58.4) [26.6 to NR]						
Rest	75/107 (43.4) [36.4 to 52.9]						
Missense mutation v rest							
Missense mutation	→ 9/10 (22.6) [7.7 to NR]						
Rest	76/113 (45.4) [36.4 to 56.9]						
Concurrent TP53 mutation							
Yes	31/39 (26.1) [18.9 to 45.9]						
No	43/64 (53) [37.3 to 72]						
Concurrent PTEN mutation							
Yes	20/23 (42.1) [17.7 to 94.9]						
No	59/87 (46) [33.6 to 57.3]						
Concurrent SPOP mutation							
Yes	→ 2/4 (104.3) [8.1 to NR]						
No	77/106 (43.4) [33.6 to 53]						
Concurrent <i>AR</i> mutation							
Yes	16/20 (24) [20 to 74.9]						
No · ·	62/89 (52.1) [42.1 to 58.4]						
Concurrent TMPRSS2-ERG fusion							
Yes	► 9/15 (52.6) [26.3 to NR]						
No	70/95 (43.1) [33.6 to 54.9]						
Median Time to Evo	nt (95% CI) Weeks						
	IL 100 /0 01/, VVGGRO						

FIG 3. (Continued).



FIG 3. (Continued).

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included in Appendix Tables A2 and A3. PSA-PFS was shorter in *BRCA1* patients compared with *BRCA2* patients (median 20 v 44 weeks; HR, 1.7; 95% CI, 0.4 to 7.3; P = .4). PFS was also shorter in *BRCA1* compared with *BRCA2* patients (median 40 v 60 weeks; HR, 2.1; 95% CI, 0.5 to 8.9; P = .3).

The median OS was 91.0 weeks (95% CI, 70.4 to 121) in the overall cohort. Again, OS was shorter in *BRCA1*compared with *BRCA2*-altered patients (median 49.6 v 104.6 weeks; HR, 3.01; 95% CI, 1.32 to 6.83; P = .008; Fig 2D). This difference persisted after adjusting for age, Gleason sum, stage, baseline PSA, and previous taxane treatment (adjusted HR, 3.50; 95% CI, 1.36 to 9.02; P = .009) and after adjusting for concurrent *TP53* and *PTEN* mutations (adjusted HR, 2.61; 95% CI, 1.07 to 6.39; P = .04; Table 2). OS was numerically shorter in patients with somatic mutations, monoallelic mutations, missense mutations, and concurrent *TP53* alterations (Fig 3D).

DISCUSSION

The advent of the PARP inhibitors, olaparib and rucaparib, represents a major breakthrough in the management of advanced prostate cancer and heralds the beginning of the precision oncology era for this disease.⁸ However, it is becoming apparent that not all mutated HRR genes display equivalent sensitivity to PARP inhibition in prostate cancer.^{17,18} Previous studies have already suggested that mCRPC patients with germline or somatic non-BRCA1/2 mutations have less favorable outcomes to a variety of PARP inhibitors compared with those with BRCA1/2 alterations.^{12,17,19} However, less attention has been given to examining the potential differential efficacy of PARP inhibitors in BRCA1-altered versus BRCA2-altered advanced prostate cancers (potentially because of the much lower relative prevalence of *BRCA1* in this disease), whereas preliminary evidence has suggested a possible blunting of PARP inhibitor sensitivity in the *BRCA1* subset.²⁰ Here, we aimed to formally examine this issue by forming a multicenter consortium to study and compare PARP inhibitor efficacy among BRCA1- versus BRCA2-associated prostate cancers.

We have found that the clinical activity of PARP inhibitors is diminished in mCRPC patients with germline or somatic *BRCA1* compared with *BRCA2* mutations. This decreased sensitivity did not appear to be driven by differences in baseline demographic or clinical characteristics in the two groups, and it persisted after adjusting for important clinical and genomic variables. Interestingly, when exploring the mutation characteristics of these *BRCA1/2*-altered patients, we observed generally improved clinical outcomes in those with biallelic (compared with monoallelic) mutations, but not in those with germline (compared with somatic) mutations. When considering *BRCA1/2* mutation mechanism, we observed broadly better clinical outcomes in patients with truncating (compared with missense) alterations,

but not in those with homozygous deletions compared with other alterations. Finally, the presence of concurrent *TP53* mutations (which were observed in 55% and 36% of *BRCA1-* and *BRCA2*-altered cancers, respectively) were associated with numerically worse outcomes to PARP inhibitor treatment. In addition to the notion that *TP53* alterations broadly portend an overall worse prognosis in many cancer types, recent reports suggest that *TP53* mutations might be more permissive of the emergence of *BRCA1/2* reversion mutations (that restore the open reading frame) in *BRCA*-altered cancers that are exposed to PARP inhibitor treatment.^{21,22} Such reversion mutations have been associated with secondary PARP inhibitor resistance in prostate and other *BRCA*-mutated cancers.

Interestingly, numerically better outcomes were observed in patients with concurrent *SPOP* mutations, although this represented a very small subset (4%) of the total population. The presence of *SPOP* mutations has also been associated with improved outcomes to a number of hormonal therapies as well.^{23,24} In addition, studies have shown that *SPOP* mutations may increase genomic instability, potentially explaining the higher PARP inhibitor sensitivity in these cancers.²⁵ These hypothesis-generating findings require further validation.

Why might patients with BRCA1-altered mCRPC respond less favorably to PARP inhibitor treatment than BRCA2altered patients? Our current data, taken together with previous findings, do not support the idea that there are differences in mutational origins (germline v somatic) when comparing BRCA1- and BRCA2-related cancers; the two genes are affected by germline alterations at equal frequencies.^{14,21} Nor are there experimental or clinical data to support the notion that biallelic BRCA1 inactivation in prostate cancer is associated with less HRR deficiency (and hence less synthetic lethality with PARP inhibition)⁶ than biallelic *BRCA2* inactivation; in fact, HRR function might be impaired more significantly from BRCA1 deficiency.^{14,21} Therefore, one might predict that patients with mCRPC harboring biallelic BRCA1 or BRCA2 mutations would respond equally to PARP inhibitor treatment. However, our data and those of other investigators suggest that biallelic mutations are less common in BRCA1- compared with BRCA2-associated prostate cancers^{11,14,26}; this appears to be one of the key differences potentially driving better responses to PARP inhibitors among the latter. Interestingly, after adjusting for zygosity status, there were no differences in outcomes among patients with biallelic BRCA1- versus BRCA2-mutated mCRPC (HR for PFS: 0.85, 95% CI, 0.20 to 3.60, P = .29; HR for OS: 1.80, 95% CI, 0.41 to 7.87, P = .77). Notably, a recent pan-cancer analysis of BRCA1/2-mutated cancers also suggested a greater amount of genome-wide loss of heterozygosity among cancers with biallelic versus monoallelic mutations, predicting enhanced PARP inhibitor sensitivity.¹⁴ Finally, another important observation (that has also been confirmed in other studies) is the greater coexistence of *TP53* mutations in *BRCA1*- versus *BRCA2*-mutated cancers^{11,20}; the presence of concurrent *TP53* mutations may blunt PARP inhibitor efficacy in prostate cancer and possibly other cancers. Notably, after adjusting for *TP53* status, there were no differences in outcomes among patients with *BRCA1*- versus *BRCA2*-mutated mCRPC (HR for PFS: 1.22, 95% CI, 0.36 to 4.13, P = .20; HR for OS: 1.75, 95% CI, 0.51 to 6.02, P = .25).

This study had not only some strengths but also several limitations. The main shortcoming was that a variety of germline and somatic DNA sequencing platforms were used for the interrogation of BRCA1/2 mutations. Furthermore, the tissue types used for tumor mutation analyses varied (sometimes involving archival primary tumor tissue, sometimes involving metastatic biopsies, and sometimes relying on ctDNA samples). Although the use of archival tissues is not likely to significantly alter the prevalence of BRCA1/2 (or SPOP or TMPRSS2-ERG) mutations, which are generally thought to be truncal events,^{27,28} archival samples would certainly underestimate the true prevalence of PTEN, RB1, and AR mutations.²⁹ However, the strict definition of BRCA1/2 pathogenicity was a strength of our study, minimizing the inclusion of patients with variants of unknown significance alterations in this analysis. In addition, because of the inclusion of patients from 12 centers, it was not possible to centrally adjudicate clinical or radiographic progression events, and we relied

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In conclusion, to our knowledge, this is the first dedicated study to examine the potential differential effect of PARP inhibitor efficacy in BRCA1- versus BRCA2-associated prostate cancers. We show that PARP inhibitor activity is attenuated in mCRPC patients with BRCA1 mutations and that sensitivity is highest in those with BRCA2 mutations. The diminished efficacy among *BRCA1*-altered patients is not due to differences in mutation origin (germline v somatic) but rather appears to be associated with a greater number of monoallelic (rather than biallelic) mutations and a higher prevalence of concurrent TP53 alterations in the BRCA1 group. Thus, additional treatment options are needed for patients with BRCA1-altered mCRPC. These findings may have broad implications for other BRCA1/2associated malignancies (breast, ovarian, and pancreatic cancers) where PARP inhibitors are used.

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APPENDIX



FIG A1. Pie charts of the biallelic inactivation mechanisms by *BRCA* mutation type: (A) *BRCA1* and (B) *BRCA2*. LOH, loss of heterozygosity.

Biallelic Inactivation Mechanism	Overall, No. (%)	BRCA1, No. (%)	<i>BRCA2</i> , No. (%)	Р
No. of patients	51	4 (8)	47 (92)	
Sequence alteration plus LOH				.20
No	28 (55)	1 (25)	27 (58)	
Yes	23 (45)	3 (75)	20 (42)	
Homozygous deletion				.15
No	35 (69)	4 (100)	31 (66)	
Yes	16 (31)	0 (0)	16 (34)	
Two sequence alterations				.90
No	39 (76)	3 (75)	36 (76)	
Yes	12 (24)	1 (25)	11 (24)	

TABLE A1. Biallelic Inactivation Mechanisms, by BRCA Mutation Type

Abbreviation: LOH, loss of heterozygosity.

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Characteristic	Overall Patients, No. (%)	BRCA1 Responders, No. (%)	BRCA1 Nonresponders, No. (%)
No. of patients	13	3	10
Gleason sum at diagnosis			
8-10	10 (77)	3 (100)	7 (70)
6-7	0		
Unknown	3 (23)	0	3 (30)
Age at start of therapy, years			
Median/mean	71/69	71/72	67/69
Baseline PSA, ng/mL	123	13	110
Median/mean	47/172	241/589	24/47
Min-max	0-1,459	68-1,459	0-143
T stage at diagnosis			
T1-T2	3 (23)	0 (0)	3 (30)
T3-T4	10 (77)	3 (100)	7 (70)
N stage at diagnosis			
NO	5 (38)	2 (66)	3 (30)
N1	8 (62)	1 (34)	7 (70)
M stage at diagnosis			
MO	2 (15)	1 (34)	1 (10)
M1	11 (85)	2 (66)	9 (90)
Prior docetaxel or cabazitaxel			
No	3 (23)	0 (0)	3 (30)
Yes	10 (77)	3 (100)	7 (70)
Prior enzalutamide or abiraterone			
No	1 (7)	0 (0)	1 (10)
Yes	12 (93)	3 (100)	9 (90)
Presence of bone metastases			
No	1 (7)	0 (0)	1 (10)
Yes	12 (93)	3 (100)	9 (90)
Presence of visceral metastases			
No	10 (77)	2 (66)	8 (80)
Yes	3 (23)	1 (34)	2 (20)
Presence of nodal metastases			
No	6 (55)	1 (34)	5 (50)
Yes	7 (45)	2 (66)	5 (50)
Origin of mutation			
Germline	6 (55)	2 (66)	4 (40)
Somatic	7 (45)	1 (34)	6 (60)
Allelic status of mutation	9	3	6
Monoallelic	5 (50)	2 (66)	3 (42)
Biallelic	4 (50)	1 (34)	3 (58)
Mutation mechanism			
Frameshift	3 (25)	0 (0)	3 (30)
Homozygous deletion	0 (0)	0 (0)	0 (0)
Missense	4 (30)	0 (0)	4 (40)

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TABLE A2.	Baseline Demographic,	, Clinical, and Genom	c Data Overall	and by Mutation	Type, in the	BRCA1-Responding and	Nonresponding	Patients
(Continued)								

Characteristic	Overall Patients, No. (%)	BRCA1 Responders, No. (%)	BRCA1 Nonresponders, No. (%)
Nonsense	3 (23)	1 (33)	2 (20)
Rearrangement	2 (15)	1 (33)	1 (1)
Splicing	1 (7)	1 (33)	0 (0)
Concurrent TP53 mutation	11		
No	5 (45)	1 (34)	4 (50)
Yes	6 (55)	2 (66)	4 (50)
Concurrent PTEN mutation	11		
No	10 (90)	3 (100)	7 (88)
Yes	1 (10)	0 (0)	1 (12)
Concurrent RB1 mutation	11		
No	11 (100)	3 (100)	8 (100)
Yes	0 (0)	0 (0)	0 (0)
Concurrent SPOP mutation	11		
No	11 (100)	3 (100)	8 (100)
Yes	0	0	0
Concurrent AR mutation	11		
No	10 (90)	3 (100)	7 (88)
Yes	1 (10)	0	1 (12)

Abbreviations: M, metastasis; N, node; PSA, prostate-specific antigen; T, tumor.

TABLE A3. Baseline Demographic, Clin Characteristic	ical, and Genomic Data Overall and Overall Patients, No. (%)	I by Mutation Type, in the <i>BRCA2</i> -Res <i>BRCA2</i> Responders, No. (%)	ponding and Nonresponding Patients BRCA2 Nonresponders, No. (%)
No. of patients	110	69	41
Gleason sum at diagnosis			
8-10	10 (77)	49 (71)	30 (73)
6-7	0	16 (23)	9 (22)
Unknown	3 (23)	4 (6)	2 (5)
Age at start of therapy, years			
Median/mean	71/69	66/65	67/65
Baseline PSA, ng/mL			
Median/mean	47/172	35/310	54/266
Min-max	0-1,459	0.04-6,394	0.07-2,026
T stage at diagnosis			
T1-T2	28 (25)	18 (26)	10 (25)
T3-T4	82 (75)	51 (74)	31 (75)
N stage at diagnosis			
NO	73 (66)	49 (63)	24 (58)
N1	37 (34)	20 (37)	17 (42)
M stage at diagnosis			
MO	52 (47)	35 (50)	17 (41)
M1	58 (53)	34 (50)	24 (59)
Prior docetaxel or cabazitaxel			
No	46 (42)	32 (46)	14 (34)
Yes	64 (38)	37 (54)	27 (66)
Prior enzalutamide or abiraterone			
No	13 (12)	8 (11)	5 (11)
Yes	97 (88)	61 (89)	36 (89)
Presence of bone metastases			
No	19 (18)	14 (20)	5 (10)
Yes	91 (82)	55 (100)	36 (90)
Presence of visceral metastases			
No	10 (77)	54 (66)	28 (80)
Yes	3 (23)	15 (34)	13 (20)
Presence of nodal metastases			
No	65 (60)	42 (60)	23 (56)
Yes	45 (40)	27 (40)	18 (44)
Origin of mutation			
Germline	56 (50)	40 (58)	16 (39)
Somatic	54 (50)	29 (42)	25 (61)
Allelic status of mutation	80	47	33
Monoallelic	33 (41)	17 (36)	16 (48)
Biallelic	47 (59)	30 (64)	17 (52)
Mutation mechanism			
Frameshift	68 (62)	44 (64)	24 (60)
Homozygous deletion	16 (14)	10 (15)	6 (15)

(Continued on following page)

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TABLE A3. Baseline Demographic, Clinical, and Genomic Data Overall and by Mutation Type, in the *BRCA2*-Responding and Nonresponding Patients (Continued)

Characteristic	Overall Patients, No. (%)	BRCA2 Responders, No. (%)	BRCA2 Nonresponders, No. (%)
Missense	6 (6)	3 (4)	3 (7)
Nonsense	9 (8)	7 (10)	2 (5)
Rearrangement	9 (8)	4 (6)	5 (12)
Splicing	2 (2)	1 (1)	1 (1)
Concurrent TP53 mutation			
No	59 (64)	42 (71)	17 (50)
Yes	33 (36)	17 (29)	16 (50)
Concurrent PTEN mutation			
No	77 (77)	51 (80)	26 (75)
Yes	22 (23)	13 (20)	9 (25)
Concurrent RB1 mutation			
No	80 (80)	53 (82)	27 (77)
Yes	19 (20)	11 (18)	8 (23)
Concurrent SPOP mutation			
No	95 (96)	60 (94)	35 (100)
Yes	4 (4)	4 (4)	0 (0)
Concurrent AR mutation			
No	79 (80)	54 (85)	25 (71)
Yes	19 (20)	9 (15)	10 (29)

Abbreviations: M, metastasis; N, node; PSA, prostate-specific antigen; T, tumor.

Adopting Consensus Terms for Testing in Precision Medicine

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abstract

PURPOSE Despite the well-understood benefits of biomarker and genetic testing in precision medicine, uptake remains low, particularly for patients with low socioeconomic status and minority ethnic backgrounds. Patients report having limited familiarity with testing terminology and may not be able to accurately explain testing's role in treatment decisions. Patient confusion and lack of understanding is exacerbated by a multiplicity of overlapping terms used in communicating about testing. A LUNGevity Foundation–led working group composed of five professional societies, 23 patient advocacy groups, and 19 industry members assessed and recommended specific terms for communicating with patients on testing for tumor characteristics and germline mutations.

METHODS Members completed a precision oncology testing framework analysis (biomarkers, germline variants, testing modalities, biospecimen, and commonly used testing terms) for nine solid tumors and blood cancers. The evaluation was segmented into terms that distinguish between somatic and germline testing. Additional data were captured in a comprehensive survey (1,650 respondents) led by FORCE (Facing Our Risk of Cancer Empowered) on patient preferences on germline testing terms.

RESULTS Thirty-three terms were noted in patient education related to biomarker, genetic, and genomic testing. Biomarker testing was selected as the preferred term for testing for somatic (acquired) alterations and other biomarkers. Genetic testing for an inherited mutation and genetic testing for inherited cancer risk were selected as the preferred terms for testing for germline variants.

CONCLUSION Democratizing comprehension about precision oncology testing through intentional use of plain language and common umbrella terminology by oncology health care providers and others in the oncology ecosystem may help improve understanding and communication, and facilitate shared decision making about the role of appropriate testing in treatment decisions and other aspects of oncology care.

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Precision medicine has transformed the practice of oncology, offering opportunities for significantly improved outcomes in an array of solid and hematologic malignancies. Indeed, professional guidelines routinely recommend the application of genomic and laboratory techniques in oncology to both direct treatment and elucidate inherited cancer risks.

Author affiliations and support information (if applicable) appear at the end of this article.

Accepted on July 19, 2021 and published at ascopubs.org/journal/ po on October 6, 2021: DOI https://doi. org/10.1200/P0.21. 00027 However, many eligible patients are not benefiting from advances in precision medicine because of low rates in both biomarker testing for tumor-specific therapies and genetic testing for inherited mutations that indicate increased cancer risk. In lung cancer, for example, a study of 5,688 patients with non–small-cell lung cancer from 2011 to 2016 demonstrated that 15.4% received broad-based genomic sequencing and 84.6% received single gene testing for *EGFR* and/ or *ALK*.¹ A more recent study evaluating testing rates showed that only 7% of patients receiving care in

community oncology settings received the recommended testing for all seven biomarkers specified in the active clinical guidelines.² Likewise, in patients with gastrointestinal stromal tumor, recent data indicate that fewer than 27% received recommended tumor testing for *KIT* mutations,³ and only 40% of patients with colorectal cancer received recommended testing for known actionable mutations.⁴ Testing according to current guidelines remains below 50% for most populations recommended for inherited cancer risk testing. This includes subgroups of patients with breast cancer, and patients with ovarian, pancreatic, and metastatic prostate cancer.⁵

There are multiple likely reasons for this pervasive undertesting, including limited availability of adequate samples, lack of provider knowledge or support (including testing and counseling resources), geographic factors, racial disparities, socioeconomic factors, limited



CONTEXT

Key Objective

Advanced diagnostic cancer risk and oncology testing that informs personalized treatment decisions for patients has been challenging to communicate effectively because of medical jargon and overlapping terminology. For the first time, a multistakeholder pan-cancer working group analyzed the landscape of precision-medicine terminology and provided recommendations for plain language terms that providers and other stakeholders can use to address gaps in patient health literacy and improve shared decision making.

Knowledge Generated

Recommended consensus umbrella testing terms for patient communication were biomarker testing (for acquired tumor characteristics) and genetic testing for an inherited mutation and genetic testing for inherited cancer risk (for germline testing).

Relevance

A recently updated CDC definition of health literacy incorporates the role of organizations in making health information equitably accessible and understandable to patients. When used consistently, common cancer testing terminology can address poor patient comprehension of the role of testing in accurate treatment selection.

insurance coverage, and reimbursement challenges.⁶ Studies suggest that demographic factors such as language, age, and insurance status may contribute to decreased access to germline genetic testing in prostate cancer.⁷ In colorectal cancer, study findings suggest that socioeconomic status, insurance status, and hospital care settings could also play a role in access to biomarker testing.⁸ Recent studies have shown lower biomarker testing rates in patients with cancer from underserved communities.^{9,10} For example, a recent retrospective observational study of patients with non--small-cell lung cancer using the Flatiron Health database showed a more than 10 percentage point difference in White (50.1%) patients receiving biomarker testing with next-generation sequencing compared with Black patients (39.8%).¹¹ Inequitable access to testing and treatment is also exacerbated by inadequate inclusion of diverse ethnicities in the diagnostic test reference cohorts compared with populations of these patients receiving testing in the clinic. One study showed that the proportion of American Indian or Alaskan Native and Native Hawaiian or Other Pacific Islander in a pan-cancer institutional cohort receiving NGS testing was significantly lower than that of patients of European ancestry.¹⁰

Managing these complex challenges will require long-term policy, process, and infrastructure solutions, but there are also more immediate opportunities at hand to address a key driver of suboptimal testing rates: confusion and lack of understanding among patients and caregivers about the language used in precision medicine. Recent preliminary results (manuscript in preparation) from Cancer Support Community, a pan-cancer patient advocacy organization, found wide variability of familiarity of terms used in patient education about precision medicine. The research surveyed 30 patients and caregivers (21 women and nine men) with education levels ranging from high school to

post-graduate school who have experience with malignancies such as breast cancer (eight), prostate cancer (six), lung cancer (three), and other cancers (13). Almost two thirds of patients with cancer and caregivers reported never having heard of or not knowing anything about the terms precision medicine (61%) and cancer subtype (66%). When asked about biomarker testing, which can also be called molecular testing, tumor profiling, somatic testing, or genomic testing of cancer cells, most patients and caregivers reported being familiar with the term and were able to articulate an accurate definition. However, although 73% indicated a basic understanding of targeted therapy, most respondents were unable to provide an accurate definition. Most respondents (90%) reported they understood the term genetic testing for inherited cancer risk and were able to articulate an accurate meaning (Table 1).

Additional data from a separate study (manuscript in preparation) by the patient advocacy group LUNGevity Foundation that surveyed patients with lung cancer about recognition of precision medicine terms found that awareness of the term targeted therapy has penetrated the patient population. When patients with lung cancer were asked whether they had heard the terms biomarker testing, mutation testing, genetic testing, genomic testing, tumor profiling, and molecular testing, 88% of patients responded that they had heard of at least one testing term. The somatic mutation testing term that had the highest level of familiarity to patients with lung cancer was biomarker testing, with 92% of patients in the LUNGevity network and 65% of patients who are unaffiliated with a patient advocacy group citing familiarity.

Patient-reported confusion about biomarker testing is likely driven, in part, by the lack of consistency and multitude of different terms used by providers, other experts, and

TABLE 1. Survey of 30 Car	ncer Patients' and Caregivers'	Familiarity With Precision	Medicine Terms
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Never Heard of It	Heard of But Do Not Know Anything About It	Heard of and Self-Reported a Basic Understanding
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Concept	(%)	(%)	(%)
Precision medicine	32	29	39
Biomarker testing	3	30	67
Targeted therapy	7	20	73
Genetic testing for inherited cancer risk	0	10	90
Cancer subtype	53	13	33

commercial companies when discussing testing.¹² When asked, patients often cite difficulty sorting out complex information about what tests to have, what tests they may have had, how results can guide treatment and care decisions, and how test results may apply to patients accessing clinical trials. In a survey of 648 patients with breast cancer from diverse communities conducted by patient advocacy groups Facing Our Risk of Cancer Empowered (FORCE) and Living Beyond Breast Cancer, respondents seemed to understand germline genetic testing the most, and tumor biomarker testing for acquired alterations the least. Almost half of the respondents (46%) reported that they did not understand their tumor biomarker test results. In addition, some respondents expressed confusion about the difference between genetic testing for inherited mutations (pathogenic variants) and tumor testing for acquired mutations only found in the tumor.¹³

PROPOSAL

Although precision medicine and testing can be complicated subjects for a lay audience, it is important that the medical community and others communicating with patients strive for language that is both accurate and accessible so that our patients can be active partners in managing their care and engaging in shared decision making about their best care options.

To assess the extent of patient and caregiver confusion about testing terminology and propose potential remedies, over the last year, LUNGevity Foundation has convened a multistakeholder pan-cancer working group of patient advocacy organizations, professional societies, medical product developers, and laboratories.

After documenting more than 33 different terms related to biomarker, genetic, and genomic testing that are currently in use within oncology clinical care and patient education, the working group sought consensus among the stakeholders on several proposed preferred terms that could be applicable across tumor types.¹⁴ These terms were evaluated by working group members, which included patient advocacy organizations with expertise in precision medicine for their disease space, professional societies such as the Association for Molecular Pathology, the Association of Community Cancer Centers, and the National Society of Genetic Counselors, and industry represented by pharma

and biotech, laboratories, and test manufacturers. In addition, for the selection of the germline testing term, terms were refined based on feedback received through surveys of more than 1,700 patients and caregivers. Although working group members did not perform an additional patient survey for the selection of a term for testing for acquired somatic and nongenomic biomarkers, a subset of member organizations had previously queried their patient communities about terms under consideration, and these insights were integrated into the discussion and selection of a preferred term.

The result of this effort was the recommendation that all stakeholders in the oncology ecosystem adopt common, consistent terms for biomarker and germline genetic testing for all cancer types. Specifically, the working group proposed the following:

- 1. For tests that identify characteristics, targetable findings, or other test results originating from malignant tissue or blood, the recommended umbrella term is *biomarker testing*.
- 2. For tests that identify germline mutations or variants, the recommendation is for *genetic testing for an inherited mutation* and *genetic testing for inherited cancer risk,* which would be used in the appropriate specific clinical scenario.

These recommendations, which are detailed in a recently released White Paper,¹⁵ are designed to be cross-cutting umbrella terms that can be used in all care settings, with the recognition that there will be important nuances relating to individual patients' specific disease states and family histories. It is expected that providers and others who communicate with patients will augment the baseline terms with necessary additional explanations, to ensure that patients receive accurate and appropriate information about their diagnosis, prognosis, and care options. It should be noted that providers who practice in diverse cross-cultural and multiracial communities where English is not the first language may benefit from additional adaptation of these terms for optimal provider-patient communication. Guiding principles for cultural adaptation include a four-step process: (1) forward translation; (2) expert panel review of the translated terms; (3) back-translation, and (4) testing the terms with the intended audience in interviews and focus groups.¹⁶

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Adopting a consistent set of clear, plain-language terms as the starting point for improved patient and provider communication and understanding is a critical step in maximizing the potential benefit of novel therapeutic

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approaches for our patients. We applaud and support the working group's commitment to this goal and encourage our oncology provider colleagues to join us in adopting these recommendations.

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Germline Testing in Prostate Cancer: When and Who to Test

Alexandra O. Sokolova, MD^{1,2} and Heather H. Cheng, MD, PhD^{3,4}

ABSTRACT: The results of multiple studies have shown that a substantial proportion of men with advanced prostate cancer carry germline DNA repair mutations. Germline testing in prostate cancer may inform treatment decisions and consideration for clinical trials. There are 2 FDA approved PARP inhibitors (PARPi), olaparib (Lynparza) and rucaparib (Rubraca), for the treatment of advanced prostate cancer with DNA repair deficiency. Increasing demand for germline testing in prostate cancer and a shortage of genetic counselors have created a need for alternative care models and encouraged oncologists to take a more active role in performing germline testing. This article summarizes recommendations for germline testing in prostate cancer and describes care models for providing counseling and testing.

Introduction

Genetic testing in men with prostate cancer has become more widespread since the discovery that men with metastatic prostate cancer are more likely to carry germline DNA repair gene mutations and the approval of PARP, or poly adenosine diphosphate-ribose polymerase, inhibitors (PARPi) for prostate tumors with DNA repair deficiency. The resulting substantial increase in men with prostate cancer who are eligible for germline testing, with time-sensitive treatment implications, challenges the traditional in-person, time- and resource-

PERSPECTIVE

Jun Gong, MD, provides perspective on page 650

intensive cancer genetics care delivery model, and calls for alternative approaches. Urologists, oncologists, and other medical providers are encouraged to take a more active role in delivering germline testing, and they should be aware of current guidelines and optimal pretest and posttest counseling components. This article focuses on the implementation of germline testing in the care of patients with prostate cancer.

Germline vs Other Genetic Testing

Germline genetic testing evaluates for inherited mutations (otherwise known as pathogenic or likely pathogenic variants) that are found in virtually all cells of the body and are derived from the fundamental DNA of an individual. DNA from no cancerous, healthy cells (eg, leucocyte or saliva/buccal swab cells) are used for germline genetic testing. The goals of germline genetic testing are to evaluate for an inherited cancer syndrome; to inform individual and family cancer risks; and to guide cancer prognosis and treatment decisions. Germline testing should be distinguished from recreational and somatic (tumor-specific) testing. Direct-to-consumer recreational genetic testing consists of an at-home test that is advertised to help understand the customer's ancestry. Recreational genetic panels look for inherited variants in saliva/buccal swab cells to inform genealogy, and they are not primarily intended to guide medical decisions as they lack gene coverage and clinical-grade precision. None of the recreational genetic tests include a comprehensive assessment of the BRCA1/2 or other DNA damage repair genes and are inadequate for medical purposes. Somatic testing panels are designed to identify alterations in a tumor's DNA. A somatic test may occasionally identify mutations expected to be germline, in which case follow-up dedicated germline tests are needed. Examples of somatic panels that reportgermline mutations include Tempus and UW-Oncoplex. However, many somatic panels use bioinformatics algorithms that may filter out, miss, and/or choose not to report germline mutations. Thus, in general, somatic panels should not be considered adequate for germline conclusions; at most, they should prompt confirmatory germline testing. This article focuses on dedicated clinical-grade germline testing.

Heritable Risks of Prostate Cancer

Germline testing in men with prostate cancer is being performed more often since an important number of prostate cancer cases have a heritable component.^{1,2} Germline mutations in DNA repair genes, such as *BRCA1/2*, contribute to hereditary prostate cancer risk and are present in up to 11.8% of men with metastatic prostate cancer,³ compared with 4.6% among men with localized prostate cancer and 2.7% in persons without a known cancer diagnosis.^{3,4}

Germline *BRCA1/2* mutations are associated with increased risk of prostate cancer: up to a 3.8-fold increase with *BRCA1* and an 8.6-fold increase with *BRCA2* mutations.⁵ Men who carry germline *BRCA1/2* mutations are not only at increased risk of developing prostate cancer but are also at risk of a more aggressive prostate cancer phenotype.

TABLE 1. Family History Criteria for GermlineTesting in Prostate Cancer Patients

Family history of high-risk germline mutations (eg, BRCA1/2, Lynch syndrome)

Ashkenazi Jewish ancestry

Personal history of breast cancer

≥1 first-, second, or third-degree relative with: breast cancer at age <50y; male breast cancer; ovarian cancer; exocrine pancreatic cancer; metastatic, regional, very-high-risk, high-risk prostate cancer at any age

 \geq 1 first-degree relative (father or brother) with prostate cancer at age \leq 60 (but not clinically localized Grade Group 1)

 \geq 2 first-, second, or third-degree relative with breast cancer or prostate cancer (but not clinically localized Grade Group 1) at any age.

≥3 first- or second-degree relatives with Lynch syndrome-related cancers, especially diagnosed at 50 years or younger: cancers of the biliary tract, endometrium, stomach, ovary, exocrine pancreas, upper tract urothelium, small bowel or colorectal cancer; or glioblastoma In their study, Castro et al found that patients with prostate cancer with germline BRCA1/2 mutations at the time of diagnosis were more likely to have higher Gleason score (≥ 8) and more advanced stage (T3/4, nodal involvement, and metastases) compared with noncarriers. Men with germline BRCA1/2 mutations also had shorter cancer-specific survival (CSS) than noncarriers (15.7 vs 8.6 years; P=.015).6 Men with localized prostate cancer and germline BRCA1/2 mutations have worse outcomes after definitive treatment with surgery or radiation compared with noncarriers: 5-year metastasis-free survival, 72% vs 94%; P<0.001; 5-year CSS, 76% vs 97%; P <0.001.⁷ The prospective PROREPAIR-B study found that germline BRCA2 status is an independent prognostic factor for CSS in patients with metastatic castration-resistant prostate cancer (mCRPC; 17.4 vs 33.2 months; $P = .027).^{8}$

NCCN Guidelines

Based on the study results above and others, the current National Comprehensive Cancer Network (NCCN) guidelines for prostate cancer (version 1.2022)⁹ recommend germline testing for the subsets of patients with prostate cancer who are more likely to have germline DNA repair mutations (**Figure 1**).

The NCCN guidelines recommend offering germline testing to the following groups of patients with prostate cancer⁹:

I. Men with node positive, high-risk or very high-risk localized prostate cancer

- **II.** Men with metastatic prostate cancer
- III. Men meeting family history criteria (Table 1)

NCCN recommends considering germline testing for men with personal history of prostate cancer and:

I. intermediate risk prostate cancer and intraductal/ cribriform histology

II. personal history of exocrine pancreatic, colorectal, gastric, melanoma, pancreatic, upper tract urothelial, glioblastoma, biliary tract or small intestinal cancers

Several commercial vendors provide germline testing panels, including Invitae, Color, and Ambry. Further details and information on available panels can be found on the vendors' websites. Panel sizes vary from dedicated *BRCA1/2* testing to 91-gene panels. The NCCN guidelines for prostate cancer⁹ recommend that germline testing panels include genes associated with Lynch syndrome (*MLH1*, *MSH2*, *MSH6*, *PMS2*) and homologous recombination genes (*BRCA1/2*, *ATM*, *PALB2*, *CHEK2*).^{9,10} Broader panels might

TABLE	2.	Care	Models	to	Deliver	Germl	ine	Testing	
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	Traditional	Provider-led	Hybrid
Pretest counseling	Genetic counselor	Provider (eg, oncologist)	Provider (eg, oncologist)
Ordering germline test	Genetic counselor	Provider (eg, oncologist)	Provider (eg, oncologist)
Posttest counseling	Genetic counselor	Provider (eg, oncologist)	Genetic counselor

FIGURE 1. Recommendations for Germline Testing in Prostate Cancer

(based on NCCN prostate cancer guidelines, version 1.2022)

PROSTATE Cancer states	LOCALIZED	BCR	mCSPC nmCRPC		
	Identify hereditary cancer syr	ndrome, inform family cancer ri	sks, determine clinical trial eligibility		
WHY TEST	In some cases, may be helpful in active surveillance discussion	Treatment implications are currently evaluated by several clinical trials	PARPi, platinum candidacy		
	Everyo	ne who meets family history cri	iteria (Table 1)		
WHO TO TEST	≥T3a Grade Group ≥4 PSA >20 N1 Intraductal/ductal histology	NCCN does now specify reccomendations for BCR*	Metastatic disease*		
WHICH GENES TO TEST	T MLH1, MSH2, MSH6, PMS2, BRCA1/2, ATM, PALB2, CHEK2**				

*NCCN does not specify recommendations for BCR and nmCRPC | **Other genes may be indicated based on personal and family history

BCR, biochemically recurrent prostate cancer; mCRPC, metastatic castration-resistant prostate cancer; mCSPC, metastatic castration-sensitive prostate cancer; NCCN, National Comprehensive Cancer Network; nmCRPC, nonmetastatic castration-resistant prostate cancer; PARPi, PARP inhibitors; PSA, prostate-specific antigen.

be appropriate for men with mCRPC, especially if clinical trial participation is being considered. Average turnaround time for germline testing is between 10 and 30 days, which varies depending on the particular panel. The cost of germline testing varies depending on insurance coverage. Some companies offer provide testing for a flat out-of-pocket fee (eg, \$250), and a benefit of participating in certain research studies may be no-cost testing.

Delivery Care Models for Germline Testing

NCCN guidelines recommend germline testing for a large

subset of patients with prostate cancer, but the best care model to offer education and testing is unclear. The traditional clinical care delivery model for cancer genetics includes 2 in-person visits with a genetic counselor, the first for pretest risk assessment and education and the second to discuss the results. This is the most established pathway and, historically, has been utilized the most. However, broadening recommendations for germline testing create great demand that cannot be currently met in a timely fashion by the approximately 4000 genetic counselors in the United States.^{11,12} Therefore, oncologists and other providers are increasingly performing pretest counseling, ordering genetic testing, and providing posttest counseling for their patients, or following hybrid models (Table 2).¹³

The provider-led germline testing model has been tested in breast and ovarian cancer but is new in prostate cancer.¹⁴⁻¹⁸ Scheinberg et al reported results of a multicenter prospective study evaluating provider-led germline testing for men with prostate cancer. Twelve oncologists received training about the role of germline testing and in counseling patients, and then offered germline testing to patients with mCRPC in their practice. Those patients who accepted germline testing received pretest counseling and educational materials, and later discussed test results in the oncologist's office. If a germline mutation was identified, the patient was referred to a genetic counselor to discuss the further implications of the results and to initiate cascade testing. Most patients (63 of 66; 95%) accepted the germline testing and high satisfaction rates were achieved among both oncologists and patients.¹⁹ A provider-led germline testing model in the Veterans Affairs health care system was also evaluated. Patients with

C ural a	0	Method of	Number of patients responding to PARPi, by mutation status				
Study	Agent	assesment	BRCA1/2	ATM	CDK12	Other HRD mut	No HRD mut
		Imaging	28/84	28/84			N/A
PROFOUND (Hussain et al, 2020) ¹	Olaparib	PSA ₅₀	66/153	66/153			N/A
		СТС	29/97		12/56		N/A
TOPARP-A (Mateo et al, 2015) ²	Olaparib	Imaging, PSA ₅₀ , 8/8		4/5	N/A	2/3	2/33
ТОРАКР-В (Mateo et al, 2020) ³	Olaparib	Imaging, PSA ₅₀ , CTC	25/30	7/19	5/20	8/27	N/A
TRITON2 (Abida et al, 2020) ^{4,5}	Rucaparib	Imaging	33/65	2/19	0/10	5/26	N/A
		PSA ₅₀	63/115	2/49	1/15	7/26	N/A
NCI study (Karzai et al, 2018) ⁶	Durvalumab + olaparib	Imaging, PSA_{50}	7/11	N/A	N/A	N/A	2/6
GALAHAD (Smith et al, 2019) ⁷	Niraparib	imaging PSA ₅₀ , CTC	18/29	N/A	N/A	5/21	N/A
KEYNOTE-365	Olaparib +	Imaging	Imaging 5/24				
(Yu et al, 2020) ⁸	pembrolizumab	PSA ₅₀	9/82				
Retrospective analysis (Marshall et al, 2019) ⁹	Off-label olaparib	PSA ₅₀	13/17	0/6	N/A	N/A	N/A

TABLE 3. Response to PARPi in mCRPC Patients Stratified by DNA Repair Gene Mutations

CTC; circulating tumor cell DNA; imaging, radiographic response measured by RECIST criteria; mCRPC, metastatic castration-resistant prostate cancer; mut, mutations; N/A, not available; PARPi, PARP inhibitors; PSA50, decline of prostate-specific antigen by 50% from baseline; rPFS, radiographic progression-free survival. metastatic prostate cancer were offered germline testing by their oncologists during regular clinic visits. Pretest counseling was provided by oncologists and study coordinators and saliva for the test was collected in the clinic. Posttest counseling sessions with genetic counselors were provided over the phone by the testing panel company. Again, most patients (190 of 227 approached veterans; 84%) accepted testing, and the test completion rate was 80% (182/227).²⁰ Results of early studies suggest that provider-led germline testing in prostate cancer could be effective and satisfactory for both patients and providers.

The need to streamline germline testing also calls for the utilization of new technologies, such as video- or phonebased counseling. The EMPOWER study (NCT04598698) assessed men's preference of in-person genetic counseling vs video-based genetic education²¹; results indicated that inperson genetic counseling was preferred by men with less education and higher anxiety levels, and it resulted in greater improvement of cancer genetics knowledge. The rates of genetic testing uptake were similar for video-based and inperson counseling groups.²¹ Video-based counseling was also evaluated by Tong et al, who compared 2 models of streamlined germline testing in prostate cancer: (a) a takehome genetic kit provided by an oncologist, followed by referral to a genetic counselor if subsequent results are concerning; and (b) a genetic testing station, at which the patient participated in a video call from a genetic counseling assistant for genetics education and collection of family history, which was followed by saliva sample collection and, later, referral to a genetic counselor if any mutation was identified. The latter approach resulted in a lower rate of incomplete tests and a higher rate of follow-up with genetic counselors for positive results. Authors suggested that utilization of video education and involvement of genetic counselor assistants may improve access to germline testing among patients with prostate cancer.22 Several studies are ongoing to evaluate other care models to provide genetic testing in prostate cancer (eg, NCT02917798, NCT03076242, NCT03328091, NCT03503097).²³

Components of Germline Testing Counseling

Oncologists who choose to perform germline testing need to be comfortable with several aspects of genetic counseling and to remain current on the ethics of informed consent and posttest counseling for germline testing (Figure 2). The 2019 Philadelphia Prostate Cancer Consensus Conference suggests that optimal pretest consent should include discussion of the purpose of testing, types of possible results (ie, pathogenic/likely pathogenic; benign/likely benign; variant of unknown significance; no variants identified), the possibility of

FIGURE 2. Germline Testing Steps

PRETEST COUNSELLING

Should include discussion of:

the goal for testing

possible results

potential to identify hereditary cancer syndrome and additional cancer risks

cost of testing

cascade family testing

Genetic Information Nondiscrimination Act (GINA) law

ORDER TEST

When choosing a panel, consider:

patient preferences genes included in the panel

Out-of-pocket cost to patient

data sharing/selling policies of genetic laboratories

genetic counselor support provided by genetic laboratories

POSTTEST COUNSELLING

Should include discussion of:

treatment implications

implications of other cancer risks

cascade genetic testing

VUS reclassification potential

family cancer risk based on family and personal history, if no mutation identified

identifying hereditary cancer syndrome and/or other cancer risks, testing's potential cost, the importance of cascade family testing, and the Genetic Information Nondiscrimination Act (GINA) law.¹² The GINA law protects against discrimination based on genetics in employment and health insurance; however, it is not applicable to life insurance, long-term care disability insurance, Indian Health services, and patients enrolled into federal employee, Veterans Administration, and US military health benefit plans.^{23,24} These gaps in protection by GINA law are important to discuss with patients, who may need to consider them before proceeding with the germline testing. Providers should also consider discussing the different panels available for testing, the privacy of genetic tests, and genetic laboratories' policies related to sharing and selling of data.12

Providers ordering germline tests also must accept responsibility to follow up with patients if reclassification occurs of a variant of (currently) unknown significance (VUS). VUS are reported in about 30% of men with prostate cancer who undergo germline testing.⁴ VUS results do not change clinical recommendations, and the majority of them end up being reclassified as benign.^{25,26} In the Find My Variant Study, 38 of 63 VUS (61%) were reclassified: 32 of 38 (84%) as benign/likely benign and 6 of 38 (16%) as pathogenic/likely pathogenic.^{27,28} In the rare case when a VUS is reclassified as pathogenic or likely pathogenic, the provider who ordered the test is notified and they are responsible for disclosing the reclassification to the patient. Regardless of the model used, genetic counselor referral is recommended if a patient has a germline mutation identified and/or if clinical suspicion is high for an inherited cancer predisposition. Collaborative efforts are needed to educate oncology providers on aspects of germline testing counseling and to create shared printed and video resources for patients to facilitate informed consent.

Cascade Testing

Germline testing in men with prostate cancer can potentially benefit not only the patient but also family members. If a germline mutation is identified in a patient, testing for the same mutation in family members (cascade testing) should be performed. For instance, identifying family members with BRCA1/2 mutations could inform potentially lifesaving risk-reducing interventions, eg, prophylactic salpingooophorectomy for female BRCA1 mutation carriers. The IMPACT study (Identification of Men with a Genetic Predisposition to Prostate Cancer: Targeted screening in gBRCA1/2 mutation carriers and controls) evaluated the utility of prostate-specific antigen (PSA) screening in men aged 40 to 69 years with germline BRCA1/2 mutations compared with its utility in noncarriers.^{29,30} The study enrolled 3027 men with no personal history of prostate cancer: 919 BRCA1 carriers, 902 BRCA2 carriers, 709 BRCA1 noncarriers, and 497 BRCA2 noncarriers. Preliminary results, reported after 3 years of follow-up, showed that BRCA2 mutation carriers, compared with noncarriers, have a higher incidence of prostate cancer and a younger age of diagnosis. The results for BRCA1 carriers were not definitive, and further investigation is needed. The results from IMPACT suggest annual PSA screening for BRCA2 mutation carriers aged between 40 and 69 years, using PSA cutoff of 3.0 ng/ ml.³⁰ Studies evaluating the predictive value of lower PSA cutoff and prostate MRI are ongoing (eg, NCT03805919, NCT01990521).



PERSPECTIVE BY

Jun Gong, MD An Evolving Relationship **Between Medical Oncologists and Genetic** Counselors in Prostate Cancer

he authors of this timely review are to be applauded for providing a comprehensive analysis of the current literature supporting guidelines-based indications for germline testing in prostate cancer. As they describe, germline mutations in DNA repair genes, including BRCA1/2, can be found in a clinically significant proportion of men with metastatic prostate cancer-up to 11.8%.1 The impact of these germline mutations on the modern care of the patient with prostate cancer is multifold.

As the authors highlight, the presence of germline mutations in DNA repair genes can guide use of FDAapproved targeted agents in refractory and advanced prostate cancer, specifically the PARP inhibitors (PARPi) olaparib (Lynparza) and rucaparib (Rubraca). In the setting of DNA repair deficiency, sensitivity to platinum chemotherapy has also been well described. These associations have direct relevance to us, as medical oncologists, in our clinical management of patients with metastatic prostate cancer. It should be noted that 2 additional PARPi, talazoparib (Talzenna) and niraparib (Zejula), are separately undergoing phase 3 trials randomizing patients with metastatic castrate-resistant prostate cancer (mCRPC) who have not received systemic therapy in the castrateesistant setting. Both of these trials seek to explore the effectiveness of moving PARPi to earlier settings in mCRPC with novel hormonal therapy in those with and without DNA damage repair deficiencies.² As mentioned in the article, PARPi are also moving into the localized, high-risk prostate cancer setting; my group is participating in the NRG-GU007 (NADIR; NCT04037254) phase 2 trial in this setting, investigating niraparib in combination

with standard-of-care radiation therapy and androgen deprivation therapy in patients with high-risk prostate cancer. As such, reasons for somatic and germline testing in prostate cancer are likely to evolve and expand in the near future.

Beyond the influence of germline testing on treatment decisions for our patients with metastatic prostate cancer, we cannot emphasize enough the importance of germline testing for patients' families in patients who are positive for germline testing with our colleagues in genetic counseling. Here, the authors importantly highlight different care models to deliver germline testing. This topic has become increasingly relevant, given concerns for broadened recommendations for genetic testing and the resultant great demand that cannot be currently met by approximately 4000 genetic counselors in the United States.

One solution to this increased demand is the provider-led testing model, in which the oncologist performs the pretest counseling and discusses posttest results, with eventual referral to genetic counseling if there is a positive genetic test result. Similar models are also being described with primary care providers and genetic counselors.3 Such provider-led models are in accordance with the American Society of Clinical Oncology's genetic testing guidelines, in that experienced clinicians who are not geneticists may provide pretest counseling so long as prior informed written consent from the patient is obtained. Important to the success of this model would likely be the degree of clinician experience (ie, how comprehensive their genetic counseling training has been), the clinician's comfort level, and the supporting staff or resources available to the clinician to operate a provider-led germline testing model.4

Members of a consensus panel discussing germline testing have pointed out that clinicians who lack genetics training may experience numerous obstacles when counseling patients, in particular obstacles related to limited knowledge of the downstream impact of genetic testing, such as health insurance coverage, implications for life insurance, and protections afforded by the Genetic Information Nondiscrimination Act.⁵ Discussions about the importance and management of variants of unknown significance could be confusing for the patient even in the posttesting stage without appropriate knowledge and training on the clinician's part. In addition, genetic counseling may not always be reimbursed by some insurers, such as Medicare and Medicaid.

The hybrid model as presented by the authors may allow oncologists to shoulder some of the burdens of pretest counseling and ordering germline testing, while the experienced genetic counselors take over in the posttest counseling stage. To additionally lessen the burdens on genetic counselors, limiting the number of in-person visits by patients may be another option. As we have all learned throughout the COVID-19 pandemic, telemedicine does have certain advantages in clinical practice. Mauer et al have described the value of virtual counseling and technological adaptations, including billing practices and coordination of education and outreach opportunities, that have been made during the pandemic and have helped genetic counselors.⁶ Such adaptations represent only a few of the evolving strategies that we as medical oncologists, in conjunction with our health care team, must seek out and implement to help our genetic counseling colleagues reach an expanding population of prostate cancer patients in need of evidence-based germline testing.

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Oncologists are encouraged to take a more active role in performing germlinetesting, but the optimal approach is unclear...joint efforts are needed to build collaborative relationships between oncologists and genetic specialists.

Treatment Implications of Germline Testing Advanced disease

PARPi. Patients with DNA repair mutations have higher response rates to PARPi and platinum chemotherapy.^{31,32} In 2020, two PARPi received FDA approval for treatment of mCRPC with germline or somatic DNA damage repair gene mutations. Rucaparib was approved based on the phase 2 TRITON2 (NCT02952534) study; it reported a 51% (50/98) radiographic response rate among men with mCRPC and BRCA1/2 alterations.33 The benefit for men with non-BRCA DNA repair mutations was less clear, and rucaparib is currently approved only for carriers of BRCA1/2 mutations. 33-35 The olaparib label includes a larger number of mutated genes eligible for treatment (BRCA1, BRCA2, ATM, BRIP1, BARD1, CDK12, CHEK1, CHEK2, FANCL, PALB2, RAD51B, RAD51C, RAD51D, RAD54L), based on results of the phase 3 ProFOUND study (NCT02987543). ProFOUND compared olaparib with enzalutamide or abiraterone and showed improved radiographic progression-free survival (5.8 months vs 3.5 months) with olaparib.36 Several other ongoing studies are evaluating the efficiency of PARPi monotherapy and combined therapies in mCRPC. Table 3 summarizes study results reporting response rates to PARPi in prostate cancer.³⁷

Platinum chemotherapy. Historically, platinum chemotherapy has been used to treat tumors, such as ovarian or pancreatic cancer, that have a high frequency of DNA repair mutations.^{38,39} Early data suggest that platinum chemotherapy is also effective in prostate tumors with DNA repair deficiency.40.43 A retrospective case series by Cheng et al showed that 3 of 3 patients with prostate cancer who had biallelic inactivation of BRCA2 had an exceptional response to platinum chemotherapy after progressing on several therapies.⁴⁰ The results of a larger retrospective study supported this observation, reporting that 75% (6/8) of patients with mCRPC and with germline BRCA2 mutations had a PSA₅₀ response (ie, decline of prostate-specific antigen by 50% from baseline) to platinum chemotherapy compared with 17% (23/133) of mCRPC patients without gBRCA2 mutations.⁴¹ Mota et al reported a 53% (8/15) PSA₅₀ response to platinum chemotherapy among men with mCRPC and DNA damage repair mutations (ie, *BRCA2*, *BRCA1*, *ATM*, *PALB2*, *FANCA*, and *CDK12*).⁴³

Localized Disease

NCCN guidelines recommend considering DNA repair mutation status when discussing the possibility of active surveillance. Germline mutations in *BRCA1/2* or *ATM* are associated with a higher likelihood of grade reclassification among men undergoing active surveillance.⁴⁴ Mutation carriers should be closely monitored; they could potentially benefit from an earlier definitive treatment approach.

BRCA1/2 carriers have worse outcomes with conventional definitive therapies. Castro et al evaluated the response of *BRCA1/2* carriers with localized prostate cancer to 2 radical treatments—definitive radiation and radical prostatectomy—and reported that *BRCA* status is an independent prognostic factor for metastasis-free survival (HR, 2.36; P = .002) and CSS (HR, 2.17; P = .016).⁷ New treatment approaches in earlier disease stages are being evaluated in clinical trials for patients with prostate cancer and DNA repair deficiency. Targeted therapies, such as PARPi, are being actively investigated in the biochemically recurrent stage of prostate cancer (eg, NCT03047135, NCT03810105, NCT04336943, NCT0353394) and as neoadjuvant therapy in localized disease (eg, NCT04030559).

Conclusions

Germline testing is becoming more commonplace with advances in precision oncology and expanding treatment implications of the results of this testing. The NCCN prostate cancer guidelines recommend germline testing for men with high-risk or very high–risk localized prostate cancer; men with metastatic prostate cancer; patients with intraductal histology of the prostate; and patients meeting family history criteria. These recommendations have created a need for germline testing of many prostate cancer patients, which calls for a change in the traditional cancer genetics delivery model to meet the new demand.⁴⁵ Oncologists are encouraged to take a more active role in performing germline testing, but the optimal approach is unclear. Until the results of larger trials focusing on various testing delivery models are available, joint efforts are needed to build collaborative relationships between oncologists and genetic specialists. Further efforts are required to create dedicated resources to support providers in this new era of genetic testing and precision oncology in prostate cancer, which is marked by near-constant change.

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Platinum Priority – Prostate Cancer Editorial by Elena Castro on pp. 251–252 of this issue

Inherited TP53 Variants and Risk of Prostate Cancer

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Article info	Abstract
<i>Article history:</i> Accepted October 28, 2021	Background: Inherited germline <i>TP53</i> pathogenic and likely pathogenic variants (g <i>TP53</i>) cause autosomal dominant multicancer predisposition including Li-Fraumeni syndrome (LFS). However, there is no known association of prostate cancer with g <i>TP53</i> .
<i>Associate Editor:</i> James Catto	Objective: To determine whether <i>gTP53</i> predisposes to prostate cancer. Design, setting, and participants: This multi-institutional retrospective study character- izes prostate cancer incidence in a cohort of LFS males and <i>gTP53</i> prevalence in a prostate cancer cohort.
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Outcome measurements and statistical analysis: We evaluated the spectrum of gTP53 variants and clinical features associated with prostate cancer.

Results and limitations: We identified 31 prostate cancer cases among 163 adult LFS males, including 26 of 54 aged \geq 50 yr. Among 117 LFS males without prostate cancer at the time of genetic testing, six were diagnosed with prostate cancer over a median (interquartile range [IQR]) of 3.0 (1.3–7.2) yr of follow-up, a 25-fold increased risk (95% confidence interval [CI] 9.2–55; *p* < 0.0001). We identified gTP53 in 38 of 6850 males (0.6%) in the prostate cancer cohort, a relative risk 9.1-fold higher than that of population controls (95% CI 6.2–14; *p* < 0.0001; gnomAD). We observed hotspots at the sites of attenuated variants not associated with classic LFS. Two-thirds of available gTP53 prostate cancer cases in this study, the median age at diagnosis was 56 (IQR: 51–62) yr, 44% had Gleason \geq 8 tumors, and 29% had advanced disease at diagnosis.

Conclusions: Complementary analyses of prostate cancer incidence in LFS males and gTP53 prevalence in prostate cancer cohorts suggest that gTP53 predisposes to aggressive prostate cancer. Prostate cancer should be considered as part of LFS screening protocols and TP53 considered in germline prostate cancer susceptibility testing.

Patient summary: Inherited pathogenic variants in the *TP53* gene are likely to predispose men to aggressive prostate cancer.

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1. Introduction

Prostate cancer (PrCa) is a highly heritable disease [1]. Recent data have demonstrated that approximately 5-20% of cases are associated with germline (inherited) pathogenic variants in genes associated with recognized cancer predisposition syndromes, such BRCA2 and ATM [2,3]. Germline TP53 pathogenic variants (gTP53) are associated with an autosomal dominant hereditary multicancer predisposition known as Li-Fraumeni syndrome (LFS) [4,5]. Patients with classic LFS develop early-onset, pediatric, and multiple primary cancers with nearly universal development of at least one cancer in their lifetime [6]; presentations with more variable penetrance are increasingly observed [5,7,8]. Panel genetic testing, largely ascertained on individuals with personal and family histories of breast cancers, has demonstrated a more expansive tumor spectrum and more variable penetrance of gTP53 variants than previously appreciated [9]. However, there has been no documented association of PrCa with gTP53, outside of one case report [10]. In a recent review of the TP53 International Agency for Research on Cancer (IARC) database [8], only 1.7% of gTP53 patients were reported to have PrCa, far lower than the 14% lifetime risk of PrCa for average men in the USA [11]. However, this analysis is misleading given that the database is heavily skewed toward men of younger ages than those relevant to typical PrCa risk.

Guidelines advise extensive cancer screening in patients with LFS, starting in childhood, for example, yearly fullbody magnetic resonance imaging (MRI) and brain imaging, targeted ultrasound, assessments for gastrointestinal and skin neoplasms, and breast screening for women [12,13]. Patients with LFS may also have an elevated risk of posttreatment secondary malignancies, for example, after radiation [14,15]. Therefore, LFS status may be considered in cancer treatment planning. For example, in women with LFS, total mastectomy is preferred to partial mastectomy to avoid the need for radiation.

Current cancer screening guidelines for LFS patients do not include PrCa. Moreover, gTP53 status is not currently considered in treatment planning for individuals with PrCa, which often includes decisions between radiation and surgery for patients with early-stage localized disease and regarding adjuvant or salvage radiation in those with later-stage or recurrent disease. Herein, we analyze LFS cohort data alongside laboratory-based clinical genetic testing data in PrCa cohorts, and we demonstrate that gTP53 is associated with the development of aggressive PrCa.

2. Patients and methods

2.1. LFS and PrCa cohorts

The LFS cohort (n = 163 males from 132 families) was created from four datasets of families with a diagnosis of LFS (Supplementary Table 1 and Supplementary material) from Dana Farber Cancer Institute, Huntsman Cancer Institute, Memorial Sloan Kettering Cancer Center, and the University of Pennsylvania. Eligibility criteria for index cases from LFS families were as follows: (1) male sex, (2) age at last follow-up ≥ 18 yr, and (3) genetic testing confirming heterozygous gTP53 or obligate carrier status within a family. Dates of genetic testing, PrCa diagnosis, or last follow-up and/or death were collected for all LFS men (Supplementary Table 1). The PrCa cohort (n = 6850 individuals) was created from four large series of PrCa patients who had undergone tumor or tumor/germline sequencing (Supplementary material). Pedigrees of patients in both cohorts were collected and examined to ensure that PrCa cases were not double counted due to enrollment in LFS registries or sequencing at more than one institution (Supplementary Fig. 1). Clinical data for both cohorts were collected in accordance with the Declaration of Helsinki guidelines and following approval from the respective institutional review boards at University of Washington, Tulane University, University of Pennsylvania, University of Utah, Memorial Sloan Kettering Cancer Institute, and Dana Farber Cancer Institute.

Keywords:

Germline

Attenuated

Genetic testing

Hypomorphic mutation

Li-Fraumeni syndrome

Pathogenic variant

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Prostate cancer

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TP53

Inherited cancer syndrome

2.2. TP53 variant review and exclusion of somatic interference

All variants in the LFS and PrCa cohorts were referenced with ClinVar [16] and classified based on *TP53*-specific American College of Medical Genetics (ACMG) guidelines (Supplementary material) [17]. Subclassification of likely pathogenic or pathogenic variants as full penetrance versus attenuated variants was based on published functional data. Patients in the LFS cohorts were confirmed to have germline variants not due to somatic interference by clonal hematopoiesis of indeterminate potential or other abnormal clonal expansion [18] by testing of ancillary tissues and/or by variant segregation in families. In the PrCa cohorts, somatic interference [18] was excluded by: first, restricting to pathogenic and likely pathogenic variants with >35% variant fraction in blood; second, tumor sequencing when available to confirm presence in the cancer and in the matched normal tissue; and finally, a comparison of variant allele fractions with other observed somatic and germline variants.

2.3. Tumor analyses

Tumor next-generation sequencing data (UW-OncoPlex and MSK-IMPACT) were available for a subset of gTP53 carriers [19,20]. Tumor data were analyzed by an expert molecular pathologist (C.C.P.) for evidence of somatic TP53 second allele inactivation, including assessment of loss of heterozygosity (L.O.H.).

2.4. Statistical analysis

To calculate PrCa risk and incidence rates, the full LFS cohort was restricted to patients without a prior PrCa diagnosis at genetic testing to avoid selection and immortality biases. Risk of PrCa diagnosis relative to the general population was then estimated using a standardized incidence ratio (SIR) comparing the observed numbers with the expected numbers of PrCa diagnoses, with the latter calculated by applying PrCa incidence rates in the population to specific ages and calendar years of follow-up. Follow-up was summarized using reverse Kaplan-Meier estimation [21], which begins at the genetic test, treats death or last followup without PrCa diagnosis as events, and censors PrCa diagnoses. This approach gives a robust summary of follow-up for all patients, which is used to calculate the expected number of PrCa diagnoses. The PrCa incidence rates were those observed in the Surveillance, Epidemiology, and End Results (SEER) program from 1997 to 2017 by calendar year and 5-yr age group. Incidence rates over the period of 2018-2020 were assumed to be equal to the rates observed in 2017. Significance of the SIR was evaluated using a two-sided exact Poisson test. Overall and agespecific PrCa incidence rates in the restricted cohort were calculated relative to observed person-years of follow-up, and corresponding rates in SEER were calculated relative to population totals. In the PrCa cohort, the relative risk of carrying gTP53 was compared with frequencies in the gnomAD database using a Fisher's exact test after excluding individuals with cancer (gnomAD v2.1.1 noncancer, 134 187 samples; Supplementary material).

3. Results

3.1. Incidence of PrCa in LFS

Among a cohort of LFS individuals created from datasets at four academic institutions, we identified 163 males aged \geq 18 yr with a confirmed gTP53 likely pathogenic/pathogenic variant or obligate carrier status from 132 families (Supplementary Tables 1 and 2, and Supplementary Fig. 1). We identified PrCa in 31 of 163 (19%) adult males in this cohort, including 26 of 54 males (48%) aged \geq 50 yr

Table 1 – Age distribution of men with prostate cancer (PrCa) in Li-Fraumeni syndrome (LFS) cohorts

Age group	Combined LFS/LFL cohorts				
	n	PrCa	%		
18–29	32	0	0		
30-39	35	1	2.9		
40-49	42	4	10		
50-59	32	15	47		
60-69	15	7	47		
70–79	7	4	57		
≥ 80	0	0	NA		
Total (w/ages)	163	31	19		
LFL = Li-Fraumeni–like syndrome; NA = not available. ⁽¹⁾ Age based on cancer diagnosis age or current age if unaffected.					

(Table 1). The frequency of PrCa within age deciles was similar in all four datasets (Supplementary Table 3). In a restricted analysis of 117 men who did not have a PrCa diagnosis at the time of genetic testing (Supplementary Table 1), six were diagnosed with PrCa over a median (interquartile range [IQR]) of 3.0 (1.3–7.2)s of follow-up. The risk of a PrCa diagnosis in this subgroup of LFS men was 25 times that in the general population (95% confidence interval [CI] 9.2–55; *p* < 0.0001), with incidence rates significantly elevated at all ages (Fig. 1, Table 2, and Supplementary Fig. 2).

3.2. Prevalence of gTP53 in individuals with prostate cancer

To determine the prevalence of gTP53 in PrCa patients, we analyzed four large germline or tumor sequencing datasets comprising 6850 PrCa patients (Table 3 and Supplementary Table 2), excluding cases suggestive of somatic interference [18]. We identified gTP53 in 38 patients overall (0.55% prevalence), with prevalence rates ranging from 0.27% to 0.84% across the four independent cohorts (Table 3). The relative risk of having gTP53 was significantly elevated at 9.1 (95% CI 6.2–14, p < 0.0001) compared with the gnomAD noncancer population database (Fig. 1). Restricting both the sequencing cohorts and the gnomAD to TP53 variants classified as likely pathogenic or pathogenic in ClinVar, the relative risk remained statistically significantly elevated at 8.7 (95% CI 4.8–16, p < 0.0001; Table 3).

3.3. *Spectrum of gTP53* variants reveals hotspots associated with attenuated mutations

To study the spectrum of *gTP53* variants and clinicopathological PrCa features, we combined *gTP53* PrCa cases from the LFS and PrCa cohorts as no significant differences were observed for any variable between cohorts (Table 4). Of 67 individuals with PrCa and *gTP53*, 20 (30%) had classic LFS variants (Table 4). Thirty-two individuals (48%) had *gTP53* variants with published evidence of being attenuated (or hypomorphic) variants, and 15 (22%) had variants suggestive of being attenuated (Table 4). Five codons associated with attenuated variants (158, 181, 282, 283, and 337) accounted for 28 of the 67 cases (42%; Fig. 1 and 2, and Supplementary Table 2). Moreover, rare attenuated variants at codon 181 (n = 10) were found in all series (except TCGA), and codons 158, 283, and 337 were enriched in four or more series (Supplementary Table 2). Specific *TP53* variants, p.



Fig. 1 – Summary of results (graphical abstract). LFS = Li-Fraumeni syndrome; PrCa = prostate cancer; SEER = Surveillance, Epidemiology, and End Results.

Table 2 – Annual prostate cancer incidence rates per 1000 in the Li-Fraumeni syndrome (LFS) and in the Surveillance, Epidemiology, and End Results (SEER) registry

Age (yr)	Restricted LFS cohort ^a		SEER		
	Rate per 1000	95% CI	Rate per 1000	95% CI	
0-49	3.9	0.48-14	0.050	0.049-0.050	
50-59	40	4.8-144	2.03	2.02-2.04	
60-74	90	11-326	7.10	7.08-7.13	
0-74	10	3.8-23	1.07	1.07-1.07	
CI = confidence interval					

Results are by post hoc age at risk and all ages combined.

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LFS cohort restricted to men with no prostate cancer diagnosis at the time of their genetic test.

R158H, p.R181H, p.R282Q, p.R283C, and p.R337H, were each significantly enriched in PrCa cohorts versus gnomAD noncancer controls, with relative risks ranging from 6.1 (for p.R283C) to 92 (for p.R158H; Supplementary Table 4).

3.4. Tumor analysis in gTP53 carriers supports role in tumorigenesis

As a biallelic loss suggests that the gTP53 variant contributed to cancer formation, we analyzed available prostate tumors

from gTP53 carriers who had adequate tumor for evaluation. Ten of 15 available tumors (67%), including nine with likely or known attenuated variants, had evidence of somatic inactivation of the second TP53 allele (Table 4 and Supplementary Table 2). The tumors without evidence of somatic inactivation had either p.R282Q or p.R283C alleles.

3.5. Clinicopathological features of gTP53 carriers with PrCa

The median age of PrCa diagnosis in males with *gTP53* in this study was 56 (IQR: 51–60) yr (Table 4). PrCa incidence was increased compared with the SEER data in each group analyzed (Table 2 and Supplementary Fig. 2). Of individuals with *gTP53* PrCa in the combined cohorts, 26% had a personal diagnosis and 55% had a family history of an LFS core cancer. Only 26% of the families in the combined cohort did not meet any LFS diagnostic criteria. Nearly all individuals had a family history of PrCa. A family history of breast cancer was reported in 61% of the combined cohort. Of men with LFS, PrCa was the only or the most recent cancer diagnosis in 58% (18 of 31).

Cohort	Total	LP/P + VUS/LP			ClinVar LP/P		
		n (%)	RR ^a (95% CI)	p value	n (%)	RR ^a (95% CI)	p value
RL	3329	23 (0.69)	11 (7.1-18)	< 0.0001	10 (0.30)	11 (5.5-23)	<0.0001
AL-1	831	7 (0.84)	14 (6.4-30)	< 0.0001	5 (0.60)	22 (8.7-57)	0.002
AL-2	2191	6 (0.27)	4.5 (2.0-10)	0.0004	1 (0.05)	NA	NA
TCGA	499	2 (0.40)	6.6 (1.6-27)	0.009	0 (NA)	NA	NA
Combined	6850	38 (0.55)	9.1 (6.2-14)	< 0.0001	16 (0.23)	8.7 (4.8-16)	< 0.0001

AL = Academic Laboratory; CI = confidence interval; RL = reference laboratory; LP/P = likely pathogenic and pathogenic mutations; RR = relative risk; TCGA = The Cancer Genome Atlas; VUS = variants of uncertain significance.

^a gnomAD v2.1.1 noncancer, 134 187 sample data for *TP53* were downloaded and *TP53* variants classified as LP/P variants as per ClinVar or VUS/LP in ClinVar, classified as likely pathogenic in this study. The rate of LP/P and VUS/LP *TP53* variants in gnomAD was 0.059%, and the rate of ClinVar LP/P *TP53* variants in gnomAD was 0.026%.

Table 4 – Characteristics of 67 PrCa patients with confirmed gTP53

	LFS		PrCa	
	n	%	n	%
Site	<i>n</i> = 31		n = 36	
LFS-1	10	32	-	-
LFS-2	3	10	-	-
LFS-3	6	19	-	
LFS-4	12	39	-	-
KL-1	-	-	/	19
RL-2	-	-	25 A	11
TCGA	_	_	2	56
Age of PrCa diagnosis	<i>n</i> = 31		n = 27	5.0
Median (IOR)	56 (50-64	1)	56 (51-60))
Mutation class	n = 31	<i>`</i>	n = 36	
Classic	12	39	8	22
Reduced penetrance	16	52	16	44
Unknown	3	10	12	33
Tumor LOH	n = 6		n = 9	
LOH present	6	100	4	44
Personal cancer history	n = 31	25	n = 12	40
Sarcoma	0	30	3	42
Adrenal cortical tumor	0	20	0	0.5
Brain	2	65	0	_
Leukemia	0	-	0	-
>1 LFS-core cancer ^a	10	32	1	8.3
Cancer timing for MP	n = 19		n = 4	
Other cancer after PrCa	7	37	3	75
Other cancer before PrCa	7	37	1	25
Both before and after PrCa	5	26	0	-
Cancer family history	n = 31		n = 13	
None	1	3.2	1	7.7
Sarcoma Adronal cortical tumor	2	29	2	15
Brain	2	10	5	28
Leukemia	3	10	2	15
Breast age <31	4	13	0	-
Any LFS core cancer ^a	16	52	8	62
Breast (any age)	21	68	6	46
Prostate	9	29	4	31
Clinical LFS criteria	n = 28		n = 7	
Classic	4	14	1	14
Chompret	13	46	4	57
Birch and/or Eeles	19	68	4	57
PrCa Classon score	8 n = 20	29	5 = 14	43
	12	60	7	50
GS 8-10	8	40	7	50
PSA at diagnosis	n = 14	10	n = 9	50
Median (IQR)	6 (4-12)		6 (3-23)	
>20	3	21	3	33
PrCa diagnosis	n = 11		n = 7	
Screening	8	73	4	57
Incidental	1	9.1	1	14
Symptoms	2	18	2	29
Stage at diagnosis	n = 21	01	n = 13	E 4
Localized (NX of NU)	17	8I 10	1	54 46
	-1	13	0	40
ACT = adrenal cortical tumor; GS	= Gleason	score; IQR	= interqua	rtile
range; LFS = Li-Fraumeni syndroi	ne; LOH	= loss of h	neterozygo:	sity;
MP = multiple primary; PrCa = pro	state cance	er; PSA = pi	ostate-spe	CITIC
^a LFS core cancers: ACT brain lo	ukemia c	arcoma and	d breast a	σ. σ.
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Of PrCa cases, 29% were diagnosed as locally advanced (N1) or de novo metastatic disease. Similarly, 44% of gTP53 individuals had high-grade disease (Gleason \geq 8; Fig. 1 and Table 4). Prostate-specific antigen (PSA) at diagnosis ranged from 1.1 to 171 ng/dl, and 68% of individuals were diagnosed by screening. Three individuals were diagnosed due to symptoms of advanced Gleason 9–10 PrCa at ages 50, 51, and 63 yr (Supplementary Table 2).

4. Discussion

We estimate the risk of PrCa diagnosis in individuals with LFS, and the frequency of rare germline pathogenic and likely pathogenic *TP53* variants in a PrCa cohort. We found that LFS men have a 25-fold increased risk of PrCa compared with the general population. Further, we found that 0.55% (range 0.27–0.84%) of individuals with PrCa in a large sequencing cohort have g*TP53*. Tumor sequencing detected second allele inactivation in a majority of available tumor cases, supporting the biological relevance of the g*TP53* variants to tumorigenesis. Collectively, these data demonstrate for the first time that g*TP53* variants contribute to PrCa risk.

There is a paucity of data on PrCa risk in individuals with gTP53 [8,10]. While an analysis of LFS males in IARC [8] suggested that PrCa was enriched among cancers diagnosed in late adulthood, comparable average ages of cancer onset in LFS patients and SEER population suggested that the contribution of gTP53 variants was minimal. More recently, Shin et al [6] reported that the incidence of non-LFS-related tumors was higher in male gTP53 carriers between ages 35 and 65 yr, but PrCa was not analyzed individually. Our findings may differ from prior literature because a larger cohort of older LFS males, including families with attenuated LFS, was included.

Over half of the gTP53 variants we reported are considered attenuated or hypomorphic variants not typically associated with classic LFS. Individuals with attenuated gTP53 likely still have a multicancer predisposition syndrome of clinical significance [22,23]. We hypothesize that these individuals are more likely to live into adulthood and be at risk for developing prostate and other adult cancers, compared with those with full-penetrance gTP53 variants who typically have a severe early-onset cancer phenotype with high mortality rates at young ages.

In the PrCa sequencing cohorts, we found the relative risk of carrying gTP53 variants to be comparable with that of BRCA2 (relative risk 4.7-8.6) [24,25], a gene for which PrCa screening recommendations are modified [26,27]. This argues for consideration of PrCa screening in LFS guidelines. Moreover, since gTP53 carriers may be at an increased risk for radiation-induced sarcomas [5,14], our data may have treatment implications for gTP53 individuals with PrCa, for example, consideration of MRI versus computed tomography screening and avoidance of therapeutic radiation. The high rate of aggressive disease in our series (29% locally advanced or de novo metastatic) is consistent with prior observations that somatic TP53 variants are associated with advanced PrCa, and supports the consideration of earlier and/or more frequent screening with PSA and attention to prostate pathology on full-body MRI screening to identify disease at a stage amenable to surgical resection in male gTP53 carriers from LFS families. For example, one LFS patient in this series had a glioblastoma at age 24 yr, developed symptomatic hematospermia at age 50 yr, and was diagnosed with Gleason score 9 de novo metastatic PrCa, a situation that might have been avoided with screening. In addition, the high rate of other LFS core cancers (61%) and breast cancer at any age (61%) in the family history of the cohort highlights the potential value of cascade familial



Fig. 2 – Distribution of *TP53* pathogenic and likely pathogenic variants. Lollipop plot depicts 67 germline P/LP variants in patients with prostate cancer. Green color represents missense variants, black represents truncating variants (frameshift, nonsense, and splice site), and black lines represent large deletion variants. Hotspots for prostate cancer were observed at sites of reduced penetrance variants at codons 158, 181, 282, 283, and 337. Classic LFS hotspot variants (R175H, G245S, R248Q, and R282W) are indicated with red asterisks. LFS = Li-Fraumeni syndrome; P/LP = pathogenic and likely pathogenic.

testing to reduce cancer risk in relatives of individuals with PrCa identified to have gTP53.

Our study has limitations-the patients represented in all series were ascertained by either clinical testing of PrCa patients or LFS status, and presumably reflect enrichment of family or personal history and younger age. Ascertainment bias is particularly important to consider for the referral laboratory series, which also had very limited clinical data. Part of the increased risk of PrCa diagnosis in the LFS cohort may be due to more frequent testing and biopsy in these men; however, it seems unlikely that this bias could explain the 25-fold increased risk relative to the general US population. In addition, the LFS cohort size is small. However, LFS is an extremely rare cancer syndrome, afflicting approximately one in 10 000–30 000 individuals [28]; therefore, centralized efforts, such as through the LiFE consortium [29], will be required to confirm the risk estimates and clinical correlations presented. It is possible that TP53mutant clonal hematopoiesis of indeterminate potential could contaminate our series [18]; however, paired tumor/ normal testing in sequencing cohorts was analyzed, variant allele fraction cutoffs were employed, and LFS males had ancillary tissue or familial testing, proving that the mutation was inherited. Although tumor sequencing results are supportive of mechanistic causality, additional studies would be needed to prove the role in tumorigenesis. Lastly, most individuals did not find out that they were a gTP53 carrier until after their PrCa diagnosis and could not be utilized in SIR calculations.

Despite these limitations, our complimentary analyses showing an increased incidence of PrCa in an LFS cohort, far higher prevalence of *gTP53* variants in a PrCa cohort than in population controls, tumor data supporting a role in tumorigenesis, and biological plausibility of observing more PrCa in attenuated *gTP53* are collectively compelling. Confirmation in larger numbers of PrCa patients with paired testing of blood and tumor will be helpful, as will better understanding of modifying factors in the context of *gTP53* variants. Exact PrCa risk estimates will likely be specific to variant and population.

5. Conclusions

This study contributes to a greater understanding of *TP53*associated cancer risk, demonstrating that adult cancers such as PrCa in LFS are understudied and merit further attention. Attenuated or hypomorphic gTP53 alleles provide a plausible hypothesis as to why some gTP53 patients develop late adulthood cancers that would not have been appreciated previously in individuals with more severe gTP53 variants that predispose to high cancer burden and earlier mortality. Screening guidelines for adults with attenuated LFS phenotypes are needed urgently. We suggest that current LFS screening guidelines be updated to consider annual PrCa screening in men with at least 10 yr of life expectancy. While gTP53 mutation rates are low in PrCa cohorts, the clinical importance of the finding for the patient and family is significant. We suggest evaluation of TP53 in germline genetic testing in PrCa patients, ideally by paired tumor-normal testing, to rule out somatic interference.

Author contributions: Colin C. Pritchard had full access to all the data in the study and takes responsibility for the integrity of the data and the accuracy of the data analysis.

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REVIEW ARTICLE Disparities in germline testing among racial minorities with prostate cancer

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Germline testing is becoming increasingly relevant in prostate cancer (PCa) screening, prognosis, and management. A subset of patients with PCa harbor pathogenic/likely pathogenic variants (P/LPVs) in genes mediating DNA-repair processes, and these P/LPVs have implications for cancer screening, treatment, and cascade testing. As a result, it is recommended that all men with high-risk localized and metastatic PCa undergo routine germline testing. As more PCa patients undergo germline testing, it is important that clinicians and genetics experts recognize current disparities in germline testing rates among racial/ethnic minorities in the United States. The reasons for these disparities are multiple and require similarly manifold consideration to close the germline testing gap and reduce inequities in PCa screening, management, and treatment.

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INTRODUCTION

Prostate cancer (PCa) is the most common cancer among men and one of the leading causes of deaths worldwide [1]. In 2021, it is estimated that 248,530 men in the United States (US) will be diagnosed with PCa and 34,130 individuals will die secondary to this disease [2]. While age, race/ethnicity, and family history are established risk factors for PCa, it is now recognized that a proportion of PCa susceptibility is attributed to genetic predisposition. Advances in molecular sequencing technologies have identified several PCa susceptibility genes, many related to known hereditary cancer syndromes, including hereditary breast and ovarian cancer (HBOC) syndrome (BRCA1, BRCA2, ATM, CHEK2, and PALB2) and Lynch syndrome (MLH1, MSH2, MSH6, and PMS2) [3]. As a result of these findings, recommendations for germline testing based on clinical features and family history have expanded. The identification of pathogenic/likely pathogenic variants (P/LPVs) in PCa predisposition genes may help inform cancer screening strategies for patients and family members, treatment options in the metastatic setting, and clinical trial enrollment.

As germline testing becomes more clinically relevant and widely available, it is important to recognize the risk of exacerbating health disparities among racial/ethnic minorities with PCa and develop systematic strategies to bridge disparities in germline testing. Reasons for these disparities are multifaceted and include patient, clinician, and system factors. Additionally, current PCa clinical trials and genetic studies do not reflect the diverse populations of individuals at-risk or suffering from this disease. In this review, we discuss the indications for germline testing in men with PCa, barriers to germline testing in diverse populations, and potential strategies to bridge the disparities gap with the expansion of germline testing for men with PCa.

DISPARITIES IN OUTCOMES OF MEN WITH PCA

There are documented disparities in the incidence, treatment, and mortality of PCa between Black and non-Black men [2, 4-6]. Notably, Black men are diagnosed with PCa at nearly twice the rate of non-Hispanic white (NHW) men [2], and Black men with local/regional PCa have been found to be less likely to receive treatment with curative intent than NHW men [7]. Further, the PCa mortality rate is twice as high in Black men compared to NHW men [2]. The National Cancer Institute estimates that Black men have a 4.72% lifetime risk of dying of PCa compared to a 2.86% risk among NHW men [5]. Although biological differences may account for a portion of the disparity in overall PCa survival, it has been suggested that improved access to care, including screening, follow-up, and therapy may be effective in reducing this disparity [8]. It is important to note that one limitation of studies of PCa incidence and mortality is that most data on Black men does not stratify them by country/region of origin—Black men are not a homogenous group and there may be differences in PCa incidence and mortality for Caribbean, African, and African-American men [9].

Similarly, despite the genetic and cultural diversity of Hispanic men in the US, individual subgroups are typically combined. Notably, significant heterogeneity has been observed among Hispanic men with PCa [10]. Overall, PCa occurs less often in Hispanic men than in NHW men [1]. However, Mexican-American men have been found to have more advanced stage PCa at diagnosis [11] and are significantly more likely to have aggressive PCa following radical prostatectomy [12]. While prostate cancerspecific mortality (PCSM) is comparable between Hispanic and NHW men, Puerto Rican men have been shown to have significantly higher PCSM than NHW men, Black men, and all

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Table 1. Representation of diverse racial/ethnic groups in prostate cancer clinical trials involving germline testing.

Race					Ethnicity (Hispanic	or Latino)
N	White	Black	Asian	Other/Unknown	No	Yes	Unknown
790	674	76	NR	40	NR	NR	NR
2962	NR	NR	NR	NR	NR	NR	NR
1199	NR	NR	NR	NR	NR	NR	NR
1917	NR	NR	NR	NR	NR	NR	NR
1052	719	19	229	85	NR	NR	NR
1150	926	16	155	53	NR	NR	NR
1125	NR	NR	NR	NR	NR	NR	NR
1006	NR	NR	NR	NR	NR	NR	NR
755	631	40	58	26	NR	NR	NR
512	461	30	NR	21	NR	NR	NR
921	865	NR	NR	NR	NR	NR	NR
1195	NR	NR	NR	NR	NR	NR	NR
1088	NR	NR	NR	NR	NR	NR	NR
1199	NR	NR	NR	NR	NR	NR	NR
1717	1324	34	167	192	1527	38	152
1200	800	68	140	192	NR	NR	NR
1401	NR	NR	NR	NR	NR	NR	NR
1509	NR	NR	NR	NR	NR	NR	NR
	Race N 790 2962 1199 1917 1052 1150 1125 1006 755 512 921 1195 1088 1199 1717 1200 1401 1509	Race N White 790 674 2962 NR 1199 NR 1199 NR 1917 NR 1052 719 1150 926 1125 NR 1006 NR 755 631 512 461 921 865 1195 NR 1088 NR 1199 NR 1200 800 1401 NR	Race White Black 790 674 76 2962 NR NR 1199 NR NR 1199 NR NR 1917 NR NR 1052 719 19 1150 926 16 1125 NR NR 1006 NR NR 755 631 40 512 461 30 921 865 NR 1195 NR NR 1199 NR NR 1200 800 68	Race N White Black Asian 790 674 76 NR 2962 NR NR NR 1199 NR NR NR 1199 NR NR NR 1917 NR NR NR 1052 719 19 229 1150 926 16 155 1125 NR NR NR 1006 NR NR NR 755 631 40 58 512 461 30 NR 1195 NR NR NR 1195 NR NR NR 1195 NR NR NR 1199 NR NR NR 1199 NR NR NR 1199 NR NR NR 1199 NR NR NR 1200 800 68	Race White Black Asian Other/Unknown 790 674 76 NR 40 2962 NR NR NR NR 1199 NR NR NR NR 1199 NR NR NR NR 1917 NR NR NR NR 1052 719 19 229 85 1150 926 16 155 53 1125 NR NR NR NR 1006 NR NR NR NR 1125 NR NR NR NR 1006 NR NR NR NR 1125 A61 30 NR 21 921 865 NR NR NR 1195 NR NR NR NR 1199 NR NR NR NR 1199 NR NR	Race Ethnicity (N White Black Asian Other/Unknown No 790 674 76 NR 40 NR 2962 NR NR NR NR NR 1199 NR NR NR NR NR 1199 NR NR NR NR NR 1917 NR NR NR NR NR 1917 NR NR NR NR NR 1052 719 19 229 85 NR 1150 926 16 155 53 NR 1125 NR NR NR NR NR 1006 NR NR NR NR NR 1125 A61 30 NR 21 NR 1195 NR NR NR NR NR 1195 NR NR NR NR	Race Ethnicity (Hispanic N White Black Asian Other/Unknown No Yes 790 674 76 NR 40 NR NR NR 2962 NR NR NR NR NR NR NR NR 1199 NR NR NR NR NR NR NR 11917 NR NR NR NR NR NR NR 1917 NR NR NR NR NR NR NR 1052 719 19 229 85 NR NR 1150 926 16 155 53 NR NR 1125 NR NR NR NR NR NR 1125 NR NR NR NR NR NR 124 461 30 NR 21 NR NR 125 NR

MCRPC metastatic castration-resistant prostate cancer, NMCRPC non-metastatic castration-resistant prostate cancer, NR not reported.

other Hispanic subgroups [10]. Ultimately, the dearth of PCa studies examining individual Hispanic subgroups makes it difficult to compare them to NHW men.

Despite these documented disparities, African-American/ Canadian, Asian/Pacific Islander, and Hispanic populations are typically underrepresented in germline testing, clinical trials (Table 1), and study cohorts [13]. One study analyzed 72 global phase III and IV prevention, screening, and treatment PCa clinical trials between 1987 and 2016: 59 trials reported race/ ethnicity data, and 96% of patients enrolled in these studies were NHW men. African and Caribbean medical centers were particularly underrepresented in these trials [14]. Concordant studies have shown that the majority of PCa patients receiving germline testing are NHW men [15, 16], with as high as 95% being English-speaking men [16]. Underrepresentation of racial/ethnic minorities in germline testing is not unique to PCa and exists among patients with various other malignancies [17–19].

Racial/ethnic minority populations in the US are expected to grow rapidly over the coming decades, underscoring the need to address and resolve these disparities. It is projected that by 2045, NHW people will make up <50% of the total US population. While NHW populations are expected to decline, all other racial/ethnic minority populations are expected to grow: in particular, Hispanic populations are the fastest growing demographic and are expected to comprise 24.6% of the US population in 2045, up from 18.7% in 2020 [20].

GENOMICS OF NON-WHITE MEN WITH PCA

P/LPVs have been found to be prevalent in men with PCa. A 2016 multi-institutional study found that the incidence of germline mutations in genes mediating DNA-repair processes (including but not limited to *BRCA2*, *ATM*, *CHEK2*, *BRCA1*,

RAD51D, and *PALB2*) among 692 men with metastatic PCa was 11.8% [3]. For patients with localized disease, the prevalence of P/LPVs ranged from 2 to 6%, with increased prevalence in men with higher Gleason scores and higher-risk PCa. Notably, 576 (83%) of the men in this study were NHW men. Additionally, a 2021 study found that 9.5% of PCa patients with high-risk localized disease had P/LPVs, most frequently in *BRCA2* and *ATM* [21].

In order to better understand the genomic landscape of racial/ ethnic minorities, there is a need to more extensively examine P/ LPV rates in non-white men with PCa. More recent studies have found that the prevalence of P/LPVs varies across racial/ethnic groups. When compared to NHW men, Hispanic men with PCa have been found to have similar rates of P/LPVs in the *ATM*, *BRCA1*, and *BRCA2* genes [22], while Black men with PCa have been found more likely to have a P/LPV in the *BRCA1* gene than their NHW counterparts [23]. Among patients with metastatic PCa, mutations in DNA-repair genes have been found to occur more often in Black men than in NHW men [24]. However, these studies were limited by small sample size.

The lack of diversity in germline testing cohorts is thought to be a contributor to higher rates of variants of uncertain significance (VUS) in racial/ethnic minorities [15, 25]. Notably, African-American, Hispanic, and Asian/Pacific Islander PCa patients have been found to be more likely to have a VUS than those with European ancestry [23, 26]. In one study of PCa patients referred to Color Genomics for germline testing, VUS rates in HBOC and Lynch syndrome genes were 21% in NHW men, while 26.6% and 33.3% in African-American/Canadian and Asian/Pacific Islander men, respectively [15]. Increasing the proportion of underrepresented groups in germline testing cohorts is predicted to result in the reclassification of VUS, which will assist in cancer risk stratification and targeted therapy strategies [15].

Tuble 2. Guidelines on germin	ie testing in prostate cancer			
Source	Regional (N1)/ metastatic prostate cancer	NCCN very high and high-risk localized prostate cancer	NCCN intermediate/low/very low risk localized prostate cancer	
National Comprehensive Cancer Network Version 1.2022 [27, 28]	Recommend	Recommend	 Recommend if a family history of: Ashkenazi Jewish ancestry High-risk germline mutations (e.g., <i>BRCA1/2</i>, Lynch mutation) PCa in brother/father/multiple family members diagnosed with PCa (not GG1) at <60 years of age or who died from PCa ≥3 cancers on same side of family, especially diagnoses ≤50 years of age: bile duct, breast, colorectal, endometrial, gastric, kidney, melanoma, ovarian, pancreatic, prostate (not GG1), small bowel, or urothelial cancer Consider for: Intraductal/cribriform histology 	
Philadelphia Prostate Cancer Consensus Meeting Publication 2019 [90]	Recommend	 Consider for T3a or higher. Consider for intraductal/ductal pathology. Consider for Gleason 4 (Gleason 8 sum) or above. Consider for Ashkenazi Jewish ancestry. Consider for family history of two or more cancers in HBOC/Lynch spectrum in any relatives on the same side of the family (especially if diagnosed at age <50 years). Recommend for family history of one brother/father/two or more male relatives with one of the following: PCa at age <60 years Died of PCa. Metastatic PCa. 		
AUA/ASTRO/SUO 2017 and 2021 [91–93]	Recommend	Recommend if a strong family history of specific cancers (e.g., breast, ovarian, pancreatic, other gastrointestinal tumors, and lymphoma).	Not recommended	

 Table 2.
 Guidelines on germline testing in prostate cancer.

PCa Prostate Cancer, HBOC Hereditary Breast and Ovarian Cancer Syndrome, NCCN National Comprehensive Network, AUA American Urological Association, ASTRO American Society of Radiation Oncology, SUO Society of Urologic Oncology, GG Grade Group.

INDICATIONS FOR GERMLINE TESTING AND IMPLICATIONS OF TESTING RESULTS

Recent studies on the incidence of P/LPVs among men with PCa have resulted in updated guidance regarding which patients should receive germline testing. The most recent iteration of the National Comprehensive Cancer Network guidelines for PCa recommends germline testing for all men with high-risk localized and metastatic PCa, Ashkenazi Jewish ancestry, a family history of high-risk germline mutations, or a positive family history of cancer [27, 28]. Given emerging data on the association between intraductal/cribriform and ductal histologies and P/LPVs, testing is considered for men with these histologic subtypes [28]. Other professional societies and expert panels have also provided recommendations for germline testing for men with PCa, largely based on evidence synthesis, consensus agreement, and expert opinion (Table 2).

Expanding germline testing uptake may help clinicians predict outcomes in men with PCa by detecting ethnicity-dependent biomarkers and mutations that drive aggressive tumor biology [29]. Germline mutations in DNA-repair genes, particularly *BRCA1/2* and *ATM*, are associated with aggressive PCa and significantly shorter survival time: mutation carriers have been found to have a higher proportion of Gleason Score \geq 7 (71%) than noncarriers (31%) and mutation frequency has been found to be significantly higher in patients that have died of PCa than in localized PCa patients [30].

Germline testing also has implications regarding candidacy of select treatments, including platinum chemotherapy, poly(ADPribose) polymerase (PARP) inhibitors, and checkpoint inhibition for patients with metastatic castration-resistant prostate cancer (mCRPC) [31]. In 2020, the PARP inhibitor Olaparib was FDA approved for the treatment of adult patients with deleterious/ suspected deleterious germline or somatic homologous recombination repair (HRR) gene-mutated mCRPC who have progressed following prior treatment with enzalutamide or abiraterone. Olaparib is FDA approved for a panel of 14 genes, including BRCA1/2. Of the patients in the PROfound trial, 69% were white, 29% were Asian, and 1% were Black [32]. Another therapy, Rucaparib, was FDA approved in 2020 for the treatment of adult patients with a deleterious BRCA1/2 mutation (germline and/or somatic)-associated mCRPC who have been treated with androgen receptor-directed therapy and a taxane-based chemotherapy. For the 115 patients enrolled in the TRITON2 study, the majority were white (73%) and 10% were Black; other racial/ethnic groups were not specified [33]. Pembrolizumab has also been FDA approved for patients with refractory metastatic cancers with MSIhigh or MMR deficiency (dMMR) status based on tumor assessment that had progressed following prior treatments [34]. Pembrolizumab has shown antitumor activity with an acceptable safety profile in an unselected subset of patients with mCRPC [35].

Another indication for germline testing is cascade testing, which refers to germline testing among relatives of patients with cancer-associated P/LPVs; it has historically had decreased uptake in the community at around 30% or less. Being a PCa patient with a germline P/LPV in a DNA-repair gene has been associated with having a first degree relative with breast or ovarian cancer [36]. Therefore, increased germline testing among PCa patients may result in increased cascade testing for family members and subsequent breast and ovarian cancer risk mitigation.

Table 3.	Challenges	and	solutions.
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5	
Challenges	Solutions
Shortage of CGCs and limitations of current GC models	 Increase clinical training capacity for CGCs Offer pretest GC and select posttest GC via alternative methods (telemedicine, group GC) Automate risk assessment
Differences in the quality of care for minority patients	Increase access to genetic services, contain costs, and address provider implicit bias
Medical mistrust	 System wide interventions to address gaps in healthcare delivery Increase representation of minorities in healthcare Community outreach
Lack of knowledge regarding testing	 Increase genetics education among patients and community health providers Culturally tailored genetic counseling
Prohibitive cost and lack of insurance coverage for germline testing	 Increase payer coverage Low-cost testing and government subsidies
Understudied link between PCa and breast/ovarian cancers	 Address similar disparities in germline testing among women with HBOC syndrome Physician and patient directed education regarding genetic link between PCa and HBOC syndrome

CGC Clinical Genetic Counselor, GC Genetic Counseling, PCa Prostate Cancer, HBOC syndrome Hereditary Breast and Ovarian Cancer Syndrome.

REASONS FOR THE DISPARITIES IN GERMLINE TESTING AMONG RACIAL/ETHNIC MINORITIES WITH PCA AND POTENTIAL STRATEGIES TO BRIDGE THE GAP

Although germline testing is now routinely recommended for high-risk localized, locally advanced, and metastatic PCa patients, there is a disparity in the proportion of white vs. non-white PCa patients receiving germline testing [15, 16, 26]. We propose several reasons and potential solutions for this disparity, including the (1) nationwide shortage of genetic counselors to facilitate germline testing within current genetic counseling models, (2) differences in access to quality healthcare between white and non-white patients, (3) healthcare system mistrust among nonwhite men leading to unfavorable attitudes towards research and reluctance to seek care, (4) lack of knowledge or education about germline testing, (5) prohibitive cost of germline testing, and (6) understudied link between PCa and breast/ovarian cancer (Table 3).

Challenge and solution: shortage of genetic counselors and limitations of current genetic counseling models

Certified Genetic Counselors (CGCs) and physicians work cooperatively to facilitate germline testing and provide counseling, risk assessment, and result interpretation to PCa patients. The shortage of clinical cancer CGCs engaged in direct patient care creates an unmet need for genetic services that disproportionately affects socioeconomically disadvantaged, rural, and racial/ethnic minority patients. As the demand for germline testing grows, CGC workforce growth limitations will need to be addressed. One such limitation is clinical training capacity. Proposed solutions include novel clinical training techniques, such as nonclinical or extra-disciplinary training placements, rural clinical placements, peer supervision/assisted learning, role-emerging placements, clinical audit, and patient simulation. Perhaps most important is the need to recruit, train, and retain clinical supervisors by providing dedicated support personnel and professional development opportunities [37].

In addition to a nationwide shortage of CGCs engaged in direct patient care, existing genetic counseling models are becoming increasingly inadequate given the number of PCa patients referred for germline testing. The current time-intensive model of assessing family histories for genetic risk, providing pretest and posttest counseling, ordering appropriate testing, and interpreting test results over multiple in-person sessions is increasingly less feasible. Increased genetic literacy among medical oncologists, urologists, and radiation oncologists, including knowledge of patient risk factors and family history, genetics and genetic conditions, and available genetic services, may alleviate bottle-necks at the genetic counseling level [38].

Modifications to existing workflows within oncology practices may expand genetic resources for patients. Automating the risk assessment would be one such modification, whereby patientcompleted family history questionnaires facilitate referral and testing processes: automated electronic medical record features can trigger genetic counseling referrals or alert clinical teams to patients with elevated cancer risks or who meet guidelines for germline testing. This would allow CGCs to prioritize posttest visits, especially those involving complex counseling or abnormal results [39]. Other practical strategies focus on increasing CGC efficiency and patient volumes, including group genetic counseling sessions. Additionally, establishing support roles, such as genetic counseling assistants, can alleviate administrative burdens [8]. Likewise, patient advocates and language interpreters in the genetic counseling setting can provide resources and translation services for non-English-speaking patients, which would further alleviate burdens on monolingual English-speaking CGCs and reduce patient miscommunication.

Rural patients are particularly disadvantaged by current genetic counseling models, given the scarcity of CGCs in more rural counties and among populations with a low median household income [40]. Telemedicine, which has been adopted by many clinics in the COVID-19 era [41], can help bridge this gap: video genetics education and genetic counseling may be as effective as traditional genetic counseling and has resulted in a similar uptake of germline testing without compromising the tenants of informed consent [42]. Telemedicine models do, however, need to adapt to potential challenges, including limited internet access, scheduling issues, billing questions, and state licensure regulations [41].

Challenge and solution: differences in the quality of care between white and non-white patients

There is overwhelming evidence that there are disparities in the quality of healthcare between white and non-white patients, even when insurance status, income, age, and severity of conditions are comparable [43]. Significant disparities have been noted for definitive therapy for PCa [6], with Black men being particularly underrepresented in PCa research, including validation studies of new clinical tools like genomic testing [15, 44]. One explanation



VUS=Variant of uncertain significance.

Fig. 1 Post-germline testing workflow depending on test result [27, 28]. VUS Variant of uncertain significance. *Genetic counseling recommended to discuss possible participation in family studies and variant reclassification studies.

for this disparity is that minority-serving physicians have been found to be significantly less likely to have ever referred a patient for germline testing or counseling, specialty services, or clinical trials [45]. This may be the result of many underlying issues, including access and cost.

Strategies to integrate genetic services into minority community health settings will be critical in ensuring the accessibility of germline testing. Because most CGCs are concentrated within large academic medical centers and hospital systems, the incorporation of satellite campuses and clinics into medically underserved communities would greatly expand access. In tandem, minority community health programs can practice evidence based medicine through the implementation of clinical pathways to ensure that all patients are receiving the minimum standard of care. This will require expanding physician knowledge and awareness of current PCa clinical practice guidelines, as well as integration of these guidelines into existing workflows (Fig. 1).

Despite the expansion of germline testing guidelines for PCa patients, germline testing is not routinely covered by insurance. Coverage policies for germline testing in PCa patients are nonspecific and nonuniform across insurance companies, and physicians may not recommend genetic services for patients who cannot afford the out-of-pocket costs [46]. Expanding insurance coverage to include PCa patients that meet recommendations for germline testing may alleviate cost barriers. Additionally, in the absence of genetic services in medically underserved communities, expanded insurance coverage for transportation costs may benefit those who cannot access such services due to geographic barriers and for whom in-person counseling may help overcome hesitation due to unfamiliarity with telemedicine and/or lack of trust in the healthcare system.

Challenge and solution: medical mistrust leading to unfavorable attitudes towards research and medicine

Healthcare disparities among racial/ethnic minorities are thought to contribute to long-standing generational mistrust in healthcareproviding entities in the US. Medical mistrust has been shown to lower utilization of routine checkups and preventive care services [47–49], including referrals for genetic counseling and testing. Delays in these services may prevent a substantial number of men from obtaining recommended services until an advanced stage of illness [47]. This mistrust becomes a barrier to an emphasis on prostate health [50] and precludes racial/ethnic minorities from seeking PCa screening, germline testing, and treatment.

The lack of representation within medical institutions, as well as subsequent language barriers, may be a contributor to medical mistrust. In 2019, 5.0% and 5.8% of physicians identified as Black and Hispanic, respectively [51]. Further, 10.0% of CGCs in the US identified as non-white in 2021 [52]. Representation improves patient-clinician communication and rapport: when provided a

doctor of the same race, Black men have been found be more likely consent to invasive services, such as blood draws and biopsies, and discuss personal matters or health issues [53]. Hispanic men, in contrast, may face language barriers with clinicians: monolingual English-speaking clinicians may have limited communication with patients or rely on interpreters or translated materials, which may convey confusing or even contradictory information [54]. Issues of representation can be addressed by actively recruiting racial/ethnic minorities to the healthcare workforce and creating student training programs targeting these populations [55]. Language challenges can be addressed by employing multilingual, culturally cognizant interpreters in clinics where the need exists [56].

Medical mistrust may also stem from implicit bias, which refers to the unconscious and unintentional attitudes and stereotypes attributed towards a group of people. Implicit bias may contribute to health disparities by shaping physician behavior and producing differences in treatment along the lines of race, ethnicity, and gender. Healthcare professionals can combat implicit bias by individuating, which involves a conscious focus on specific information about a patient instead of their race, ethnicity, or gender [57]. Addressing implicit bias early is essential: genetic counseling and nursing programs, medical schools, and healthcare professional training programs can expand and emphasize coursework in racial sensitivity and implicit bias. Additionally, addressing implicit bias in continuing medical education may help minimize biases.

Medical mistrust may also result from a lack of trust regarding the use of genetic information. Despite the passage of the Genetic Information Nondiscrimination Act in 2008, which was designed to protect Americans against discrimination in health insurance and employment based on their genetic information [58], utilization of genetic services among racial/ethnic minorities is disproportionately low [59]. In response, providers need to anticipate and dispel patient fears about germline testing. Patients may believe that their results are not confidential or that positive results will leave them susceptible to discrimination, reduced access to care, or insurance coverage loss [44]. Patients may also conflate germline testing ordered by a clinician with direct-to-consumer DNA testing provided by companies that have faced controversy for sharing customers' data with law enforcement and pharmaceutical companies.

Outreach and community support may help combat medical mistrust. Distributing medical literature directly to underserved populations has been shown to have positive results; however, personalized interactions between clinicians and racial/ethnic minority communities may further build trust and assuage fears about genetic services in order to encourage participation in germline testing and clinical trials [59]. Outreach and educational efforts within community institutions (such as churches) that involve partners and spouses, as well as cancer survivors within the community, may play a pivotal role [60].

Challenge and solution: lack of knowledge regarding testing A lack of knowledge regarding germline testing and its implications for PCa screening, diagnostics, and treatment may present further barriers [38]. The availability of reliable, easy-to-understand information regarding the effects of P/LPVs on disease, as well as the importance of personal or family history of disease, is crucial [56].

Access to clear, concise tools about genetics is important because the complexity of such tools may compromise their effectiveness in identifying individuals at-risk for PCa. Genetics education among the general public is also important because individuals who are aware of and ask for specialized genetic services are the most likely to receive them [25]. Clear, simple, prescriptive education on genetics needs to be widely available to all PCa patients, and physicians will need to communicate the 6

advantages of genetic counseling and germline testing when they encounter high-risk localized and metastatic PCa patients who may benefit from it [40].

A lack of cross-cultural communication may also prevent racial/ ethnic minorities from seeking or consenting to germline testing. The cultural impact of cancer can have an effect on patients' attitudes towards germline testing: some South Asian and African-American communities have been found to take on a fatalistic view of cancer, associating the diagnosis with death; they may not wish to pursue testing if they believe nothing can be done to prevent or treat it [61]. Culture can also have an effect on the acceptance of test results: patients who receive germline testing may fear that their results will ostracize them from their family or community. Additionally, patients may not understand what a positive, negative, or inconclusive result means in the context of their own health and their family's health. One solution could be culturally tailored genetic counseling (CTGC) and testing programs, which have been developed and evaluated to improve access to risk assessment services, subsequently enhancing the quality of care among patients from racial/ethnic minority groups. CTGC consists of education about risk factors for hereditary disease, personalized risk information, and discussions about the benefits, limitations, and risks of germline testing [56].

Challenge and Solution: prohibitive cost and lack of insurance coverage for germline testing

Access to germline testing is often limited by access to guality, affordable health insurance, which varies by race/ethnicity: NHW people are more likely to have health insurance than racial/ethnic minorities [62]. Additionally, NHW people are more likely to have private health coverage as opposed to public health coverage, such as Medicare and Medicaid [62]. Patients who are uninsured, underinsured, or insured by government programs may face significant barriers to obtaining care-for example, they may be denied care by private physicians, leading them to seek care in emergency departments, public hospital systems, or local health departments which may not offer the same referrals or specialty and preventative services as private practices [63]. Overall, having health insurance is strongly associated with undergoing PCa screening, lower stage of cancer at diagnosis, treatment for local/ regional disease, prostatectomy, PCa survival, and guality of life [5]. Without health insurance, the cost of germline testing is often prohibitive. And, even when germline testing is covered by insurance, there may be prohibitive out-of-pocket costs, including deductibles and copayments. Additionally, not all insurers cover germline testing for PCa [46], including some private insurers and public options such as Medicare and Medicaid [64].

There are programs that increase PCa patient access to genetic services by offering free or reduced cost germline testing. Color Genomics offers a relatively low-cost risk analysis of several genes associated with PCa, as well as access to CGC and physician services [65]. Additionally, Invitae offers free germline testing and counseling for hereditary PCa through their Detect Hereditary Prostate Cancer program, in which eligible patients work with a genetic counselor or physician to order testing [66]. These, along with research studies such as the patient-driven PROMISE registry, which offers medical Color Genomics germline testing by mail to men with any stage of PCa [67], can reduce cost and access barriers.

Additional strategies for increasing payer coverage for germline testing and reducing test costs are necessary in order to create equitable access for all PCa patients. Strategies to increase insurance coverage may include clarifying and expanding Current Procedural Terminology codes to allow coverage for more specific tests and adding genetic specialists to insurance company staff to address shortages of genetic expertise. To address the costs of genetic tests, government subsidy programs and cost caps may be helpful in mitigating the cost to both the patient and insurers. Ultimately, there is a need for healthcare coverage reform in the US. In the absence of publicly funded healthcare, improving provider discussions about out-of-pocket costs is critical for ensuring informed patient testing and treatment decisions [64].

Challenge and solution: understudied link between PCa and breast/ovarian cancers

P/LPVs of *BRCA1/2* have been found to increase the risk of multiple cancers, including those of the breast, ovary, and prostate. These P/LPVs have clinical implications for PCa patients as well as their families. *BRCA1/2* associated HBOC should be suspected in individuals with family history of PCa and other cancers associated with HBOC syndrome [68], and likewise, PCa risk should be considered in individuals with a personal history of male breast cancer and/or family history suggestive of HBOC syndrome [69].

As with PCa, there are disparities in germline testing rates among racial/ethnic minority women with HBOC syndrome. These disparities are thought to be a result of multiple factors, including medical mistrust and fears of discrimination on the basis of genetic information [70]. Such disparities are thought to contribute to concordant disparities among racial/ethnic minority men with PCa. Therefore, addressing germline testing disparities among women with HBOC syndrome may aid in identifying male family members at-risk for developing PCa, as well as those already diagnosed with PCa who would benefit from germline testing's impact on treatment options.

One particular challenge for PCa patients is that the names of certain PCa predisposition genes and familial risk factors (e.g., *BRCA1/2* and HBOC syndrome) do not make obvious their link to PCa. As a result, it may not be clear to PCa patients that hereditary mutations in these genes affect them, as their names only indicate a link to breast and ovarian cancers. To address this misconception, one proposal is to change the name of HBOC syndrome to remove the sex specificity of the name [71], which may reduce confusion about its relevance to men.

CONCLUSION

It is widely accepted that a subset of PCa susceptibility is attributed to inherited predisposition. Because the identification of alterations in PCa predisposition genes may help inform screening strategies for patients and family members, treatment options in the metastatic setting, and clinical trial enrollment, it will become increasingly important to bridge the gap for PCa patients who are underserved with regard to germline testing. Issues to be addressed include a shortage of genetics professionals, disparities in care, medical mistrust, misinformation, and misunderstanding regarding germline testing, costs, and the understudied link between PCa and breast/ovarian cancer.

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COMPETING INTERESTS

HHC received research funding to her institution from Astellas, Clovis Oncology, Color Foundation, Janssen, Medivation, Phosplatin, and Sanofi; is a consultant for AstraZeneca. RRM received research funding from Bayer, Pfizer, Tempus; serves on Advisory Board for AstraZeneca, Bayer, Bristol Myers Squibb, Calithera, Exelixis, Janssen, Merck, Novartis, Pfizer, Sanofi, Tempus; is a consultant for Dendreon, Myovant, Vividion; serves on the molecular tumor board at Caris. The remaining authors declare no competing interests.

ADDITIONAL INFORMATION

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Circulating and Intratumoral Adrenal Androgens Correlate with Response to Abiraterone in Men with Castration-Resistant Prostate Cancer

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ABS<u>TRACT</u>

Purpose: In metastatic castration-resistant prostate cancer (mCRPC) low serum androgens prior to starting abiraterone acetate (AA) is associated with more rapid progression. We evaluated the effect of AA on androgens in castration-resistant prostate cancer (CRPC) metastases and associations of intratumoral androgens with response.

Experimental Design: We performed a phase II study of AA plus prednisone in mCRPC. The primary outcome was tissue testosterone at 4 weeks. Exploratory outcomes were association of steroid levels and genomic alterations with response, and escalating AA to 2,000 mg at progression.

Results: Twenty-nine of 30 men were evaluable. Testosterone in metastatic biopsies became undetectable at 4 weeks (P < 0.001). Serum and tissue dehydroepiandrosterone sulfate (DHEAS) remained detectable in many patients and was not increased at

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Introduction

While initially effective, treatment of prostate cancer with androgen deprivation therapy (ADT) is uniformly characterized by progression to castration-resistant prostate cancer (CRPC). Despite castrate-serum testosterone (T) levels, levels of T and DHT in CRPC metastases and patient-derived xenografts (PDX) are sufficient for androgen receptor (AR) activation (1, 2). Residual androgens in CRPC tumors may reflect *de novo* androgen synthesis or intratumoral uptake and conversion of adrenally derived steroid precursors to T and DHT (3, 4). In particular, serum levels of dehydroepiandrosterone sulfate (DHEAS), the primary circulating form of the adrenal androgen DHEA, are extremely high and are not suppressed by ADT (5, 6).

progression. Serum and tissue DHEAS in the lowest quartile

(pretreatment), serum DHEAS in the lowest quartile (4 weeks), and

undetectable tissue DHEAS (on-therapy) associated with rapid

progression (20 vs. 48 weeks, P = 0.0018; 20 vs. 52 weeks, $\hat{P} =$

0.0003; 14 vs. 40 weeks, P = 0.0001; 20 vs. 56 weeks, P = 0.02, respectively). One of 16 men escalating to 2,000 mg had a 30% PSA

decline; 13 developed radiographic progression by 12 weeks. Among patients with high serum DHEAS at baseline, wild-type (WT) PTEN

status associated with longer response (61 vs. 33 weeks, P = 0.02).

strongly associated with an androgen-poor tumor microenviron-

ment and with poor response to AA. Patients with CRPC with

higher serum DHEAS levels may benefit from dual androgen

receptor (AR)-pathway inhibition, while those in the lowest quartile

may require combinations with non-AR-directed therapy.

Conclusions: Low-circulating adrenal androgen levels are

CYP17A, expressed in the adrenal gland, testes, and ovary, catalyzes sequential reactions converting pregnenolone and progesterone to the adrenal androgens DHEA and androstenedione (AED). The role of adrenal androgens in promoting CRPC is supported by the efficacy of the CYP17A inhibitor abiraterone acetate (AA) in decreasing circulating adrenal androgens and improving overall survival (OS) in CRPC (7-10). The proposed mechanism is suppression of androgen levels in tumor tissue as a result of suppressing testicular, adrenal, and tumoral CYP17A activity. This regimen markedly decreases prostate androgens below that achieved by standard ADT in the neoadjuvant setting (5) and studies using CRPC xenografts similarly demonstrate suppression of tissue androgens below castration alone (11). However, the efficacy of AA and prednisone in reducing intratumoral androgens in CRPC metastases has not been reported. Moreover, lower serum androgen levels prior to starting this regimen have been associated with worse outcomes in patients with CRPC (12, 13). Whether a similar association exists with intratumoral androgen levels prior to



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Translational Relevance

In men with metastatic castration-resistant prostate cancer (CRPC), low-circulating adrenal androgens levels are strongly associated with an androgen-poor tumor microenvironment, with lower androgen levels while on-therapy, and with poor response to abiraterone acetate (AA) plus prednisone. While response to AA is clearly linked with its ability to suppress circulating and intratumor androgen levels, the paradoxical association of lower adrenal androgen levels while on-therapy with more rapid radiographic progression suggests an intrinsic resistance to androgen receptor (AR)-pathway therapy related to tumor outgrowth in a low androgen microenvironment. These data suggest that clinical benefit from dual-AR pathway inhibition is likely to be observed in patients with higher serum adrenal androgen levels, but will be limited in those with low/undetectable levels in whom treatment combinations with non-AR-directed therapy are likely to be required. Assessment of baseline and on-treatment androgen levels can inform the stratification and interpretation of trials evaluating the efficacy of AR pathway-directed therapy.

starting therapy, or with on-treatment androgen levels in serum or tissue is unknown.

We carried out a phase II study to evaluate the efficacy of AA plus prednisone in reducing androgen levels in CRPC metastases. The primary outcome was tissue T levels at 4 weeks. Exploratory outcomes were the association of steroid levels and genomic alterations with response, and the impact of escalating AA to 2,000 mg at progression.

Materials and Methods

Study design and patient population

This was an investigator-initiated open-label single-center threearm study of AA (1,000 mg daily) and prednisone (5 mg twice daily) followed by escalation of AA to 2,000 mg daily at disease progression in men with metastatic castration-resistant prostate cancer (mCRPC). Eligible patients had metastatic prostate cancer resistant to ADT comprised of medical or surgical castration \pm standard antiandrogen (bicalutamide, flutamide, or nilutamide) and were not previously treated with AA or enzalutamide. Prior ketoconazole and docetaxel were allowed.

Study procedures and treatment

Patients underwent pretreatment biopsy of a bone, node, or softtissue metastasis and were then alternately enrolled in cohorts undergoing repeat biopsy at 4 weeks (cohort 1) or 12 weeks (cohort 2) until 10 patients were enrolled in each cohort (Study Schema provided in Supplementary Fig. S1). Patients with radiographic or clinical progression prior to planned biopsy were reassigned to cohort 3 (biopsy at progression) and another patient placed in cohort 1 or 2. After cohorts 1 and 2 were filled, patients were sequentially assigned to cohort 3 with biopsy at progression, until a total of 10 patients were enrolled in cohort 3 (of these, 2 had been reassigned from cohort 1 or 2 for clinical progression at 4 and 8 weeks). Patients remained on ADT and received AA 1,000 mg orally daily with prednisone 5 mg orally twice daily until development of radiographic or clinical progression. CT of the chest, abdomen, and pelvis, and bone scan were obtained before enrollment and every 12 weeks while on study treatment. Radiographic progression was determined based on Prostate Cancer Working Group 2 (PCWG2) criteria. Serum for PSA was drawn monthly. At radiographic progression asymptomatic patients were offered dose escalation of AA to 2,000 mg daily. Therapy with standard or dose-escalated AA was continued until radiographic or clinical progression or for a maximum of 2 years (104 weeks).

Steroid and abiraterone measurements

Methods for determination of steroids and abiraterone in serum and prostate tissue by mass spectrometry were as previously reported (14). Similar methods were used for detection of the abiraterone metabolites D4-abiraterone, and 3-keto-5 α -abiraterone. Additional information on assay methodology and limits of detection and quantitation is provided in Supplementary Fig. S2. For purposes of calculation, analyte values below the lower limit of detection were set at the lower limit of quantitation specific for that analyte.

Genomic analysis

Genomic DNA was prepared from clinical samples (buffy coat, mCRPC tumor tissue) using DNeasy Blood and Tissue Kit (QIAGEN). Next-generation sequencing (NGS) was performed on CRPC tissue biopsies using the clinically validated UW-OncoPlex platform (15). We determined *HSD3B1* genotype in DNA extracted from buffy coat using a melting assay with an unlabeled, locked, nucleic acid oligonucleotide probe in an asymmetric PCR as previously described (16).

Statistical analysis

A sample size of 6 patients per arm provided 94% power to detect the anticipated 0.660 pg/mg difference in tissue T levels relative to baseline, based on a 2-sided paired *t* test with alpha 5%. Ten patients per cohort were enrolled to account for potentially unproductive biopsies. Demographic and clinical characteristics were summarized using descriptive statistics. Comparisons of continuous variables among groups were assessed using the nonparametric Wilcoxon rank–sum test (Mann–Whitney test). Comparison of continuous variables between baseline and subsequent timepoints were assessed using the Wilcoxon matched-pairs test. Progression-free survival (PFS) was estimated using Kaplan–Meier methods and compared using the Gehan–Wilcoxan test. The statistical significance was set at *P* < 0.05. Due to the small sample size, all findings were considered hypothesis generating and no multiple-testing adjustments were performed. All statistical analyses were done using GraphPad Prism (version 8.3.0).

Study approval

All procedures were carried out in accordance with the U.S. Common Rule and approved by the institutional review board of the University of Washington. All subjects signed written informed consent. The trial was registered with the clinicaltrials.gov identifier NCT01503229.

Results

Patient characteristics

Thirty patients enrolled and 29 were evaluable for analysis (**Fig. 1**). Baseline characteristics are shown in **Table 1**. Median age was 71 years (range 44–83 years). The median PSA was 78 ng/mL (range 2–908). In the 18 patients with soft-tissue \pm bone disease, the biopsy site was equally divided between bone and lymph node based solely on tumor location most accessible to biopsy. Eleven patients had received previous definitive therapy for localized disease while 19 were metastatic at diagnosis. Eleven patients had received one or more treatments beyond bicalutamide for CRPC.

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Analyzed (n = 29)

- Efficacy evaluable population (*n* = 29)
- Safety evaluable population (*n* =29)
- Excluded from analysis (n = 0)

Figure 1.

Flow diagram of patient recruitment, enrollment, and participation. Diagram depicts participant flow through the study process from patient screening to data analysis.

Clinical response to standard and dose-escalated AA and prednisone

The median time-to-radiographic/clinical progression in the entire cohort was 36 weeks (range 4-104; Fig. 2A). Twenty of 29 (69%) achieved a PSA decline of ≥30% (PSA30) after 12 weeks of standarddose AA plus prednisone (Fig. 2B), with 22 (75%) eventually doing so. The median time-to-progression was longer in those achieving PSA30 decline at 12 weeks (40 vs. 34 weeks; P = 0.05; with a similar but nonsignificant trend in those achieving a PSA50 decline; Supplementary Fig. S3A and S3B; ref. 17). Notably, 4 of the 9 patients without PSA30 at 12 weeks had responses lasting 36, 40, 41, and 104 months, underscoring the importance of radiographic progression versus PSA decline as a primary endpoint. Three patients withdrew while responding to therapy (1 each to pursue alternative therapy, for religious reasons, and due to diagnosis of an unrelated malignancy) and were censored at the time of study withdrawal (at 28, 24, and 20 months). Three patients did not progress on standard-dose therapy by the end of the 2-year treatment period and were censored at 104 months.

 Table 1. Baseline clinical characteristics at time of study enrollment.

Patients, <i>n</i>	29
Median age (range), years	71 (44-83)
Median PSA (range), ng/mL	78 (2-908)
Extent of disease	
Bone only	10 (33%)
Bone and LAD	15 (50%)
Bone and LAD/visceral disease	3 (10%)
LAD only	2 (7%)
Median tumor fraction in prestudy biopsy	55% (4-88%)
Previous therapies, <i>n</i>	
Radical prostatectomy	5
Definitive radiotherapy	6
Neither (metastatic at diagnosis)	19
Systemic therapy	
Combined androgen blockade	8
Bicalutamide	9
Nilutamide/flutamide	3
High-dose ketoconazole	5
Diethylstilbestrol	2
Sipuleucel-T	4
Docetaxel	4 (1 CSPC)
Lines of therapy for CRPC	
0	7
1	14
2	3
3-4	5

Abbreviations: CSPC, castration-sensitive prostate cancer; LAD, lymphadenopathy.

At radiographic progression, 16 of 29 patients underwent dose escalation of AA to 2,000 mg per day (with continuation of prednisone). There was no decrease in the median PSA (Supplementary Fig. S3C), with only 1 patient achieving a PSA30 decline (**Fig. 2C**). Thirteen patients had clinical or radiographic progression and discontinued therapy by week 12 after dose escalation. Two patients remained on dose-escalated therapy for 56 weeks and 36 weeks, respectively, prior to second radiographic progression, while 1 patient remained on dose-escalated therapy for 20 weeks at which time he reached the end of the 2-year treatment period and was censored at 104 months. No consistent findings with regards to PSA, steroid, or abiraterone levels, or tumor genomic alterations were observed in these 3 patients.

Steroid and abiraterone levels during standard and doseescalated AA therapy

Steroid levels in serum and tissue prior to and during AA and prednisone therapy are summarized in Supplementary Tables S1 and S2. Serum levels showed a significant increase in steroids upstream of CYP17A (pregnenolone) and decreases in downstream steroids (DHEAS, DHEA, AED, T, and DHT) at all timepoints (**Fig. 2D**; see steroid metabolism schema, Supplementary Fig. S4), consistent with prior observations in serum and urine (7). While median levels of DHEAS and DHEA decreased by over two orders of magnitude in response to therapy in all patients, there appeared to be two modes of response. In one, levels became undetectable by week 4 and remained undetectable, while in the other subset, levels were still detectable at week 4 and remained detectable at all time points of treatment. AED, T, and DHT in serum were largely undetectable at all time points after starting therapy. Serum steroids were not increased at progression compared with earlier time points.

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Figure 2.

Clinical response and steroid levels in serum and metastatic tissue on AA plus prednisone. **A**, Kaplan-Meier plot of time to radiographic progression on standard dose AA. **B**, Waterfall plot showing percent change in PSA at 12 weeks. **C**, Kaplan-Meier plot of time to radiographic progression comparing patients with or without a 30% PSA decline at 12 weeks. **D**, Waterfall plot comparing the original change in PSA (blue bars) to the percent change in PSA after dose escalation of AA to 2,000 mg per day (red bars). **E**, Change in serum steroid levels after standard dose AA plus prednisone at baseline (0 weeks); at 4, 8 and 12 weeks (4wk, 8wk, 12wk); and at end of study (EOS) at the time of radiographic progression. **F**, Change in steroid levels in metastatic tissue (tx) biopsies prior to therapy (biopsy 1, bx1) and while on therapy (biopsy 2, bx2). Biopsy 2 was taken at either 4 weeks (4wk bx), 12 weeks (12wk bx), or at progression (Progr bx). *P* values for the indicated comparison calculated via the Wilcoxon matched-pairs test. Data are shown as box and whisker plots, where horizontal lines indicate median values, white boxes denote the 75th (upper margin) and 25th percentiles (lower margin), and upper and lower bars indicate the minimum and maximum values, respectively. AED, androstenedione; DHEA, dehydroepiandrosterone; DHEAS, dehydroepiandrosterone sulfate.

In tissue as in serum, steroids upstream of CYP17A (pregnenolone) were increased in the on-treatment tissue biopsies, while downstream steroids [DHEAS, AED, T, androsterone (ASD)] were significantly decreased (**Fig. 2E**). Levels of AED, T, and ASD in tissue fell below the limit of detection by week 4 and remained essentially undetectable. DHEAS in tissue remained detectable in the majority of biopsies obtained at 4 and 12 weeks (6 of 9 and 6 of 7, respectively), but was undetectable in 6 of 9 samples at progression. DHT levels were below the limit of detection in 24 of 29 tissue samples at baseline and undetectable in all tissue after therapy. These observations suggest that an increase in tissue levels of androgens is not responsible for resistance to AA and prednisone and explains the lack of response to AA dose escalation.

AA is a prodrug that rapidly dissociates to abiraterone once ingested, therefore, all serum and tissue measurements are of abiraterone, not AA (summarized in Supplementary Table S3). Abiraterone is converted by 3β HSD1 to D4-abiraterone, and then by SRD5A to 3-keto- 5α -abiraterone, metabolites with AR antagonist and ARagonist activity, respectively (18). Levels of abiraterone metabolites in serum and tissue were similar at all time points and were not decreased at progression compared with earlier time points (Supplementary Fig. S5A and S5B). These observations suggest that resistance to AA is not associated with an increase in serum steroid levels or decrease in serum or tissue drug levels at the time of progression.

Dose escalation of AA from 1,000 mg to 2,000 mg resulted in the expected pharmacokinetic changes with a nonsignificant increase in

the median level of abiraterone (22.4 to 78.2 ng/mL), and a significant increase in D4-abiraterone (1.48 to 4.0; P = 0.012) and 3-keto-5 α -abiraterone (10.6 to 14.3 ng/mL; P = 0.005) at 4 weeks (Supplementary Fig. S5C). Accordingly, serum levels of DHEAS and DHEA decreased in 9 of 16 patients, and AED levels remained or became undetectable in 15 of 16 (Supplementary Fig. S5D), although the overall decrease in median levels was nonsignificant for DHEAS and DHEA, and of borderline significance for AED (P = 0.21, 0.36, and 0.06, respectively). These observations suggest that the lack of clinical response to AA dose escalation is not accounted for by a failure of pharmacokinetic or pharmacodynamic responses in serum. Moreover, in the 3 patients that experienced prolonged responses, serum abiraterone and androgen levels after dose escalation were variably altered (decreased in 2 and increased in 1), although changes in tissue levels before and after dose escalation were not assayed.

Correlation of steroid levels in serum and metastatic tissue before and after therapy with AA and prednisone

Serum levels of DHEAS, DHEA, AED, ASD, T, and DHT, were highly correlated with each other and with levels of DHEAS, AED, and ASD in pretreatment biopsies (**Fig. 3A**). Tissue levels of DHEAS and AED, DHEAS and ASD, and AED and ASD correlated with each other (r = 0.51, 0.56, and 0.46, respectively; P < 0.05 for all), while tissue T levels were not significantly correlated with steroid levels in either serum or tissue. After starting AA plus prednisone, levels of DHEAS,



Figure 3.

Correlation of steroid levels in serum and metastatic tissue before and after treatment with AA plus prednisone. **A**, Heatmap of steroid correlations in pretreatment serum (day 0) and metastatic tissue biopsies (Biopsy 1). The Spearman *r* value for each correlation is shown in the box. Correlations with P < 0.05 in black, P < 0.10 in italics, P > 0.10 in gray. **B**, Heatmap of Spearman correlations for steroids in serum at week 4 (wk4), week 8 (wk8), and week 12 (wk12). **C**, Comparison of baseline serum steroid levels stratified by serum DHEAS levels above (blue) versus below (red) the median at baseline (d0). **D** and **E**, Comparison of DHEAS levels (**D**) and DHEA levels (**E**) in serum stratified by baseline serum DHEAS levels at baseline (0 weeks); at 4, 8, and 12 weeks; and at EOS. Significant Spearmen correlations between on-treatment and baseline values at each time point is indicated below the timepoint. **F**, Comparison of tissue (by DHEAS levels above (blue) vs. below (red) the median at baseline. **G**, Comparison of steroid levels in pretreatment tissue biopsies (bx1 and bx2). *P* values for the indicated comparison calculated via nonparametric Mann-Whitney *t* tests. ABI, abiraterone; D4 ABI, D4-abiraterone; Keto ABI, 3-keto-5\alpha-abiraterone; Preg, pregnenolone; Preg, progesterone.

DHEA, and AED remained significantly correlated with each other and showed the expected inverse correlations with abiraterone and its metabolites (**Fig. 3B**), while progesterone showed the expected positive correlation with abiraterone and its metabolites. These treatmentrelated correlations were present by 4 weeks and became notably more pronounced at 8 and 12 weeks. Abiraterone and metabolite levels were strongly correlated with each other in serum and tissue at all time points (Supplementary Fig. S6A).

These baseline and on-treatment steroid correlations are further illustrated by the observation that subjects with baseline serum DHEAS levels above versus below the median also had higher baseline levels of DHEA, AED, T, DHT, and ASD (**Fig. 3C**) and maintained significantly higher serum levels of DHEAS (**Fig. 3D**) and DHEA (**Fig. 3E**) at all time points [including, for DHEAS, at the end-of-study (EOS) measurement taken at progression]. Moreover, strong correlations between baseline and on-treatment serum levels were observed at all time points for DHEAS (**Fig. 3D**), and at 4 and 8 weeks for DHEA (**Fig. 3E**). Likewise, subjects with baseline serum DHEAS above versus below the median had higher tissue levels of DHEAS, AED, and ASD at baseline (Fig. 3F), as well as higher DHEAS in on-treatment tissue biopsies (Fig. 3G). These observations demonstrate that serum DHEAS levels prior to AA therapy can identify patients with CRPC with concomitantly higher levels of all androgens in serum and tissue, and that this subset of patients with high baseline androgen levels maintains persistently higher serum and tissue DHEAS levels after treatment with AA and prednisone.

Association of steroid and abiraterone levels with PSA decline and PFS

Compared with patients who achieved a PSA30 decline at 12 weeks, those with less than a PSA30 decline had numerically lower pretreatment levels of serum and tissue androgens (**Fig. 4A**). These differences were strongest for T (P = 0.055) and DHT (P = 0.069) in serum, and for AED (P = 0.063), T (P = 0.034), and ASD (P = 0.088) in tissue. Accordingly, the rate of achieving a PSA30 decline at 12 weeks was 37% (3/8) in patients in the lowest quartile of serum DHEAS, but 81% (17/21) in patients in the top 3 quartiles (**Fig. 4C**; PSA levels at baseline were not associated



Figure 4.

Association of steroid and abiraterone levels with PSA decline and radiographic progression on AA plus prednisone. **A** and **B**, Comparison of steroid levels in serum (**A**) and metastatic tissue biopsies (**B**), based on achieving a 30% PSA decline at 12 weeks. **C**, Distribution of pretreatment PSA levels and waterfall plot showing percent change in PSA at 12 weeks by quartile (Q1-Q4) of pretreatment serum DHEAS levels. *P* values for the indicated comparison calculated via nonparametric Wilcoxon rank-sum test (Mann-Whitney test). **D**, Radiographic PFS (rPFS) as a function of baseline serum androgen levels comparing subjects in the lowest vs. highest 3 quartiles (Q4 vs. Q1-3). **E**, rPFS as a function of on-treatment serum DHEAS levels at week 4 (wk4) and week 8 (wk8) comparing subjects in the lowest vs. highest 3 quartiles (Q4 vs. Q1-3). **F**, rPFS as a function of pretreatment tissue DHEAS and AED levels comparing subjects in the lowest vs. highest 3 quartiles (Q4 vs. Q1-3). **F**, rPFS as a function of pretreatment tissue DHEAS and AED levels. The quartiles were separately assessed in the pre- and on treatment populations. **G**, rPFS comparing subjects with detectable vs. undetectable levels of DHEAS in tissue biopsies taken at 4 and 12 weeks of therapy. **H**, rPFS as a function of serum 3-keto-5α-abiraterone levels (keto-Abi) at wk4 and wk8 comparing subjects above vs. below the median. PFS was estimated using Kaplan-Meier methods and compared using the Gehan-Wilcoxan test. Androst, androsterone; Q, quartile.

with serum DHEAS levels). These observations suggest that being in the lowest quartile of serum androgens prior to starting AA therapy is associated with a decreased incidence of PSA30 decline at 12 weeks.

Consistent with these observations, serum steroid levels in the lowest quartile prior to therapy were associated with more rapid progression. This was highly significant for DHEAS (20 vs. 48 weeks, P = 0.0018) with less significant trends noted for DHEA, T, and ASD (P = 0.13, 0.041, and 0.049 respectively; **Fig. 4D**). Notably, ontreatment levels of DHEAS in the lowest quartile remained associated with more rapid progression (14 vs. 40 weeks, P = 0.0001 at 4 weeks; 20 vs. 40 weeks, P = 0.02 at 8 weeks; **Fig. 4E**). Low adrenal androgens in pretreatment tissue biopsies were even more strongly associated with worse outcomes (20 vs. 52 weeks, P = 0.0003 for DHEAS; 14 vs. 41 weeks, P = 0.0002 for AED; **Fig. 4F**). Likewise, undetectable vs.

detectable DHEAS levels in biopsies taken at 4 and 12 weeks were associated with shorter time-to-progression (20 vs. 56 weeks, P = 0.023; **Fig. 4G**). These observations demonstrate that the association of lower serum adrenal androgen levels with more rapid progression on AA plus prednisone holds true for lower adrenal-androgen levels in pretreatment metastasis biopsies, and for lower on-treatment levels of DHEAS in serum and tissue.

Levels of abiraterone and D4-abiraterone in serum were not associated with differences in time-to-progression, nor were levels of abiraterone and its metabolites in tissue (Supplementary Fig. S6B and S6C). However, serum levels of 3-keto-5 α -abiraterone above the median at week 4 and 8 were associated with more rapid progression (24 vs. 48 weeks, P = 0.04, and 24 vs. 48 weeks, P = 0.008, respectively; **Fig. 4H**), consistent with the ability of this metabolite to act as an AR agonist.



Figure 5.

Association of *PTEN* status with radiographic progression on AA plus prednisone. **A**, rPFS as a function of *PTEN* status alone or as a function of baseline serum DHEAS levels stratified by *PTEN* status, comparing subjects in the lowest vs highest three quartiles (Q4 vs Q1-3). **B**, rPFS as a function of *MYC*, *TP53*, or *AR* status.

Association of genomic alterations with radiographic PFS on AA and prednisone

All patients had pretreatment tumor biopsy tissue that was adequate for sequencing. The frequency and distribution of pathogenic alterations were consistent with mCRPC (Supplementary Table S4). Wild-type (WT) PTEN was weakly associated with longer time-to-progression (52 vs. 33 weeks, P = 0.06; Fig. 5A). Patients in the lowest quartile of serum DHEAS (3 PTEN WT, and 5 PTEN loss) were previously shown to have a poor response to AA (Fig. 4D) and this was not influenced by PTEN status. However, in the top 3 quartiles of serum DHEAS (with median survival 48 weeks; Fig. 4D), WT PTEN versus PTEN loss distinguished patients with a significantly more prolonged versus intermediate response (61 vs. 33 weeks; P = 0.02) versus those in the lowest quartile of DHEAS (20 weeks; P < 0.001 for trend; Fig. 5A). These findings demonstrate that patients in the lowest quartile of serum DHEAS levels have the most rapid progression on AA, regardless of PTEN status, while those with DHEAS levels in the top 3 quartiles can be meaningfully stratified by PTEN status. In this small study WT MYC was also weakly correlated with longer survival (40 vs. 16 weeks, P = 0.08) while TP53 status or the presence of AR mutation or amplification were not associated with progression (Fig. 5A).

As inhibition of AR signaling has been associated with reciprocal induction of PTEN signaling (19, 20), we determined if lower androgens were associated with PTEN loss. Median serum levels of T and DHT at baseline were numerically but not statistically lower in patients with *PTEN* loss versus WT *PTEN* (P = 0.09 and 0.084, respectively; Supplementary Fig. S7B), as were on-treatment levels of DHEAS in tissue (P = 0.09). Median serum levels of DHEAS and DHEA at baseline were also numerically lower in patients with *TP53* loss versus WT *TP53* (P = 0.053 and 0.047, respectively; Supplementary Fig. S7C). These observations suggest that while specific AR-independent tumor drivers such as *PTEN* and *TP53* may be selected to emerge in a low-androgen environment, a low-androgen environment is likely to promotes a more aggressive tumor biology by multiple mechanisms not limited to specific pathway alterations.

Association of *HSD3B1* genotype with steroid and abiraterone levels and radiographic PFS

The 1245C variant of HSD3B1 produces a more stable enzyme, increasing conversion of DHEA to AED, a precursor of T and DHT (Supplementary Fig. S4), as well as increasing conversion of abiraterone to D4-abiraterone (21). Germline DNA testing identified 14 men who were homozygous WT (48%), 10 men who were heterozygous (34%), and 6 who were homozygous for the allelic variant (21%). Consistent with the impact of the variant on enhancing conversion of abiraterone to D4-abiraterone, serum levels of this metabolite were highest in subjects with two variant alleles (median 2.7 ng/mL) versus one variant allele (2.1 ng/mL) versus two WT alleles (1.2 ng/ mL; ANOVA P = 0.02; Supplementary Fig. S8A). Serum levels of 3-keto-5α-abiraterone did not differ by HSDB1 genotype, nor did levels of abiraterone metabolite in tissue (Supplementary Fig. S8A). There was no difference in serum or tissue-androgen levels based on HSD3B1 status (including the five tissue samples with detectable levels of DHT; Supplementary Fig. S8B), nor in time-to-progression (Supplementary Fig. S8C).

Discussion

In this phase II study we demonstrate that in mCRPC AA plus prednisone decreases T levels in metastatic tissue biopsies to undetectable by 4 and 12 weeks of therapy, consistent with the predicted mechanism of activity. Steroid and abiraterone levels in serum and tissue remained stable at progression compared with earlier time points, consistent with prior reports regarding serum adrenal androgens (8), but demonstrating for the first time that tissue-androgen levels also remain unchanged at progression. Overall, these findings suggest that the development of resistance to AA plus prednisone is not accounted for by a decrease in serum or tissue drug levels below the levels originally achieved in response to therapy. Nor is it accounted for by an increase in serum or intratumoral androgens above the levels originally achieved in response to AA plus prednisone. The observations that tumor steroid levels do not become reelevated at progression and that persistent serum DHEAS levels do not become undetectable after dose escalation of AA to 2,000 mg likely accounts for the lack of clinical response to high-dose AA at progression, now reported in two studies (22).

At baseline, serum levels of DHEAS and DHEA varied by over an order of magnitude (range 36–2,659 ng/mL) and demonstrated two patterns of response to treatment. While median levels of steroids downstream of CYP17A decreased by a similar order of magnitude in all patients, the subset of patients defined by higher serum DHEAS levels prior to therapy also had higher serum levels of other steroids at baseline; higher levels of DHEAS, AED, and ASD in pretreatment tissue biopsies; and maintained higher DHEAS levels in on-treatment serum samples and tissue biopsies. These observations demonstrate that serum DHEAS levels prior to therapy can distinguish patients with correspondingly lower or higher serum and tissue levels of all androgens and can identify those likely to maintain persistent serum and tissue DHEAS levels while on treatment with AA plus prednisone.

The correlation of low baseline with low on-treatment adrenalandrogen levels is of particular interest as lower adrenal androgens prior to therapy have been consistently associated with worse response to AA plus prednisone (13, 23–25). We show for the first time that this association with worse outcomes extends to low on-treatment level of DHEAS in serum and tissue, and with low adrenal androgens in pretreatment metastasis biopsies. At baseline, the association of worse response with lower levels was highly significant for DHEAS in serum (P = 0.0018) and for DHEAS and AED in pretreatment tissue biopsies (P = 0.0003 and P = 0.0002, respectively). On therapy, serum DHEAS in the lowest quartile at 4 and 8 weeks (P = 0.0001 and 0.024, respectively), as well as undetectable versus detectable DHEAS levels in metastatic biopsies taken at 4 and 12 weeks (P = 0.023 and P = 0.04, respectively) all associated with more rapid progression on AA therapy. These specific associations with DHEAS are consistent with the fact that DHEAS is the predominant steroid in serum and tissue prior to therapy, and remains the only steroid consistently present at measurable levels in metastatic tissue after AA therapy.

While response to AA is clearly linked with suppression of circulating and intratumor androgens, the paradoxical association of better outcomes with higher on-treatment androgen levels suggests that response to AA is not dictated solely by a pharmacodynamic effect on serum or tissue androgens, but may reflect an intrinsic resistance to AR-pathway therapy associated with tumor outgrowth in a low androgen microenvironment (26). These observations suggest that baseline serum androgen levels, by identifying patients with a more aggressive tumor biology that is less androgen dependent, may be prognostic as well as predictive of response to AR-pathway-directed therapy. As such, patients with higher androgens may have better survival independent of an effect of AA. This is consistent with the association of lower serum androgen levels with decreased survival in both the placebo and AA arms of the phase III study of AA plus prednisone in men with mCRPC (13), and with a recent meta-analysis demonstrating that PFS and OS were lower in patients with CRPC with lower versus higher T levels (27).

Importantly, the observation that lower androgen levels in CRPC associate with worse outcomes is not incompatible with data linking the achievement of lower T levels with improved time-to-progression in men with CSPC treated with ADT (28, 29). While time-to-development of CRPC may be delayed, CRPC tumors that emerge

in patients with lower T levels (due to low adrenal contribution and/or optimally suppressed T levels while on ADT) are likely to represent a more aggressive, less androgen-dependent phenotype compared with tumors that emerge with more rapid kinetics in context of higher androgen levels (due to more robust adrenal contribution and/or suboptimally suppressed T levels). While this may not influence response to subsequent non–AR-specific agents such as docetaxel, it is likely to adversely influence response to next-generation ARtargeted therapy. This is consistent with findings in the metaanalysis discussed above, in which lower T levels were a consistently poor prognostic factor for OS in patients with CRPC treated with AR-targeting agents, but not in those treated with chemotherapy (27).

The significant variation in adrenal androgen levels is not well understood. Functional polymorphisms in genes encoding critical steroidogenic enzymes such as CYP17A, HSD3B1, SULT2A1, AKR1C3, SRD5A, and UGT2B17 influence enzyme activity and/or production of downstream steroids (21, 30–32). Population-based studies will be required to determine whether a composite haplotype of genes involved in adrenal androgen production exists that may account for the observed spectrum of serum androgen levels. Alternatively, the variability might reflect genetic variation in regulatory factors such as *CYB5A1*, *NR5A1* (also known as SF-1 or steroidogenic factor 1), or *MC2R* [the adrenocorticotropic hormone (ACTH) receptor] that are upstream of adrenal steroid synthesis (33–35).

We found no association of abiraterone levels with PSA decline or with time-to-radiographic progression, with nearly all patients having serum levels above the 8.4 ng/mL value previously proposed as a cutoff for PSA response (36). This contrasts with the observation of Friedlander and colleagues who found in a study of 41 men with mCRPC that patients who failed to show a PSA response to AA had lower abiraterone levels after 4 weeks and at progression (22). This difference may reflect variability in timing of the blood draws, which, while mandated before the daily dose, were not specifically recorded precluding correction for differences based on pharmacokinetics (18). However, our findings are consistent with the work of Smulewitz and colleagues, who also found no correlation between abiraterone levels and change in PSA in a study of 72 men with mCRPC randomized to standard or low-dose AA (37), as well as with an analysis performed by the FDA in which no association was found between trough abiraterone levels and OS (38).

The adrenal-permissive variant of HSD3B1 (promotes conversion of AED and T to downstream androgens, and of abiraterone to D4abiraterone and 3-keto-5\alpha-abiraterone) has been consistently associated with more rapid progression on ADT (39), and potentially with worse outcomes in response to AA and enzalutamide in some but not all studies (40-43). Although we did find an association of HSD3B1 status with D4-abiraterone (the immediate downstream product of HSD3B1), we did not observe an association of HSD3B1 genotype with response to abiraterone, nor the previously reported association with 3-keto-5 α -abiraterone, potentially reflecting that serum levels were not corrected for differences based on pharmacokinetics. (18) However, we did observe that serum levels of 3-keto-5 α -abiraterone above the median at weeks 4 and 8 were associated with a more rapid time-toprogression. These observations are consistent with the ability of this metabolite to act as an AR agonist, and suggest that dose escalation of AA may in fact be detrimental to patient outcomes. These findings provide support for the low-dose AA strategy proposed by Smulewitz (37), and provide impetus for clinical trials combining AA therapy with an SRD5A inhibitor to prevent conversion of D4-abiraterone to 5α -keto metabolite (44, 45).

NGS of CRPC tumors has identified aberrations in multiple genes including AR, TP53, PTEN, and SPOP which have been explored as predictive biomarkers of response to AR-pathway inhibition. In this small study we found no association of AR, TP53, or SPOP status with response to AA (46-48). In our cohort, WT PTEN was weakly associated with longer time-to-progression on AA plus prednisone, consistent with Ferraldeschi and colleagues who reported a retrospective study of 144 patients in which PTEN loss was associated with shorter OS (14 vs. 21 months; P = 0.004) and shorter duration of abiraterone treatment (24 vs. 28 weeks; P = 0.009; ref. 49). Moreover, whereas poor response to AA in men with the lowest serum DHEAS levels was not additionally influenced by PTEN status, in those with higher androgen levels WT PTEN versus PTEN loss conferred a significantly longer time-to-progression (61 vs. 33 weeks; P = 0.02). While our study is too small to meaningfully predict genomic alterations associated with response to AR-pathway inhibition, these data suggest that interpretation of tumor sequencing data may be more informative if analyzed in context of the risk conferred by low versus high serum androgen levels.

This study has several important limitations, including small sample size, that abiraterone and metabolite levels were not corrected for pharmacokinetic differences based on timing of trough blood draws, and that analyses were exploratory with no attempt to correct for multiple testing. As such, our observations must be considered hypothesis generating and require validation in larger data sets.

Our data show that higher circulating adrenal androgens in patients with CRPC are strongly associated with an androgenrich tumor microenvironment before and during therapy with AA and prednisone, and suggest that ambient androgen levels in the castrate tumor microenvironment are an important determinant of prostate-tumor biology and response to therapy (13). Baseline and on-treatment androgen levels are likely to be important in the stratification and interpretation of trials evaluating AR-pathwaydirected therapy. In particular, while addition of AA to enzalutamide did not prolong survival in metastatic CRPC (50), higher baseline DHEAS levels may distinguish a subset of patients who do benefit from dual-AR therapy. Conversely, patients with CRPC in the lowest quartile of serum DHEAS levels may warrant stratification to regimens that include non-AR-directed therapy. Whether adrenal androgens associate with response to AA in metastatic CSPC is unknown but requires exploration. Prospective studies evaluating baseline and on-treatment androgen levels as predictive biomarkers of response to AR-directed therapy are required to test these hypotheses.

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Authors' Contributions

E.A. Mostaghel: Conceptualization, resources, data curation, formal analysis, funding acquisition, methodology, writing-original draft, writing-review and editing. B.T. Marck: Data curation, formal analysis, investigation, methodology, writingreview and editing. O. Kolokythas: Resources, writing-review and editing. F. Chew: Resources, writing-review and editing. E.Y. Yu: Resources, writing-review and editing. M.T. Schweizer: Resources, writing-review and editing. H.H. Cheng: Resources, writing-review and editing. P.W. Kantoff: Resources, writing-review and editing. S.P. Balk: Resources, writing-review and editing. M.E. Taplin: Resources, writing-review and editing. N. Sharifi: Resources, methodology, writing-review and editing. P.S. Nelson: Conceptualization, resources, funding acquisition, writing-review and editing. R.B. Montgomery: Conceptualization, resources, supervision, funding acquisition, writing-review and editing.

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Niraparib in patients with metastatic castration-resistant prostate cancer and DNA repair gene defects (GALAHAD): a multicentre, open-label, phase 2 trial

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Summary

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Background Metastatic castration-resistant prostate cancers are enriched for DNA repair gene defects (DRDs) that can be susceptible to synthetic lethality through inhibition of PARP proteins. We evaluated the anti-tumour activity and safety of the PARP inhibitor niraparib in patients with metastatic castration-resistant prostate cancers and DRDs who progressed on previous treatment with an androgen signalling inhibitor and a taxane.

Methods In this multicentre, open-label, single-arm, phase 2 study, patients aged at least 18 years with histologically confirmed metastatic castration-resistant prostate cancer (mixed histology accepted, with the exception of the small cell pure phenotype) and DRDs (assessed in blood, tumour tissue, or saliva), with progression on a previous nextgeneration androgen signalling inhibitor and a taxane per Response Evaluation Criteria in Solid Tumors 1.1 or Prostate Cancer Working Group 3 criteria and an Eastern Cooperative Oncology Group performance status of 0-2, were eligible. Enrolled patients received niraparib 300 mg orally once daily until treatment discontinuation, death, or study termination. For the final study analysis, all patients who received at least one dose of study drug were included in the safety analysis population; patients with germline pathogenic or somatic biallelic pathogenic alterations in BRCA1 or BRCA2 (BRCA cohort) or biallelic alterations in other prespecified DRDs (non-BRCA cohort) were included in the efficacy analysis population. The primary endpoint was objective response rate in patients with BRCA alterations and measurable disease (measurable BRCA cohort). This study is registered with ClinicalTrials.gov, NCT02854436.

Findings Between Sept 28, 2016, and June 26, 2020, 289 patients were enrolled, of whom 182 (63%) had received three or more systemic therapies for prostate cancer. 223 (77%) of 289 patients were included in the overall efficacy analysis population, which included BRCA (n=142) and non-BRCA (n=81) cohorts. At final analysis, with a median follow-up of 10.0 months (IQR 6.6–13.3), the objective response rate in the measurable BRCA cohort (n=76) was 34.2%(95% CI 23.7-46.0). In the safety analysis population, the most common treatment-emergent adverse events of any grade were nausea (169 [58%] of 289), anaemia (156 [54%]), and vomiting (111 [38%]); the most common grade 3 or worse events were haematological (anaemia in 95 [33%] of 289; thrombocytopenia in 47 [16%]; and neutropenia in 28 [10%]). Of 134 (46%) of 289 patients with at least one serious treatment-emergent adverse event, the most common were also haematological (thrombocytopenia in 17 [6%] and anaemia in 13 [4%]). Two adverse events with fatal outcome (one patient with urosepsis in the BRCA cohort and one patient with sepsis in the non-BRCA cohort) were deemed possibly related to niraparib treatment.

Interpretation Niraparib is tolerable and shows anti-tumour activity in heavily pretreated patients with metastatic castration-resistant prostate cancer and DRDs, particularly in those with BRCA alterations.

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Introduction

Patients with metastatic castration-resistant prostate cancer who have progressed on a next-generation androgen signalling inhibitor and taxane chemotherapy (docetaxel, cabazitaxel, or both) have few treatment options.^{1,2} DNA repair gene defects (DRDs), seen in approximately 12-23% of tumours in patients with metastatic prostate cancer when considering both germline and somatic alterations,3-5 are associated with cancer development, aggressiveness, and progression.6

These DRD-altered tumours are not only frequent in metastatic disease, but are also associated with poor prognosis and potential resistance to systemic therapies.7 Developing more effective treatments to improve survival for these patients is therefore a critical unmet need.

Cancers with DRDs, particularly those with defects in homologous recombination repair, are highly sensitive to the blockade of DNA single-strand break repair via inhibition of the PARP family of nuclear proteins, which

Research in context

Evidence before this study

At the time that the GALAHAD study was designed, docetaxel and the androgen signalling inhibitors abiraterone acetate and enzalutamide were the only established treatment options for patients with metastatic castration-resistant prostate cancer, but there remained a subset of patients who either did not initially respond or became refractory to these agents and for whom no approved therapeutic options were available. Given that genomic instability is a hallmark of cancer that has been documented in this patient population, we evaluated the medical literature by searching PubMed from database inception up to Aug 31, 2016, with (castration) AND (resistant) AND ("prostatic neoplasm" OR "prostate cancer") AND ("genomic instability" OR "DNA repair" OR "DNA repair defect") as search terms of interest with no additional restrictions (eq, to English language publications only). The search yielded 33 results. Only two of these were clinical trial publications, which presented results from an early phase 1 study of veliparib and the phase 2 TOPARP study of olaparib—both PARP inhibitors-in this disease setting. Veliparib was reported to have low efficacy, but the high response rate observed among patients with specified DNA repair gene defects (DRDs) in the TOPARP study provided a compelling rationale for assessing the clinical activity and safety of other such agents in a genetically selected patient population. Coauthors of the current study also contributed appropriate citations of importance that were not detected by the original search strategy or that were found in subsequent literature, with an emphasis on randomised clinical

are involved in single-strand DNA break repair.⁸ PARP inhibitors, such as olaparib, rucaparib, and talazoparib, have been studied in patients with metastatic castration-resistant prostate cancer and DRDs in previous phase 2 and 3 studies.⁹⁻¹³ Olaparib is approved in the EU for *BRCA1*-mutated or *BRCA2*-mutated metastatic castration-resistant prostate cancer¹⁴ and by the US Food and Drug Administration (FDA) for patients with metastatic castratic castration-resistant prostate cancer and DRDs progressing after treatment with enzalutamide, abiraterone, or both,¹⁵ whereas rucaparib is approved for patients with *BRCA1*-mutated or *BRCA2*-mutated metastatic castration-resistant prostate cancer who have been treated with an androgen signalling inhibitor therapy and a taxane.¹⁶

Niraparib, a potent and highly selective inhibitor of PARP-1 and PARP-2, is approved by the FDA for the maintenance treatment of select patient populations with ovarian, fallopian tube, and primary peritoneal cancers.^{17,18} Here, we report the final anti-tumour activity and safety results of a multicentre, open-label, phase 2 study of niraparib in patients with metastatic castration-resistant prostate cancer and tumour DRDs, whose disease had progressed on androgen signalling inhibitor therapy and taxane chemotherapy (docetaxel, cabazitaxel, or both).

trials, systematic reviews, meta-analyses, and prospective observational studies. Taken together, the findings indicated that PARP inhibitors show notable activity in cancers with DRDs. In articles published since the GALAHAD study was initiated, further clinical activity has since been reported in metastatic castration-resistant prostate cancers with selected DRDs for the PARP inhibitors olaparib, rucaparib, and talazoparib (for which key primary publications are cited in the present work), but not yet for niraparib, which is also a potent and highly selective PARP inhibitor with established efficacy and tolerability in other cancers.

Added value of this study

To our knowledge, the GALAHAD study is the first to show the anti-tumour activity of niraparib in patients with metastatic castration-resistant prostate cancer and DRDs who previously progressed on both androgen signalling inhibitors and taxanes, with notable activity particularly in the cohort of patients with defects in *BRCA1* or *BRCA2*.

Implications of all the available evidence

This final analysis of the GALAHAD study suggests that in patients with heavily pretreated metastatic castration-resistant disease, niraparib could offer promising clinical activity with a manageable safety profile. These findings motivate the further assessment of niraparib alone or in combination with other agents to improve treatment options and underscore the importance of biological disease profiling in informing treatment decisions.

Methods

Study design and participants

GALAHAD is an open-label, phase 2 study at 115 hospitals or health-care centres in 15 countries (appendix pp 8–9), which consisted of the following phases: prescreening, screening, treatment, follow-up, and long-term extension.

Male patients aged at least 18 years with histologically confirmed metastatic castration-resistant prostate cancer (mixed histology was acceptable, with the exception of the small cell pure phenotype, which was excluded) were eligible if they had a predefined DRD and disease progression on an androgen signalling inhibitor and taxane chemotherapy (docetaxel, cabazitaxel, or both). Disease progression was defined as progression of metastatic prostate cancer in the setting of castrate levels of testosterone of up to 50 ng/dL on a gonadotropinreleasing hormone analogue or with history of bilateral orchiectomy at study entry, with progression specifically defined as prostate-specific antigen (PSA) progression or radiographic progression of soft tissue by Response Evaluation Criteria in Solid Tumors (RECIST) version 1.1 or bone disease by Prostate Cancer Working Group 3 (PCWG3) criteria.^{19,20} Patients were also required to have an Eastern Cooperative Oncology Group (ECOG)

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See Online for appendix

performance status of 2 or less. Patients with measurable and non-measurable disease were enrolled. Exclusion criteria included previous treatment with a PARP inhibitor or platinum-based chemotherapy regimen, and a known history or current diagnosis of myelodysplastic syndrome or acute myeloid leukaemia. The full eligibility criteria are available in the protocol (appendix).

All patients provided written informed consent. Independent ethics committees or institutional review boards of each participating institution approved this study. The study was conducted according to Good Clinical Practice guidelines and the Declaration of Helsinki. The study protocol is available in the appendix.

Procedures

Patients were prescreened using a blood sample (Resolution Bioscience, Kirkland, WA, USA) or tumour tissue sample (Foundation Medicine, Cambridge, MA, USA²¹) for evaluation of DRD alterations. The Resolution Bioscience assay, Resolution HRD, is a targeted hybrid capture, nextgeneration sequencing assay that detects single-nucleotide variants, indels, and copy number variation (including homozygous deletions) in genes involved in homologous recombination repair using cell-free DNA from plasma. The specific genes of interest for DRD consisted of eight candidates: ATM, BRCA1, BRCA2, BRIP1, CHEK2, FANCA, HDAC2, and PALB2. In addition, three genes that are commonly mutated in metastatic castration-resistant prostate tumours were evaluated: AR, CDKN2A, and TP53. This Resolution Bioscience assay can also identify patients with monoallelic and biallelic pathogenic alterations in the genes of interest. Patients were eligible to enter the screening phase if a deleterious germline or somatic alteration was found in at least one of the following genes: ATM, BRCA1, BRCA2, BRIP1, CHEK2, FANCA, HDAC2, and PALB2. Patients were considered DRD-positive if they had an alteration with known pathogenic consequences including homozygous deletions; rearrangements; and nonsense, missense, frame-shift, and splice-site mutations. After the assay was developed to distinguish between biallelic and monoallelic DRD, patients who had been enrolled with monoallelic or non-pathogenic DRD were excluded from the final analysis according to an approved protocol amendment (amendment 3; October, 2017). As such, only patients with germline pathogenic or biallelic pathogenic alterations in BRCA1 or BRCA2 (BRCA cohort) or other prespecified non-BRCA genes (non-BRCA cohort) were included in the final analysis. Additional details on testing methods are available in the appendix (p 4).

All patients received niraparib 300 mg orally in the form of 100 mg capsules (Quotient Sciences, Boothwyn, PA, USA) starting on day 1 of cycle 1 (once daily dosing, with a cycle defined as 28 days) until treatment discontinuation due to disease progression, unacceptable toxicity or adverse events, diagnosis of myelodysplastic syndrome or acute myeloid leukaemia, investigator decision in the best interest of the patient, patient withdrawal of consent, death, or study termination. Monitoring for the need of dose adjustments or interruptions (eg, with laboratory measurements) was at the discretion of the investigator, based on the severity of the adverse events experienced. Patients who were not surgically castrated continued regularly prescribed gonadotropin-releasing hormone analogue.

During the treatment phase, study visits occurred weekly for the first month, biweekly for the second month, and monthly thereafter. CT or MRI and ⁹⁹"technetium bone scans were performed during screening, every 8 weeks for 24 weeks, and then every 12 weeks thereafter. Circulating tumour cell (CTC) counts were assessed at every cycle until cycle 7 and then at the end-of-treatment visit. PSA assessments were done every 4 weeks until cycle 7 and then every three cycles thereafter.

The follow-up phase began after completion of the treatment phase. If a patient discontinued treatment without radiographic progression, imaging was done every 12 weeks (or within 2 weeks before or after this timepoint) until radiographic progression was documented. The longterm extension phase began after completion of the primary analysis, at which point patients could elect to discontinue treatment or continue niraparib until disease progression. Throughout the study, adverse events were evaluated and graded using the National Cancer Institute Common Terminology Criteria for Adverse Events (version 4.03 or later). Safety evaluations included incidence, severity, and types of adverse events, as well as deaths. Adverse events were classified as treatmentemergent adverse events if they were reported on or after the date of first dose until 30 days (inclusive) after the last dose of study drug. Drug-related adverse events were determined by investigators if they were considered related to the study drug. Appropriate supportive measures to address adverse events could be administered at the discretion of investigators per institutional standards of care. A full schedule of study assessments and procedures is available in the protocol in the appendix.

Outcomes

The primary endpoint was investigator-assessed objective response rate (defined as the proportion of patients with a confirmed partial response or complete response as defined by RECIST version 1.1,¹⁹ according to the sum of target tumour lesion diameters, with no evidence of bone progression on bone scan per PCWG3 criteria²⁰) in patients with BRCA alterations and measurable disease (the measurable BRCA cohort). The primary endpoint was amended early on in this study (amendment 2; January, 2017) from a composite response endpoint to objective response rate to comply with feedback from health authorities, and hence the primary efficacy analysis included only these participants with measurable disease; additional details regarding this amendment are available in the study protocol in the appendix. Patients with non-measurable disease were still included in the study to increase the size of the safety population and to assess the activity of niraparib in this population.

Secondary efficacy endpoints were objective response rate in patients with non-BRCA alterations (ATM, BRIP1, CHEK2, FANCA, HDAC2, and PALB2) and measurable disease; CTC response (CTC0) defined as CTC=0 per 7.5 mL blood at 8 weeks post-baseline in patients with CTC count greater than $\overline{0}$ (1 or more) at baseline;^{22,23} overall survival (time from enrolment to death from any cause); radiographic progression-free survival (time from enrolment to radiographic progression or death from any cause, whichever occurred first); time from enrolment to radiographic progression; time to PSA progression (defined as time from enrolment to first date of documented PSA progression based on PCWG3 criteria); time to symptomatic skeletal event (defined as time from enrolment to tumour-related spinal cord compression, radiotherapy to bone to relieve skeletal symptoms, surgery to bone or need for tumour-related orthopaedic surgical intervention, or symptomatic or pathological fracture); duration of objective response (defined as time from complete response or partial response to radiographic progression of disease, unequivocal clinical progression, or death, whichever occurred first); and safety. With the exception of objective response rate in patients with non-BRCA alterations and measurable disease, all secondary endpoints were assessed in both the BRCA and non-BRCA populations.

Prespecified exploratory endpoints included the composite response rate, defined as either an objective response for patients with measurable disease, CTC conversion (defined as CTC count \geq 5 per 7 · 5 mL blood at baseline and <5 per 7 · 5 mL blood post-therapy nadir), or at least a 50% decline in PSA (PSA₅₀). Both CTC conversion and PSA₅₀ were also assessed separately as prespecified exploratory analyses.

Statistical analysis

Statistical analysis followed Simon's two-stage design for phase 2, single-arm clinical trials.²⁴ Specifically for the non-BRCA cohort, a futility analysis for objective response rate based on this design was implemented, in which Simon's stage 1 was assessed after approximately 14 patients with measurable disease were evaluated for objective response rate with at least one post-treatment scan and a confirmatory scan; enrolment was to be terminated for this cohort if two or fewer responses were observed in the first stage. Otherwise, enrolment was specified to proceed to the second stage with a total of 45 patients enrolled for the two stages combined, and the null hypothesis was to be rejected if ten or more responses were observed. For the primary endpoint, the null hypothesis of an objective response rate of 15% or less was tested against the alternate hypothesis of an objective response rate of 32% or higher. With approximately 120 patients with biomarker-positive measurable disease (75 BRCA and 45 non-BRCA) planned for enrolment, the study had more than 90% power to show that the lower limit of the 95% CI for the primary endpoint of objective response rate exceeded 15% in the measurable *BRCA* cohort. Activity of niraparib was to be declared if the lower bound of the two-sided 95% exact CI for objective response rate was higher than 15% in this cohort. For the secondary endpoint of objective response rate in patients with non-*BRCA* alterations, the null hypothesis of an objective response rate of 15% or less was tested against the alternate hypothesis of an objective response rate of 32% or higher, with a one-sided α of 0.05 and power of 80%.

Objective response in soft tissue disease was evaluated in both BRCA and non-BRCA patients with measurable disease within the efficacy analysis population of patients who fulfilled the final biomarker assay criteria for this study; however, as prespecified, the primary endpoint was specifically evaluated in the cohort of BRCA patients with measurable disease, and the final primary endpoint analysis was planned for approximately 6 months after the last patient with measurable disease in the BRCA cohort was enrolled. For analysis of objective response rate, patients who discontinued treatment before any efficacy assessments were considered non-responders; patients with no imaging available for a particular study visit were considered not evaluable for that visit, and patients without valid baseline data were considered not evaluable. Anti-tumour activity, such as PSA response, CTC conversion or response, and composite response rate, was analysed separately for the BRCA and non-BRCA cohorts, with corresponding criteria for identification of nonresponders and non-evaluable patients based on discontinuation or availability of laboratory measurements. Response rates were calculated along with exact two-sided 95% CIs. Time-to-event endpoints were summarised by Kaplan-Meier curves with median times and 95% CIs, as well as descriptive event-free rates analysed as prespecified. Analyses of additional study outcomes, such as the prespecified calculation of treatment compliance in the form of relative dose intensity, are described in further detail in the appendix (p 4).

Post-hoc analyses included objective response rate by baseline characteristics of interest (such as in subgroups of patients with visceral disease at baseline, patients who experienced stable disease for more than 6 months, or patients with three or more previous lines of therapy), specific evaluation of stable disease (defined as neither sufficient decrease in target lesions to qualify for partial response, nor sufficient increase to qualify for progressive disease, with respect to smallest sum of target lesion diameters while on study), and biomarker analyses for non-DRD alterations of interest (AR and TP53 alteration) were also done using the available data. For the post-hoc analysis of patients with AR and TP53 alterations, differences in objective response rates were assessed using Pearson's χ^2 test and p values were adjusted using false discovery rate correction for multiple testing (Benjamini-Hochberg procedure).



Figure 1: Trial profile DRD=DNA repair gene defect.

Safety and treatment compliance were analysed in the safety analysis population (ie, all patients who received at least one dose of the study drug). Adverse events and serious adverse events were reported and summarised. Sensitivity analyses with censoring rules were done if warranted. Additional details from the statistical analysis plan are available in the appendix. Statistical analyses were performed using SAS (version 15.1).

This study is registered with ClinicalTrials.gov, NCT02854436, and with the European Clinical Trials database, EudraCT 2016-002057-38).

Role of the funding source

The sponsor and employees of the sponsor of this study participated in the study design, data collection, data analysis, and data interpretation, with writing and editorial assistance also funded by the sponsor. All authors participated in the writing process and provided critical input.

Results

385 patients were screened for this study; of these, 289 (75%) patients were enrolled between Sept 28, 2016, and June 26, 2020. All 289 patients were included in the safety analysis population, and 223 (77%) of 289 patients were included in the efficacy analysis population, based on DRD eligibility from the validated biomarker assay (142 with BRCA alterations [139 biallelic, three monoallelic germline pathogenic] and 81 with biallelic non-BRCA alterations; figure 1). 66 (23%) of 289 patients with monoallelic or non-pathogenic DRD from the safety analysis were not included in the final efficacy analysis. Additional information on the prescreening results is available in the appendix (p 5). For patients with measurable disease, 76 with BRCA alterations (primary efficacy population) and 47 with non-BRCA alterations were enrolled, which fulfilled the numbers required per study sample size estimation for evaluation of objective response rate. The types and frequencies of genotypes observed in the efficacy analysis are reported in the appendix (p 10).

Based on the Simon's two-stage design, enrolment proceeded through both stages to fulfill the estimated sample size requirements. At the clinical cutoff date of Jan 26, 2021, 271 (94%) of 289 patients had discontinued treatment, with reasons summarised in the appendix (p 11). Seven (9%) of 76 patients in the primary efficacy cohort (patients with BRCA alterations and measurable disease) discontinued therapy before their first study evaluation due to progressive disease (n=4), urosepsis leading to death (n=1), or withdrawal of consent (n=1 due to fear of COVID-19; n=1 received radium-223 due to bone disease burden). The median treatment duration was 6.5 months (IQR 3.3-9.4) in the BRCA cohort and 3.6 months (1.8-5.6) in the non-BRCA cohort. Dose adjustments and interruptions are summarised in the appendix (p 12), with most treatment dose reductions occurring due to an adverse event.

Patients were heavily pretreated and showed advanced disease in both the *BRCA* and non-*BRCA* populations (table 1). Nearly all patients had bone metastases and, in the primary efficacy population (the measurable *BRCA* cohort), a notable proportion of patients had visceral disease, including liver and lung metastases, as well as many patients having nodal disease.

At baseline, 182 (63%) of 289 patients in the safety analysis population had received at least three previous systemic therapies for metastatic prostate cancer; 94 (33%) had received two previous androgen signalling inhibitor therapies, and 107 (37%) had received two previous taxanebased chemotherapies. The demographics and baseline characteristics of the safety analysis population are presented in the appendix (p 13). The final activity results for the overall *BRCA* cohort (with a median follow-up of $10 \cdot 1$ months [IQR $7 \cdot 5-13 \cdot 4$]) are shown in tables 2 and 3 and the appendix (pp 6, 7, 14).

The primary endpoint, objective response rate per protocol in the measurable *BRCA* cohort, was met in 26 of 76 patients ($34 \cdot 2\%$, 95% CI $23 \cdot 7$ – $46 \cdot 0$; table 2) with a median follow-up of $10 \cdot 0$ months (IQR $6 \cdot 6$ – $13 \cdot 3$). Of the 76 patients in the measurable *BRCA* cohort, 35 (46%) had at least a 30% decrease of maximum change from baseline in the sum of longest target lesion diameters relative to baseline (appendix p 6). Median duration of objective response was $5 \cdot 55$ months (95% CI $3 \cdot 91$ – $7 \cdot 20$; table 3); eight (31%) of 26 responses were ongoing at the time of data cutoff.

Figure 2 and table 3 present radiographic progression-free survival, with 87 (61%) events at the time of data cutoff, and overall survival, with 88 (62%) events in the overall *BRCA* cohort. 12-month event-free survival in the overall *24*-month event-free survival was $15 \cdot 2\%$ ($7 \cdot 7 - 25 \cdot 1$). Approximately a quarter of patients reached CTC0 (table 3). 85 (60%) of 142 patients in the *BRCA* cohort and 42 (55%) of 76 patients in the measurable *BRCA* cohort experienced PSA progression, and 46 (32%) of 142 patients and 23 (30%) of 76 patients had a documented symptomatic skeletal event in these cohorts, respectively.

The exploratory endpoint of composite response rate in the overall *BRCA* cohort is also presented in table 3. More than 40% of patients in the overall *BRCA* cohort had PSA₅₀ and CTC conversion (also exploratory), and approximately two thirds of evaluable patients experienced a decrease in PSA levels from baseline (table 3; appendix p 7). Similar outcomes in composite response rate were obtained in the *BRCA* cohort for patients with measurable and non-measurable disease (appendix p 14).

Of note, two patients (both with biallelic alterations) in the measurable BRCA cohort had a complete response. One patient with visceral (adrenal) and nodal disease at baseline maintained the complete response for $9{\cdot}7$ months, and a second patient with nodal disease at baseline experienced a complete response that persisted for 9.5 months based on imaging, despite having received only 2.1 months of treatment that was discontinued due to an adverse event of anaemia (grade 3). In a post-hoc analysis, of the 30 patients in the measurable BRCA cohort who had visceral disease at baseline, 11 (37%) had an objective response. Furthermore, a post-hoc analysis of the 20 patients who experienced stable disease for more than 6 months in this study showed that 14 (70%) were in the BRCA cohort. 16 (21%) of the 76 patients in the measurable BRCA cohort continued treatment after radiographic progression with no unequivocal clinical progression because they were considered to still be benefiting from therapy.

For the measurable non-*BRCA* cohort (n=47; median follow-up of 8.6 months [IQR 4.8-14.0]), objective response rate per protocol and median duration of

response (none of which are ongoing) are shown in table 2. An objective response was recorded in five of 47 patients (10.6%; 95% CI 3.5-23.1) in this cohort.

The corresponding maximum changes in the sum of target tumour lesion diameters from baseline in the

	BRCA cohort (n=142)	Measurable BRCA cohort (n=76)	Non-BRCA cohort (n=81)	Measurable non-BRCA cohort (n=47)
Age, years	67·0 (63·0–73·0)	66·0 (62·0–73·0)	70·0 (66·0–75·0)	71·0 (59·0–86·0)
Bodyweight, kg	82·7 (15·5)	80.5 (13.4)	79·9 (16·1)	77.6 (13.0)
Race				
White	101 (71%)	57 (75%)	54 (67%)	33 (70%)
Asian	9 (6%)	6 (8%)	6 (7%)	3 (6%)
Black or African American	5 (4%)	3 (4%)	0	0
Other	3 (2%)	0	2 (2%)	0
Multiple	1(1%)	0	2 (2%)	1 (2%)
Not reported	11 (8%)	5 (7%)	8 (10%)	4 (9%)
Unknown	12 (8%)	5 (7%)	9 (11%)	6 (13%)
PSA at baseline, ng/mL	141·5 (41·0–512·4)	197·0 (40·1–653·9)	161·7 (43·7–611·1)	196·0 (43·7–662·3)
Patients with alterations in a sin	ngle gene*			
BRCA1	4 (3%)	3 (4%)		
BRCA2	127 (89%)	69 (91%)		
ATM			37 (46%)	21 (45%)
BRIP1			1 (1%)	1 (2%)
CHEK2			5 (6%)	2 (4%)
FANCA			18 (22%)	10 (21%)
HDAC2			8 (10%)	5 (11%)
PALB2			0	0
ECOG performance status score	2			
0	48 (34%)	25 (33%)	18 (22%)	9 (19%)
1	78 (55%)	44 (58%)	47 (58%)	27 (57%)
2	16 (11%)	7 (9%)	16 (20%)	11 (23%)
Extent of disease progression at	t study entry			
Bone	127 (89%)	61 (80%)	79 (98%)	45 (96%)
Visceral	33 (23%)	30 (39%)	20 (25%)	16 (34%)
Liver	24 (17%)	23 (30%)	13 (16%)	12 (26%)
Lung	15 (11%)	13 (17%)	10 (12%)	7 (15%)
Lymph node	79 (56%)	67 (88%)	39 (48%)	33 (70%)
Soft tissue	22 (15%)	21 (28%)	16 (20%)	15 (32%)
Disease status				
Measurable	76 (54%)	76 (100%)	47 (58%)	47 (100%)
Non-measurable	66 (46%)	0	34 (42%)	0
Gleason score at diagnosis				
<8	39/135 (29%)	20/73 (27%)	26/77 (34%)	15/43 (35%)
≥8	96/135 (71%)	53/73 (73%)	51/77 (66%)	28/43 (65%)
Previous therapies for prostate	cancer†			
Two	59 (42%)	29 (38%)	22 (27%)	10 (21%)
Three	54 (38%)	31 (41%)	31 (38%)	18 (38%)
Four	21 (15%)	12 (16%)	19 (23%)	12 (26%)
Five	7 (5%)	3 (4%)	9 (11%)	7 (15%)
Six	1 (1%)	1 (1%)	0	0
			(Table 1 contin	iues on next page)

	BRCA cohort (n=142)	Measurable BRCA cohort (n=76)	Non-BRCA cohort (n=81)	Measurable non-BRCA cohort (n=47)
(Continued from previous page	:)			
Previous androgen signalling in	hibitor therapies			
One	97 (68%)	51 (67%)	45 (56%)	23 (49%)
Two	44 (31%)	25 (33%)	31 (38%)	21 (45%)
Three	1 (1%)	0	5 (6%)	3 (6%)
Previous taxane-based chemot	herapies			
One	100 (70%)	51 (67%)	41 (51%)	21 (45%)
Two	42 (30%)	25 (33%)	40 (49%)	26 (55%)

Data are reported as median (IQR), mean (SD), n (%), or n/N (%). The measurable BRCA cohort (n=76) is the primary efficacy population and the BRCA and non-BRCA cohorts combined (n=223) is the overall efficacy analysis population. PSA=prostate-specific antigen. ECOG=Eastern Cooperative Oncology Group. *All patients with PALB2 had co-occurring alterations and are thus not listed here; patient numbers and percentages might not add up to 100% because some patients had more than one gene alteration and are thus not listed here. †Number of androgen signalling inhibitors, taxane-based chemotherapies, cytotoxic chemotherapies, and other therapies received; specifically, previous therapies could include taxane-based chemotherapy for metastatic prostate cancer with evidence of disease progression, or next-generation androgen signalling inhibitor therapy for either metastatic prostate cancer with evidence of subsequent metastasis.

Table 1: Baseline characteristics of patients in the overall efficacy analysis population

	Measurable BRCA cohort* (n=76)	Measurable non-BRCA cohort† (n=47)				
Objective response rate	26 (34·2%; 23·7–46·0)	5 (10.6%; 3.5–23.1)				
Complete response	2 (3%)	0				
Partial response	24 (32%)	5 (11%)				
Data are n (%; 95% Cl) or n (%). *Primary efficacy analysis cohort. †Objective response rate in measurable non- <i>BRCA</i> patients was a secondary efficacy endpoint.						

overall non-*BRCA* cohort (n=81) are presented in the appendix (p 6).

Figure 2 and table 3 also present radiographic progression-free survival in the non-*BRCA* cohort, with 57 (70%) events at the time of data cutoff, and overall survival, with 65 (80%) events. 12-month event-free survival was $41 \cdot 3\%$ (95% CI $30 \cdot 0-52 \cdot 2$), and 24-month event-free survival was $11 \cdot 1\%$ ($4 \cdot 4-21 \cdot 2$). Fewer than 10% of patients reached CTC0 in this cohort; 39 (48%) of 81 patients had PSA progression, and 19 (23%) of 81 patients had a documented symptomatic skeletal event.

The exploratory endpoint of composite response rate in the non-*BRCA* cohort is also presented in table 3, and the maximum change in PSA from baseline is presented in the appendix (p 7). Response by either PSA₅₀ or CTC conversion (also exploratory) among non-*BRCA* patients with non-measurable disease is provided in the appendix (p 14).

In post-hoc analyses of the non-*BRCA* cohort, two (13%) of 16 patients with visceral disease and four (80%) of five patients who had received three or more lines of therapy experienced an objective response in the

non-*BRCA* cohort; six patients in this cohort experienced stable disease for more than 6 months. 15 (32%) of 47 patients continued treatment after radiographic progression with no unequivocal clinical progression.

Of note, 11 (8%) of 142 patients in the *BRCA* cohort and seven (9%) of 81 patients in the non-*BRCA* cohort had coexpression of two or more eligible DRD biomarkers. Moreover, in addition to being DRD-positive, 162 (74%) of 220 patients with available plasma DNA results had alterations in the *AR* gene and 49 (22%) of 220 had alterations in *TP53*, of whom 42 (19%) had both *TP53* and *AR* alterations. These additional alterations in plasma DNA were similarly distributed between the *BRCA* and non-*BRCA* cohorts, and no substantial difference in objective response rate was observed in subgroups of patients with or without co-occurring alterations (appendix pp 15–16).

Safety results are summarised in table 4 and the appendix (pp 17-25, 28-30). Almost all patients in the safety population experienced at least one treatmentemergent adverse event. The most common adverse events (of any grade) were nausea (169 [58%] of 289), anaemia (156 [54%]), and vomiting (111 [38%]). Of the grade 3 or worse treatment-emergent adverse events reported in 217 (75%) of 289 patients, most were haematological, with both the most common grade 3 or worse adverse events overall and grade 3 or worse adverse events of special interest being anaemia (95 [33%] of 289), thrombocytopenia (47 [16%]), and neutropenia (28 [10%]). These events were manageable with one or more of: treatment interruptions, dose reductions, or supportive measures such as blood transfusions. One patient experienced neutropenic sepsis. The most common non-haematological grade 3-4 treatment-emergent adverse events were fatigue and nausea. 134 (46%) of 289 patients had at least one serious treatment-emergent adverse event, with haematological events being the most common (17 [6%] of 289 with thrombocytopenia and 13 [4%] of 289 with anaemia; appendix pp 21-23). Similarly, of 43 (15%) of 289 patients with drug-related serious treatment-emergent adverse events, the most common were thrombocytopenia (four [3%] of 142 in the BRCA cohort and seven [9%] of 81 in the non-BRCA cohort) and anaemia (three [2%] of 142 in the BRCA cohort and three [4%] of 81 in the non-BRCA cohort; appendix p 24). The most common adverse events overall by BRCA and non-BRCA cohorts are also summarised in the appendix (p 20).

Estimated relative dose intensities are presented in the appendix (pp 26–27), including a breakdown of relative dose intensities in responders versus nonresponders in the primary efficacy analysis population (appendix p 26). In the safety population, 128 (44%) of 289 patients had an adverse event leading to a dose reduction; consistent with the aforementioned findings, 87 (68%) of 128 patients had haematological events

	BRCA cohort (n=142)	Measurable BRCA cohort (n=76)	Non-BRCA cohort (n=81)
CTC response*, n/N (%)	31/131 (24%)	18/71 (25%)	6/71 (8%)
Overall survival, months	13.01 (11.04–14.29)	10.87 (9.49–13.77)	9.63 (8.05–13.44)
Radiographic progression-free survival, months	8.08 (5.55-8.38)	5.52 (5.29-7.59)	3.71 (1.97-5.49)
Time to radiographic progression, months	8.08 (5.75-8.97)	5.55 (5.36-8.08)	3.78 (2.00-5.55)
Time to PSA progression, months	5·13 (4·60–5·59)	5.55 (4.60-8.31)	3.65 (2.83–3.71)
Time to symptomatic skeletal event, months	13·80 (10·41-NE)	13·80 (9·07-NE)	10·35 (8·18-NE)
Duration of objective response, months	6.28 (3.65-9.23)	5.55 (3.91-7.20)	5·16 (2·14-NE)
Composite response rate†, n/N (%; 95% CI)	82/142 (58%; 49·2-66·0)	46/76 (61%; 48·7–71·6)	12/81 (15%; 7·9–24·5)
CTC conversion‡, n/N (%; 95% CI)	55/117 (47%; 37·7–56·5)	28/64 (44%; 31·4–56·7)	9/60 (15%; 7·1–26·6)
PSA ₅₀ , n/N (%; 95% CI)	61/142 (43%; 34·7-51·5)	31/76 (41%; 29·7–52·7)	4/81 (5%; 1·4–12·2)

Data are median (95% CI) unless otherwise indicated. CTC=circulating tumour cell. PSA=prostate-specific antigen. NE=not estimable. PSA_{so}=at least 50% decline in prostate-specific antigen. *Defined per protocol and statistical analysis plan as CTC=0 per 7.5 mL blood at 8 weeks post-baseline in patients with baseline CTC count >0. †Defined as an objective response for patients with measurable disease, CTC conversion (defined as CTC count \geq 5 per 7.5 mL blood at baseline and <5 per 7.5 mL blood post-therapy nadir), or PSA_{so}. ‡Among patients with baseline CTC count \geq 5.

Table 3: Secondary and exploratory efficacy endpoints

(appendix p 28), which were manageable with one or more of the following: dose reductions, interruptions, or appropriate supportive measures (administered at the discretion of investigators per institutional standards of care). Among patients evaluated for antitumour activity, 70 (95%) of 74 patients with dose reductions in the BRCA cohort and 37 (93%) of 40 patients with dose reductions in the non-BRCA cohort had dose reductions due to adverse events versus other reasons; 103 (46%) of 223 patients received at least one transfusion (platelets or packed red blood cells), and the incidence of transfusions was similar between the BRCA and non-BRCA cohorts (data not shown). Other supportive measures included colonystimulating factors, which were administered to 12 (4%) of 289 patients, and erythropoietin, which was administered to 15 (5%) of 289 patients. 37 (13%) of 289 patients were deemed to have discontinued treatment due to drug-related toxicities (treatment-emergent adverse events deemed related to study drug). The most common drug-related toxicities leading to discontinuation were thrombocytopenia (in seven patients with BRCA alterations and three patients with non-BRCA alterations) and anaemia (in six patients with BRCA alterations and one patient with non-BRCA alteration; appendix p 25).

Adverse events leading to death are summarised in the appendix (p 29). Of the 16 deaths related to adverse events, two events (one patient with urosepsis in the *BRCA* cohort and one patient with sepsis in the non-*BRCA* cohort) were deemed possibly related to niraparib treatment. 208 (72%) of 289 patients died during the study; reasons for deaths are summarised in the appendix (p 30). The only sensitivity analysis warranted was for COVID-19, but there was only one patient with a COVID-19-related adverse event (non-serious) and one death due to COVID-19 in this study (appendix p 30).



Figure 2: Radiographic progression-free survival (A) and overall survival (B) in the BRCA and non-BRCA cohorts Symbols represent censored patients.

	Grade 1–2	Grade 3	Grade 4	Grade 5
Nausea	154 (53%)	15 (5%)	0	0
Vomiting	101 (35%)	10 (3%)	0	0
Constipation	95 (33%)	5 (2%)	1 (<1%)	0
Fatigue	87 (30%)	19 (7%)	0	0
Decreased appetite	85 (29%)	8 (3%)	0	0
Anaemia	61 (21%)	92 (32%)	2 (1%)	1(<1%)
Thrombocytopenia	52 (18%)	24 (8%)	23 (8%)	0
Back pain	51 (18%)	13 (4%)	0	0
Arthralgia	38 (13%)	6 (2%)	0	0
Asthenia	37 (13%)	11 (4%)	0	0
Neutropenia	27 (9%)	17 (6%)	11 (4%)	0
Bone pain	23 (8%)	9 (3%)	0	0
Hypertension	22 (8%)	12 (4%)	0	0
Blood alkaline phosphatase increased	15 (5%)	11 (4%)	0	0
Stomatitis	15 (5%)	6 (2%)	0	0
Leukopenia	14 (5%)	11 (4%)	3 (1%)	0
γ-glutamyl transferase increased	13 (4%)	11 (4%)	1 (<1%)	0
Lymphopenia	11 (4%)	12 (4%)	1 (<1%)	0
Hypophosphataemia	7 (2%)	6 (2%)	1 (<1%)	0
Spinal cord compression	1 (<1%)	7 (2%)	0	0
General physical health deterioration	1 (<1%)	7 (2%)	1 (<1%)	4(1%)

Data are shown as n (%). A total of 288 patients had one or more recorded treatment-emergent adverse events. Data are presented for grade 1–2 treatment-emergent adverse events with a combined incidence of \geq 20% or any higher-grade (grade 3–5) treatment-emergent adverse events with an incidence of \geq 2%.

Table 4: Treatment-emergent adverse events in the safety analysis set (n=289)

Discussion

The results of this multicentre, open-label, phase 2 study establish the anti-tumour activity of niraparib in patients with metastatic castration-resistant prostate cancer and DRDs who have progressed on both androgen signalling inhibitors and taxanes. Treatment with niraparib was manageable, and adverse events observed were consistent with the known safety profile of niraparib, with no new safety signals.

The activity of niraparib in the measurable BRCA cohort is notable given the heavily pretreated, end-stage patient population with few therapeutic options. These findings are especially remarkable considering the high percentage of patients with visceral metastasis, in particular to the liver, which is strongly associated with poor survival;25 the high percentage of patients with three or more lines of previous therapy; and that some patients in the BRCA cohort even achieved a complete response. Further evidence of benefit was shown by the proportion of patients experiencing stabilisation of disease for more than 6 months in both the BRCA and non-BRCA cohorts, which is a clinically meaningful finding given this heavily pretreated advanced disease state. Also notable was that patients in both cohorts, some with multiple poor prognostic features, continued to derive clinical benefit from niraparib after radiographic progression (in line with the importance of considering the totality of a patient's disease before discontinuing a

drug rather than strictly at the first evidence of progression in any site, as recommended by PCWG3²¹). Objective response rate, median radiographic progression-free survival and overall survival, and composite response rate were greater in the BRCA cohort than in the non-BRCA cohort, including a median radiographic progression-free survival time that was approximately double that in the non-BRCA cohort. Interestingly, our exploratory endpoint of composite response rate was largely similar between the subgroups of patients with measurable versus nonmeasurable disease in both cohorts (particularly in the BRCA cohort). Taken together, these results extend the evidence on the activity of PARP inhibitors in patients with metastatic castration-resistant prostate cancer and DRD-altered tumours whose disease has progressed on approved life-prolonging therapies, and also highlight the importance of biological profiling of an individual patient's disease in metastatic castration-resistant prostate cancer.^{8,21} Of note, to our knowledge, this trial is the first to prospectively test the CTC0 endpoint, which has been shown to strongly associate with survival.²²

The dose of niraparib used in this study (300 mg oral; once daily dosing) was chosen based on the previously evaluated pharmacokinetics, clinical activity, and safety profile of niraparib and is the approved dose for patients with ovarian cancer.^{17,26} As expected, grade 3 or worse treatment-emergent adverse events were largely haematological and manageable with supportive measures (such as blood transfusions and growth factor treatment), dose interruptions, and dose reductions. Rates of treatment interruptions and reductions were higher than the previously reported rates for other PARP inhibitors.9-13 This finding is consistent with the more advanced disease stage of patients in the GALAHAD trial, who had all progressed on androgen signalling inhibitor therapy and taxane chemotherapy and also tended to be on later lines of therapy, with the majority having received three or more lines of previous therapy. Moreover, the present study applied more stringent dose interruption criteria (for example, skipping a dose was also considered a dose interruption). Thus, the finding that at least half of the patients in both the BRCA and non-BRCA cohorts maintained the full dose (300 mg) of niraparib throughout the study supports the overall tolerability of this regimen. Relative dose intensity was also generally high, including in the primary efficacy cohort, and was higher for those who had an objective response in that cohort compared with those who did not.

The clinical activity of niraparib shown in this study's specific patient population (noting particular activity observed in the *BRCA* cohort) can be further contextualised by results of studies of other PARP inhibitors that point to a benefit for both minimally and heavily pretreated patients with metastatic castration-resistant prostate cancer and particular DRD alterations. Of note, in the phase 3 PROfound study that evaluated patients treated with the PARP inhibitor olaparib versus those treated with the

physician's choice of an androgen signalling inhibitor, olaparib treatment resulted in a median radiographic progression-free survival of 7.4 months versus 3.6 months (hazard ratio 0.34, 95% CI 0.25-0.47; p<0.001), median overall survival of 19.1 months versus 14.7 months (0.69, 0.50-0.97; p=0.02 at final analysis), and confirmed objective response rate of 33% (28 of 84) versus 2% (one of 43; odds ratio 20.86, 95% CI 4.18-379.18; p<0.001) compared with the control treatment in a cohort of patients with alterations in BRCA1, BRCA2, or ATM.^{10,11} Rucaparib, which was investigated in the phase 2 TRITON-2 study, led to an objective response rate of 47.5% and a median time to PSA progression of 6.5 months, with a better response seen in patients with BRCA alterations compared with those with alterations in other genes such ATM or CDK12.12,13 In the phase 2 TALAPRO-1 study, patients with certain gene alterations reported to sensitise to PARP inhibitors were enrolled and treated with talazoparib. The objective response rate was 29.8% (31 of 104; 95% CI 21.2-39.6) with talazoparib treatment after a median follow-up of 16.4 months.9

The limitations of the present study include that some patients developed progressive disease before completing their first disease evaluation, consistent with the advanced stage and aggressiveness of the disease in the enrolled population. Additionally, tissue-based assays rely on sufficient high-quality biopsy samples, which might be difficult to obtain, and further challenges ensue when archival samples are found to be unsuitable or unavailable for analysis. In this study, a commercially available tissuebased assay was initially used to select patients, but due to the aforementioned challenges, a blood-based assay was subsequently implemented, with early prescreening rates and biomarker logic finalisation then addressed during a brief study pause. As such, a notable number of patients in GALAHAD were prescreened using blood-based assay. Such assays could offer valuable data, especially for metastatic prostate cancer for which tumour biopsies are challenging to acquire and biopsies are largely limited to bone that has considerable issues with the quality of materials. However, liquid biopsies also have limitations. Given the lack of parallel next-generation sequencing of corresponding white blood cells in this study, clonal haematopoietic alterations of indeterminate potential could have presented as a biological confounding factor.²⁷ Additionally, blood-based assays might show false negative results in blood samples with low plasma circulating tumour DNA content, especially for mutations that are difficult to detect such as homozygous deletions. Conversely, circulating tumour DNA assays could select for patients with higher percentages of circulating tumour DNA, which was previously found to be a predictive factor for a poorer prognosis.28 Nevertheless, the number of patients enrolled for efficacy evaluation in GALAHAD (n=223 with specifically germline pathogenic or biallelic DRD alterations, of a total of 4218 with any biomarker sample submitted) represents an incidence of DRD alterations that is within expectations. Finally, 22% of the GALAHAD study population had *TP53* alterations, which are also associated with overall poor prognosis.

Additional studies, including those designed to evaluate niraparib-based regimens in appropriate biomarkeridentified populations at earlier stages of disease, are underway to expand on the present findings. The phase 3 MAGNITUDE study is evaluating niraparib in combination with abiraterone acetate plus prednisone as firstline therapy in patients with metastatic castration-resistant disease with or without DRD.²⁹ The phase 3 AMPLITUDE study will also evaluate niraparib in combination with abiraterone acetate plus prednisone in a biomarkerselected population with metastatic castration-sensitive disease.³⁰

In conclusion, these results suggest that niraparib has promising clinical activity with a manageable safety profile when administered as a monotherapy for treatmentrefractory metastatic castration-resistant prostate cancer with *BRCA* alterations or select non-*BRCA* alterations. Such findings underscore the need for and importance of molecular testing to inform management along with continued research to establish treatment paradigms with appropriately targeted therapies for patients with prostate cancer. Efforts to investigate and better understand predictive markers and signatures of both response and resistance to treatment with PARP inhibitors such as niraparib are needed to guide therapy selection and optimise treatment outcomes.

Contributors

All authors in their role as GALAHAD study investigators or Janssen Research & Development investigators contributed to study design, study conduct, data analysis, and data interpretation. All authors participated in drafting and revising the manuscript and approved the final version before submission. MRS, GEM, and XZ verified all data. All authors had full access to all data for the study and had final responsibility for the decision to submit for publication.

Declaration of interests

MRS has received grants or contracts to their institution from Bayer, Janssen, Pfizer, AstraZeneca, and Lilly; has received consulting fees from Astellas Pharma, Novartis, Janssen, AstraZeneca, Bayer, Lilly, and Pfizer; and has participated on data safety monitoring boards, advisory boards, or both for Janssen, Pfizer, and AstraZeneca. HIS has a leadership role in Asterias Biotherapeutics; holds stock and other ownership interests in Asterias Biotherapeutics; received grants or contracts to their institution from Epic Sciences, Illumina, Menarini Silicon Biosystems, ThermoFisher, and AIQ Pharma; provided consulting to Ambry Genetics Corporation/Konica Minolta, Amgen (uncompensated), Bayer, ESSA Pharma (uncompensated), Menarini Silicon Biosystems (uncompensated), Pfizer, Sun Pharmaceuticals, and WCG Oncology; has received payment or honoraria for lectures, presentations, speakers bureaus, manuscript writing, or educational events from Sidney Kimmel Cancer Center-Jefferson Health: has received support for attending meetings or travel from Amgen, Bayer, ESSA Pharma, Menarini Silicon Biosystems, Epic Sciences, Pfizer, WCG Oncology, and Phosplatin; has patents planned, issued, or pending via their institution with BioNTech, Elucida Oncology, MabVax Therapeutics, and Y-mAbs Therapeutics; and has other financial or non-financial interests in Elsevier, Prostate Cancer Foundation (via institution), National Cancer Institute (via institution), Department of Defense (via institution), MabVax Therapeutics, and BioNTech. SS has received grants from Amgen, Advanced Accelerator Applications (a Novartis company), Merck Sharp & Dohme,

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presentations, speakers bureaus, manuscript writing, or educational events from Astellas, AstraZeneca, Bayer, Janssen, Novartis, Merck Sharp & Dohme, Bristol Myers Squibb, and Orion; and has participated on data safety monitoring boards, advisory boards, or both for Astellas, AstraZeneca, Bayer, Novartis, Janssen, Amgen, Pfizer, Sanofi, Orion, and Curevac. OS declares no competing interests.

Data sharing

The full study protocol is available in the appendix. The data sharing policy of Janssen Pharmaceutical Companies of Johnson & Johnson is available at https://www.janssen.com/clinical-trials/transparency. As noted on this site, requests for access to the study data can be submitted through the Yale Open Data Access Project site at http://yoda. yale.edu. De-identified patient-level data will be made available to qualified researchers upon request, after signing of a data transfer agreement with Janssen Research & Development. Requests for data sharing, including a research proposal, can also be made to the corresponding author.

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Article Whole-Body [¹⁸F]-Fluoride PET SUV Imaging to Monitor Response to Dasatinib Therapy in Castration-Resistant Prostate Cancer Bone Metastases: Secondary Results from ACRIN 6687

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Copyright: © 2021 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (https:// creativecommons.org/licenses/by/ 4.0/). **Abstract:** ACRIN 6687, a multi-center clinical trial evaluating differential response of bone metastases to dasatinib in men with metastatic castration-resistant prostate cancer (mCRPC), used [¹⁸F]-fluoride (NaF) PET imaging. We extend previous ACRIN 6687 dynamic imaging results by examining NaF whole-body (WB) static SUV PET scans acquired after dynamic scanning. Eighteen patients underwent WB NaF imaging prior to and 12 weeks into dasatinib treatment. Regional VOI analysis of the most NaF avid bone metastases and an automated whole-body method using Quantitative Total Bone Imaging software (QTBI; AIQ Solutions, Inc., Madison, WI, USA) were used. We assessed differences in tumor and normal bone, between pre- and on-treatment dasatinib, and evaluated parameters in association with PFS and OS. Significant decrease in average SUV_{max} and average SUV_{peak} occurred in response to dasatinib. Univariate and multivariate analysis showed NaF uptake had significant association with PFS. Pharmacodynamic changes with dasatinib in tumor bone can be identified by WB NaF PET in men with mCRPC. WB PET has the benefit of examining the entire body and is less complicated than single FOV dynamic imaging.

Keywords: ACRIN 6687; metastatic castration-resistant prostate cancer (mCRPC); bone metastases; [¹⁸F]-Fluoride; PET; dasatinib; progression-free survival (PFS); Quantitative Total Bone Imaging (QTBI)

1. Introduction

Approximately 70% of men with advanced prostate cancer harbor osteoblastic bone metastases [1]. Imaging of bone metastases typically relies on bone scintigraphy and anatomic modalities such as CT and MRI. However, these methods measure qualitative changes in bone turnover (bone scan) or bone structure (MRI, CT) but not direct metastatic tumor cell activity. Clinically meaningful prostate cancer treatment response has been difficult to define quantitatively, as there is no uniformly accepted surrogate marker that correlates with long-term outcomes to optimally guide patient management and new drug development.

The use of positron emission tomography (PET) to monitor response to therapy in prostate cancer is inherently quantitative. PET can measure in vivo tumor and normal tissue biology using tracers to map many metabolic pathways, including bone osteoblastic metabolism using [¹⁸F]-fluoride (NaF) PET [2,3]. NaF PET offers a quantitative measure of osteoblastic bone formation and remodeling, and is appropriate for imaging the blastic lesions observed in prostate cancer [4]. Additionally, when compared to standard ^{99M}Tc-

based bone scintigraphy, NaF PET offers improved sensitivity of detection and when combined with CT, specificity is also improved [5–7].

ACRIN 6687 was a prospective, multi-center phase 2 trial that used NaF PET to probe the response of dasatinib (SPRYCEL[®]; Bristol-Myers Squibb) treatment, a SRC kinase inhibitor that decreases bone turnover, in men with metastatic castration-resistant prostate cancer (mCRPC) [8]. The trial was designed to evaluate differential response of normal and tumor bone to dasatinib treatment using NaF PET using a protocol that began with dynamic single field-of-view (FOV) imaging and then was followed by static whole-body (WB) scans with multiple FOVs. Previous kinetic modelling results from single FOV dynamic imaging found significant differences in changes of the PET kinetic parameters from tumor bone compared to normal bone in response to dasatinib treatment. Changes in the 30–60 min summed SUV metrics from the dynamic acquisition had a modest association (p = 0.056, n = 12 patients) with progression-free survival (PFS), where progression was determined by the Prostate Cancer Working Group 2 (PCWG2) [9] criteria.

Although the initial results for the ACRIN 6687 trial were intriguing, we recognize the potential limitations of dynamic single FOV analyses for general use and widespread adoption. Specifically, although dynamic studies may offer breadth of analysis, the level of complexity and lack of standardization are not practical for broad utilization. In the initial set of analyses using the 30-60 min SUV images, changes in the average SUV_{max} for up to 5 tumors (SUV_{maxavg}) in a patient not only had significant differential changes to dasatinib therapy in tumor vs. normal bone, but those changes had marginal association with progression free survival (PFS); these were features not displayed by dynamic Ki (metabolic flux) or K_1 (tracer transport) kinetic parameters. This lends further credence to the concept of simplifying the NaF PET image analysis with SUV only. Additionally, the previously reported limited FOV may have omitted important information from metastatic lesions outside of the single FOV. As part of a post-hoc analysis not proposed in the original ACRIN 6687 clinical trial, we sought to determine if important information obtained from outside of the dynamic FOV could offer additional clinical and prognostic information, comparable and/or incremental to earlier published dynamic data. Previous reports using WB fluoride analysis also showed a relationship of SUV measures to PFS for patients that received either a docetaxel-based chemotherapy regimen or an androgen receptor pathway inhibitor [10]. Here we examine SUV analysis results from multi-FOV WB static NaF PET imaging scans, acquired after a one-hour dynamic scan, in mCRPC patients recruited to ACRIN 6687 at baseline and after receiving 12 weeks of dasatinib treatment. Statistical analysis of the clinical and PET imaging data was undertaken in order to identify potentially interesting associations between various biomarkers (PET and blood borne) and patient outcomes. As is the nature of secondary investigations, the reported data analysis and relationships cannot be interpreted in the same way that the analysis for the primary hypothesis of the underlying clinical trial that has been reported [8].

2. Materials and Methods

2.1. Study Design

Study design and treatments (Supplementary Materials, Figure S1), patient eligibility, imaging protocol, regulatory approval, radiochemistry and study endpoints have been previously described [8]. Briefly, American College of Radiology Imaging Network (ACRIN) 6687 was a phase 2 trial conducted by ACRIN at 4 Prostate Cancer Clinical Trials Consortium (PCCTC) centers: University of Washington, Duke University, Oregon Health Sciences University and the Dana-Farber Cancer Institute (NCT00936975). ACRIN 6687 protocol was approved at each site's institutional review board and other local regulatory agencies. Informed consent was obtained from all individual participants included in the study prior to trial enrollment. Patients enrolled on the study had to have metastatic castration-resistant prostate cancer with at least one convincing bone metastasis defined by bone scintigraphy, CT scan or plain X-ray. All patients eligible for ACRIN 6687 were first enrolled in a clinical trial (NCT00918385) where patients were selected either for nilutamide or dasatinib based

on a 300-gene signature found on a metastatic biopsy. Only patients receiving dasatinib were imaged on ACRIN 6687. The PET imaging protocol included a single field-of-view (FOV) low-dose CT scan for attenuation correction, a one-hour dynamic PET emission scan consisting of 45 time frames over 60 min immediately following the NaF injection, a multiple FOV (range 5–7 FOV) WB PET emission scan from base of skull to mid-thigh and a multiple FOV WB low-dose CT scan. Eligible patients with bone mCRPC underwent the WB NaF PET scan, that occurred starting at approximately 75 min (range 53 to 95 min) after NaF injection, with an on-average mid scan time of 90 min (range 64–110 min) prior to and 12 weeks after the onset of treatment with dasatinib therapy to determine if the nature of the drug effect could be ascertained through PET/CT imaging. The WB scans were approximately 25-40 min in duration, making the uptake time range from the start to the end of the scan 53–130 min after injection with a mean mid scan time of 90 min. Individual patient WB PET scan acquisition parameters and reconstructed image resolution values appear in Supplementary Materials Table S1 and the WB time profile in Figure S2. Additional scanning before and while on dasatinib treatment included a clinical CT scan and a ^{99m}Tc-methylene diphosphonate (^{99m}Tc-MDP) bone scan.

2.2. Clinical Assessments

Patients were clinically followed after initiation of dasatinib with clinical visits every 4 weeks and repeated bone and CT scan imaging every 12 weeks until radiographic or clinical progression, significant toxicity necessitating cessation of dasatinib or until patient withdrawal from the trial. Baseline pathologic Gleason grade scores from archival prostate tissue was obtained from local participating sites. Biomarkers from blood and urine samples obtained at baseline and throughout therapy included bone alkaline phosphatase (BAP), an indicator of bone metabolism, urine N-telopeptide (uNTX), an indicator of bone resorption and prostate specific antigen (PSA), an indicator of progressive disease.

2.3. PET Image Analysis

Unlike the previous single dynamic FOV investigation surrounding the pelvis and lower spinal column, WB image analysis used both a traditional lesion-level volume-of-interest (VOI) method and a whole-body patient-level assessment. The lesion-level VOI method collected up to 5 of the most NaF avid bone metastases using the highest NaF SUV_{max} uptake value, the maximal voxel within a 1cc VOI, on the baseline scan. The average activity from a 1cc spherical VOI placed over the hottest region of the tumor as described in the PERCIST protocol [11] was the SUV_{peak}. These VOIs were placed in the same anatomical location on the mid-therapy scan. Based on previous reports, only tumors with a SUV_{peak} threshold of 15 g/mL were included in the analysis [10,12]. Although Kurdziel et al. used a segmentation SUV threshold of 10 g/mL [13], a later study by Rohren et al. showed that lesion ROIs identified using this threshold still included normal bone activity [14]. Lesions smaller than 1.5 cc as measured by PET volume were also excluded.

Each selected tumor region from the NaF PET and corresponding CT images was reviewed by an experienced PET image nuclear medicine radiologist and a prostate cancer oncologist and confirmed as malignant. Bone lesion VOIs, along with matched areas of normal bone, were used for intensity analysis by SUV_{max} and SUV_{peak} . Tumor assessments were performed using the average of up to 5 tumors from each patient, using the notation from the original ACRIN 6687 report of SUV_{maxavg} and $SUV_{peakavg}$ and the index lesion SUV_{max} for each patient. The index lesion was the single lesion with the most NaF avidity. These SUV metrics have been shown to be useful in prior studies of NaF PET imaging of mCRPC patients for evaluation of treatment response [8,10,15,16]. Tumor-matched normal bone regions identified by both CT and NaF PET of identical volume to tumor regions were also constructed.

2.4. Quantitative Total Bone Imaging (QTBI) Analysis

Whole-body patient-level image analysis utilized the bone metastases software application from the University of Wisconsin and AIQ Solutions (Madison, WI, USA) [12,17]. Briefly, CT images were segmented into skeletal regions using an atlas-based segmentation approach [18], then region-specific optimized thresholds were used to detect lesions [19] on the PET image. Following lesion detection, a random forest model and manual review were applied to exclude lesions that were likely to be benign [20]. Patient-level PET parameters used for tumor assessment included qSUV_{max}, qSUV_{peak}, qSUV_{total} (total tumor burden) and qVF (volume fraction), where the q indicates that the parameters are derived from QTBI analysis. The peak SUV was determined by placing 1cc spheres on each of the 5 lesions with the highest SUV_{max} and averaging the extracted values.

2.5. Statistics

Pre- and on-treatment differences of lesion-level and patient-level PET parameters were assessed using standard paired t-tests. Repeatability studies showed that SUV_{max} from lesion level analysis coefficient of variation was 14.1%, while at the patient level, it was slightly smaller: 12.0% [12]. Variation of other PET SUV metrics from repeatability analysis were similar in magnitude. While the data have limited power to properly verify normality of the underlying data, the Shapiro-test of normality showed little evidence of departure from such an assumption. *p*-values obtained by the t-test were found to be in close agreement with those obtained using a non-parametric Wilcox rank test approach. Pairwise comparisons were summarized in terms of rank correlations. Rank correlation was used because it has the ability to evaluate monotone relations, not just linear ones. Note that overall, 96 separate *p*-values were generated in this analysis. It is important to appreciate that the *p*-values reported are without adjustment for multiple comparisons. Our justification for this is that results presented are not offered as definitive resolutions to the 96 hypotheses being considered, instead they are presented as a way to guide the selection of a much more limited set of hypotheses that might merit further investigation in a prospective clinical trial. See the discussion for further comment.

Pre-treatment PET values and the change from pre- to on-treatment PET values were evaluated in association with PFS and overall survival (OS), both of which are continuous variables measured in days from the onset of dasatinib treatment. PFS is determined as the number of days from dasatinib treatment to the first progression event as evaluated by PCWG2 criteria. The relationship between PET parameters and outcome measures of PFS was evaluated by univariate and multivariate regression analysis. The overall survival (OS) data are incomplete (censored) and so a Cox proportional hazards model was used for both univariate and multivariate analysis.

For multivariate regressions, we report *p*-values associated with the PET parameter combined with the base model. This approach assesses the additional prognostic contribution of the PET parameter, after adjustment for a base model of established clinical variables; age and baseline ln(BAP). The *p*-values reported for the SUV variables in multivariate analysis assess the added impact of the SUV variables in a context where there is adjustment (by the multivariate method) for the ln(BAP) and age covariates. These are not *p*-values for the overall model. The multivariate analysis gives a more precise appreciation of the 'added-benefit' of the PET information. In the case of OS, the effects of the PET variables are reported in terms of the excess risk, or hazard ratio (HR), associated with a 1-SD change in the PET variable.

As a result that the PFS data were complete (no censoring), the relation between prognostic factors, such as age, BAP or PET variables, and PFS was analyzed by multiple linear regression. Cox modeling analysis was also considered, but given the more precise nature of regression analysis, the multiple regression analysis was used in this report. Given the limited sample size and the consequent concerns regarding the adequacy of standard asymptotic Gaussian approximations for inferences, Efron's Bootstrap [21] with 500 replicates was used in multivariate outcome analysis.

Effects were assessed using a two-sided z-test based on the bootstrap estimated mean and standard error (SE) values. Additionally, changes in PET uptake parameters in response to dasatinib treatment, were compared with changes in markers of bone turnover, urinary N-telopeptide (uNTX), bone alkaline phosphatase (BAP) and PSA using Kendall's tau-b correlation. All statistical tests were performed in R, and acronyms are defined in Table 1.

Table 1. Definition of acronyms.

Acronym	Definition
Δ	The difference of a parameter between scan 2 and scan 1
^{99m} Tc-MDP	^{99m} Tc-methylene diphosphonate
ACRIN	American College of Radiology Imaging Network
AR	Androgen receptor
BAP	Bone alkaline phosphatase
СТ	Computed tomography
Diff	The difference of a parameter between scan 2 and scan 1
FOV	Field of view, usually axial
HR	Hazard ratio
index SUV _{max}	The hottest baseline lesion (index lesion) SUV _{max} value
index SUV _{peak}	The hottest baseline lesion (index lesion) SUV _{peak} value
K1	A model parameter estimating transport of the tracer from blood to tissue
Ki	Metabolic flux determined from the model parameters $(K_1 \times k_3)/(k_2 + k_3)$
mCRPC	Metastatic castration resistant prostate cancer
MIP	Maximal image projection flattening a 3D image series to 2D
MRI	Magnetic resonance imaging
NaF	¹⁸ F-sodium fluoride
OS	Overall survival
PCWG2	Prostate cancer working group 2
PET	Positron emission tomography
PFS	Progression free survival
Pval	The <i>p</i> -value of a comparison between two arrays of data
qSUV _{max}	QTBI analysis of SUV _{max} , the maximum uptake in the tumor volume (g/mL)
qSUV _{peak}	QTBI analysis of SUV _{peak} (g/mL)
qSUV _{total}	QTBI analysis of total tumor burden, the sum of voxel SUVs in the tumor volume.
QTBI	Quantitative total bone imaging analysis software, AIQ Solutions, Madison, WI
qVF	QTBI analysis of the tumor volume fraction compared to the total bone volume
ROI	Region of interest
SE	Standard Error
SUV	Standard uptake value
SUV _{max}	The maximum SUV voxel within a tumor (g/mL)
SUV _{maxavg}	The average of up to 5 tumor SUV _{max} values (g/mL)
SUV _{peak}	The average activity of a 1cc spherical VOI over maximal tumor activity (g/mL)
SUV _{peakavg}	The average of up to 5 tumor SUV _{peak} values (g/mL)
uNTX	Urinary N-telopeptide
VOI	Volume of interest
WB	Whole-body PET scan

3. Results

3.1. Patients

Of the 18 patients enrolled in the trial (median age 69 years range 48–86), one withdrew from the study with no follow-up on PFS or OS after the first PET scan, and was excluded from this analysis leaving 17 evaluable patients for WB PET baseline imaging. Three patients, with worse baseline prognostic features, did not undergo an on-treatment PET imaging study due to clinical progression while on dasatinib; this resulted in early discontinuation from the trial prior to the second imaging time point. In our initial ACRIN 6687 publication on dynamic imaging results, two studies were omitted due to technical issues with the dynamic scan, but their WB scan was useable for this analysis and therefore were included. Seventeen patients had either met progression criteria or death by the time of this investigation. Thus, 14 patients had evaluable pre- and on-treatment dasatinib WB NaF PET imaging. The baseline patient and PET imaging characteristics appear in Supplemental Materials Table S1.

3.2. PET Findings

In the original single FOV report for ACRIN 6687 [8], up to 5 bone lesions were selected by the local site physician, which occurred in the pelvis or along the lower spinal column. The WB tumor selection criteria at the lesion level presented in this report was determined by averaging up to 5 of the highest NaF SUV_{max} uptake bone lesions using a lower threshold of 15 g/mL. However, only 19 WB regions of the 70 dynamic regions (27%) overlapped between the dynamic and static PET series (Figure 1). Thus, many of the hottest lesions from the WB SUV images acquired at an average mid-acquisition time of 90 min after injection were not present in the single FOV SUV image acquired precisely at 45 min (30–60 min summed SUV) from the dynamic series. A summary of the lesion-level PET parameter values before and while on-dasatinib treatment appear in Table 2. Individual patient NaF PET SUV uptake values appear in Supplementary Materials Table S2. The average uptake values for all tumors from a patient study were represented as SUV_{peakavg} and SUV_{maxavg}, while the values for the hottest single index lesion from each patient were represented as index SUV_{max} and index SUV_{peak}. Fifteen of the 17 evaluable patients had 5 tumor sites above the threshold, while 1 patient had 2 tumor sites and 1 patient had 1 tumor site above the SUV_{peak} threshold of 15 g/mL. Significant average decreases were observed in SUV_{maxavg} ($-20\% \pm 12\% 95\%$ CI, p = 0.001), SUV_{peakavg} ($-17\% \pm 14\% 95\%$ CI, p = 0.013), index SUV_{max} (-16% ± 14% 95%CI, p = 0.025) and index SUV_{peak} (-16% ± 15% 95%CI, p = 0.049) in bone metastases in response to dasatinib, while no significant change was observed in normal bone (Figure 2). Significance was based on repeatability results of NaF in mCRPC patients [12]. Significant differences in changes from tumor bone compared to normal bone in response to dasatinib were noted for SUV_{maxavg} (p = 0.004) and SUV_{peakavg} (p = 0.028).

Table 2.	[¹⁸ F]-Fluoride	uptake	parameters	in	bone	tumors
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Parameters	Baseline NaF PET (SD)	On-Dasatinib NaF PET (SD)	Change On-Dasatinib (SD)	% Change (<i>p-</i> Value)
⁺ Lesion-level				
SUV_{maxavg} (g/mL)	47.1	38.3	-9.5	-20.1%
0.0	(16.7)	(17.0)	(9.6)	(0.001)
SUV _{peakavg} (g/mL)	34.5	28.8	-5.8	-16.2%
1 0 -	(13.3)	(13.0)	(8.3)	(0.013)
Index SUV _{max} (g/mL)	60.0	52.8	-9.8	-14.3%
5	(27.3)	(24.9)	(14.7)	(0.025)
Index SUV _{peak} (g/mL)	45.8	40.3	-7.1	-12.9%
1	(21.6)	(18.8)	(11.3)	(0.049)
[‡] Patient-Level				
$qSUV_{max}$ (g/mL)	61.2	64.5	-2.7	0.3%
1	(27.4)	(26.1)	(13.9)	(0.569)
qSUV _{peak} (g/mL)	37.6	37.8	-0.6	2.2%
I from 0	(15.7)	(12.5)	(7.0)	(0.470)
$qSUV_{total}$ (g/mL × cc)	8234	7307	576	30.0%
	(8914)	(6950)	(1553)	(0.176)
qVF	9.9	8.8	0.3	25.8%
•	(10.2)	(8.3)	(0.5)	(0.120)

[†] Lesion-level average results and average change for 17 patient values at baseline and 14 patients that were scanned while on-dasatinib with standard deviation below in parentheses. Lesion-level Index is the single hottest lesion for the patient. [‡] Patent-level parameters from QTBI analysis, indicated by a q preceding the parameter, was performed on 16 patients at baseline and 12 while on-dasatinib. Patient-level qVF is the volume fraction of the tumor from QTBI analysis. Boldface type indicates a significant ($p \le 0.05$) decrease in the PET value from baseline.



Figure 1. Example of an 82-year-old patient scan 1 (**top** row) and scan 2 (**bottom** row). Panels left to right, NaF overlaid on CT, NaF alone and with NaF PET maximal image projection (MIP) of the entire WB volume. The red box is the single FOV for the dynamic scan. Three of the 5 hottest tumors were not located in the single dynamic FOV, the results of which were reported previously [8]. An example WB patient with none of the hottest tumors in the dynamic FOV appears in Supplementary Materials Figure S3.

Results of patient-level QTBI analysis used only 15 patient scans at baseline and 12 s time point on-treatment scans due to technical issues related to image scaling and image quality for 2 patients between the dual time point scans. No significant change between pre-dasatinib and on-treatment NaF uptake for $qSUV_{max}$, $qSUV_{peak}$, $qSUV_{total}$ and VF was observed for the 12 patients (Table 1). Individual patient-level QTBI uptake values appear



in Supplementary Materials Table S3 with a patient example analysis in Supplementary Materials Figure S4.

Figure 2. Change in regional ¹⁸F uptake in response to dasatinib treatment in mCRPC bone metastases measured by SUVpeak, SUVmax. No significant changes were seen in normal bone. Diff = Scan2—Scan1; Pval = p-value. * Difference = Δ in tumor bone— Δ in normal bone.

3.3. Statistical Analyses

In the case of progression, the data are complete (no censoring) so standard multiple linear regression analysis was used. However, for OS, 3 patients were censored of the 17 evaluable patients and a Cox proportional hazard model was applied to account for censoring.

In univariate analysis of PET variables as predictors of PFS (Table 3), only elevated baseline qSUV_{total} and baseline qVF were significantly associated with PFS (p = 0.023 and p = 0.011, respectively), where higher values lead to earlier progression. There was no clear association of the change in any other lesion-level or patient-level PET parameter with PFS or OS for univariate analysis unlike the univariate analysis results of the original ACRIN 6687 report that showed a borderline correlation of change in SUV_{maxavg} to PFS (p = 0.056). Bootstrap results are not reported for univariate analyses, but they are provided in Supplementary Materials Table S4.

In multivariate analyses (Table 4), the regression model included age, the logarithm of baseline bone alkaline phosphatase (ln(BAP)) and the PET parameter as covariates. Age and ln(BAP) were found to be strong predictors of disease progression in univariate analysis [8]. Baseline lesion-level SUV_{maxavg} and SUV_{peakavg} values from the 17 patients showed an association with PCWG2 PFS (p = 0.043 and p = 0.018, respectively) using multivariate analysis. The multivariate analysis used for QTBI parameters had the same

base model of age and ln(BAP) described above, and showed that baseline qSUV_{peak} also had a significant relationship with PFS (p = 0.025). The multivariate analysis showed no relationships to OS for any PET parameter at baseline or change in the parameter while on-dasatinib. The original report for ACRIN 6687 [8] did not perform multivariate analysis.

PET Parameter	PFS	OS	HR
⁺ Lesion-Level			
SUV _{maxavg} 1	0.549	0.547	1.199
ΔSUV_{maxavg}	0.836	0.253	0.659
SUV _{peakavg} 1	0.437	0.494	1.229
$\Delta SUV_{peakavg}$	0.622	0.443	0.765
Index SUV _{max} 1	0.631	0.726	1.112
Index ΔSUV_{max}	0.760	0.407	0.739
Index SUV _{peak} 1	0.630	0.678	1.128
Index ΔSUV_{peak}	0.884	0.336	0.716
[‡] Patient-Level			
qSUV _{max} 1	0.850	0.745	1.101
$\Delta qSUV_{max}$	0.780	0.634	0.848
qSUV _{peak} 1	0.553	0.454	1.285
$\Delta q SUV_{peak}$	0.781	0.485	0.787
qSUV _{total} 1	0.023	0.061	1.884
$\Delta qSUV_{total}$	0.889	0.260	0.668
qVF1	0.011	0.104	1.687
ΔqVF	0.680	0.704	0.869

Table 3. Univariate analysis of PET variables to PFS and OS (p-values, HR).

[†] The lesion-level analyses were performed on up to 5 tumors per patient selected by uptake intensity for 17 patients at baseline. The change (Δ) while on-dastinib was determined on 14 of the 17 patients. The PFS column has the *p*-value for the PET parameter in analysis of PCWG2 progression free survival. The OS column has the *p*-value for the PET parameter in the analysis of overall survival, and HR has the associated hazard ratio corresponding to a 1-SD increase in the PET parameter. [‡] The patient-level whole-body QTBI analyses were performed on 16 patients at baseline, while change was determined on 12 of the 16 patients. Boldface type indicates a significant ($p \leq 0.05$) association with outcome.

Table 4. Multivariate analysis of PET variables to PFS and OS (p-values, HR).

† PFT Parameter		PFS			OS	
T ET T utumeter	Days	SE	<i>p</i> -Value	HR	SE	<i>p</i> -Value
Lesion-Level						
SUV _{maxavg} 1	26.5	13.1	0.043	1.135	0.856	0.875
ΔSUV_{maxavg}	-2.1	21.5	0.923	0.800	1.081	0.853
SUV _{peakavg} 1	32.0	13.5	0.018	1.421	2.770	0.879
$\Delta SUV_{peakavg}$	-10.4	21.9	0.635	1.142	3.486	0.968
Index SUV _{max} 1	17.3	14.2	0.222	1.296	2.552	0.908
Index ΔSUV_{max}	0.7	18.3	0.971	1.196	4.299	0.964
Index SUV _{peak} 1	21.5	15.4	0.163	1.443	3.250	0.892
Index ΔSUV_{peak}	-2.4	17.4	0.888	0.874	0.874	0.885
Patient-Level						
qSUV _{max} 1	17.6	19.2	0.359	1.321	2.759	0.908
$\Delta qSUV_{max}$	0.9	27.2	0.972	1.341	4.186	0.935
qSUV _{peak} 1	36.9	18.3	0.044	1.646	3.191	0.840
$\Delta qSUV_{peak}$	-15.4	18.8	0.413	1.003	1.609	0.999
qSUV _{total} 1	0.7	20.9	0.972	2.911	6.061	0.753
$\Delta qSUV_{total}$	14.1	25.4	0.580	0.635	1.396	0.794
qVF1	-11.2	21.6	0.606	1.977	4.017	0.808
$\overline{\Delta} \mathbf{q} \mathbf{V} \mathbf{F}$	15.7	21.2	0.458	0.708	1.063	0.783

[†] The multivariate model used age, ln(BAP) and the PET parameter. For association with PFS multiple linear regression was used as the data were not censored. PFS days are the number of days corresponding to a 1-SD increase in the PET parameter, and SE is the standard error of Days. Cox proportional hazard modeling was used to determine association of the multivariate model to OS, where 4 patients were censored. The hazard ratio (HR) is the associated hazard ratio corresponding to a 1-SD increase in the PET parameter. The lesion-level analyses were performed on 17 patients at baseline (indicated by 1 after the parameter), while change on-dasatinib was determined on 14 of the 17 patients. The patient-level whole-body QTBI analyses were performed on 16 patients at baseline, while change was determined on 12 of the 16 patients. Boldface type indicates a significant ($p \le 0.05$) association with outcome.

The actual PFS versus the predicted progression based on multivariate regression analysis is shown in Supplementary Materials Figure S5. The predicted progression relies on the multivariate base model that includes the covariates of age and baseline ln(BAP) with the addition of a PET parameter and shows a high correlation (r = 0.83) between the actual and predicted progression (*p* = 0.001).

Changes in patient and lesion-level NaF PET uptake parameters in response to dasatinib in bone metastases to the change in PSA and bone biomarkers appear in Table 5. Specifically, change in BAP had a significant negative correlation with baseline NaF PET assessed by lesion-level SUV_{peakavg} and SUV_{maxavg}. Universally, PET uptake parameters decreased from before to while on-dasatinib treatment, while BAP levels increased or stayed the same. Change in uNTX was correlated to the SUV_{max} of the index lesion, but no other PET variables. PSA had no correlation with changes in any NaF PET uptake values.

⁺ PET Parameter	ΔuNTX	ΔΒΑΡ	ΔΡSΑ
ΔSUV_{maxavg}	0.31	-0.41	0.08
	(0.142)	(0.047)	(0.747)
$\Delta SUV_{peakavg}$	0.26	-0.45	0.12
	(0.221)	(0.026)	(0.591)
Δ Index SUV _{max}	0.44	-0.21	0.14
	(0.037)	(0.331)	(0.518
Δ IndexSUV _{peak}	0.23	-0.36	-0.01
	(0.270)	(0.080)	(1.00)
$\Delta qSUV_{max}$	0.11	0.00	0.15
	(0.630)	(1.000)	(0.545)
$\Delta q SUV_{peak}$	0.02	-0.27	0.12
	(0.945)	(0.250)	(0.638)
$\Delta qSUV_{total}$	-0.17	0.03	0.42
	(0.450)	(0.947)	(0.063)
ΔqVF	0.17	-0.06	0.39
	(0.450)	(0.841)	(0.086)

Table 5. Correlations between change of NaF PET parameters and change in biomarkers.

⁺ Kendall tau β rank correlation values (and *p*-values) between the change of NaF PET parameters and the change in PSA and bone biomarkers. Significant correlation of *p*-values ($p \le 0.05$) appear in boldface type.

4. Discussion

Similar to the results in our previous report of ACRIN 6687 evaluating a limited dynamic FOV, NaF PET WB uptake also reveals the distinct patterns of pharmacodynamic changes in bone mCRPC from normal bone in response to therapy with dasatinib, as displayed in Figure 2. There appears to be a differential effect of dasatinib on normal compared to tumor bone in men with mCRPC, as measured by fluoride uptake and fluoride bone incorporation.

The previous ACRIN 6687 report [8] showed that SUV_{maxavg} from a single FOV NaF image summed exactly from 30–60 min had a large decrease in bone mCRPC uptake in response to treatment with dasatinib, and that a decrease in SUV_{maxavg} marginally correlated with shorter PFS (p = 0.056), indicating that patients with a lower decline in SUV_{maxavg} had longer PFS. In the current WB lesion-level SUV analysis, baseline or changes in uptake measures collected later, on average WB imaging starting approximately 75 min after injection (range 53 to 95 min), failed to find significance with PFS or OS in univariate analysis. The later WB scan acquired with a mid-scan average of 90 min after injection (range 65 to 110 min) might be different from the single FOV dynamic scan collected precisely at mid-scan 45 min (30 to 60 min SUV image) due to tracer clearance that is independent of the disease, fewer counts with increased noise and the large variability of uptake time between patient WB scans, that all have the effect of increasing variability.

The wide range in the time of WB image acquisition from the injection time in this multicenter trial can increase variability in SUV measurements by as much as 25% for 15 min deviations [22,23] and may significantly affect the correlation of WB NaF measures to PFS where uptake times differ by more than 40 min.

The assessment of up to the 5 hottest tumors with a threshold SUV, is similar to prior methods, but may not be as useful as the selection of tumors and imaging FOV by local clinicians that utilized information based on their clinical impression of the patients in the ACRIN 6687 primary aim report [8]. Averaging the SUV_{peak} or SUV_{max} over 5 tumors may capture the intensity, but not the spatial distribution of a tumor and [10,15] therefore may be unable to determine total tumor burden, as the QTBI analysis offers. Using QTBI analysis, Harmon et al. [10] have found that total tumor burden determining a SUV_{total} metric via bone segmentation followed by thresholding the NaF SUV at 15g/mL has been valuable in assessing response in mCRPC patients using an effective therapy, such as androgen receptor pathway inhibitors or a docetaxel-based chemotherapy regimen. Patient-level WB assessment using QTBI software for the patients presented here did show that large baseline total tumor burden (qSUV_{total}) and tumor volume fraction (qVF) were significantly associated with shorter PFS in univariate analysis, suggesting that a large, intense tumor burden at baseline indicates poor clinical outcome. However, in univariate analysis the change in patient-level PET parameters from QTBI analysis failed to show a relationship to PFS, and no patient-level parameter showed association with OS.

The inability to observe a definitive relationship between changes in NaF PET uptake and PFS or OS may also be because the effect of dasatinib in mCRPC patients is marginal. Dasatinib has not been successful in demonstrating overall survival benefit in phase 3 trials of men with mCRPC [24]. Although the effects of dasatinib on bone have been clearly documented, it does not appear to offer significant anti-tumor efficacy [25,26]. The lack of association of changes in PET parameters to PFS or OS may be that the disease burden was so high in these mCRPC patients, that any response was buried in either PET measurement variability or dasatinib is an ineffective antineoplastic treatment against mCRPC.

However, a multiple variable statistical model that has covariates of age, a clinical biomarker (baseline ln(BAP)) and an NaF PET uptake measure showed that lesion-level baseline SUV_{maxavg}, baseline SUV_{peakavg} and patient-level baseline qSUV_{peak} were all significantly associated with longer PFS in this small cohort (Table 4). No PET parameter used in multivariate modeling analysis showed significant association with OS. The major multivariate model driving component is ln(BAP), which along with age and measures of NaF uptake aids in optimizing the estimates of progression. BAP and NaF uptake are expected to be closely related, as bone turnover (BAP) goes hand-in-hand with new bone formation and matrix mineralization (fluoride uptake on NaF PET). High baseline BAP and high NaF uptake might indicate a more favorable blastic phenotype and longer progression, while baseline BAP and lower NaF might indicate a more lytic phenotype and more aggressive clinical behavior.

The statistical results for the multivariate analysis might be affected by the large variation in image acquisition times between patients (see Supplementary Materials Figure S2), which can increase variability by as much as 75% for over 40 min deviation in uptake time between patient scans [22,23]. Outcomes using NaF PET have been different when more efficacious agents, with proven survival benefit, such as androgen axis inhibiting therapeutics or docetaxel chemotherapy have been used. In prior published studies with a larger cohort of patients (n = 56), mid-treatment findings with NaF imaging alone have association with PFS [10]. This suggests that NaF PET imaging has potential for assessment of treatment efficacy of some therapies in men with mCRPC.

Interestingly, we observed a negative correlation between a decreasing change in lesion-level SUV parameters (Δ SUV_{maxavg}, Δ SUV_{peakavg}, Δ Index SUV_{max}) and an increase in bone alkaline phosphatase (Δ BAP). This relationship was noted in the initial report on the ACRIN 6687 trial that patients with the largest decrease in PET uptake parameters had worse outcome than those that stayed the same or increased [8]. An increase in BAP

levels may be due to dasatinib treatment, which has been shown previously to promote osteoblast differentiation [27] and mineralization that could lead to a relative activation and a transient increase in BAP levels indicative of a healing or reparative response [28–30]. Increased osteoblastic activity would also be expected to lead to a relative increase of NaF uptake. We did not follow these patients after completion of dasatinib treatment with repeat measurements of BAP, thus it is speculative to associate a decrease in BAP levels in this small cohort of patients with better outcome; however, this finding indicates some mechanistic consistency between prior findings based on dynamic imaging and the current WB analysis. Change in uNTX and PSA had no correlation with changes by NaF PET.

Given the very limited capacity of the dataset (n = 17 at baseline, n = 14 with an additional scan at 12 weeks into therapy) and the many measurements carried out, there is no real scope to carry out any type of internal cross-validation. The bootstrapping approach used in evaluating the relationship between PET variables and outcomes (PFS and OS) provides more defensible estimates of statistical significance of the reported effects and provides some measure of adjustment for the limited sample size. Nevertheless, our exploratory analysis is mainly offered to provide some guidance on what relationships may be worth future investigation via a prospective clinical trial. The most glaring limitation of this study, however, was the small number of evaluable patients recruited and an even smaller subset that completed the second PET scan during dasatinib treatment, limiting statistical power for prediction of PFS and OS.

5. Conclusions

The preferential effect of dasatinib in tumor bone over normal bone is well characterized by static WB imaging using NaF PET before and while on dasatinib treatment, and was largely confirmatory of the dynamic results from these same patients [8]. The association of changes in NaF uptake while on dasatinib treatment and PFS or OS were not evident. Dasatinib had some enhanced targeting to involved disease sites but the impact on the disease overall progression was minimal. However, baseline total tumor burden and tumor volume fraction was predictive of a shorter PFS. We had hoped to observe greater effect on tumor bone, disease progression and overall survival but dasatinib showed limited efficacy as a therapeutic for mCRPC patients.

Supplementary Materials: The following are available online at https://www.mdpi.com/article/ 10.3390/tomography7020013/s1, Figure S1: Study design for ACRIN 6687. ¹⁸F-fluoride PET was obtained at baseline before therapeutic introduction of dasatinib and at 12 ± 4 weeks into therapy. [†] Nilutamide-only patients are not eligible. Patients must be receiving dasatinib to be eligible. However, if a nilutamide patient crosses over at progression to add dasatinib, he may be eligible, Figure S2: The acquisition times for whole-body scans for each patient are represented by lines to indicate the variation in start time and duration of imaging of each scan for the ACRIN 6687 multi-center clinical trial. Paired lines of the same color represent the baseline scan (left) and the on-dasatinib scan (right) imaged 12 weeks later. Some patients had a different number of FOV between their two scans, Figure S3: 74-year-old patient with heterogeneous bone lesions imaged before and after dasatinib. Red box indicates the single dynamic FOV from prior report. Baseline PSA was relatively stable (pre-157, post 185) following 6 cy dasatinib (PFS was 3.0 mos). Arrows indicate the 5 hottest lesions in units of SUV_{max}. None of the 5 hottest lesions were assessed in the initial dynamic single FOV imaging study, Figure S4: The same patient described in Figure 1 using the Quantitative Total Bone Imaging (QTBI) analysis software with tumor regions outlined in red. Briefly, CT images were segmented into skeletal regions using an atlas-based approach, then region-specific optimized thresholds were used to detect lesions on the PET image segmentation A random forest model and manual review were applied to exclude lesions that were likely to be benign. The response assessment following dasatinib stratified changes in tumor uptake based off of repeatability measures (Lin 2016), Figure S5: Actual versus predicted time to progression based on multivariate regression analysis. The predicted progression model has age and baseline $\ln(BAP)$ and adds in PET SUV_{peak} as covariates. The line shows the standard deviation used for assessment of the correlation ($\rho = 0.83$) between true and predicted progression and determining

hazard ratios. The correlation is highly significant (p-value = 0.001), Table S1: The individual PET scanning characteristics are listed for all 18 enrolled patients in the study. Case 5 chose to withdraw from the study after the first scan. Three cases (3, 12 and 16) that progressed early, did not receive the second scan. Uptake time (UptakeT), the time between dose injection and WB scanning, is a sensitive parameter in the assessment of SUV from PET scans. The difference between the uptake times (Δ UT) shows the consistency in the protocol for the scanning institution. The iterative reconstructed image resolution for in-plane X/Y pixel size and slice thickness appears in the last two columns The BLUE highlighted cases are those reported in the original publication using the dynamic PET data. SD is the standard deviation of the group, Table S2: $SUV_{peakavg}$ and SUV_{maxavg} value is the average of up to the 5 hottest tumors that were above the threshold of 15 g/mL in the first scan. Only two patients had less than 5 tumors that met threshold criteria; Case 9 had one tumor and Case 13 had 2 tumors above the threshold. The index SUV is the hottest lesion for the patient. SD is the standard deviation of the group. Case 5 withdrew from the study, so was lost to follow-up for PFS and OS assessment, Table S3: Patient-level analysis results using QTBI software (AIQ Solutions, Inc.) for (A) scan 1 and (B) scan 2. SD is the standard deviation of the group. Case 15 had image quality and scaling issues that prevented analysis. Case 5 withdrew from the study, so was lost to follow-up for PFS and OS assessment, Table S4: Gaussian approximations for inferences using a Bootstrap approach with 500 replicates was used in univariate outcome analysis The change (Δ) while on-dastinib was determined on 14 of the 17 patients. The PFS section has correlation (tau), standard error (SE), and the *p*-value for each PET parameter. The OS section has the hazard ratio (HR), standard error (SE) of HR and the p-value for each PET parameter. In the analysis of overall survival, HR has the associated hazard ratio corresponding to a 1-SD increase in the PET parameter. The lesion-level analyses were performed on the average of up to 5 tumors per patient selected by uptake intensity for 17 patients at baseline. The patient-level whole-body QTBI analyses were performed on 16 patients at baseline, while change was determined on 12 of the 16 patients. Boldface type indicates a significant ($p \le 0.05$) association with outcome.

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Institutional Review Board Statement: All procedures performed in studies involving human participants were in accordance with the ethical standards of the multiple institutions' participation in ACRIN 6687 multi-center clinical trial and with the 1964 Helsinki declaration and its later amendments or comparable ethical standards. This report is a secondary analysis using the data originally collected by the ACRIN clinical trial team.

Informed Consent Statement: Informed consent was obtained from all subjects involved in the multi-center ACRIN 6687 clinical trial.

Data Availability Statement: PET image extracted data for individual patients appears in supplementary martials located on the MDPI website.

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Phase 2 multicenter study of enzalutamide in metastatic castration resistant prostate cancer to identify mechanisms driving resistance

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Authors	Concept/ Design	Collection/Data Assembly	Data Analysis/ Interpretation	Manuscript Writing/Editing	Final Approval
RRM	Х	X	Х	X	Х
LK	Х	X	Х	X	Х
JPC		X	Х	X	Х
JMS		X	Х	X	Х
SGZ		X	Х	X	Х
WX		X	Х	X	Х
LW		X	Х	X	Х
RL		X		X	Х
ZZ		X		X	Х
XXW		X	Х	Х	Х
JML		X	Х	Х	Х
EVA		X	Х	X	Х
RSB		X		X	Х
EYY		X		X	Х
PSN		X		X	Х
GJB		X		X	Х
RBM		X		Х	Х
MET	Х	X	Х	X	Х

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Abstract

Purpose: Enzalutamide is a second-generation androgen receptor (AR) inhibitor which has improved overall survival (OS) in metastatic castration resistant prostate cancer (CRPC). However, nearly all patients develop resistance. We designed a phase 2 multicenter study of enzalutamide in metastatic CRPC incorporating tissue and blood biomarkers to dissect mechanisms driving resistance.

Experimental Design: Eligible patients with metastatic CRPC underwent a baseline metastasis biopsy and then initiated enzalutamide 160 mg daily. A repeat metastasis biopsy was obtained at radiographic progression from the same site when possible. Blood for circulating tumor cell (CTC) analysis was collected at baseline and progression. The primary objective was to analyze mechanisms of resistance in serial biopsies. Whole exome sequencing was performed on tissue biopsies. CTC samples underwent RNA sequencing.

Results: 65 patients initiated treatment, of whom 22 (33.8%) had received prior abiraterone. Baseline biopsies were enriched for alterations in *AR* (mutations, amplifications) and tumor suppression genes (*PTEN*, *RB1*, and *TP53*) which were observed in 73.1% and 92.3% of baseline biopsies, respectively. Progression biopsies revealed increased *AR* amplifications (64.7% at progression versus 53.9% at baseline) and *BRCA2* alterations (64.7% at progression versus 38.5% at baseline). Genomic analysis of baseline and progression CTC samples demonstrated increased AR splice variants, AR regulated-genes, and neuroendocrine markers at progression.

Conclusions: Our results demonstrate that a large proportion of enzalutamide-treated patients have baseline and progression alterations in the AR pathway and tumor suppressor genes. We demonstrate an increased number of *BRCA2* alterations post-enzalutamide highlighting importance of serial tumor sampling in CRPC.

Precis:

We report on a phase 2, multicenter, open-label, single-arm study of enzalutamide in men with metastatic castration resistant prostate cancer incorporating baseline and progression metastasis tissue sampling and serial analyses of circulating tumor cells (CTCs) to dissect mechanisms driving clinical resistance to enzalutamide. Our results demonstrate that a substantial proportion of enzalutamide-treated metastatic CRPC patients harbor alterations in the AR pathway and tumor suppressor genes which contribute to the resistance phenotype.

Keywords

Androgen receptor; Castration resistance; Circulating tumor cells; Enzalutamide; Metastases; Prostate cancer; Resistance

Introduction:

Metastatic castration resistant prostate cancer (CRPC) is a lethal disease with a relative 5year survival of 29%.[1] While novel treatments, including androgen receptor (AR) directed therapies, have improved overall survival for patients with CRPC, resistance is observed in nearly all patients. Enzalutamide is a rationally designed second generation AR inhibitor which competitively binds to AR with great potency and also inhibits active AR nuclear translation, DNA binding, and coactivator recruitment.[2] Two large phase 3 trials demonstrated the efficacy of enzalutamide over placebo resulting in routine clinical use in metastatic CRPC.[3, 4] However, 10–25% of patients receiving enzalutamide have primary resistance and at 18-months 50–80% of patients have developed radiographic progression.[3, 4] Therefore, strategies to understand determinants of primary and acquired resistance are essential to developing therapeutic approaches to prolong the activity and durability of treatment.

Several preclinical and clinical studies have examined mechanisms of resistance to AR targeting agents. AR dependent mechanisms hypothesized to cause resistance to enzalutamide include *AR* mutations[5], amplifications[6, 7], splice variant emergence[8, 9], and altered steroidogenesis[10, 11]. Additionally, resistance may also be mediated by activation of parallel AR-independent signaling pathways[12]. While these studies have been informative, they did not integrate paired baseline and progression tumor sampling with comprehensive molecular analysis. Prospective studies embedding tumor tissue and blood-based analyses which are placed in the context of patient outcomes are needed to understand mechanisms that drive resistance to treatment. We report the results of a phase 2, multicenter, open-label, single-arm study of enzalutamide in men with metastatic CRPC incorporating baseline and progression metastasis tumor sampling and serial analyses of circulating tumor cells (CTCs) to dissect mechanisms driving *de novo* and acquired clinical resistance to enzalutamide.

Materials and Methods:

Patients:

This is a phase 2, single arm, open-label study of enzalutamide in metastatic CRPC (NCT01942837). Eligible patients had CRPC defined as disease progression despite a serum total testosterone <50 ng/dL and: 1) PSA progression as defined by the Prostate Cancer Clinical Trials Working Group (PCWG) 2[13], 2) soft tissue disease progression as defined by Response Evaluation Criteria In Solid Tumors (RECIST) version 1.1[14], or 3) bone disease progression as defined by PCWG2[13]. Additionally, patients had evidence of metastases with at least one metastatic site amendable to biopsy. Patients were required to have prostatic adenocarcinoma. Variant histologies, including neuroendocrine differentiation, were not permitted.

Patients may have received prior hormonal therapies (including ketoconazole, abiraterone, first-generation anti-androgens) and up to two cytotoxic therapies. Prior enzalutamide, apalutamide or darolutamide was not allowed. Other eligibility criteria included an Eastern Cooperative Oncology Group performance status 2 and adequate organ and bone marrow

function. The study was conducted after Institutional Review Board approval at each of the participating institutions in accordance with the principals outlined in the Declaration of Helsinki. All patients provided written informed consent.

Treatment:

Following enrollment, patients had a baseline biopsy of a metastasis. Biopsies were performed after informed consent in the interventional radiology department. Subsequently, patients received enzalutamide 160 mg by mouth daily. Patients continued enzalutamide until radiographic progression, significant toxicity or patient/physician requested withdrawal. A repeat metastasis biopsy, with ongoing enzalutamide, was obtained at radiographic progression in patients completing 3 cycles (1 cycle=28 days). The protocol specified that when possible the progression biopsy should target the same site as the baseline biopsy. Though baseline and progression biopsies were mandatory, not all patients underwent biopsy at progression given lack of feasible biopsy site, clinical disease progression, or patient study withdrawal. Imaging assessments occurred every twelve weeks. PSA was measured every four weeks.

Tumor Tissue Genomic Sequencing:

Biopsies were prioritized for pathologic assessment followed by whole exome sequencing. Whole exome sequencing was performed on tumor biopsies and collected blood normal using a customized version of a previously described protocol.[15] After DNA shearing, hybridization and exome capture were performed using either Illumina's Rapid Capture Exome Kit or the Agilent SureSelect Human All Exon 44Mb v2.0 bait set (Supplementary Table 1S).[16] Libraries were sequenced with 76 bp paired-end reads on an Illumina instrument.

Reads were aligned using BWA v0.5.9 and somatic mutations called using a customized version of the Getz Lab CGA WES Characterization Pipeline (https://portal.firecloud.org/ #methods/getzlab/CGA_WES_Characterization_Pipeline_v0.1_Dec2018/). [17] Briefly, we used ContEst to estimate contamination, MuTect and Strelka to call SNVs and indels, DeTiN to estimate tumor-in-normal contamination, and Orientation Bias Filter and MAFPoNFilter to filter sequencing artifacts.[18-23] For target intervals, we used an intersection of Illumina Rapid Capture Exome and Agilent SureSelect regions, created using bedtools.[24] Variants were annotated using VEP, Oncotator, and vcf2maf v.1.6.17 (https://github.com/mskcc/ vcf2maf). [25, 26] Copy number alterations, purity, ploidy, and whole genome doubling status were called using FACETS v0.5.14.[27] In cases where FACETS fit an incorrect copy number profile, ABSOLUTE with manual review was used instead.[28] Copy number alterations were evaluated with respect to whole genome doubling status. Samples were included in the final cohort if they had contamination <4%, purity >20%, tumor coverage >50x, and normal coverage >30x. Presence of biallelic alterations was defined as 1) the presence of a loss of function mutation in addition to allelic full deletion, or 2) two allelic full deletions.

To compare mutations between distinct samples from the same patient, we used a previously described method designed to recover evidence for mutations called in one sample in all

other samples derived from the same individual.[29] In brief, the 'force-calling' method uses the strong prior of the mutation being present in at least one sample in the patient to more sensitively detect and recover mutations that might otherwise be missed. Successfully sequenced tissue samples were part of larger cohort analyses.[30, 31]

Circulating Tumor Cell Analysis:

Blood for CTC gene expression analysis was collected in vacutainer tubes (BD Biosciences) with EDTA anticoagulant at baseline and off treatment. Mononuclear cells were isolated with a Ficoll-Pacque Plus (GE Healthcare) gradient before undergoing CD45 depletion (Miltenyi Biotec). The VERSA platform[32] was used for the live cell capture of CTCs using an anti-EpCAM antibody (R&D) conjugated to paramagnetic particles (Life Technolgies). Cells were lysed in the VERSA with a modified LIDs buffer (10 mM Tris-HCL, 500 mM lithium chloride, 1 % Igepal® CA-630 (Sigma-Aldrich, USA), 5 mM ethylenediaminetetraacetic acid (EDTA), 5 mM dithiothreitol, pH 7.5) and mRNA was extracted with olgio(dt)25 Dynabeads® (Life Technologies, USA)[33].

Extracted mRNA was reverse transcribed using a High Capacity cDNA Reverse Transcriptase kit (Life Tech, USA), according to manufacturer's directions using Bio-Rad C1000 Thermo Cycler (Bio-Rad, USA). The RT reaction was amplified for 14 cycles using TaqMan® PreAmp (Life Tech) according to manufacturer's directions and diluted 1:20 in 1x TE (10 mM Tris-HCL pH8, 1 mM EDTA). For TaqMan® assays, 5 μ L of diluted cDNA template was mixed with 10 μ L iTaq® master mix (Bio-Rad), 1 μ L TaqMan® Gene Expression Assay (Life Technologies) and 4 μ L nuclease free (NF) water. Each reaction was amplified for 45 cycles (denatured at 95 °C for 15 seconds followed by annealing at 60°C for 1 minute) using a CFX Connect® Real-Time PCR System (Bio-Rad). A table of genes of interest and primers used is available in Supplementary Table 2S. Samples are reported as 38-cycle threshold value with cycle threshold values less than 38 considered positive for expression.

Statistical Analysis:

The primary objective was to analyze mechanisms of *de novo* and acquired resistance to enzalutamide in serial CRPC tumor biopsies. This was assessed by tumor exome sequencing. The trial design assumed AR related resistance parameters to be measured as continuous variable. Sample size of 40 with serial biopsies was targeted to detect a standardized effect size of 0.454 for the changes in a set of resistance parameters at progression compared to baseline having 80% power with 1-sided alpha=0.025 using the paired t-test. The planned enrollment was 66 patients to obtain 40 evaluable patients with paired samples.

Secondary endpoints included toxicity, PSA and investigator-assessed radiographic response, time to PSA and investigator-assessed radiographic progression. Toxicity was summarized using Common Terminology Criteria for Adverse Events version 4.0. Radiographic response as defined by RECIST version 1.1 was summarized with 95% exact binomial confidence interval (CI)[14]. PSA response and progression were defined by PCWG2 criteria[13]. Time to PSA progression was defined from treatment initiation to PSA

progression or censored at the date of last PSA evaluation. Radiographic progression was defined by RECIST version 1.1 for soft tissue and visceral disease and PCWG2 for bone disease[13, 14]. Progression-free survival (PFS) was defined as time from treatment initiation to radiographic progression or death from any cause, whichever came first, or censored at the date of last evaluation. Time to event endpoints were summarized using Kaplan-Meier method. We evaluated outcomes in the overall cohort, by type of prior therapy, and by CTC biomarker status. Patients with a positive CTC biomarker were defined as those positive for expression of AR variants, synaptophysin, and/or two or more AR-regulated genes (KLK2, LKL3, TMPRSS2, FOLH1, or NKX3.1). Comparisons between biomarker groups were conducted using the log-rank test.

Results:

Baseline Characteristics:

At data lock in April 2020, 67 patients were enrolled. The final analysis cohort for clinical outcomes consists of 65 men who received 1 dose of enzalutamide, and three patients remained on treatment; two men who never initiated treatment were excluded. Patient were enrolled between November 2013–May 2017: Dana-Farber Cancer Institute (n=39), University of Washington (n=19), Beth Israel Deaconess Medical Center (n=6), and South Shore Hospital (n=1) (Table 1). The median age was 70 years. Sixteen patients (24.6%) received prior chemotherapy, 22 (33.8%) prior abiraterone, and nine (13.8%) prior ketoconazole. All patients had metastases, of whom 32 (49.2%) had measurable disease.

PSA and Radiographic Response:

Thirty-eight patients (58.5%) achieved a 50% PSA reduction and 20 patients (30.8%) had a 90% decline in PSA (Figure 1). The PSA response rates in patients having received prior abiraterone, ketoconazole, or chemotherapy were 22.7% (n=5/22), 33.3% (n=3/9), and 68.8% (n=11/16), respectively (Supplementary Table 3S). Of the 32 patients with measurable disease, 11 (34.4%) had an objective response (Supplementary Table 4S).

PSA and Radiographic Progression:

Forty-three (66.1%) patients experienced PSA progression. Median time to PSA progression was 5.6 months (95% CI 3.7, 10.1) (Supplementary Figure 1S) in the overall cohort and 2.8 months (95% CI 1.9, 5.6; n=14 events/22 patients), 11.0 months (95% 1.8, not reached; n=5/9), and 6.4 months (95% CI 1.8, 13.8; n=10/16) in patients having received prior abiraterone, ketoconazole, and chemotherapy, respectively (Supplementary Table 5S).

Overall, 33 patients (50.8%) experienced radiographic progression. Median radiographic PFS was 11.0 months (95% CI 8.1, 19.6) (Supplementary Figure 1S): 5.3 months (95% CI 2.7, 8.1; n=13/22) for prior abiraterone (Supplementary Table 5S) and 19.1 months (95% CI 2.1, not reached) for prior chemotherapy.

Toxicity:

Patients received a median nine cycles of enzalutamide (range <1-56) with a median duration of 8.6 months (range 0.1–51.6). Five patients (7.7%) had a dose reduction to 120

mg daily and 8 patients (12.3%) experienced a treatment hold. Six patients (9.7% among 62 patients who discontinued therapy of any reason) discontinued treatment due to unacceptable toxicity.

Overall, 24.6% (n=16), 36.9% (n=24), 30.8% (n=20), and 4.6% (n=3) reported maximum grade 1, 2, 3, and 4 toxicity of any attribution. There were no grade 5 events. The most common treatment-associated adverse events of any grade included fatigue, pain, hypertension, and back pain. The most common grade 3 toxicity was hypertension. Falls occurred in six patients and all were grade 1 or 2.

Metastasis Biopsy Samples:

Overall, 66 patients underwent a baseline biopsy (including one patient who consented but did not initiate treatment) and 28 patients underwent a biopsy at progression (Supplementary Table 7S; Supplementary Figure 2S). The majority of biopsies were from bone (n=65, 68%) followed by lymph nodes (n=25, 26%). Following quality control including assessment of tumor purity, tumor and normal coverage, and contamination, successful sequencing analysis was performed on 26 (39%) baseline and 17 (61%) progression biopsies. Successful sequencing analysis was performed on 42% of bone biopsies (n=27/65) and 64% (n=16/25) of soft tissue biopsies.

Tumor Sequencing Analysis:

Androgen Receptor Alterations—Of patients with baseline biopsies (n=26), 14 (53.9%) had *AR* amplifications and seven (26.9%) had *AR* mutations of whom four (28.6%) and three patients (42.9%) had a PSA response (50% PSA reduction from baseline), respectively (Figure 2, Supplementary Table 8S). Of the seven *AR* mutations presents at baseline, patients with a T878S, T979A, L702H or W742L did not experience a PSA response (Supplementary Table 9S). The PSA response rate in patients without *AR* mutations. Of the nine patients who received prior abiraterone, four (44.4%) had *AR* mutations and six (66.7%) had *AR* amplifications at baseline biopsy. PSA responses to enzalutamide were low in abiraterone pretreated individuals with *AR* amplifications (n=2/6, 33.3%) or *AR* mutations (n=1/4, 25.0%).

With regards to individuals with progression biopsies (n=17), 11 patients had *AR* amplifications (64.7%) and three (17.6%) had *AR* mutations (Figure 2, Supplementary Table 8S, Supplementary Table 9S). Of the six patients who received prior abiraterone, five (83.3%) demonstrated *AR* amplifications and one (16.7%) demonstrated an *AR* mutation. PSA responses were observed in seven patients (63.6%) with *AR* amplifications and all patients with *AR* mutations at progression.

In analyzing the paired baseline and progression samples (n=10), baseline *AR* alterations (n=2 mutations (W552C, T695A), n=5 allelic amplification] were present in seven patients (70%) of whom five (71.4%) experienced a PSA response (Figure 2). The two patients who did not experience a PSA response were abiraterone exposed. Acquired *AR* alterations present in progression metastases only were observed in four patients (40%) [n=1 mutation

(S234C), n=3 allelic amplification] and all individuals experienced a PSA response to enzalutamide

Tumor Suppressor Genes Alterations—Of individuals with a baseline metastasis biopsy (n=26), alterations in tumor suppressor genes were present in 24 patients (92.3%) [*TP53* n=18 (69.2%); *RB1* n=18 (69.2%); *PTEN* n=17 (65.4%)] (Figure 2, Supplementary Table 8S). Biallelic alterations were observed in eight patients (30.7%) [*TP53* n=4/26 (15.4%); *RB1* n=1/26 (3.8%); *PTEN* n=5/26 (19.2%)]. The PSA response rate was 50.0% for patients with *TP53* alterations (n=9/18), 50.0% for *RB1* (n=9/18), and 47.1% for *PTEN* (n=8/17). The PSA response was 50% (n=4/8) in patients with biallelic alterations [*TP53* n=2/4 (50%); *RB1* n=0/1 (0%); *PTEN* n=3/5 (60%)]. PSA response rates were similar to those without tumor suppressor gene alterations [50.0% *TP53* wildtype/neutral (n=4/8), 50.0% *RB1* wildtype/neutral (n=4/8), and 55.6% *PTEN* wildtype/neutral (n=5/9)]. The frequency of tumor suppressor gene alterations was similar between patients with or without abiraterone with abiraterone with tumor suppressor gene alterations 25% of patients (n=2/8) pretreated with abiraterone with tumor suppressor gene alterations; 25% of patients (n=2/8) pretreated with abiraterone with tumor suppressor gene alterations had a PSA response.

With regards to individuals with a progression metastasis biopsy (n=17), all patients (100%), including those with (n=6) and without (n=11) prior abiraterone exposure, had a tumor suppressor gene alteration [*TP53* n=12/17 (70.6%); *RB1* n=13/17 (76.5%); *PTEN* n=13/17 (76.5%)] (Figure 2, Supplementary Table 8S). Biallelic alterations at progression were observed in five patients (29.4%) [*TP53* n=4/17 (23.5%); *RB1* n=0/17 (0%); *PTEN* alterations n=1/17 (5.9%)]. The PSA response rate was 75.0% for patients with *TP53* alterations (n=9/12), 61.5% for *RB1* (n=8/13), and 61.5% for *PTEN* (n=8/13). The frequency of tumor suppressor gene alterations in progression biopsies was numerically higher in patients with prior abiraterone exposure compared to those naïve to abiraterone. Of patients pretreated with abiraterone with tumor suppressor gene alterations at progression (n=6), one patient (20%) experienced a PSA response.

From the paired biopsy samples (n=10), tumor suppressor gene alterations were present at baseline in nine patients (90.0%) [*TP53* n=7/10 (70.0%); *RB1* n=7/10 (70.0%); *PTEN* n=6/10 (60.0%)], including all three patients exposed to abiraterone (Figure 2). Acquired tumor suppressor gene alterations not present at baseline were observed in eight patients (80%) [(*PTEN* alteration n=4/10 (40.0%), *RB1* alteration n=4/10 (40.0%), *TP53* alteration n=2/10 (20.0%)].

DNA Repair Gene Alterations—Of individuals with a baseline biopsy (n=26), DNA repair genes alterations were present in 15 patients (57.7%) [*BRCA2* n=10/26 (38.5%); *CKD12* n=4/26 (15.4%); *ATM* n=1/26 (3.5%)] (Figure 2, Supplementary Table 8S). Biallelic alterations were observed in three patients (11.5%) [*BRCA2* n=3/26 (11.5%)]. The PSA response rate was 50.0% (n=5/10), 25% (n=1/4), and 100% (n=1/1) for patients with *BRCA2*, *CDK12*, and *ATM* alterations, respectively. The PSA response was 0% in the three patients with biallelic alterations. In wildtype/neutral patients, PSA response rates were 50.0% (n=8/16), 54.5% (n=12/22), and 48.0% (n=12/25) for patients without *BRCA2*,

CDK12, and *ATM* alterations. Of the patients pretreated with abiraterone with DNA repair alterations (n=7), only one patient (14.3%) with a *CDK12* alteration had a PSA response.

Of those with a progression metastasis biopsy (n=17), 64.7% (n=11/17) had DNA repair alteration: 64.7% *BRCA2* (n=11/17), 5.9% *CDK12* (n=1/17), and 5.9% *ATM* (n=1/17) (Figure 2, Supplementary Table 8S). PSA response rates were observed in 54.5% of patients with *BRCA2* alterations (n=6/11). One patient had a biallelic alteration in *BRCA2* and did not experience a PSA response. Of the six patients with prior abiraterone exposure and a progression biopsy, five (83.3%) had DNA repair alterations at progression (n=5/6 with *BRCA2* alterations, n=1/6 with a *CDK12* alteration), of whom two experienced a PSA response (33.3%).

From the paired metastasis samples (n=10), *BRCA2* gene alterations were observed in four patients (40.0%) at baseline (Figure 2). One patient each had a baseline *CDK12* and *ATM* alteration. Acquired *BRCA2* alterations not observed at baseline were seen in four patients (40%), in whom none were bilallelic and all co-occurred with *RB1* alterations. No patient was previously exposed to a PARP inhibitor.

SPOP and CHD1 Alterations—In the baseline biopsy samples (n=26), *SPOP* alterations were observed in nine patients (34.6%) of whom four (44.4%) experienced a PSA response (Figure 2, Supplementary Table 8S). In patients having received prior abiraterone (n=9), *SPOP* alterations were present in four individuals (44.4%) of whom two (50.0%) had a PSA response to enzalutamide. *CHD1* alterations were observed in 10 patients (38.5%) and seven (70.0%) experienced a PSA response to enzalutamide. Three patients (11.5%) had co-occurring *SPOP* and *CHD1* alterations at baseline, two (66.7%) of whom had a PSA response.

In patients with evaluable progression biopsies (n=17), *SPOP* alterations were observed in five individuals (29.4%) (Figure 2, Supplementary Table 8S). Two patients (40.0%) with progression *SPOP* alterations experienced a PSA response. *CHD1* alterations were present in nine (52.9%) patients at progression of whom seven (77.8%) had a PSA response to enzalutamide. Two patients (11.8%) had co-occurring *SPOP* and *CHD1* alterations at progression and one of these individuals experienced a PSA response.

In assessing the paired metastasis biopsies (n=10), *SPOP* alterations were present at baseline in four patients (40.0%) of whom two (50.0%) had been previously exposed to abiraterone and two (50.0%) had a PSA response to enzalutamide (Figure 2). Acquired *SPOP* alterations, not present at baseline but present at progression, were observed in two individuals (20.0%), both of whom developed emergent co-occurring *RB1* alterations and one developed emergent *AR* amplification.

Association of Tumor Gene Status with Outcomes—In evaluating baseline and progression biopsy samples, *AR* amplification was more prevalent in tumors samples at progression compared to baseline (Figure 3); no other gene was associated with presence in the progression biopsy in this analysis.

Circulating Tumor Cell Analysis:

Of the 65 patients who received at least one dose of enzalutamide, 52 had blood samples collected at baseline of whom 21 patients (40%) had adequate CTCs for gene expression analysis (Supplementary Figure 2S). Progression samples were collected from 37 patients of whom 23 (62%) had adequate samples. Reasons for the inability to perform the CTC assay for the remainder of patients included shipping delays/shipping protocol deviations (17% baseline, 5% progression) and inadequate blood volume or reagent issues (43% baseline, 22% progression). Collection methods were revised mid study that resolved these issues. Paired baseline and progression samples were available from 11 patients. Matched biopsy and CTC samples were available for six patients at baseline and 10 at progression (Supplementary Figure 3S).

We measured gene expression of splice variant AR, AR-regulated genes, and neuroendocrine markers. In swimmer plots, we observe shorter survival in patients who had detectable expression, either at baseline or progression, of genes in these pathways related to enzalutamide resistance (Figure 4). Overall survival was shorter in patients positive for enzalutamide resistant gene expression at baseline (median overall survival 17.7 months versus not reached in patients positive or negative for enzalutamide resistant gene expression respectively, HR 6.29 95% CI 1.22 to 32.5, p=0.01) (Supplementary Figure 4S). When comparing the paired baseline and progression CTC samples (n=11), there was increased frequency of AR splice variants, AR regulated genes, and neuroendocrine markers in progression samples compared to baseline (Figure 5).

Discussion:

In this phase 2 study, embedding tissue and CTC-based genomic analyses, we investigate mechanisms of resistance to enzalutamide in metastatic CRPC. This analysis is important to understanding therapy selection and developing strategies to overcome resistance. Our analysis of tumor genomics with tissue and blood-based assays, confirms the landscape of CRPC alterations and reveals several insights about mechanisms of resistance to enzalutamide.[30]

A critical initial step to the molecular characterization of metastatic CRPC is the procurement of tumor tissue for genomic profiling. Successful sequencing of a metastasis biopsy requires sufficient tumor for isolation of high-quality nucleic acid. The majority of prostate cancer patients have bone metastases and bone-predominant disease. Bone metastases are frequently associated with a dense sclerotic reaction making biopsy itself and DNA preparation technically challenging; decalcification procedures may have a negative impact on nucleic acid quality and quantity. While use of archival primary prostate tumor tissue could overcome some of these challenges, treatment-naïve tumors will not capture alterations that emerge as a consequence of systemic therapy.[34]

In our study, of the 94 biopsies performed, 46% underwent successful whole exome sequencing. Larger efforts profiling the genomic landscape of metastatic CRPC, either do not report on successful sequencing yield from patients who underwent metastasis biopsy or report slightly higher yields than documented in our series.[30, 31, 35] Ongoing refinement

of tissue biopsy and processing procedures will maximize the success of future genomic analyses in CRPC; these efforts are especially important in the current era of PARP inhibitor therapy. Given the challenges associated with metastasis biopsy and limitations in capturing the scope of tumor heterogeneity from an isolated metastatic site, minimally invasive bloodbased "liquid" biopsies have emerged as an alternative to tissue sampling. Liquid biopsies enable frequent and sequential monitoring of tumor molecular dynamics; however, the concordance of tissue and blood-based methods for genomic assessment has varied.[36] In our study, we utilize an integrated molecular CTC assay to complement tissue analyses. Of the 89 patients with blood samples collected for CTC analysis, 49% underwent successful gene expression analysis. Because of an initial low success rate, we refined our methods for sample collection, shipping, and processing which resulted in higher yields in collected progression samples.

While only 25% of patients in our cohort (n=16/65) had biopsies with matched CTC analysis and the methodologies of analysis differed by specimen source, there were notable similarities in tissue and CTC molecular profiles. Specimens with *AR* alterations in tissue had increased expression of AR and AR regulated genes in CTCs. Our work aligns with other studies demonstrating conservation of AR alterations between CTCs and biopsies suggesting that CTCs can serve as a non-invasive surrogate for characterizing tumor molecular alterations.[37–39]

We demonstrate that *BRCA2* alterations were acquired in 40% (n=4/10) of patients with paired metastasis biopsies following treatment with enzalutamide. Whether these alterations are true driver events remains to be determined given that most were monoallelic losses co-occurring with *RB1* alterations. Prior reports have demonstrated the presence of alterations in homologous recombination repair (HRR) genes in tumors post AR signaling inhibitors (ARSIs), however these reports were without analysis of tumor samples prior to ARSI exposure.[31] *BRCA2* and *RB1* are both located on chromosome 13q, 16 megabases apart, thus there is a tendency for co-occurrence of alterations in these genes.[30] Moreover, while our numbers are small, these data underscore the value of serial tumor sampling in patients with CRPC to identify potential molecular targets with vulnerabilities to systemic treatment and also to evaluate for the emergence of neuroendocrine prostate cancer. Patients with HRR alterations, particularly *BRCA2* mutations, can be responsive to PARP inhibitors or platinum chemotherapy, therefore testing for the emergence of such alterations is critical to therapy selection for patients. Our RNA-based CTC assay did not integrate HRR gene status, though continued assay refinement to integrate assessment of DNA and RNA is currently in process.

We confirm that AR pathway alterations, namely amplifications and mutations, are drivers of resistance to enzalutamide. Point mutations in the *AR* ligand-binding domain have been associated with resistance to AR-targeted therapy, including F877L and T878A, which have been associated with resistance to ARSIs.[5, 40–42] Other mutations, including T878S, have been associated with receptor promiscuity with increased sensitivity to steroids or AR antagonists.[42] L702H has been observed to emerge following glucocorticoid exposure and confers resistance to enzalutamide.[43] In our study, patients harboring baseline T878A, T878S, W742L, and L702H did not have a PSA response to enzalutamide. This raises the question of whether alternate AR antagonists, such as darolutamide, which have

demonstrated *in vitro* activity against mutant *AR*, would be more effective in metastatic CPRC harboring these mutations or in the post abiraterone setting.[44] Our work highlights the difficulty of individual real-time tumor analysis, however targeted patient/tumor specific therapy remains a laudable goal.

We demonstrate that CTC transcriptomic interrogation is feasible and results in meaningful information that can elucidate both primary and secondary resistance mechanisms to enzalutamide. The CTC gene set analyzed in this cohort included splice variant *AR*, *AR* regulated genes, and neuroendocrine markers. While the well-studied AR variant-7 has clinical relevance given that detection in CTCs is predictive of resistance to enzalutamide and abiraterone, additional AR variants have been discovered that confer resistance to ARSIs[45]. In our CTC analysis, expression of AR variants and AR-regulated genes was seen in a higher proportion of progression CTC samples, consistent with findings observed from tumor genomic profiling. Given that CTCs are shed from tumor into circulation, it is expected that some concordance between tissue and CTC profiling would exist. Prior studies have demonstrated conservation between CTC and tissue AR pathway alterations, including AR variants and amplifications.[38] We confirm that possible AR dependency remains a persistent mechanism of resistance in CPRC and can be recapitulated in CTC analysis.

It is recognized that a proportion of CRPC tumors develop histologic neuroendocrine transformation as an AR-independent mechanism of treatment resistance. These tumors often have low or absent AR and/or AR-regulated genes and increased expression of classic neuroendocrine markers, including chromogranin and synaptophysin[46]. Frequently, these tumors harbor loss of RB1 and TP53, however these alterations are not specific to neuroendocrine CRPC[47]. In our CTC analysis, we demonstrate that progression samples exhibit increased expression of markers of resistance including neuroendocrine markers, AR variants but also increase in AR-regulated genes. This result likely reflects the heterogeneity of both AR-dependent and independent resistance mechanisms observed in advanced CRPC and lineage plasticity occurring in a subset of resistance clones. ARSI exposed tumors have a higher percentage of histologic neuroendocrine features and have higher neuroendocrine expression scores[30]. A recent study demonstrated that a targeted genomic and epigenomic gene set applied to cfDNA was capable of identifying patients with neuroendocrine CRPC with high concordance between cfDNA and tissue[48]. Patients with neuroendocrine CPRC are candidates for platinum chemotherapy, although subsequent effective treatments are limited for this poor risk population.

We evaluate the relevance of *SPOP* alterations in baseline and progression samples and demonstrate a PSA response rate of 55% (n=6/11) in patients with baseline *SPOP* alterations. Furthermore, two of the three abiraterone pretreated patients with *SPOP* alterations demonstrated a response to enzalutamide. Prior studies have demonstrated that *SPOP*-mutated prostate cancer is associated with more favorable prognosis, enrichment in earlier stage disease relative to CRPC, and improved responses to ARSI[30]. While our numbers are low, our data corroborate these findings.

Lastly, we confirm that prior exposure to CYP-17 inhibition, including abiraterone or ketoconazole, results in blunted efficacy to enzalutamide. In patients without abiraterone

and/or ketoconazole exposure, PSA 50% responses were observed in 79.5% (n=31/39), while 26.9% of abiraterone and/or ketoconazole exposed patients (n=7/26) and 13.2% of abiraterone exposed patient (n=5/22) experienced a PSA response. This is consistent with prior studies which have demonstrated that sequential use of ARSIs results in cross-resistance and decreased efficacy[49, 50]. In a randomized, phase 2 crossover trial evaluating abiraterone followed by enzalutamide, PSA responses to second-line enzalutamide were seen in 36% of patients compared to 68% in patients receiving first-line abiraterone[49]. Additionally, a meta-analysis of eight studies including 643 patients demonstrated decreased PSA responses to second-line ARSIs[50].

Despite this being a prospective, multicenter phase 2 study interrogating mechanisms of resistance to enzalutamide, several limitations exist. The study required blood and tissue collection at baseline and progression; however, samples passing quality control were limited, resulting in a smaller sample size than projected. Additionally, the small sample size limited our ability to make inferences regarding less common genomic events.

Despite limitations our results confirm previously published data that resistance to enzalutamide is driven by alterations in the AR pathway and tumor suppressor genes. Our work was performed within the framework of a prospective, multicenter phase 2 trial leveraging paired tissue sampling and minimally invasive liquid biopsies in a patient population representative of standard enzalutamide treatment. Larger prospective studies, with integrated tissue analyses, are ongoing to validate the CTC gene expression panel utilized in this study. This panel has the potential to guide therapy selection between AR targeting agents, PARP inhibitors, chemotherapy, and clinical trials. Our data underscore the need for novel treatments and combinations to enhance efficacy to AR targeting agents and overcome or prolong resistance.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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Conflict of Interest:

RRM received research funding from Bayer, Pfizer, Tempus; serves on Advisory Board for AstraZeneca, Bayer, Bristol Myers Squibb, Calithera, Exelixis, Janssen, Merck, Novartis, Pfizer, Sanofi, Tempus; is a consultant for Dendreon, Vividion. PSN served received renumeration for consultant/advisory services to Bristol Myers Squibb, Astellas, and Janssen. XW received research funding from Bristol Myers Squibb. EMV received renumeration for consultant/advisory services to Tango Therapeutics, Genome Medical, Invitae, Enara Bio, Janssen, Manifold Bio, Monte Rosa, and received research funding from Novartis, Bristol Myers Squibb. MET served on the Advisory Board for Bayer, AstraZeneca, Janssen, Abbvie, and Astellas. The remaining authors have no disclosures.

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Figure 1. Waterfall plot of best PSA response to therapy with enzalutamide.

Each bar represents an individual patient. Best percent change of PSA was calculated using date of first cycle of PSA as reference. Each green, blue and red bar indicates those who received prior therapies of abiraterone acetate/ketoconazole only (n=20), chemotherapy only (n=10) and both (n=6), respectively. The gray bars represent patients without prior treatment with chemotherapy, abiraterone acetate, or ketoconazole.

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Figure 2. Integrative landscape analysis of somatic alterations obtained through DNA sequencing from baseline metastasis biopsies prior to treatment with enzalutamide and progression metastasis biopsies following treatment with enzalutamide.

Columns represent an individual metastasis biopsy. The left panel of columns represents paired baseline and progression metastasis biopsies obtained from the same individual (total 10 patients). The middle panel represents baseline biopsies only (total 16 patients). The right panel represents progression biopsies only (total 7 patients). Mutations per Mb are shown in the upper histogram. Biopsy type, prior abiraterone exposure, and presence of PSA 50% response from baseline are delineated in the first three rows. The remaining rows represent specific genes of interest. Color legend of the alterations are displayed. Multiple mutations in a gene are represented by triangles. Copy number calls are allelic and relative to whole genome doubling status, with calls for the two alleles indicated by two triangles. Allelic deletions that are not complete deletions are possible in samples with whole genome doubling. Because AR is on the X chromosome and has only a single allele in men, its copy number is represented as a box. Complex indicates that a copy number breakpoint occurred within the body of the gene. Putative loss of function (LoF) missense mutations were annotated as LoF or likely LoF in OncoKB or mutated the same amino acid as a LoF mutation. This plot was created using the CoMut software.

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Figure 3. Association of AR amplification in progression samples (n=17) compared to baseline samples (n=26).

To assess significant changes in copy number before and after enzalutamide exposure, we combined p-values from a paired, two-sided Mann-Whitney U test for paired biopsies (n=10 pairs) and an unpaired, two-sided Mann-Whitney U test using unpaired biopsies (n=16 baseline, n=7 progression). The p-values were combined using a partially-mixed pooling approach designed to enable robust analysis of combined paired and unpaired data. AR=Androgen receptor, WGD=Whole genome duplication.

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Figure 4. CTC gene expression analysis at baseline (A) and at progression (B).

Left panel: Heatmap showing expression of genes of interest. Each row represents an individual patient. Each column represents an individual gene. Red denotes increased expression. Middle panel: Swimmer plot of patient outcomes. Each row represents an individual patient. Column to the left of the Swimmer plot denotes best objective response on radiographic imaging (PR=partial response; SD=stable disease; PD=progressive disease). Right panel: Pie chart demonstrating percent expression of *AR* splice variants, AR regulated genes, and synaptophysin.

A) Baseline CTC expression analysis correlated with patient outcomes.

B) Progression CTC expression analysis correlated with patient outcomes.

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Figure 5. CTC gene expression analysis of paired baseline and progression samples.

A: Heatmaps showing expression of genes of interest. Each row represents an individual patient. Each column represents an individual gene. Red denotes increased expression. Left panel denotes baseline pre-treatment CTC samples. Right panel denotes progression CTC samples. B: Pie chart demonstrating percent expression of *AR* splice variants, synaptophysin, and AR regulated genes. Left pie chart denotes baseline pre-treatment CTC samples. C: Swimmer plot of patient outcomes. Each row represents an individual patient. Column to the left of the Swimmer plot denotes best objective response on radiographic imaging (PR=partial response; SD=stable disease; PD=progressive disease).

Table 1.

Baseline patient and disease characteristics.

Characteristic	N	Median (q1-q3) or %
Institution		
Dana-Farber Cancer Institute	39	60.0%
University of Washington	19	29.2%
Beth Israel Deaconess Medical Center	6	9.2%
South Shore Hospital	1	1.5%
Age at baseline (years)	65	70 (66–75)
ECOG performance status		
0	44	67.7%
1	21	32.3%
Gleason score at diagnosis		
6	6	9.2%
7	22	33.8%
8	9	13.8%
9	22	33.8%
10	3	4.6%
Missing	3	4.6%
Metastases at diagnosis	18	27.7%
Prior chemotherapy	16	24.6%
Prior docetaxel	15	23.1%
Prior abiraterone [*]	22	33.8%
Prior ketoconazole	9	13.8%
Prior sipuleucel-T	15	23.1%
Prior first-generation anti-androgens **	53	81.5%
Measureable disease at baseline	32	49.2%
Non-measurable disease at baseline	65	100%
Sites of metastasis at baseline ***		
Bone	58	89.2%
Lymph nodes	32	49.2%
Lung	8	12.3%
Liver	1	1.5%
Other ****	9	13.8%

Characteristic		Median (q1-q3) or %
Laboratory data at baseline		
PSA (ng/mL)	65	14.2 (6.9–140.6)
Albumin (g/dL)	65	4.2 (4.0–4.4)
Alkaline phosphatase (U/L)	65	80 (66–116)
Calcium (mg/dL)	65	9.6 (9.2–9.8)
Hemoglobin (g/dL)	65	12.8 (11.7–13.6)
Platelets (K/UL)	65	211 (183–268)
White blood cells (K/uL)	65	6.4 (5.5–7.6)

ECOG=Eastern Oncology Cooperative Group, PSA=prostate specific antigen.

*17 patients received prior abiraterone without ketoconazole; 5 patients received prior abiraterone and ketoconazole.

** First-generation anti-androgens include bicalutamide or nilutamide,

*** Percentage for each category is calculated based on N=65, regardless of measurable/non-measurable disease.

**** Others include bladder, pelvis, paraspinal lesion, peritoneum/omentum or prostate.

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Platinum Priority – Prostate Cancer Editorial by Maxton E. Thoman, Keyan Salari on pp. 31–33 of this issue

Pembrolizumab Plus Docetaxel and Prednisone in Patients with Metastatic Castration-resistant Prostate Cancer: Long-term Results from the Phase 1b/2 KEYNOTE-365 Cohort B Study

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Article info	Abstract
Article history:	Background: Patients with metastatic castration-resistant prostate cancer (mCRPC) frequently receive docetaxel after they develop resistance to abiraterone or enzalutamide
Accepted rebidary 22, 2022	and need more efficacious treatments.
Associate Editor:	Objective: To evaluate the efficacy and safety of pembrolizumab plus docetaxel and

Objective: To evaluate the efficacy and safety of pembrolizumab plus docetaxel and prednisone in patients with mCRPC.

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0302-2838/© 2022 Merck Sharp & Dohme Corp., a subsidiary Merck & Co., Inc., Kenilworth, NJ, USA and The Author(s). Published by Elsevier Inc. This is an open access article under the CC BY-NC-ND license (http://creativecommons.org/licenses/by-nc-nd/4.0/).



Keywords: Docetaxel Metastatic castration-resistant prostate cancer Pembrolizumab Prednisone **Design, setting, and participants:** The trial included patients with mCRPC in the phase 1b/2 KEYNOTE-365 cohort B study who were chemotherapy naïve and who experienced failure of or were intolerant to ≥ 4 wk of abiraterone or enzalutamide for mCRPC with progressive disease within 6 mo of screening.

Intervention: Pembrolizumab 200 mg intravenously (IV) every 3 wk (Q3W), docetaxel 75 mg/m² IV Q3W, and prednisone 5 mg orally twice daily.

Outcome measurements and statistical analysis: The primary endpoints were safety, the prostate-specific antigen (PSA) response rate, and the objective response rate (ORR) according to Response Evaluation Criteria in Solid Tumors version 1.1 (RECIST v1.1) by blinded independent central review (BICR). Secondary endpoints included time to PSA progression; the disease control rate (DCR) and duration of response (DOR) according to RECIST v1.1 by BICR; ORR, DCR, DOR, and radiographic progression-free survival (rPFS) according to Prostate Cancer Working Group 3–modified RECIST v1.1 by BICR; and overall survival (OS).

Results and limitations: Among 104 treated patients, 52 had measurable disease. The median time from allocation to data cutoff (July 9, 2020) was 32.4 mo, during which 101 patients discontinued treatment, 81 (78%) for disease progression. The confirmed PSA response rate was 34% and the confirmed ORR (RECIST v1.1) was 23%. Median rPFS and OS were 8.5 mo and 20.2 mo, respectively. Treatment-related adverse events (TRAEs) occurred in 100 patients (96%). Grade 3–5 TRAEs occurred in 46 patients (44%). Seven AE-related deaths (6.7%) occurred (2 due to treatment-related pneumonitis). Limitations of the study include the single-arm design and small sample size.

Conclusions: Pembrolizumab plus docetaxel and prednisone demonstrated antitumor activity in chemotherapy-naïve naive patients with mCRPC treated with abiraterone or enzalutamide for mCRPC. Safety was consistent with profiles for the individual agents. Further investigation is warranted.

Patient summary: We evaluated the efficacy and safety of the anti-PD-1 antibody pembrolizumab combined with the chemotherapy drug docetaxel and the steroid prednisone for patients with metastatic prostate cancer resistant to androgen deprivation therapy, and who never received chemotherapy. The combination showed antitumor activity and manageable safety in this patient population.

This trial is registered on ClinicalTrials.gov as NCT02861573.

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1. Introduction

Despite significant advances in the treatment of prostate cancer, the primary systemic treatment for regional or metastatic prostate cancer is androgen deprivation therapy (ADT) [1]. Most patients with metastatic disease develop resistance to ADT within 1-2 yr and progress to metastatic castration-resistant prostate cancer (mCRPC) [2]. Several treatment options show a survival benefit after development of mCRPC-including abiraterone [3], enzalutamide [4], docetaxel [5], cabazitaxel [6], sipuleucel-T [7], and radium-223 [8]-but are not curative. Next-generation hormonal agents (NHAs) such as abiraterone and enzalutamide are often used following disease progression after ADT, but there is no consensus regarding the optimal sequence for therapy after progression. Docetaxel is a recommended treatment after initial progression on abiraterone or enzalutamide despite the lack of prospective data for docetaxel after NHA therapy [1]. To date, docetaxel combination regimens have not shown a survival benefit over sequential monotherapies with docetaxel [1]. With a 5-yr survival rate estimated at 30% for patients with distant metastases [9,10], there is a need for therapies that prolong survival.

The tumor microenvironment is immunosuppressive in patients with prostate cancer, and therefore restoring the T-cell antitumor response via programmed death 1 (PD-1) or programmed death ligand 1 (PD-L1) blockade is a promising treatment approach [11,12]. Elevated expression of PD-L1 on tumor-infiltrating T cells has been associated with disease progression in prostate cancer [13]. Furthermore, a recent immunohistochemical study showed that metastases from CRPC tumors in patients previously treated with NHAs had increased PD-L1 expression and immunoreactivity [14]. Pembrolizumab is a highly selective humanized monoclonal antibody that blocks interaction between PD-1 and its ligands, PD-L1 and PD-L2, and is approved for the treatment of multiple tumor types [15]. In the phase 2 KEYNOTE-199 trial, pembrolizumab monotherapy showed antitumor activity with manageable safety in patients with mCRPC previously treated with docetaxel and one or more targeted endocrine therapies [16]. Preclinical studies have shown that many chemotherapeutic agents, including taxanes such as docetaxel, can have immunostimulatory effects [17]. Combining immunotherapy and standard chemotherapy may therefore enhance antitumor activity.

The phase 1b/2 KEYNOTE-365 trial (NCT02861573) evaluated the safety, tolerability, and efficacy of pembrolizumab combination therapy in patients with mCRPC. We describe the results for cohort B, which included chemotherapy-naïve patients with mCRPC who experienced disease progression on abiraterone or enzalutamide for mCRPC and who were treated with the combination of pembrolizumab, docetaxel, and prednisone.

2. Patients and methods

2.1. Study design and patients

KEYNOTE-365 is a multicohort, nonrandomized, multicenter, open-label, phase 1b/2 trial. Patients in eight countries (Australia, Canada, France, Germany, New Zealand, Spain, UK, and USA) were enrolled in cohort B. The trial was conducted in accordance with good clinical practice and the Declaration of Helsinki. The protocol and its amendments were approved by the appropriate ethics body at each participating institution. All patients provided written informed consent.

Key eligibility criteria included age \geq 18 yr; histologically or cytologically confirmed adenocarcinoma of the prostate without small-cell histology; disease that progressed within 6 mo before screening (prostatespecific antigen [PSA] progression or radiologic bone/soft tissue progression); Eastern Cooperative Oncology Group performance status score of 0 or 1; received \geq 4 wk of treatment with either abiraterone or enzalutamide (but not both) for mCRPC and with treatment failure or intolerance to the drug; no previous chemotherapy; and serum testosterone level <50 ng/dL. The full inclusion and exclusion criteria are listed in the Supplementary material.

Pembrolizumab 200 mg was administered intravenously (IV) every 3 wk (Q3W) with docetaxel 75 mg/m² IV Q3W and prednisone 5 mg orally twice daily. Pembrolizumab was administered for up to 35 cycles (\sim 2 yr), and docetaxel was administered for up to ten cycles.

2.2. Assessments and endpoints

On-study computed tomography or magnetic resonance imaging and radionuclide bone imaging were performed every 9 wk from the date of allocation through week 54, and then every 12 wk thereafter. The response and radiographic progression for soft tissue lesions were assessed according to Response Evaluation Criteria in Solid Tumors version 1.1 (RECIST v1.1), and radiographic progression for bone lesions was determined according to Prostate Cancer Working Group 3 (PCWG3)-modified RECIST v1.1. Imaging continued until confirmed disease progression, the start of a new anticancer treatment, withdrawal of consent, or death, whichever occurred first. PSA was assessed by a central laboratory at screening and every 3 wk after allocation. Follow-up time began at allocation. PD-L1 positivity was defined as a combined positive score (CPS) \geq 1, where CPS is defined as the number of PD-L1-staining cells (tumor cells, lymphocytes, macrophages) divided by the total number of viable tumor cells, multiplied by 100.

Adverse events (AEs) were monitored throughout the study through 30 d after the last dose of trial treatment (90 d for serious AEs), graded according to the National Cancer Institute Common Terminology Criteria for Adverse Events version 4.0. Immune-mediated AEs were determined by the sponsor on the basis of a list of terms specified by the sponsor as potentially associated with immunologic causes.

Primary efficacy endpoints included the PSA response (PSA reduction of \geq 50% from baseline, measured twice \geq 3 wk apart) and the objective response rate (ORR; complete response [CR] or partial response [PR]) according to RECIST v1.1 as assessed by blinded independent central review (BICR). The primary safety objective was to characterize the safety and tolerability. Secondary endpoints included time to PSA progression; ORR according to PCWG3-modified RECIST v1.1 by BICR; the disease control rate (DCR; CR, PR, stable disease [SD] or non-CR/nonprogressive disease [PD] \geq 6 mo) and the duration of response (DOR) according to RECIST v1.1 and PCWG3-modified RECIST v1.1 by BICR; radiographic progression-free survival (rPFS) according to PCWG3-modified RECIST v1.1 by BICR; and overall survival (OS).

2.3. Statistical considerations

Efficacy and safety populations included all patients who received at least one dose of study treatment (all patients as treated [APaT]). APaT for ORR included only patients with measurable disease at baseline; APaT for DOR included only patients with an objective response. The Clopper-Pearson method was used to provide point estimates and 95% confidence intervals (Cls) for the PSA response rate, ORR, and DCR. The Kaplan-Meier method was used to provide median point estimates and 95% Cls for DOR, time to PSA progression, rPFS, and OS.

Safety and tolerability were assessed via clinical review of all relevant parameters, including AEs, laboratory tests, and vital signs. Counts and percentages for AEs are provided.

Table 1 – Patient demographics and baseline characteristics for the 104 patients treated with pembrolizumab + docetaxel + prednisone

Parameter	Result
Median age, yr (interquartile range)	68 (64-74)
Age ≥ 65 yr, <i>n</i> (%)	77 (74)
Race, n (%)	
White	79 (76)
All others	9 (8.7)
Unknown	16 (15)
Geographic region of enrolling site, n (%)	
North America	41 (39)
Europe	54 (52)
Rest of the world	9 (8.7)
Eastern Cooperative Oncology Group performance status, n (%)	
0	56 (54)
1	48 (46)
Median prostate-specific antigen, ng/mL (interquartile	44.1 (17.1-
range)	131.4)
PD-L1 status, n (%)	
Positive ^a	24 (23)
Negative	76 (73)
Unknown	4 (3.8)
Disease measurable according to RECIST v1.1, n (%)	52 (50)
Median baseline tumor size, mm (interquartile range) ^b	49.9 (26.9-
Marco and Marcona	73.8)
Visceral disease, n (%) ^c	
With liver	8 (7.7)
Without liver	18 (17)
No visceral disease	78 (75)
Metastatic staging, n (%)	
M1	61 (59)
M1A	4 (3.8)
M1B	34 (33)
M1C	5 (4.8)
History of brain metastases, n (%)	
No	101 (97)
Unknown	3 (2.9)
Previous use of abiraterone/enzalutamide, n (%)	
Abiraterone only	51 (49)
Enzalutamide only	52 (50)
Abiraterone and enzalutamide	1 (1.0)
RECIST v1.1 = Response Evaluation Criteria in Solid Tum	ors version 1.1.

^a PD-L1 positivity was defined as a combined positive score (CPS) ≥1.
CPS was calculated as the number of PD-L1-staining cells (tumor cells, lymphocytes, macrophages) divided by the total number of viable tumor cells, multiplied by 100.

^b Assessed by blinded independent central review according to RECIST v1.1.

^c Soft tissue (not in brain, bone, or lymph nodes).

3. Results

3.1. Disposition, demographics, and exposure

As of July 9, 2020, cohort B enrolled 105 patients; 104 patients whose median age was 68.0 yr (interquartile range [IQR] 64-74) with median PSA of 44.1 ng/mL (IQR 17.1-131.4) were treated (Table 1). Median time from allocation to data cutoff was 32.4 mo (IQR 12.2-27.8). At data cutoff, 101 patients (97%) had discontinued treatment (Supplementary Fig. 1). Among those patients, 81 (78%) discontinued because of disease progression and 15 (14%) because of AEs. Patients received a median of 12 cycles (IOR 7.5-15) of pembrolizumab, and 8.5 cycles (IQR 6-10) of docetaxel. All treated patients received at least two cycles of both treatments; 65 (63%) received at least ten cycles of pembrolizumab and 86 (83%) received at least six cycles of docetaxel. The median duration on therapy, defined as the time between the first dose date and the last dose date, was 7.7 mo (IQR 4.8-9.7).

3.2. Efficacy

The confirmed PSA response rate in patients with a baseline PSA measurement was 34% (35/103) for the total population and 27% (14/51) for patients with RECIST-measurable dis-



Fig. 1 – (A) Percentage PSA change from baseline (confirmed and unconfirmed; one patient did not have a baseline PSA measurement). (B) Kaplan-Meier estimate of time to PSA progression. PSA = prostate-specific antigen; RECIST = Response Evaluation Criteria in Solid Tumors.

ease. Seventy-six patients (74%) exhibited any reduction in PSA from baseline, and 45 patients (44%) experienced a PSA reduction of \geq 50% from baseline (Fig. 1A). Of 24 patients with PD-L1–positive tumors, 16 (67%) experienced a reduction in PSA from baseline and nine (38%) experienced a reduction of \geq 50%. Overall, 56/75 patients (75%) with PD-L1–negative tumors experienced a reduction in PSA from baseline, whereas 35 patients (47%) experienced a reduction of \geq 50%. The median time to PSA progression was 29.3 wk (95% CI 21–32; Fig. 1B). PSA response rates were generally consistent across subgroups (Supplementary Fig. 2A).

The confirmed ORR for patients with RECIST-measurable disease was 23% (CR, n = 0; PR, n = 12; Table 2). DCR was 54% for the total population by BICR according to RECIST v1.1. ORRs and DCRs were largely similar between subgroups (Supplementary Fig. 2B,C). Forty-seven of 52 patients (90%) experienced reductions in target lesion size from baseline, and 22 patients (42%) experienced reductions of >30% by BICR according to RECIST v1.1 (Fig. 2A). BICR assessment according to PCWG3-modified RECIST v1.1 revealed a DCR of 68% overall and a confirmed ORR of 33% for patients with measurable disease (Supplementary Table 1). For the 12 patients with a response, the estimated median DOR by BICR according to RECIST v1.1 was 6.3 mo (range 3.4-9.0+), and eight patients (67%) had a response duration ≥ 6 mo according to Kaplan-Meier estimates (Fig. 2B,C). BICR assessment according to PCWG3modified RECIST v1.1 revealed a median DOR of 6.8 mo (range 3.4–10.4), and nine patients (62%) had a response duration >6 mo. Median rPFS was 8.5 mo (95% CI 8.3–10); the 6-mo rPFS rate was 77% and the 12-mo rPFS rate was 26% (Fig. 3A). Median OS was 20.2 mo (95% CI 17-24); the 6-mo OS rate was 96% and the 12-mo OS rate was 76% (Fig. 3B).

3.3. Safety

Treatment-related AEs (TRAEs) attributed by the investigator occurred in 100 patients (96%) (Supplementary Table 2).

Table 2 – Confirmed be review according to REC	st response by IST v1.1	blinded	independent	central

Parameter	$\frac{\text{RECIST-MD}}{(n = 52)}$	$\frac{\text{RECIST-NMD}}{(n = 52)}$	Total (n = 104)
Objective response rate, % (95% CI)	23 (13–37)	NA	NA
Disease control rate, % (95% CI) ^a	52 (38-66)	56 (41-70)	54 (44-64)
Best response, n (%)			
CR	0 (0)	NA	NA
PR	12 (23)	NA	NA
SD of any duration	26 (50)	0(0)	26 (25)
Non-CR/non-PD	0 (0)	41 (79)	41 (39)
SD or non-CR/non-PD $\geq 6 \text{ mo}$	15 (29)	29 (56)	44 (42)
PD	14 (27)	11 (21)	25 (24)
CI = confidence interval; CR = complete response; MD = measurable disease; NA = not applicable; NMD = non-measurable disease; PD = pro- gressive disease; PR = nartial response; SD = stable disease; RECIST v1 1 =			

ease; NA = not applicable; NMD = non-measurable disease; PD = pro gressive disease; PR = partial response; SD = stable disease; RECIST v1.1 Response Evaluation Criteria in Solid Tumors version 1.1. ^a Disease control rate defined as CR + PR + SD or non-CR/non-PD ≥ 6 mo.



Fig. 2 – (A) Target lesion change from baseline (confirmed and unconfirmed), (B) time to response for responders by BICR according to RECIST version 1.1, and (C) Kaplan-Meier estimate of the duration of response for responders by BICR according to RECIST version 1.1. APaT = all patients as treated; BICR = blinded independent central review; PD = progressive disease; PR = partial response; RECIST = Response Evaluation Criteria in Solid Tumors.

Grade 3–5 TRAEs occurred in 46 patients (44%). The most frequent TRAEs (incidence \geq 20%) were diarrhea, fatigue, alopecia, dysgeusia, nausea, peripheral neuropathy, and asthenia (Table 3). The most frequent grade 3–5 TRAEs



Fig. 3 – Kaplan-Meier estimates of (A) radiographic progression-free survival according to Prostate Cancer Working Group 3-modified Response Evaluation Criteria in Solid Tumors version 1.1 and (B) overall survival.

(incidence $\geq 2\%$) were febrile neutropenia, decreased neutrophil count, anemia, neutropenia, diarrhea, fatigue, pneumonitis, and decreased lymphocyte count. Serious TRAEs occurred in 24 patients (23%; Supplementary Table 3), and 28 (27%) discontinued because of TRAEs (pembrolizumab, n = 13 [13%]; docetaxel, n = 24 [23%]; prednisone, n = 10 [9.6%]).

Sponsor-defined immune-mediated AEs occurred in 34 patients (33%); nine (8.7%) experienced grade 3–5 events (pneumonitis, n = 4; colitis, n = 4; severe skin reaction, n = 1; Supplementary Table 4). The most common immune-mediated AEs (incidence $\geq 5\%$) were infusion reactions, hyperthyroidism, pneumonitis, colitis, and hypothyroidism. Of 46 immune-mediated AE episodes, ten (22%) necessitated concurrent systemic corticosteroids with a high starting dose (\geq 40 mg/d prednisone or equivalent).

Overall, seven patients (6.7%) died of AEs. Five deaths (4.8%) were unrelated to treatment (cerebrovascular accident, n = 1; pneumonia, n = 2; malignant neoplasm progression, n = 2). Two deaths (1.9%) from AEs (both pneumonitis, an immune-mediated AE) were related to treatment as

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Table 3 – Treatment-related adverse events with ${\geq}5\%$ incidence among the 104 patients treated with pembrolizumab + docetaxel + prednisone

Treatment-related adverse event	Patients, n (%)		
	Any grade	Grade 3–5	
Any	100 (96)	46 (44)	
Diarrhea	43 (41)	3 (2.9)	
Fatigue	43 (41)	3 (2.9)	
Alopecia	42 (40)	0 (0)	
Dysgeusia	28 (27)	0 (0)	
Nausea	27 (26)	0 (0)	
Peripheral neuropathy	23 (22)	0 (0)	
Asthenia	22 (21)	2 (1.9)	
Anemia	19 (18)	5 (4.8)	
Decreased appetite	16 (15)	0 (0)	
Peripheral edema	15 (14)	1 (1.0)	
Mucosal inflammation	13 (13)	0 (0)	
Febrile neutropenia	12 (12)	12 (12)	
Dyspepsia	11 (11)	0 (0)	
Paresthesia	11 (11)	0(0)	
Arthralgia	10 (9.6)	1 (1.0)	
Dyspnea	10 (9.6)	0 (0)	
Decreased neutrophil count	10 (9.6)	6 (5.8)	
Peripheral sensory neuropathy	10 (9.6)	0 (0)	
Hyperthyroidism	8 (7.7)	0 (0)	
Nail discoloration	8 (7.7)	0(0)	
Nail disorder	8 (7.7)	0 (0)	
Neutropenia	8 (7.7)	5 (4.8)	
Pruritus	8 (7.7)	0(0)	
Pyrexia	8 (7.7)	0 (0)	
Constipation	7 (6.7)	0 (0)	
Cough	7 (6.7)	0 (0)	
Dry skin	7 (6.7)	0 (0)	
Infusion reaction	7 (6.7)	0(0)	
Insomnia	7 (6.7)	0 (0)	
Pain in extremity	7 (6.7)	0 (0)	
Pneumonitis	7 (6.7)	3 (2.9)	
Exertional dyspnea	6 (5.8)	0(0)	
Flushing	6 (5.8)	0 (0)	
Decreased lymphocyte count	6 (5.8)	3 (2.9)	
Muscle spasms	6 (5.8)	0 (0)	
Myalgia	6 (5.8)	0(0)	
Maculopapular rash	6 (5.8)	1 (1.0)	

determined by the investigator. One death from pneumonitis occurred 40 d after the patient's last exposure to treatment (4 d after AE onset), and the other occurred 63 d after the patient's last exposure to treatment (13 d after AE onset).

4. Discussion

Combination therapy with pembrolizumab plus docetaxel and prednisone showed a clinical benefit for chemotherapy-naïve patients previously treated with abiraterone or enzalutamide for mCRPC in cohort B of the KEYNOTE-365 study. The confirmed PSA response rate was 34% for patients with baseline PSA measurements, with an ORR of 23% by BICR for those with measurable disease. Antitumor activity was noted in RECIST-measurable and bone-predominant disease, and in PD-L1-positive and PD-L1-negative tumors. The benefit was similar regardless of whether the previous NHA was abiraterone or enzalutamide. Among the patients with RECIST-measurable disease, none experienced CR, and 12 experienced PR as the best response. The target lesion size was reduced in 90% of patients in the current study, with 42% of patients experiencing reductions >30% by BICR. The safety profile of the

combination was manageable and consistent with the profiles of the individual agents. The PSA response rate, ORR, and OS observed in the present study are higher than those observed in two cohorts of patients with RECISTmeasurable mCRPC in the phase 2 KEYNOTE-199 study of pembrolizumab monotherapy

(cohort 1 [PD-L1–positive]: PSA response, 6%; ORR, 6%; OS, 9.5 mo; cohort 2 [PD-L1–negative]: PSA response, 8%; ORR, 3%; OS, 7.9 mo) [18]. However, patients in KEYNOTE-199 previously received docetaxel, whereas patients in KEYNOTE-365 cohort B had chemotherapy-naïve mCRPC.

The efficacy of docetaxel was established in the phase 3 study of docetaxel and prednisone versus mitoxantrone and prednisone in patients with mCRPC who experienced progression during hormone therapy and subsequently received antiandrogen therapy [19]. Docetaxel Q3W led to a 2.4-mo improvement in OS versus mitoxantrone (18.9 vs 16.5 mo; hazard ratio [HR] 0.76, 95% CI 0.62–0.94; p = 0.009). Confirmed PSA levels decreased by \geq 50% from baseline in 45% of patients receiving docetaxel and 32% receiving mitoxantrone. In the current study, the confirmed PSA response rate was 34%. The docetaxel versus mitoxantrone study took place before the development of abiraterone and enzalutamide; hence, the data are limited regarding the efficacy of docetaxel after NHA treatment, and the optimal order of therapies is not clear.

The phase 3 FIRSTANA trial compared OS after cabazitaxel (two dose schedules) versus docetaxel in 1168 patients with chemotherapy-naïve mCRPC [20]. For the docetaxel group, the median OS was 24.3 mo, the median time to tumor progression was 12.1 mo, and the tumor response rate (CR or PR) was 31%. However, few patients enrolled in FIRSTANA had previously received enzalutamide or abiraterone. In one retrospective study that included patients from a phase 1/2 abiraterone trial, median OS for patients who received docetaxel after abiraterone was 12.5 mo (95% CI 10.6-19.4), and 13 patients (37%) experienced a PSA decrease of \geq 30% [21]. By contrast, the current study showed longer OS after pembrolizumab plus docetaxel and prednisone (20.2 mo, 95% CI 16.9-24.2) than previously reported. Cross-resistance between abiraterone and docetaxel could be the reason why patients receiving docetaxel after abiraterone are more likely to experience disease progression, but additional studies are needed to confirm this hypothesis [21,22]. Enzalutamide has also been used in patients with mCRPC with disease progression after abiraterone. Although the sample size was small (n = 61), a retrospective analysis compared docetaxel (n = 31) and enzalutamide (n = 30) in patients with mCRPC whose disease had progressed on abiraterone [23]. In a multivariable logistic model controlled for baseline and primary refractoriness to previous abiraterone therapy, there was no significant difference between the groups in the odds of a PSA decline of \geq 30% (odds ratio 2.17, 95% CI 0.68–7.30; p = 0.20) or >50% (odds ratio 1.68, 95% CI 0.51-5.66; p = 0.40). Median PSA PFS was 4.1 mo for both the docetaxel and enzalutamide cohorts (HR 1.35, 95% CI 0.53-3.656); median PFS was 4.7 mo for the enzalutamide cohort and 4.4 mo for the docetaxel cohort (HR, 1.44, 95% CI 0.77-2.71; p = 0.257 [23]. A mouse model of CRPC showed lower

efficacy of docetaxel in mice with enzalutamide-resistant tumors compared with enzalutamide-naïve tumors, similar to the hypothesized cross-resistance between abiraterone and docetaxel [24]. These findings suggest that further study of the optimal sequencing of NHA and chemotherapy agents such as docetaxel may be warranted.

The current study is limited by its small sample size and single-arm design. However, the promising ORR (23%; *n* = 12 with PR) and OS (20.2 mo) served as a rationale to further investigate this treatment combination in KEYNOTE-921 (NCT03834506). KEYNOTE-921 is a randomized, global, parallel-group, double-blind, phase 3 trial to investigate pembrolizumab (200 mg IV Q3W) plus docetaxel (75 mg/m² IV Q3W) and prednisone (5 mg orally twice daily) versus placebo plus docetaxel and prednisone in patients with histologically or cytologically confirmed chemotherapy-naïve mCRPC with disease progression after NHA therapy [25].

The phase 2 CheckMate 9KD study examined the PD-L1 inhibitor nivolumab combined with docetaxel and prednisone. The ORR was 36.8%, with median rPFS of 8.2 mo after minimum follow-up of 28 wk for patients with chemotherapy-naïve mCRPC (65% previously received abiraterone or enzalutamide), similar to the rPFS in the current study (8.5 mo) with comparable safety results [26]. The subsequent phase 3 CheckMate 7DX trial will further investigate this combination.

Mismatch repair deficiency (dMMR), microsatellite instability, and/or hypermutation are believed to be potential enrichment biomarkers for response to immunotherapy in patients with solid tumor malignancies. However, the microsatellite instability-high/dMMR phenotype is rare in mCRPC, affecting only 3–4% of patients [27,28]. There is limited information about and there are no trial data for the response rate to pembrolizumab for this rare prostate cancer population. Therefore, we feel it is unlikely that our findings were significantly affected by these potential enrichment factors.

5. Conclusions

Pembrolizumab plus docetaxel and prednisone demonstrated antitumor activity in chemotherapy-naïve patients with mCRPC previously treated with abiraterone or enzalutamide for mCRPC. OS was longer than observed in previous studies in this population, and the ORR is similarly promising. The safety profile was manageable and consistent with the known profiles of each agent. Our results show activity for this combination, which will be confirmed in the phase 3 KEYNOTE-921 trial.

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Astex, AstraZeneca, Aveo Pharmaceuticals, Bayer, BeiGene, Blueprint, BMS, Boehringer Ingelheim, Celgene, Chugai, Clovis, Daiichi Sankyo, Debiopharm, Eisai, Eos, Exelixis, Forma, GamaMabs, Genentech, Gortec, GSK, H3 Biomedicine, Incyte, Innate Pharma, Janssen, Kura Oncology, Kyowa, Lilly, Loxo, Lysarc, Lytix Biopharma, MedImmune, Menarini, Merus, MSD, Nanobiotix, Nektar Therapeutics, Novartis, Octimet, OncoEthix, Oncopeptides AB, Orion, Pfizer, PharmaMar, Pierre Fabre, Roche, Sanofi, Servier, Sierra Oncology, Taiho, Takeda, Tesaro, and Xencor. Xin Tong Li is an employee of MSD China. Charles Schloss and Christian H. Poehlein are employees of Merck Sharp & Dohme Corp., a subsidiary of Merck & Co., Inc., Kenilworth, NJ, USA, and own stock in Merck & Co., Inc., Kenilworth, NJ, USA. Johann S. de Bono has received personal fees and travel expenses for serving as an advisor for Amgen, Astellas, Astra-Zeneca, Bayer, BioXcel Therapeutics, Boehringer Ingelheim, CellCentric, Daiichi, Eisai, Roche/Genentech, Genmab, GlaxoSmithKline, Harpoon, Janssen, Menarini Silicon Biosystems, Merck Serono, Merck Sharp & Dohme, Orion Pharma, Pfizer, Qiagen, Sanofi Aventis, Sierra Oncology, Taiho, Terumo, and Vertex Pharmaceuticals; has received institutional grants from Astellas, AstraZeneca, Bayer, CellCentric, Daiichi, Roche/ Genentech, Genmab, GlaxoSmithKline, Harpoon, Janssen, Merck Serono, Merck Sharp & Dohme, Orion Pharma, Pfizer, Sanofi Aventis, Sierra Oncology, Taiho, and Vertex Pharmaceuticals; and holds patents WO 2005 053662 licensed to AstraZeneca and US5604213 licensed to Janssen, for which he receives no personal income.

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Data sharing statement: Merck Sharp & Dohme Corp. (MSD), a subsidiary of Merck & Co., Inc., Kenilworth, NJ, USA, is committed to providing qualified scientific researchers access to anonymized data and clinical study reports from the company's clinical trials for the purpose of conducting legitimate scientific research. MSD is also obligated to protect the rights and privacy of trial participants and, as such, has a procedure in place for evaluating and fulfilling requests for sharing company clinical trial data with qualified external scientific researchers. The MSD data sharing website (available at: http://engagezone.msd.com/ds_documentation.php) outlines the process and requirements for submitting a data request. Applications will be promptly assessed for completeness and policy compliance. Feasible requests will be reviewed by a committee of MSD subject matter experts to assess the scientific validity of the request and the qualifications of the requestors. In line with data privacy legislation, submitters of approved requests must enter into a standard data-sharing agreement with MSD before data access is granted. Data will be made available for request after product approval in the US and EU or after product development is discontinued. There are circumstances that may prevent MSD from sharing requested data, including country or regionspecific regulations. If the request is declined, it will be communicated to the investigator. Access to genetic or exploratory biomarker data requires a detailed, hypothesis-driven statistical analysis plan that is collaboratively developed by the requestor and MSD subject matter experts; after approval of the statistical analysis plan and execution of a datasharing agreement, MSD will either perform the proposed analyses and share the results with the requestor or will construct biomarker covariates and add them to a file with clinical data that is uploaded to an analysis portal so that the requestor can perform the proposed analyses.

Appendix A. Supplementary data

Peer Review Summary and Supplementary Data associated with this article can be found online at https://doi.org/10. 1016/j.eururo.2022.02.023.

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Appendix 3

Curricula vitae:

Heather H. Cheng – PI [2020-2022] Evan Y. Yu - co-investigator Michael T. Schweizer - co-investigator Celestia Higano – PI [2017-2020]

UNIVERSITY OF WASHINGTON SCHOOL OF MEDICINE

CURRICULUM VITAE HEATHER H. CHENG, MD, PhD

1.	Personal Data: Place of birth: Citizenship:	
2.	Education: 1994-1998	Bachelor of Arts, Molecular Biology Princeton University, Princeton, NJ
	2000-2005	Doctor of Philosophy, Molecular and Cellular Biology University of Washington, Seattle, WA
	1998-2007	Doctor of Medicine (NIH Medical Scientist Training Program) University of Washington School of Medicine, Seattle, WA
3.	Postgraduate Training: 06/2007-06/2009	Internship and Residency, Internal Medicine University of Washington, Seattle, WA
	07/2009-08/2014	Fellowship, Hematology-Oncology (ABIM Research Pathway) University of Washington, Seattle, WA
4.	Faculty Positions Held: 03/2014-06/2019	Assistant Professor, Division of Medical Oncology, Department of Medicine, University of Washington, Seattle, WA
	03/2014-06/2019	Assistant Professor, Clinical Research Division, Fred Hutchinson Cancer Research Center, Seattle, WA
	07/2019-present	Associate Professor, Division of Medical Oncology, Department of Medicine University of Washington, Seattle, WA
	07/2019-present	Associate Professor, Clinical Research Division, Fred Hutchinson Cancer Research Center, Seattle, WA
	04/2021-present	Adjunct Associate Professor, Department of Laboratory Medicine and Pathology, University of Washington, Seattle, WA
5.	Hospital Positions Held: 03/2014-present	Attending Physician, Genitourinary Medical Oncology Clinics Seattle Cancer Care Alliance, Seattle, WA
	03/2014-present	Attending Physician, Inpatient Oncology Service, Oncology Consult Service, University of Washington Medical Center, Seattle, WA
	09/2016-present	Director, Prostate Cancer Genetics Clinic Seattle Cancer Care Alliance, Seattle, WA
	02/2019-present	Attending Physician, Genitourinary Cancer Risk Management (GU/GICP) Seattle Cancer Care Alliance, Seattle, WA

6. Current (non-UW) Employment: n/a

7. Honors:

- 1998 Sigma Xi Society, Princeton, NJ
- 1998 New Jersey Cancer Commission Research Fellowship
- 2000 Paul Allen Research Fellowship
- 2009 University of Washington School of Medicine: Resident Teaching Award
- 2012 American Society of Clinical Oncology/National Cancer Institute Markers in Cancer Meeting, Merit Award
- 2014 American Society of Clinical Oncology Genitourinary Oncology Symposium, Merit Award
- 2014 American Society of Clinical Oncology Annual Meeting, Merit Award
- 2015 Prostate Cancer Foundation Young Investigator Award
- 2015 SWOG Integrated Translational Science Workshop, Cold Spring Harbor
- 2017 Becker's Healthcare, Rising Stars: Healthcare Leaders Under 40
- 2020 National Cancer Institute, Cancer Clinical Investigator Team Leadership Award

8. Board Certification:

- 2010 American Board of Internal Medicine, Certification in Internal Medicine
- 2013 American Board of Internal Medicine, Certification in Medical Oncology

9. Current License(s) to Practice:

Washington State Medical License #MD60095549	expires 11/03/2024
DEA #FC2472328	expires 08/31/2025

10. Diversity, Equity and Inclusion Activities:

2020-present	Prostate Cancer Clinical Trials Consortium Diversity and Outreach Committee
2022	Ad hoc mentor for Fred Hutchinson Cancer Center Eddie Méndez Scholar Awardee,
	Aileen Fernandez PhD, post-doctoral fellow, Yale University
2022-present	Career advisor for Morehouse School of Medicine/University Washington Medical
	Scientist Training Program student, Gygeria Manuel

11. Professional Organizations:

2022-present	American Urological Association
2009-present	American Society of Clinical Oncology
2005-present	American Association of Cancer Research
2013-present	Southwest Oncology Group (SWOG)
2005-2009	American College of Physicians
1998-2009	Physicians for Social Responsibility

12. Teaching Responsibilities:

2020-present	Associate Program Director, University of Washington/Fred Hutchinson Cancer
	Center Medical Scientist Training Program

University of Washington School of Medicine:
HUBIO 513, 522 and 535, Intro to Clinical Medicine, Small Group Leader
MEDECK 614, Medical Oncology Clerkship, Richard Stein, MS4 (Fall 2014).
HUBIO 550, Introduction to Clinical Medicine, panelist
MED 505, Dept of Medicine Preceptorship, clinical preceptor: Dilip Nagakar, MS1
(Fall 2014); Caroline Jackson, MS1 (Fall 2015); J.D. Neumeister, MS2 (Fall 2016)
MEDSCI 540A, Blood and Cancer, small group leader

TEACHING/COMMITTEES:

A. Residents, Graduate Students & Medical Students (*primary mentor)

2017 Paul Katangole, MD, MS, (Uganda Cancer Institute), mentor for NCI Fogarty International Center Fellow Candidate
2018-2019	*Darren Pouv, 1 st year medical student, University of Washington School of Medicine, primary research mentor, Independent Investigative Inquiry			
2020	Emiko M. Oshima, University of Washington School of Medicine: MPH candidate, research mentoring committee member			
2022	Sunny Ren, University of Washington Genetic Counseling Program, Masters candidate, research project co-mentor			
B. Subspecialty Fellows (*primary/co-primary mentor)				
2014-2015	Faculty advisor for UW/FHCRC Heme/Onc Fellows' Solid Tumor Conference			
2014-present	Teaching Faculty for Heme/Onc fellows and Internal Medicine residents in Genitourinary			
	Oncology and Bladder Multi-disciplinary Clinics and Inpatient Oncology service.			
2018-2021	*Alexandra Sokolova, MD, University of Washington/Fred Hutch Heme/Onc fellow, primary research mentor, current position: Assistant Professor at Oregon Health Sciences University (as of 2022)			
2019-present	Faculty Champion for Hematology/Oncology Fellowship, Outpatient Genitourinary Oncology Block			
2019-2022	Risa Wong, MD, University of Washington/Fred Hutch Heme/Onc fellow, research co- mentor, current position: Assistant Professor at University of Pittsburg			
2021-present	*Hiba Khan, MD, MPH, University of Washington/Fred Hutch Hematology/Oncology fellow, primary research co-mentor			
2022-present	Ruben Raychaudry, MD, University of Washington/Fred Hutch Hematology/Oncology fellow, research project co-mentor			

13. Editorial Responsibilities: n/a

14. Special National Responsibilities:

June 2017	Organizing Chair, Coffey-Holden Prostate Cancer Academy*, Carlsbad, CA
	(*prestigious invitation-only annual meeting for \sim /5 prostate cancer researchers)
June 2017-	Chair, Prostate Cancer Clinical Trials Consortium/PCF Genetics Working Group
2017-2018	Co-Leader, Prostate Cancer Foundation DNA Repair Working Group
October 2017	Session Chair, DNA Repair, Prostate Cancer Foundation 24 th Scientific Retreat,
	Washington D.C.
February 2018	Prostate Cancer Foundation Delegation on Prostate Cancer Genetics, Tel Aviv, Israel
April 2018-	Healthcare and Scientific Advisory Board, FORCE: Facing Hereditary Cancer
	Empowered Organization
June 2018	Education Session Chair, American Society for Clinical Oncology, 2018 Annual
	Meeting, Practical Methods for Integrating Genetic Testing into Clinical Practice for
	Advanced Prostate Cancer, Chicago, IL
August 2019-	Member, Prostate Cancer Guidelines Panel, National Comprehensive Cancer
	Network, (NCCN)
2020-2021	Board of Directors, Us-TOO International Prostate Cancer Education and Support
	Network (private, non-profit 501(c)3)
October 2020-	Member, Prostate Cancer Task Force, National Cancer Institute Genitourinary
	Steering Committee
June 2021-	Member, American Society for Clinical Oncology, Annual Meeting Education
	Committee: Genitourinary Cancer—Prostate, Testicular, and Penile Track (3-year term)
August 2021-	Member, Germline and Somatic Genomic Testing for Advanced and Metastatic Prostate
	Cancer Guideline Panel, American Society for Clinical Oncology
March 2022-	Member, American Urological Association Salvage Therapy for Prostate Cancer Panel
May 2022-	Member, Genetic/Familial High-Risk Assessment: Breast, Ovarian, and Pancreatic Panel
	Guidelines Panel, National Comprehensive Cancer Network, (NCCN)
Oct 2022-	Chief Scientific Officer, BRCA Research & Cure Alliance (CureBRCA)

June 2023 Education Session Chair, American Society for Clinical Oncology, 2023 Annual Meeting, Genetic and Genomic Testing for Prostate Cancer: Beyond DNA Repair Deficiencies, Chicago, IL

15. Special Local Responsibilities:

University of Washington Hematology-Oncology Fellowship, fellow representative University of Washington Hematology-Oncology Fellows Orientation Handbook, first	
editor and author	
University of Washington Hematology-Oncology Solid Tumor Conference, fellow organizer	
Genitourinary Cancer Clinical Research Database, faculty lead	
Seattle Cancer Care Alliance Schwartz Center Rounds Planning Committee	
Fred Hutchinson Cancer Center/University of Washington Cancer Consortium	
Data Safety Monitoring Committee	
Fred Hutch/Clinical Research Division, Appointments and Promotions Committee	
Fred Hutch/Human Biology Division, Prostate Program Faculty Search Committee	
Fred Hutch/UW Cancer Consortium Pilot Award Review Committee	
SCCA Genitourinary Medical Oncology Community Research Working Group lead	
Faculty search committee for University of Washington, Department of Urology	

16. Research Funding

CURRENT RESEARCH SUPPORT

Title: 2021 Prostate Cancer Clinical Consortium Clinical Research Site: University of Washington **Major Goals:** The proposed study will 1) characterize advanced prostate cancer using new genotypic and phenotypic methods and inform the design of precision oncology clinical trials, 2) define and address mechanisms of therapeutic resistance by developing clinical trials of novel therapeutic combinations, and 3) advance equitable delivery of precision oncology clinical trials to men with prostate cancer from high-risk, underserved and/or military populations.

Status of Support: Active

Project Number: W81XWH-22-2-0016 Name of PD/PI: Heather Cheng Source of Support: US Department of Defense (DOD) Primary Place of Performance: Fred Hutch Cancer Center – Seattle, WA Project/Proposal Start and End Date: 09/30/2022 – 09/29/2026 Total Award Amount:

Title: Pacific Northwest (PNW) Prostate Cancer Sponsored Program of Research Excellence (SPORE) Project 1: Molecular Predictors of Prostate Cancer Progression and Mortality **Major Goals:** The proposed study will ascertain and recruit germline cancer risk mutation carriers from: 1) population- and clinic-based incident cases of metastatic PC to find index cases with germline cancer risk mutations; 2) to conduct a PC early detection study incorporating novel biomarkers for unaffected, male germline mutation carriers (including first degree relatives of those with metastatic PC who are mutation carriers); and 3) to understand the cascade genetic testing process what will facilitate an innovative recruitment strategy for recruiting men at highest genetic risk of aggressive prostate cancer. **Status of Support:** Active **Project Number:** 5 P50 CA097186-16 **Name of PD/PI:** Peter Nelson **Source of Support:** NIH/NCI **Primary Place of Performance:** Fred Hutch Cancer Center – Seattle, WA **Project/Proposal Start and End Date:** 09/01/18 to 08/31/23 **Total Award Amount:** Title: 2020 Cancer Clinical Investigator Team Leadership Award (CCITLA)

Major Goals: To work with cancer consortium staff and colleagues to harmonize genitourinary cancer clinical trial portfolio and transfer to media-friendly formats. To expand cancer genetics care delivery to newer formats to expand delivery of care and disseminate research opportunities to the cancer center catchment and region.

Status of Support: Active Project Number: CCITLA - Yr 4 2023 Name of PD/PI: Heather Cheng Source of Support: Fred Hutchinson Cancer Center Primary Place of Performance: Fred Hutchinson Cancer Center – Seattle, WA Project/Proposal Start and End Date: 01/01/2020 – 12/31/2023 Total Award Amount:

Title: ACT PROMISE (Cheng)

Major Goals: The major goal of this study, in collaboration with Dr. Channing Paller, is to design, implement, recruit patients, and identify prostate cancer patients who carry germline pathogenic variants, assessing frequency, family history, outcomes, longitudinal treatment response, treatment sequences and therapy combinations. Status of Support: Active Project Number: ACT c19-235-Promise Registry Name of PD/PI: Heather Cheng Source of Support: DOD PROSTATE CANCER CLINICAL TRIALS CONSORTIUM Primary Place of Performance: Fred Hutch Cancer Center – Seattle, WA Project/Proposal Start and End Date: 06/19/2020 to 06/30/2024 Total Award Amount:

Title: PLATI-PARP: A phase 2 study of induction docetaxel and carboplatin followed by maintenance rucaparib in treatment of patients with metastatic castration resistant prostate cancer with homologous recombination DNA repair deficiency

Status of Support: Active Project Number: 338-IIT-071 Name of PD/PI: Heather Cheng Source of Support: Clovis Oncology, Inc Primary Place of Performance: Fred Hutch Cancer Center – Seattle, WA Project/Proposal Start and End Date: 07/26/2018 to 08/30/2023 Total Award Amount:

Title: Enhanced Genetic Awareness and Genetic Evaluation for Men Through Technology - The ENGAGEMENT Study

Major Goals: The project will 1) Develop and implement a web-based virtual PCA genetics board across academic, community, and VA settings. Perceived usefulness, acceptability, self-efficacy for genetically-based recommendations, and genetics knowledge from dynamic case-based learning will be assessed. 2) Establish a web-based, national, patient-driven registry for any male who has undergone PCA genetic testing to assess men's experience with the genetic evaluation process and inform patient centered genetics practice and resource development. 3) Utilize digital media to share updated information on genetic testing and precision management of PCA through a public-facing podcast series. **Status of Support:** Active

Project Number: W81XWH2010310 Name of PD/PI: Veda Giri Source of Support: US Department of Defense (DOD) Primary Place of Performance: Fred Hutch Cancer Center – Seattle, WA Project/Proposal Start and End Date: 09/30/2020-09/29/2023 Total Award Amount:

Title: A Study of Rucaparib Versus Physician's Choice of Therapy in Patients With Metastatic Castration-resistant Prostate Cancer and Homologous Recombination Gene Deficiency (TRITON3)

Major Goals: The major goal of this study is to assess the efficacy of rucaparib versus physician's choice of treatment based on radiographic progression free survival (rPFS) in mCRPC patients with HRD who progressed on prior AR-directed therapy and have not yet received chemotherapy in the castration-resistant setting.

Status of Support: Active Project Number: CO-338-063 Name of PD/PI: Celestia Higano (2018-2021) Heather Cheng (2021 – Present) Source of Support: Clovis Oncology Primary Place of Performance: Fred Hutch Cancer Center – Seattle, WA Project/Proposal Start and End Date: 8/21/2018 – 4/30/2023 Total Award Amount:

Title: AMPLITUDE A Study of Niraparib in Combination With Abiraterone Acetate and Prednisone Versus Abiraterone Acetate and Prednisone for the Treatment of Participants With Deleterious Germline or Somatic Homologous Recombination Repair (HRR) Gene-Mutated Metastatic Castration-Sensitive Prostate Cancer

Major Goals: The major goal of this study is to assess the primary endpoint, rPFS, and defined as the time from the date of the randomization to the date of radiographic progression, or death. Status of Support: Active Project Number: 67652000PCR3002 Name of PD/PI: Heather Cheng Source of Support: Janssen Research & Development, LLC Primary Place of Performance: Fred Hutch Cancer Center – Seattle, WA Project/Proposal Start and End Date: 8/16/2021 – 1/31/2026 Total Award Amount:

Title: A Phase 1, open label study evaluating the safety, pharmacokinetics and clinical effects of intravenously administered PT-112 injecting in patients with advanced solid tumors and subsequent expansion cohorts

Major Goals: Define the recommended dose level for PT-112, administered on Days 1 and 15 of each 28-day cycle, for pivotal studies based on the risk/benefit ratio of 360 mg/m2 (Arm 1) and 250 mg/m2 (Arm 2) dose levels.

Status of Support: Active Project Number: PT-112-101 Name of PD/PI: Heather Cheng Source of Support: Phosplatin Therapeutics LLC Supporting Agency: Phosplatin Therapeutics LLC Primary Place of Performance: Fred Hutch Cancer Center – Seattle, WA Project/Proposal Start and End Date: 9/28/21 – 7/31/2026 Total Award Amount:

Title: Prostate Cancer Outcomes: An International Registry to Improve Outcomes in Men with Advanced Prostate Cancer (IRONMAN) Major Goals: The major goal of this study is to create an international, population-based, prospective registry of at least 5,000 men with advanced prostate cancer. Status of Support: Active Project Number: C16-170 Name of PD/PI: Heather Cheng Source of Support: Movember (via PCCTC, LLC) Primary Place of Performance: Fred Hutch Cancer Center – Seattle, WA

Project/Proposal Start and End Date: 08/18/17 to 01/31/2029 Total Award Amount:

Title: IRONMAN: An International Registry and/or the PMC Sub-Study for Men with Advanced Prostate Cancer

Major Goals: The primary objective of this substudy is to describe the response and DOR to olaparib

among subjects with mCRPC whose disease has progressed following prior treatment with an NHA. Subjects with a mutation in one of the nine HRR genes (BARD1, BRIP1, CHEK1, FANCL, PALB2, RAD51B, RAD51C, RAD51D, and RAD54L) that were evaluated in five or fewer subjects within cohort B of the PROfound study will be included in the study.

Status of Support: Active

Project Number: C16-170a Name of PD/PI: Heather Cheng Source of Support: AstraZeneca Pharmaceuticals, LP (via PCCTC, LLC) Primary Place of Performance: Fred Hutch Cancer Center – Seattle, WA Project/Proposal Start and End Date: 08/18/17 to 01/31/2029 Total Award Amount:

Title: Long-read DNA-sequencing and targeted RNA-Seq to identify previously undetectable classes of mutations in families with lethal prostate cancer.

Major Goals: We intend our approach to improve genetic testing for inherited predisposition to prostate cancer, particularly in families with a severe history of the disease but no genetic diagnosis. We will Inform all patients with positive test results and integrate new genetic information into their care following NCCN guidelines for mutation carriers and offer genetic testing to their family members. As such, our proposal specifically addresses the overarching challenge of reducing lethal prostate cancer in high risk populations.

Status of Support: Active

Project Number: W81XWH-21-1-0343 Name of PD/PI: Tomas D. Walsh Source of Support: US Department of Defense (DOD) Primary Place of Performance: University of Washington Medical Center – Seattle, WA Project/Proposal Start and End Date: 06/01/2021 – 05/31/2024 Total Award Amount:

PENDING RESEARCH SUPPORT

Title: Pacific Northwest (PNW) Prostate Cancer Sponsored Program of Research Excellence (SPORE) Project 1: Molecular Predictors of Prostate Cancer Progression and Mortality **Major Goals:** The major goals of the study are to define the independent and combined effect of multiancestry PRS (PRS_m) and gDRG with clinical characteristics of prostate cancer aggressiveness and prognosis across diverse populations. To develop clinical-grade paired tumor-germline molecular profiling assays to prospectively interrogate multi-ancestry PRS and gDRG. And to conduct a tailored prostate cancer screening clinical trial for at-risk men with gDRG and determine patterns of enrollment and adherence.

Status of Support: Pending Project Number: PAR-20-305 Name of PD/PI: Peter Nelson Source of Support: NIH/NCI Primary Place of Performance: Fred Hutch Cancer Center – Seattle, WA Project/Proposal Start and End Date: 09/01/23 - 08/31/28 Total Award Amount:

Title: NCI R50 Research Specialist (Clinician Scientist)

Major Goals: The project goals are to continue contribution to NCI and NCTN supported clinical/translational research, mentoring clinical scientists, and developing novel approaches to clinical research and to education and outreach for patients with the goal of accruing a more representative cohort of patients to the next generation of targeted and patient-partnered clinical trials.

Status of Support: Pending Project Number: PAR-20-306 Name of PD/PI: Heather Cheng

Source of Support: NIH/NCI

COMPLETED RESEARCH SUPPORT

1998	New Jersey Cancer Commission Research Fellowship
1998-2000	NIH Medical Scientist Training Program Fellowship
2000-2004	Paul Allen Research Fellowship
2010-2013	NIH T32 Training in Cancer Biology and Transplantation Fellowship

Title: SWOG 1216: A phase III randomized trial comparing androgen deprivation therapy + TAK-700 with androgen deprivation therapy + bicalutamide in patients with newly diagnosed metastatic hormone sensitive prostate cancer

Supporting Agency: NIH/NCI (U10 CA180828) Performance Period: 05/20/14 – 02/28/18

Level of Funding:

Project Goals: Compare overall survival in newly diagnosed metastatic prostate cancer patients randomly assigned to androgen deprivation therapy (ADT) (LHRHa or orchiectomy) + TAK-700 versus ADT (LHRHa or orchiectomy) + bicalutamide.

Title: Genitourinary Cancer Clinical Research Database Support
Supporting Agency: Institute for Prostate Cancer Research (IPCR)
Performance Period: 09/01/14 – 12/31/19
Level of Funding:
Project Goals: The GU Cancer Clinical Research Database (GUCCRD) is designed to inventory, display, aggregate, and integrate comprehensive clinical information derived from patients with prostate cancer (and potentially other GU malignancies).

Title: Cancer Center Support Grant: New Investigator Award **Supporting Agency:** NIH/NCI (P30 CA015704) **Performance Period:** 12/15/14 – 12/31/19 **Level of Funding:**

Project Goals: The major goal of this project is to recruit new investigators who will further the strategic objectives of the University of Washington/Fred Hutchinson Cancer Consortium. Specifically, this project will develop infrastructure to study the underlying genetic causes of early onset prostate cancer and familial prostate cancer.

Title: Defining the role of cancer risk genes in early-onset, lethal prostate cancer
Supporting Agency: NIH/NCI (P50 CA097186)
Performance Period: 01/01/15 – 12/31/15
Level of Funding:
Project Goals: The major goal of this project is to examine the role of germline cancer risk genes in early-onset, lethal prostate cancer and parlay the resulting data into future research projects.

Title: Identifying germline cancer risk genes in advanced prostate cancer **Supporting Agency:** NIH/NCI (P50 CA097186) **Performance Period:** 01/01/15 – 08/31/16 **Level of Funding:**

Project Goals: The major goal of this project is to identify the underlying genetic cause in some hereditary prostate cancer families--especially those with early-onset, aggressive prostate cancer-by examining tumor suppressor genes known to be involved in other familial cancer syndromes.

Title: A precision clinical trial targeting DNA repair defects **Supporting Agency:** Institute for Prostate Cancer Research (IPCR)

Performance Period: 07/01/15 - 12/31/19**Level of Funding:**

Project Goals: The major goal of this project is to determine if men with tumors that harbor DNA repair defects will exhibit the hypothesized enhanced sensitivity to platinum-based chemotherapy.

Title: 2016 Challenge Award: Exploiting DNA repair vulnerabilities as a precision oncology target in metastatic prostate cancer

Supporting Agency: Movember Foundation & Prostate Cancer Foundation

Performance Period: 07/31/15 – 07/31/18

Level of Funding:

Project Goals: The major goal of this project is to test the hypothesis that aberrations in key genes that repair DNA strand breaks by homologous repair are predictive of meaningful clinical responses to FDA-approved genotoxic therapeutics.

Title: 2015 PCF Young Investigator Award: Identifying high-penetrance prostate cancer risk genes: leveraging families for next generation discovery and prevention

Supporting Agency: Prostate Cancer Foundation

Performance Period: 10/01/15 – 09/30/18

Level of Funding:

Project Goals: The major goals of this project are to collect families affected by prostate cancer and discover new prostate cancer risk genes, to collect men with prostate cancer who are found via tumor testing to carry high-penetrance germline cancer risk mutations, and to provide both groups of men and their family members with access to better educational materials, genetic counseling resources, and research opportunities.

Title: PCa-001: Phase I, open-label trial to evaluate the safety and immugenicity of INO-5150 alone or in combination with INO-9012 in men with biochemically relapsed (PSA) prostate cancer

Supporting Agency: Inovio Pharmaceuticals

Performance Period: 11/12/15 – 11/11/18

Level of Funding:

Project Goals: The major goal of this study is to test the study drug INO-5150 (plasmid DNA vaccine) for prostate specific proteins alone or in combination with INO-9012 (plasmid DNA vaccine for human interleukin 12) to see how safe they are and if they cause any side effects or generate an immune response against prostate cancer cells when given by intramuscular injection followed by electroporation.

Title: Pharmacogenetic dissection of protein synthesis control across the spectrum of PI3K pathway mutations in prostate cancer

Supporting Agency: Movember Foundation & Prostate Cancer Foundation (2016CHAL1523) **Performance Period:** 10/01/16 – 09/30/18

Level of Funding:

Project Goals: The major goal of this project is to delineate the biology of various PI3K pathway mutations that occur in CRPC and develop strategies to effectively target tumors harboring these mutations.

Title: CRISPR-excision and long-read sequencing of BRCA1, BRCA2, PALB2 and ATM to identify previously undetectable classes of mutations in families severely affected with advanced prostate cancer (PIs Tom Walsh, Heather Cheng) Level (%) of effort: 10%

Funding Agency: Brotman Baty Institute **Performance period:** 02/01/2020 to 01/31/2021

Total level of Funding:

Goals of the project: The goal is to identify complex structural mutations in advanced prostate cancer families that have been missed by current sequencing approaches.

Title: Telehealth to Reduce Prostate Cancer Burden in Rural Underserved Communities **Effort:** 0.30 calendar

Supporting Agency: Fred Hutchinson Cancer Research Center CCSG (NIH)

Contracting/Grants Officer: Heidi Tham **Performance Period:** 07/01/18 to 12/31/21 **Level of Funding:**

Project Goals: The major goal of this study is to provide prostate cancer patients in rural areas with access to treatment options and resources they may not otherwise receive from a general practitioner. **Specific Aims:** 1) Evaluate the telehealth program through patient-reported outcomes, 2) assess some clinician-directed and health system-responsiveness outcomes, and 3) specifically assess the outcomes in the prostate cancer Genetics Clinic, with an eye toward developing a model on which to base other niche clinics in genitourinary oncology.

Title: A phase 1b study of enzalutamide plus CC-115 in men with castration-resistant prostate cancer **Effort:** 0.60 calendar

Supporting Agency: PCCTC, LLC (Celgene) Performance Period: 10/01/17 to 12/31/21

Level of Funding:

Project Goals: The major goal of this study is to determine the safety, pharmacokinetics, and the Maximum Tolerated Dose and/or Recommended Phase 2 Dose of the combination of CC-115 plus enzalutamide.

Title: A ph I/II trial of concurrent chemohormonal therapy using enzalutamide (MDV-3100) and cabazitaxel in patients with metastatic castration resistant prostate cancer

Effort: 0.60 calendar

Supporting Agency: PCCTC, LLC (Medivation and Sanofi)

Performance Period: 07/14/16 to 11/30/21

Level of Funding:

Project Goals: The major goal of this project is to test the safety and efficacy of combination treatment with enzalutamide (MDV3100) and cabazitaxel chemotherapy of prostate cancer.

Specific Aims: To determine safe dosing level. To collect correlative biospecimens to understand the biological effects of the treatment and to evaluate for potential prognostic biomarkers.

Title: The Galahad Study: A phase 2 efficacy and safety study of niraparib in men with metastatic castration-resistant prostate cancer and DNA-repair anomalies **Effort:** 0.60 calendar

Supporting Agency: Janssen Research & Development, LLC

Performance Period: 12/28/16 to 12/27/21

Level of Funding:

Project Goals: The major goal of this project is to assess the efficacy of niraparib in men with mCRPC and DNA-repair anomalies who have measurable disease by looking at the objective response rate. **Specific Aims:** To assess the efficacy of niraparib in subjects with mCRPC and DNA-repair anomalies.

Title: A ph I/II trial of concurrent chemohormonal therapy using enzalutamide (MDV-3100) and cabazitaxel in patients with metastatic castration resistant prostate cancer.

Major Goals: To determine safe dosing level. To collect correlative biospecimens to understand the biological effects of the treatment and to evaluate for potential prognostic biomarkers. The major goal of this project is to test the safety and efficacy of combination treatment with enzalutamide (MDV3100) and cabazitaxel chemotherapy of prostate cancer.

Status of Support: Active

Project Number: MDV3100 Name of PD/PI: Heather Cheng Source of Support: PCCTC, LLC (Medivation and Sanofi) Primary Place of Performance: Fred Hutch Cancer Center – Seattle, WA Project/Proposal Start and End Date: 07/14/16 to 11/30/22 Total Award Amount:

Title: PROSTATE CANCER CLINICAL TRIALS CONSORTIUM, W81XWH-17-2-0043 (Cheng) **Major Goals:** The Department of Defense provides funding for infrastructure to support participation as a clinical site in the Prostate Cancer Clinical Trials Consortium. **Status of Support:** Active **Project Number:** W81XWH-17-2-0043 **Name of PD/PI:** Heather Cheng **Source of Support:** US Department of Defense (DOD) **Primary Place of Performance:** Fred Hutch Cancer Center – Seattle, WA **Project/Proposal Start and End Date:** 09/30/2017 to 09/29/2022 **Total Award Amount:**

Title: Technology-Enhanced Acceleration of Germline Evaluation for Therapy - The TARGET Study **Major Goals:** The proposed study will 1) evaluate understanding of providers around genetic testing in prostate cancer patients and uncover barriers to identifying patients who meet the NCCN guidelines for genetic testing. 2) develop a mobile app to assist providers in educating patients and identifying candidates for genetic testing. 3) devise a randomized clinical trial comparing mobile-assisted app to traditional, in-person genetic counseling for men with metastatic prostate cancer in different practice settings.

Status of Support: Active Project Number: 080-27000-U23201 Name of PD/PI: Heather Cheng Source of Support: Prostate Cancer Foundation Primary Place of Performance: Fred Hutch Cancer Center – Seattle, WA Project/Proposal Start and End Date: 08/06/20 – 12/31/2022 Total Award Amount:

Title: Clinical qualification of DNA repair defects as biomarkers in metastatic prostate cancer using integrated genomics and tissue-based functional assays.

Major Goals: We aim to evaluate tissue-based tests of HR proficiency to stratify patients to receive DNA repair targeting agents. In a two-step approach, we will optimize the test and study the correlation with genomic data in a cohort of mCRPC biopsies, to then implement the assay into a clinical trial to stratify patients for receiving treatment with carboplatin, a DNA damaging chemotherapy.

Status of Support: Active Project Number: W81XWH-15-1-0430 Name of PD/PI: Colin Pritchard Source of Support: US Department of Defense (DOD) Primary Place of Performance: Fred Hutch Cancer Center – Seattle, WA Project/Proposal Start and End Date: 09/30/18 to 09/29/22 Total Award Amount:

Title: A phase 1b study of enzalutamide plus CC-115 in men with castration-resistant prostate cancer. **Major Goals:** The major goal of this study is to determine the safety, pharmacokinetics, and the Maximum Tolerated Dose and/or Recommended Phase 2 Dose of the combination of CC-115 plus enzalutamide.

Status of Support: Active Project Number: CC-115 Name of PD/PI: Heather Cheng Source of Support: PCCTC, LLC (Celgene) Primary Place of Performance: Fred Hutch Cancer Center – Seattle, WA Project/Proposal Start and End Date: 10/01/17 to 12/31/22 Total Award Amount:

17. Bibliography:

Scopus Index (1/5/2023) h-index: 26 Cumulative citations: Google Scholar, All (1/5/2023) h-index: 30 Cumulative citations: 10,019

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- 5. **Cheng, H.** The Problem with Direct to Consumer Genetic Tests. Scientific American, March 10, 2020. https://blogs.scientificamerican.com/observations/the-problem-with-direct-to-consumer-genetic-tests/

g) Manuscripts Submitted:

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- Sekar, R.R., Diamantopoulos, L.N., Bakaloudi, D.R., Khaki, A.R., Grivas, P., Winters, B.R., Vakar-Lopez, F., Tretiakova, M.S., Psutka, S.P., Holt, S.K., Gore, J.L., Lin, D.W., Schade, G.R., Hsieh, A.C., Lee, J.K., Yezefski, T., Schweizer, M.T., Cheng, H.H., Yu, E.Y., True, L.D., Montgomery, R.B., Wright, J.L. Sarcomatoid Urothelial Carcinoma is Associated with Limited Response to Neoadjuvant Chemotherapy and Poor Oncologic Outcomes after Radical Cystectomy (*submitted*) [original work]
- Graff, J.N., Sokolova, A.O., Smith, C.E., Beer, T.M., Latour, E., Chen, Y., Bailey, S., Kreitner, D., Petreaca, D., Grivas, P., Schweizer, M.T., Higano, C.S., Alumkal, J.J., Vuky, J., Yu, E.Y., Cheng, H.H. A Phase I/II Trial of Concurrent Chemo-hormonal Therapy Using Enzalutamide and Cabazitaxel in Patients with Metastatic Castration Resistant Prostate Cancer. (*submitted*) [original work]
- Zhao, J.L., Antonarakis, E.S., Cheng, H.H., George, D., Aggarwal, R., Riedel, E., Sumiyoshi, T., Schonhoft, J., Mao, N., Haywood, S., Decker, B., Curley, T., Abida, A., Feng, F.Y., Knudsen, K., Carber, B., Lacouture, M.E., Wyatt, A., Rathkopf, D., Phase 1b Study of Enzalutamide plus CC-115, a dual mTORC1/2 and DNA-PK inhibitor, in Men with Metastatic Castration-Resistant Prostate Cancer. (*submitted*) [original work]
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- Rencsok, E.M., Slopen, N., Autio, K., Morgans, A., McSwain, L., Barata, P., Cheng, H.H., Dreicer, R., Heath, E., McKay, R., Pomerantz, M., Rathkopf, D., Tagawa, S., Whang, Y., Ragin, C., Folakemi O.T., George, D.J., Kantoff, P.W., Vinson, J., Villanti, P., Haneuse, S., Mucci[,] L.A. Quality of life in the year after diagnosis with advanced prostate cancer for Black and White individuals living in the US. (*submitted*) [original work]
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- 25. Sokolova, A., Cheng, H.H., Hintze, B., Kelley, M., Spector, N., Duffy, J., Lynch, J., Rettig, M., Montgomery, B., *The Veterans Health Administration Precision (VHA) Oncology Program for Advanced Prostate Cancer Patients: expanding tumor NGS opportunities to a broader patient population*, Genitourinary Cancers Symposium, San Francisco, CA (2019). [Abstract]
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- Sokolova, A.O., Miyamoto, A.N., Pouv, D.L., Cheng, H.H., Montgomery, R.B. Implementation of Systematic Germline Genetic Testing (GT) for Metastatic Prostate Cancer (mPC) Patients at the Puget Sound VA Prostate Oncology Clinic. American Society for Clinical Oncology Annual Meeting, Chicago, CA (2020). [Poster abstract]
- Wong, R.L., Lin, D.W., Pritchard, C.C., Nelson, P.S., Stanford, J.L., Cheng, H.H. Genetic Information to Inform Treatment and Screening (GIFTS) Study for Prostate Cancer: Characterizing Germline DNA Alterations in Men with Metastatic Prostate Cancer and their First-Degree Male Relatives. European Society for Medical Oncology, virtual (2020). [Poster abstract]
- 51. Loeb, S., Thakker, S., Falge, E., Taneja, S., Byrne, N., Walter, D., Katz, M., Wong, R., Leader, A., Selvan, P., Rose, M., Joy, M., Cheng, H.H., Massey, P., and Giri, V.N. *Twitter Discussions about Genetic Testing and BRCA Awareness in the Context of Prostate Cancer and Breast Cancer*. Prostate Cancer Foundation Annual Retreat, virtual (2020). [Poster abstract]
- 52. Rathkopf, D., Chi, K.N., Olmos, D., **Cheng, H.H.,** Agarwal, N., Graff, J., Sandhu, S., Hayreh, V., Lopez-Gitlitz, A., Francis, P., Attard, G. AMPLITUDE: A Study of Niraparib (Nira) in Combination With Abiraterone Acetate and Prednisone (AAP) Versus AAP for the Treatment of Patients With Deleterious Germline or Somatic Homologous Recombination Repair (HRR) Gene-mutated Metastatic Castrationsensitive Prostate Cancer. Genitourinary Cancers Symposium, San Francisco, CA (2021). [Abstract]
- 53. Wong, R.L., Cheng, H.H., Holt, S.K., Conrad, N., Fernandez, S., Sahoo, R., Bauer, Z., Toulouse, A.E., Grivas, P., Yezefski, T., Russell, K.J., Wright, J.L, Schweizer, M.T., Montgomery, R.B., Lee, J.H., Chen, D.L., Zeng, J., Lin, D.W., Yu, E.Y. Use of Fluciclovine PET/CT (FluPET) for Prostate Cancer: Initial Results from a Prospective Registry at the University of Washington/Seattle Cancer Care Alliance. Genitourinary Cancers Symposium, San Francisco, CA (2021). [Abstract]
- 54. Loeb, S., Li, R., Sanchez Nolasco, T., Byrne, N., Cheng, H.H., Leader, A., Giri, V., Barriers and Facilitators of Germline Genetic Evaluation for Prostate Cancer. Genitourinary Cancers Symposium, San Francisco, CA (2021). [Abstract]

- 55. Taza, F., Holler, A., Adra, N., Albany, C., Ashkar, R., Cheng, H.H., Sokolova, A.O., Agarwal, N., Nussenzveig, R., Bryce, A., Nafissi, N., Barata, P., Sartor, O., Bastos, D., Smaletz, O., Berchuck, J., Taplin, M., Aggarwal, R., Sternberg, C., Vlachostergios, P.J., Alva, A.S., Su, C., Marshall, C.H., Antonarakis, E.S. *Differential activity of PARP inhibitors in BRCA1- vs BRCA2-altered metastatic castration-resistant prostate cancer (mCRPC)*. Genitourinary Cancers Symposium, San Francisco, CA (2021). [Abstract]
- 56. Karzai, F., Couvillon, A., McKinney, Y., Lee-Wisdom, K., Choyke, P.L., Giri, V.N., Morgan, T.M., Cheng, H.H., Merino, M.J., Pinto, P.A., Turkbey, B., Dahut, W.L., *A Natural History Study of Men with High-Risk Genetics for Prostate Cancer (PCa) Using Multiparametric MRI (mpMRI)*. American Association for Cancer Research Annual Meeting, Washington, D.C. (2021). [Abstract]
- 57. Rathkopf, D.E., Chi, K.N., Olmos, D., Cheng, H.H., Agarwal, N., Graff, J.N., Sandhu, S.K., Hayreh, V., Lopez-Gitlitz, A., St. John, P., Attard, G., AMPLITUDE: A Study of Niraparib in Combination With Abiraterone Acetate Plus Prednisone (AAP) vs AAP Alone for the Treatment of Metastatic Castration-Sensitive Prostate Cancer (mCSPC) in Patients With Deleterious Germline orSomatic Homologous Recombination Repair (HRR) Gene Alterations. American Society for Clinical Oncology Annual Meeting, Chicago, CA (2021). [Abstract]
- 58. Zhao, J.L., Antonarakis, E.S., Cheng, H.H., George, D.G., Aggarwal, R.A., Abida, W., Decker B., Curley, T., Schonhoft, J., Haywood, S., Riedel, E., Carver, B., Wyatt, A., Feng, F.Y., Knudsen, K., Rathkopf, D. A Phase 1b Study of Enzalutamide (Enza) plus CC-115 in Men with Metastatic Castration-Resistant Prostate Cancer (mCRPC). American Society for Clinical Oncology Annual Meeting, Chicago, CA (2021). [Abstract]
- 59. Wong, R.L., Holt, S.K., Zeng, J., Graham, L., Kang, R., Conrad, N., Toulouse, A.E., Fernandez, S., Bauer, Z., Lai, M.Y., Yezefski, T., Wright, J.L, Weg, E.S., Hsieh, A.C., Cheng, H.H., Lee, J.H., Chen, D.L., Lin, D.W., Yu, E.Y. *The fluciclovine (FACBC) PET/CT site-directed therapy of oligometastatic prostate cancer (Flu-BLAST-PC) trial*. American Society for Clinical Oncology Annual Meeting, Chicago, CA (2021). [Abstract]
- 60. Su, C.T., Nizialak, E., Berchuck, J.E., Vlachostergios, P., Ashkar, R., Sokolova, A.O., Barata, P., Aggarwal, R., McClure, H., Sartor, O., Cheng, H.H., Adra, N., Sternberg, C.N., Taplin, M.E., Cieslik, M., Antonarakis, E., Alva, A. Differential responses to taxanes and PARP inhibitors (PARPi) in ATM-versus BRCA2-mutated metastatic castrate-resistant prostate cancer (mCRPC) patients (pts). American Society for Clinical Oncology Annual Meeting, Chicago, CA (2021). [Abstract]
- 61. Giri, V.N., Walker, A., Gross, L., Fisher, C., Cheng, H.H., Loeb, S. *HELIX: Development and Testing of New Digital Tool to Facilitate Guideline-Concordant Prostate Cancer Genetic Testing in Clinical Practice.* American Urological Association (2021). [Abstract]
- 62. Maldonado, R., Jan Marquardt, J., Fintelmann, F., O'Malley, R., Holt, S., Ngo, S., Diamantopoulos, L., Laidlaw, G., Schade, G., Lin, D.W., Wright, J.L., Gore, J.L., Nyame, Y., Grivas, P., Yu, E.Y., Montgomery, B., Hsieh, A., Yezefski, T., Schweizer, M., Cheng, H.H., Psutka, S.P. Change in Skeletal Muscle (SMI), Subcutaneous (SFI) and Visceral Fat Indices (SFI) with Neoadjuvant Chemotherapy (NAC) in patients with Muscle Invasive Bladder Cancer (MIBC): Associations with Adverse Events (AEs) and Oncologic Outcomes. American Urological Association (2021). [Abstract]
- 63. Szymaniak, B.M., Facchini, L.A., Cheng, H.H., Morgans, A.K., Integrating Genetic Counseling and Testing into Genitourinary (GU) Oncology & Urology Clinics. BRCA Conference (2021). [Abstract]
- 64. Couvillon, A., Karzai, F., Choyke, P.L., Giri, V.N., Morgan, T.M., **Cheng, H.H.,** Kesserwan, C., Merino, M.J., Pinto, P.A., Turkbey, B., Dahut, W.L., *Inherited Risk for Prostate Cancer: How to Follow and Image the Natural History of Men with High-Risk Genetics*. BRCA Conference (2021). [Abstract]

- 65. Schweizer, M.T., Roman Gulati, R., Yezefski, T., Cheng, H.H., Sievers, C., Ruth Dumpit, Alexander, K., McDonald, N., Lai, M., Nega, K., Hammond, J., Grivas, P., Hsieh, A., Montgomery, B., Nelson, P.S., Yu, E.Y. Bipolar Androgen Therapy (BAT) plus Olaparib in Men with Metastatic Castration-resistant Prostate Cancer (mCRPC). European Society of Medical Oncology (2021). [Abstract]
- 66. Cheng, H.H., Powers, J., Gulati, R., Le, A., Ledet, E., Van Allen, E., Vijai, J., Nicolosi, P., Nussbaum, R.L., Garber, J.E., Offit, K., Schiffman, J., Sartor, O., Nelson, P.S., Walsh, M.F., Pritchard, C.C., Maxwell, K.N. *TP53* variants are associated with an increased risk of prostate cancer. American Society of Human Genetics (2021). [Poster Abstract]
- 67. Maldonado, R., Marquardt, J.P., Fintelmann, F.J., O'Malley, R., Holt, S.K., Ngo, S., Diamantopoulos, L., Laidlaw, G., Schade, G.R., Lin, D.W., Wright, J.L., Gore, J.L., Nyame, Y., Grivas, P., Yu, E.Y., Montgomery, B., Hsieh, A.C., Yezefski, T.A., Schweizer, M., Cheng, H.H., Psutka, S.P. Changes in Body Composition During Platinum-based Neoadjuvant Chemotherapy (NAC) Prior to Radical Cystectomy (RC and Association with Outcomes. Society for Urologic Oncology (2021). [Abstract]
- 68. Zhao, J.L., Antonarakis, E.S., Cheng, H.H., George, D.G., Aggarwal, R.A., Abida, W., Decker B., Curley, T., Schonhoft, J., Anderson, A., Haywood, S., Riedel, E., Carver, B., Wyatt, A., Feng, F.Y., Knudsen, K., Rathkopf, D. *A Phase 1b Study of Enzalutamide (Enza) plus CC-115 in Men with Metastatic Castration-Resistant Prostate Cancer (mCRPC)*. European Society of Medical Oncology (2021). [Abstract]
- 69. Mita, A.C., Mayer, I., Conley, B., Harris, L., Arteago, C., Maican, T., Cheng., H.H. Erdafitinib in patients with tumors harboring FGFR gene mutations or fusions: results from the NCI-MATCH arm K2 trial. AACR-NCI-EORTC Molecular Targets and Cancer Therapeutics Virtual Conference (2021). [Abstract]
- Selvan, P., Leader, A., Hunter, A., Massey, P., Cheng, H.H., Loeb, S., Giri, V.N., Assessing the Impact of Messaging about Prostate Cancer and Genetics on Facebook. Prostate Cancer Foundation Annual Retreat, virtual (2021). [Poster abstract]
- 71. Sokolova, A.O., Gulati, R., Cheng, H.H., Beer, T., Graff, J.N., Vuky, J., Yezefski, T., Grivas, P., Yu, E.Y., Schweizer, M.T. *Trial in progress: Durvalumab and Olaparib for the Treatment of Prostate Cancer in Men Predicted to Have a High Neoantigen Load.* Genitourinary Cancers Symposium, San Francisco, CA (2022). [Abstract]
- 72. Giri, V.N., Cheng, H.H., Paller, C., Weg, E., Johnson, J., Gross, L., Russo, J., Loeb, S., *Virtual Genetics Board for Enhancing Knowledge and Practice of Prostate Cancer Genetic Testing: The ENGAGEMENT Study.* Genitourinary Cancers Symposium, San Francisco, CA (2022). [Poster Abstract]
- 73. Paller, C.J., Lorentz, J., DeMarco, T.A., Stadler, W.M., Armstrong, A.J., Taplin, M., Hussain, M.H., Pili, R., Mao, S., Elrod, J.B., Sokolova, A.O., Heath, E.I., McKay, R.M., Vinson, J., Tran, C., Macario, N., Cook, A., Chiang, J., Cheng, H.H. PROMISE Registry: A Prostate Cancer Registry of Outcomes and Germline Mutations for Improved Survival and Treatment Effectiveness. Genitourinary Cancers Symposium, San Francisco, CA (2022). [Abstract]
- 74. Clark, N.M., Roberts, E.A., Fedorenko, C., Sun, Q., Dubard-Gault, M., Handford, C., Yung, R., Cheng, H., Norquist, B., Flanagan, M.R. *Guideline concordant genetic testing in patients with breast, ovarian, pancreatic and prostate cancer*. International Conference on Surgical Cancer Care, Dallas, TX (2022) [e-poster, Abstract]
- 75. Makrakis, D., Roudier, M.P., Wang, Y., Vakar-Lopez, F., Garcia, J., Dash, A., Lin, D., Schade, G., Mostaghel, E.M., Cheng, H.H., Schweizer, M.T., Gore, J.L., Yu, E.Y., Lam, H.M., Wright, J.L., Montgomery, B. A Phase 1/2 Study of Rapamycin and Cisplatin/Gemcitabine for Treatment of Patients With Bladder Cancer (NCT01938573). American Urological Association (2022). [Abstract]

- 76. Garcia, J., Vakar-Lopez, F., Roudier, M., Grivas, P., Yu, E.Y., Cheng, H.H., Schweizer, M.T., Haffner, M., Lee, J.K., Corey, E., Montgomery, B., Hsieh, A.C., Wright, J.L., Lam, H. An update on the Urothelial Cancer Rapid Autopsy Program: Biospecimens and Patient-derived Preclinical Models. American Urological Association (2022). [Abstract]
- 77. Noonavath, M., Muney, K., Marquandt, J.P., Fintelmann, F.J., O'Malley, R., Holt, S.K., Dwyer, E., Maldonado, R., Diamantopoulos, L., Makrakis, D., Laidlaw, G., Schade, G.R., Lin, D.E., Wright, J.L., Nyame, Y., Grivas, P., Yu, E.Y., Montgomery, B., Hsieh, A.C., Yezefski, T.A., Schweizer, M.T., Cheng, H.H., Psutka, S.P. Skeletal Muscle Gauge: A Novel Assessment of Muscle Mass and Quality: Associations with Outcomes Following Radical Cystectomy for Bladder Cancer. American Urological Association (2022). [Abstract]
- 78. Gulhane, A. Lin, D., Dash, A., Nyame, Y., Schade, G., Wright, J., Chen, J., Liao, J., Wallner, K., Weg, E., Cheng, H.H., Hawley, J., Montgomery, B., Nelson, P.S., Schweizer, M.T., Yu, E.Y., Chen, D.L. [⁶⁸Ga]-PSMA-11 clarifies equivocal lesions on conventional imaging and affects management for men with prostate cancer. Society of Nuclear Medicine and Molecular Imaging Annual Meeting (2022). [Abstract]
- 79. Wong, R.L., Cheng, H.H., Fann, J.R., Hnida, J., Chakoian, M., Schenker, Y., Yu, E.Y., Gore, J.L. Longitudinal Screening for Depression and Anxiety in Prostate Cancer and Association with Disease and Treatment Factors. American Society of Clinical Oncology Annual Meeting (2022). [Abstract]
- 80. Khan, H.M., Wong, R.L., Darst, B.F., Pritchard, C.C., Nelson, P.S., Stanford, J.L., Lin, D.W., Cheng, H.H. Cancer Registry-Based Recruitment of Men with Incident Metastatic Prostate Cancer and their First-Degree Male Relatives for Germline Genetic Testing: Genetic Information to Inform Treatment and Screening (GIFTS) Study. American Society of Clinical Oncology Annual Meeting (2022). [Oral Abstract Presentation] (*HHC senior author)
- 81. Gulhane, A., Talukder, R., Dash, A., Ellis, W., Nyame, Y.A., Schade, G., Wright, J.L., Apisarnthanarax, S., Chen, J., Liao, J.J., Wallner, K., Weg, E.S., Cheng, H.H., Grivas, P., Hawley, J., Hsieh, A.C., Lee, J.K., Montgomery, B., Nelson, P.S., Schweizer, M.T., Yezefski, Y., Yu, E.Y., Lin, D.W., Chen, D.L. Clinical Impact of PSMA PET in patients with biochemical recurrence of prostate cancer after local definitive therapy. American Society of Clinical Oncology Annual Meeting (2022). [Abstract]
- 82. Liao, J.J., Mostaghel, E.A., Russell, K.J., Dalkin, B.L., Ellis, W.J., Lin, D., Wright, J., Schade, G., Nyame, Y., Yu, E.Y., Nelson, P., Grivas, P., Schweizer, M.T., Cheng, H.H., Yezefski, T., Hawley, J.E., Chen, J.J., Weg, E., Nguyen, M., Montgomery, B., *Abiraterone, Androgen Deprivation Therapy, and Radiotherapy for Localized High Risk and Intermediate Risk Prostate Cancer: Long-term follow up of the RAD1 Phase 2 trial.* American Society of Radiation Oncology, Annual Meeting (2022). [Abstract]
- 83. Garcia, J., Vakar-Lopez, F., Roudier, M., Grivas, P., Yu, E.Y., Cheng, H.H., Schweizer, M.T., Haffner, M., Lee, J.K., Corey, E., Montgomery, B., Hsieh, A.C., Wright, J.L., Lam, H. Bladder Cancer Rapid Autopsy Program provides a critical resource for the biological study of advanced bladder cancer. American Urological Association (2022). [Abstract]
- 84. Gulhane, A., Talukder, R., Dash, A., Ellis, W., Nyame, Y.A., Schade, G., Wright, J.L., Apisarnthanarax, S., Chen, J., Liao, J.J., Wallner, K., Weg, E.S., Cheng, H.H., Grivas, P., Hawley, J., Hsieh, A.C., Lee, J.K., Montgomery, B., Nelson, P.S., Schweizer, M.T., Yezefski, Y., Yu, E.Y., Lin, D.W., Chen, D.L. Utility of PSMA PET for Initial Staging of Prostate Cancer. Radiological Society of North America (2022). [Abstract]
- 85. Lorentz, J., Appleman, L., Armstrong, A.J., Barata, P., DeMarco, T.A., Dreicer, R., Elrod, J.B., Fleming, M., George, C., Heath, E.I., Hussain, M.A., Mao, S., McKay, R.R., Metwalli, A., Morgans, A., Orton, M., Pili, R., Saraiya, B., Sigmond, J., Sokolova, A.O., Stadler, W.M., Tran, C., Macario, N., Vinson, J., Green, R., Paller, C.J., Cheng, H.H. Utilization of a decentralized national genetic registry to address

informational needs caused by expanded testing recommendations and recently approved treatments for prostate cancer: the PROMISE Registry. National Society for Genetic Counseling (2022) [Abstract]

- Wong, R.L., Cheng, H.H., Fann, J.R., Hnida, J., Chakoian, M., Schenker, Y., Yu, E.Y., Gore, J.L. Depression Screening in Prostate Cancer and Use of Supportive Care Services. ASCO Quality Care Symposium (2022) [Abstract]
- 87. Rathkopf, D.E., Chi, K.N., Olmos, D., Cheng, H.H., Agarwal, N., Graff, J.N., Sandu, S.K., Kim, W., Lopez-Gitlitz, Francis, P.S., Attard, G., AMPLITUDE: Niraparib and Abiraterone Acetate Plus Prednisone to Treat Patients with Metastatic Castration Sensitive Prostate Cancer and Deleterious Germline or Somatic Homologous Recombination Repair Gene Alterations. Society for Urology Oncology (2022) [Abstract]
- 88. Paller, C.J.*, Barata, P.C., Lorentz, J., Appleman, L.J., Armstrong, A.J., DeMarco, T.A., Dreicer, R., Elrod, J.B., Fleming, M., George, C., Heath, E.I., Hussain, M.H., Mao, S., McKay, R.M., Metwalli, A.R., Morgans, A., Stadler, W.M., Tran, C., Macario, N., Vinson, J., Green, R., Cheng, H.H.* *PROMISE Registry: A Prostate Cancer Registry of Outcomes and Germline Mutations for Improved Survival and Treatment Effectiveness.* Prostate Cancer Foundation Annual Retreat (2022). [Poster abstract]
- 89. Couvillon, A., Turkbey, B., Choyke, P.L., Lee-Wisdom, K., McKinney, Y., Sidlow, R., Mullane, M., Giri, V.N., Morgan, T.M., **Cheng, H.H.,** Merino, M.J., Figg, W., Pinto, P.A., Dahut, W.L., Karzai, F. *Inherited Risk for Prostate Cancer (PCa): Following the Natural History of Men with High-Risk Genetics using Multiparametric MRI (mpMRI)*. ASCO Genitourinary Cancer Symposium (2023). [Abstract]
- 90. Giri, V.N., Gross, L., Hartman, R., Reader, A.E., Whang, Y.E., Couvillon, A., Cheng, H.H., Paller, C.J., Loeb, S., Karsh, L.I., Friedman, S., Beer, T.M., Keith, S. *Factors Impacting Men's Experience with Prostate Cancer Germline Testing: Results from PROGRESS Registry*. ASCO Genitourinary Cancer Symposium (2023). [Abstract]
- 91. Koehne, E., Vakar-Lopez, F., Roudier, M., Garcia, J., Arora, S., Cheng. H.H., Schweizer, M.T., Haffner, M., Lee, J.K., Yu, E.Y., Grivas, P., Montgomery, B., Hsieh, A., Wright, J.L., Lam, H. *Molecular Characterization of Plasmacytoid Urothelial Carcinoma Metastases from Rapid Autopsy*. American Urological Association (2023). [Abstract]
- 92. Erickson, M.S., Scherzer, Z., Toderas, L., Schweizer, M., Yu, E.Y., Cheng, H.H., Yezefski, T.A., Hsieh, A.T., Montgomery, B., Nelson, P.S., Hawley, J., Chen, D.L., Iravani, A., *Best Practices for Limiting Treatment Cancellations of Lutetium-177 PSMA-617*. Society of Nuclear Medicine and Molecular Imaging Annual Meeting (2023). [Abstract]

18. Invited Talks, including CME presentations

a. National/International Invited Lectures

- 1. 12/2002: *Identifying the Requirements and Mechanisms of FeLV-T Entry*. 2002 International Workshop on Retroviral Pathogenesis, Indian Wells, CA [invited lecture]
- 2. 05/2003: Determinants of Receptor Specificity for Feline Leukemia Virus Variants. Cold Spring Harbor Meeting on Retroviruses, Cold Spring Harbor, NY [invited lecture]
- 3. 06/25/2016: Germline DNA Repair Gene Mutations in Metastatic Prostate Cancer. 2016 Prostate Cancer Foundation Coffey-Holden Academy, Coronado, CA [invited lecture]

- 11/30/2016: Clinical Implications for Prostate Cancer Screening and Treatment of Men with Germline Mutations in BRCA and other DNA Repair Genes. The 17th Annual Meeting of the Society of Urologic Oncology, San Antonio, TX [invited lecture]
- 5. 06/05/2017: *Clinical Implications of Genomic Sequencing in Prostate Cancer*. American Society for Clinical Oncology Annual Meeting, Chicago, IL [invited abstract discussant]
- 10/06/2017: Beyond the Androgen Receptor II: New Approaches to Understanding and Treating Metastatic Prostate Cancer; Report from the 2017 Coffey-Holden Prostate Cancer Academy Meeting. 24th Annual Prostate Cancer Foundation Scientific Retreat, Washington, D.C. [invited oral presentation]
- 7. 10/06/2017: *Implementing Germline Genetics into Prostate Cancer Clinical Care*. 24th Annual Prostate Cancer Foundation Scientific Retreat, Washington, D.C. [invited oral presentation]
- 8. 02/09/2018: A New Era in Prostate Cancer Treatment? Understanding DNA Repair Deficiencies and the *Therapeutic Rationale for PARP Inhibition*. Genitourinary Cancers Symposium CME, San Francisco, CA. [invited CME faculty]
- 9. 02/11/2018: The Changing Landscape of Prostate Cancer Genetics Care and the GENTleMEN Study, Morris Kahn and Maccabi Research and Innovation Institute, Tel Aviv, Israel [invited oral presentation]
- 10. 02/12/2018: *The Changing Landscape of Prostate Cancer Genetics Care and the GENTleMEN Study,* **Sheba Medical Center/Tel Hashomer Hospital, Tel Aviv, Israel** [invited oral presentation]
- 11. 03/29/2018: *Expanding Clinical and Research Horizons in Prostate Cancer Genetics*. Koch Center Seminar Series, **MD Anderson Cancer Center**, Houston, TX. [invited faculty speaker]
- 12. 05/20/2018: Genetic Testing in Prostate Cancer: Understanding Clinical Implications for Early Detection, Localized disease, and CRPC. Annual Meeting of the American Urological Association, San Francisco. [educational course faculty]
- 13. 06/01/2018: Genomics Versus Genetics, and Implications for Prostate Cancer Care. American Society of Clinical Oncology Annual Meeting, Chicago, IL [invited session chair and oral presentation]
- 09/15/2018: Genetics and Genomics in Prostate Cancer: Realizing the Promise of Precision Medicine and Other Very Important Benefits. Prostate Cancer Symposium, Barbara Ann Karmanos Cancer Institute, Wayne State University School of Medicine, Detroit, MI [invited Keynote Lecture]
- 15. 05/03/2019: Genetic Testing in Prostate Cancer: Understanding Clinical Implications for Early Detection, Localized disease, and CRPC. Annual Meeting of the American Urological Association, San Francisco. [educational course faculty]
- 05/31/2019: The Genetic Landscape and Prognostic/Predictive Implications. 2019 ASCO Genetics and Genomics Pre-Annual Meeting Seminar, American Society of Clinical Oncology Annual Meeting, Chicago, IL [invited faculty speaker]
- 17. 09/11/2019: *Expanding Clinical and Research Horizons in Prostate Cancer Genetics*. Oncology Grand Rounds, **University of Wisconsin/Carbone Cancer Center**, Madison, WI [invited Grand Rounds speaker]
- 10/04/2019: Germline Contribution to Metastatic Prostate Cancer. Implementation of Genetic Testing for Inherited Prostate Cancer, Philadelphia Prostate Cancer Consensus Conference 2019. [invited speaker]

- 10/26/2019: Prostate Cancer Genetics. Prostate Cancer Foundation and UsTOO International Prostate Cancer Support Network, 26th Prostate Cancer Foundation Annual Scientific Retreat. Carlsbad, CA. [invited speaker]
- 20. 11/06/2019: *Molecular-Driven Therapy in GU Cancers*. **37**th Annual CFS®: Innovative Cancer Therapy for Tomorrow, New York, NY [invited faculty speaker]
- 21. 04/18/2020: Prostate Cancer, DNA Repair Pathways and Predictive Testing for Inherited Cancers. 9th Annual International Clinical Cancer Genetics and Genomics Conference, University of Chicago; Chicago, IL [invited faculty speaker]
- (cancelled due to COVID19) 05/20/2020: Genetic Testing in Prostate Cancer: Understanding Clinical Implications for Early Detection, Localized disease, and CRPC. Annual Meeting of the American Urological Association, Washington, D.C. [educational course faculty]
- 23. 10/14/2020: *Prostate Cancer Genetics: Testing, Targeted Therapy and Early Detection.* **Dana-Farber Genitourinary Oncology Seminar Series**, Boston, MA [invited faculty speaker]
- 24. 10/15/2020: *Genetics, Genomics, and Prostate Cancer*. USToo International, Chicago, IL [invited webinar speaker]. <u>https://www.youtube.com/watch?v=WjkAF1xixOA&feature=youtu.be</u>
- 25. 11/20/2020: Genetic Testing in Prostate Cancer. Facing Our Risk of Cancer Empowered Annual Conference, Philadelphia, PA. [invited faculty]. <u>https://www.youtube.com/watch?v=m515URd9uYk&feature=youtu.be</u>
- 26. 04/29/2021: Integrating Genetic Testing into Clinical Practice for Advanced Prostate Cancer. Genitourinary (GU) Medical Oncology Series: The Impact of Genomic Profiling on Patients with Prostate Cancer. LUGPA Webinar [invited faculty speaker]
- 27. 07/29/2021: What is Right for Me in My Prostate Cancer Treatment Genetics & Genomics. USToo International, Chicago, IL [invited national webinar speaker]
- 28. 09/20/2021: Genetic Testing in Prostate Cancer: Understanding Clinical Implications for Early Detection, Localized Disease, and CRPC. Annual Meeting of the American Urological Association, Washington, D.C. [educational course faculty]
- 29. 09/20/2021: Germline Genetics for Prostate Cancer Prognosis: Predicting Drug Treatment Response for Men with Advanced Prostate Cancer (Urologic Oncology Research Symposium) Annual Meeting of the American Urological Association, Washington, D.C. [invited faculty speaker]
- 30. 09/29/2021: *What's New in Prostate Cancer Treatment*. **12th Annual FORCE Hereditary Cancer Conference, Philadelphia, PA** [invited national webinar faculty]
- 31. 04/29/2022: *How to take care of muscle strength for prostate cancer patients*. Advanced Prostate Cancer Consensus Conference 2022, Lugano, Switzerland [invited faculty speaker and session chair]
- 32. 05/15/2022: Genetic Testing in Prostate Cancer: Understanding Clinical Implications for Early Detection, Localized Disease, and CRPC. Annual Meeting of the American Urological Association, New Orleans, LA. [educational course faculty]
- 33. 06/06/2022: *AR and PARP: Partners in Crime*. American Society of Clinical Oncology 2022 Annual Meeting, Chicago, IL [invited oral poster discussant]
- 34. 10/13/2022: *What's New in Prostate Cancer Treatment*. 13th Annual FORCE Hereditary Cancer Conference, Philadelphia, PA [invited national webinar faculty]

- 35. *(anticipated)* 01/28/2023: *Testing for Hereditary Cancer Predisposition.* University of California at San Diego Prostate Cancer Patient Summit, San Diego, CA [invited speaker]
- 36. (anticipated) 05/05/2023: Bringing Prostate Cancer Risk Assessment to the Community: A GENTleMEN's PROMISE. City of Hope/University of Chicago 11th Annual Clinical Cancer Genomics Conference, Los Angeles, CA [invited speaker]
- 37. (anticipated) 05/15/2023: Genetic Testing in Prostate Cancer: Understanding Clinical Implications for Early Detection, Localized Disease, and CRPC. Annual Meeting of the American Urological Association, New Orleans, LA. [educational course faculty]
- 38. *(anticipated)* 06/05/2023: *Genetics and Genomics: Beyond DNA Repair.* American Society for Clinical Oncology 2023 Annual Meeting, Chicago, IL, [invited session chair and speaker]

b. Regional Invited Lectures

- 1. 07/15/2012: *Circulating microRNA Biomarkers in Prostate Cancer*. Oral presentation for Department of Defense/Prostate Cancer Clinical Trials Consortium. Teleconferenced nationally from Memorial Sloan Kettering Cancer Center, New York, NY
- 2. 11/20/2013: A Phase I/II Trial of Concurrent Chemohormonal therapy using Enzalutamide and Cabazitaxel in Patients with Metastatic Castration Resistant Prostate Cancer. Oral presentation, teleconferenced nationally from Memorial Sloan Kettering Cancer Center, New York, NY
- 3. 04/12/2014: *Circulating Biomarkers in Advanced Disease*. Institute for Prostate Cancer Research 2014 Symposium, Fred Hutchinson Cancer Research Center, Seattle, WA.
- 4. 05/01/2014: Comparison of plasma microRNAs with CTCs and PSA in patients treated on SWOG S0925. Oral presentation at 2014 SWOG Genitourinary Working Group Meeting, San Francisco, CA
- 06/20/2014: Recent Developments and Clinical Trials in Prostate Cancer. Oral presentation for the Seattle Cancer Care Alliance/National Comprehensive Cancer Network "Breakthroughs in Solid Tumor Oncology" Symposium; June 20, 2014, Seattle, WA
- 10/31/2014: Comparison of plasma microRNAs with CTCs and PSA in patients treated on SWOG S0925. Prostate Cancer SPORE Seminar, Fred Hutchinson Cancer Research Center, teleconferenced to Oregon Health Sciences and University of British Columbia
- 7. 06/29/2016: *Emerging Therapies in Cancer: Cancer Genetics*. Seattle Cancer Care Alliance CME lecture for Skagit Valley Hospital, Mount Vernon, WA
- 8. 10/27/2016: *Prostate Cancer Foundation Women's Networking Forum*. Junior Investigator Panelist at the 2016 Prostate Cancer Foundation Retreat, Carlsbad, CA
- 9. 04/13/2017: *Metastatic Prostate Cancer*. Cases From Kampala, hosted by Uganda Cancer Institute/Hutchinson Cancer Center Alliance; WebEx between Seattle, WA, and Kampala, Uganda
- 10. 09/23/2017: The Genetics of Inherited Prostate Cancer Risk: Why what has always mattered matters even more in 2017. 17th Annual Pacific NW Prostate Cancer Conference, Seattle, WA
- 11. 02/01/2018: Genetic Testing for Men with Metastatic Prostate Cancer: Changing Landscape and the GENTleMEN Study. PPCR SPORE Seminar Series, Fred Hutch Cancer Research Center, Seattle, WA
- 12. 03/08/2018: *Precision Medicine for Older Adults: Delivering on a Promise*. Plein Research Symposium in Geriatric Pharmacy, Center for Urban Horticulture, Univ of Washington, Seattle, WA

- 13. 06/23/2018: Prostate Cancer Pathways for Patients and Caregivers: Updates in Prostate Cancer Genetics. UsTOO International Prostate Cancer Support Network Patient Symposium and Webcast, Evergreen Hospital, Kirkland, WA
- 14. 07/17/2018: *Molecular Predictors of Prostate Cancer Progression and Mortality*. PNW SPORE Symposium, Fred Hutch Cancer Research Center, Seattle, WA, , teleconferenced to Oregon Health Sciences and University of British Columbia
- 15. 10/12/2018: *Prostate Cancer*. Transitions in Oncology Care: Pearls for the Primary Care Provider Conference, Talaris Conference Center, Seattle, WA.
- 10/15/2018: Expanding Clinical and Research Horizons in Prostate Cancer Genetics. Fred Hutch Clinical Research/University of Washington Medical Oncology/Seattle Cancer Care Alliance, Clinical Research Division Seminar Series, Seattle, WA
- 17. 05/11/2019: *Genetics: The GENTleMEN study and extending potential benefit to families.* Prostate Cancer Symposium, hosted by the Institute for Prostate Cancer Research; Fred Hutch Cancer Research Center, Seattle, WA
- 07/22/2020: Prostate Cancer Genetics. Medscape CME Webinar; Seattle Cancer Care Alliance, Seattle WA
- 19. 09/24/2020: *Prostate Cancer Genetics in 2020: Testing, Targeted Therapy and Early Detection.* PPCR SPORE Seminar Series, Fred Hutch Cancer Research Center, Seattle, WA, teleconferenced to Oregon Health Sciences and University of British Columbia
- 20. 03/06/2021: Updates in Genetics for Bladder and Urinary Tract Cancer. Updates in Bladder and Urinary Tract Cancers; Seattle Cancer Care Alliance, Seattle WA
- 21. 7/30/2022: *Risk-Based Screening and Hereditary Prostate Cancer*. Breakthroughs in Prostate Cancer Research. Institute for Prostate Cancer Research Symposium; Seattle, WA
- 22. 10/15/2022: What You Should Know About the Growing Importance of Genetic Testing in Prostate Cancer. 22nd Annual Pacific NW Prostate Cancer Conference; Seattle, WA [invited webinar faculty]

c. Local Invited Lectures

- 1. 09/25/2014: *Prostate Cancer: New Treatments and Ongoing Research*. Fred Hutchinson Cancer Research Center Diversity/Outreach Program to local African American Community, NW African American Museum, Seattle, WA.
- 2. 11/12/2014: *The Surprising Ways in Which Patients Shape our Lives*. Schwarz Center Rounds, hosted by The Schwarz Center for Compassionate Healthcare; Seattle Cancer Care Alliance, Seattle, WA
- 3. 04/11/2015: Lessons from Breast Cancer: How Genes May Affect Risk, Treatment and Outcomes in Prostate Cancer. Prostate Cancer Symposium, hosted by the Institute for Prostate Cancer Research; Fred Hutchinson Cancer Research Center, Seattle, WA
- 4. 05/07/2015: Prostate Cancer: Progress Made and Research in Progress. Research Matters Series, Seattle Cancer Care Alliance, Seattle, WA
- 5. 03/24/2016: Leveraging DNA Repair Defects for Treatment of Prostate Cancer. PPCR SPORE Seminar Series, Fred Hutchinson Cancer Research Center, Seattle, WA

- 6. 10/11/2016: New Discoveries in Prostate Cancer Genetics (or: Why Breast Cancer Genes Are Not Just for Women)". Fred Hutch Clinical Research/University of Washington Medical Oncology/Seattle Cancer Care Alliance Grand Round, Seattle, WA
- 7. 11/17/2016: *Prostate Cancer Genetics: Leveraging Family Traits for Early Detection*. Fred Hutchinson Cancer Research Center Innovators Network. Seattle, WA
- 8. 12/23/2016: *Testicular Cancer/Germ Cell Tumors*. UW/Fred Hutch Hematology/Oncology Fellows Lecture Series, Seattle, WA.
- 9. 03/18/2017: *Inherited Risk and Prostate Cancer Behavior*. Prostate Cancer Symposium, Institute for Prostate Cancer Research; Fred Hutchinson Cancer Research Center, Seattle, WA
- 10. 05/24/2017: *Prostate Cancer Genetics*. UsTOO Greater Seattle Area Prostate Cancer Patient Support Group; Greenwood Community Center, Seattle, WA.
- 11. 10/26/2017: *Clinical Implementation of Quality of Life Measurement in Prostate Cancer Care*. PPCR SPORE Seminar Series, Fred Hutchinson Cancer Research Center, Seattle, WA
- 12. 11/06/2017: *Genetics and Genomics*. CCSG Prostate Program Cancer Retreat, Fred Hutchinson Cancer Research Center, Seattle, WA
- 13. 01/19/2018: *Testicular Cancer/Germ Cell Tumors*. UW/Fred Hutch Hematology/Oncology Fellows Lecture Series, Seattle, WA.
- 14. 01/26/2018: *Expanding Clinical and Research Horizons in Prostate Cancer Genetics*. UW Medical Genetics Division Grand Rounds, Seattle, WA
- 23. 04/28/2018: *Inherited Risk and GENTleMEN*. Prostate Cancer Symposium, hosted by the Institute for Prostate Cancer Research; Fred Hutch Cancer Research Center, Seattle, WA
- 24. 05/04/2018: *Genetic Testing for Men with Metastatic Prostate Cancer: GENTleMEN.* Seattle Cancer Care Alliance Network Summit, Fred Hutch Cancer Research Center, Seattle, WA
- 25. 05/07/2018: *Prostate Cancer: Screening, Treatment and Genetics.* UW Internal Medicine Residents Report, University of Washington Medical Center, Seattle, WA
- 26. 05/23/2018: *Prostate Cancer Genetics and the GENTleMEN Study*. CCSG Breast and Ovary Cancer Research Program Retreat, Fred Hutch Cancer Research Center, Seattle, WA
- 27. 08/09/2018: *Prostate Cancer Genetics and the GENTleMEN Study*. Overbaugh Lab 30th Year Symposium Retreat, Islandwood, Bainbridge Island, WA
- 28. 10/05/2018: *Testicular Cancer/Germ Cell Tumors*. UW/Fred Hutch Hematology/Oncology Fellows Lecture Series, Seattle, WA.
- 29. 09/06/2019: Germline and Somatic DNA repair mutations in Prostate Cancer. Genitourinary Medical Oncology Research Team Staff Education Series; Fred Hutch Cancer Research Center, Seattle, WA
- 30. 09/06/2019: *Updates in Prostate Cancer Genetics*. Seattle Cancer Care Alliance Community Site Dinner Clinical Research Partnership Series; Seattle, WA
- 31. 01/09/2020: From Cat Viruses to Men's Prostates: An Ongoing Research Journey. UW Medical Scientist Training Program Monthly Research Meeting; Seattle, WA.

- 32. 01/24/2020: *Mutational Testing for Solid Tumors*. UW/Fred Hutch Hematology and Oncology Fellowship Solid Tumor Conference; Seattle, WA.
- 33. 01/29/2020: *Prostate Cancer: Screening, Side Effects and Survivorship.* Genitourinary Medical Oncology Research Team Staff Education Series; Fred Hutch Cancer Research Center, Seattle, WA
- 34. 05/27/2020: *Prostate Cancer Genetics through a Medical Oncologist's Lens*. University of Washington, Radiation Oncology Grand Rounds, Seattle, WA. [invited Grand Rounds]
- 35. 07/15/2020: Olaparib for Metastatic Castration Resistant Prostate Cancer. Clinical Research Division Journal Watch; Fred Hutch Cancer Research Center, Seattle, WA
- 36. 02/22/2021: *Prostate Cancer Genetics and Risk.* Seattle Cancer Care Alliance Board Enrichment Series; Seattle Cancer Care Alliance, Seattle WA
- 37. 06/06/2021: *Molecular Subtypes and Prostate Cancer Treatments*. Prostate Cancer Symposium, hosted by Institute for Prostate Cancer Research; Fred Hutch Cancer Research Center, Seattle, WA
- 38. 08/25/2021: *Role of Genes in Prostate Cancer and the PROMISE Study*. USToo Support Group Meeting, Seattle, WA
- 39. 7/21/2022: *Genetics and Genomics of Prostate Cancer*. Genitourinary Medical Oncology Research Staff Education Series; Seattle, WA

CURRICULUM VITAE

EVAN YA-WEN YU, MD

825 Eastlake Ave E, G4-830 Seattle, WA 98109

Personal Data		
Place of birth:		
Citizenship:		
Date of Birth:		
Languages:	English, Mandarin Chinese	
EDUCATION		
B.S. (Zoology) Unive	rsity of Washington, Seattle, WA	1989-1994
M.D. University of W	Vashington, School of Medicine, Seattle, WA	1994-1998
Postgraduate Training		
Clinical Fellow in Me	dicine, Harvard Medical School, Boston, MA	1998-2004
Intern in Medicine, E	3righam and Women's Hospital, Boston, MA	1998-1999
Junior Assistant Resi	1999-2000	
Senior Assistant Res	ident, Brigham and Women's Hospital, Boston, MA	2000-2001
Fellow in Hematolog	2001-2004	
Clinical Fellow in Me	dicine, Brigham and Women's Hospital, Boston, MA	2001-2004
Post-doctoral Basic S	Science Research Fellow, Dana-Farber Cancer Institute	
William C. Hahn, I	M.D., Ph.D., Boston, MA	2002-2004
AACR/ASCO Method	ls in Clinical Cancer Research Workshop	2006
FACULTY POSITIONS HELD		
Assistant Professor,	Department of Medicine, School of Medicine	
University of Washir	ngton, Seattle, WA	2004-2010
Assistant Member, C	Clinical Research Division	
Fred Hutchinson Car	ncer Research Center, Seattle, WA	2004-2010
Assistant Fellowship	Director	
Medical Oncology ar	nd Hematology Fellowship Program	
University of Washir	ngton / Fred Hutchinson Cancer Research Center, Seattle, WA	2006-2017
Associate Professor,	Department of Medicine, School of Medicine	
University of Washir	igton, Seattle, WA	2010-2016
Associate Member,	Clinical Research Division	
Fred Hutchinson Car	icer Research Center, Seattle, WA	2010-2016
Clinical Trials Core D	irector	
Genitourinary Medic	cal Oncology Research Group	
University of Washir	igton / Fred Hutchinson Cancer Research Center, Seattle, WA	2012-2022

Full Professor, Department of Medicine, School of Medicine University of Washington, Seattle, WA	2016-present
Full Member, Clinical Research Division Fred Hutchinson Cancer Research Center, Seattle, WA	2016-present
Clinical Research Director Genitourinary Oncology Research Group University of Washington / Fred Hutchinson Cancer Research Center, Seattle, WA	2017-2022
Medical Director Clinical Research Support Fred Hutchinson Cancer Consortium, Seattle, WA	2018-present
Section Head Medical Oncology, Division of Cancer Medicine Fred Hutchinson Cancer Center, Seattle, WA	2022-present
 <u>Hospital Positions Helo</u> Member, Medical Staff, Pembroke Psychiatric Hospital, Pembroke, MA Member, New England Sinai Rehabilitation Hospital, Stoughton, MA Member, Medical Staff, Anna Jacques Hospital, Newburyport, MA Member, Medical Staff, South Shore Hospital, Weymouth, MA Member, Medical Staff, Emerson Hospital, Concord, MA Member, Medical Staff, Jordan Hospital, Plymouth, MA Member, Medical Staff, Faulkner Hospital, Boston, MA Member, Medical Staff, Brigham and Women's Hospital, Boston, MA Member, Medical Staff, University of Washington Medical Center, Seattle, WA 	2000-2001 2000-2002 2001-2002 2001-2004 2000, 2004 2004 2004 2004
 Alpha Omega Alpha, School of Medicine, University of Washington Graduation with Honors, School of Medicine, University of Washington Chief Resident, Faulkner Hospital (Subsidiary of Brigham and Women's Hospital) Seattle Magazine's "Top Doctor" Who's Who in Medicine and Healthcare Seattle Met Magazine's "Top Doctor" U.S. News and World Report "Top Doctor" Castle Connolly America's Top Doctors Invited Faculty for "Fellows, Residents and Junior Faculty Networking Luncheon" Genitourinary Cancers Symposium Asian Journal of Andrology "Excellent Editorial Board Member Award" Albert Nelson Marquis Lifetime Achievement Award Who's Who in Academia "Triple Threat Award," Fred Hutchinson Cancer Research Center Assistant Fellows! "Best of the Best," Top 1% America's Most Honored Professionals William J. Bremner Endowed Department of Medicine Mentorship Award Nominee Outstanding Research Mentor Award, E17 University of Washington School of Medicine 	1997 1998 2001 2010, 2018, 2022 2011-2012 2011 2011-present 2012, 2013 2016 2017 2017-present nip Director 2018 2018-present e 2018 dicine 2019 2021
Philip Saccoccia Montana WWAMI Translational Medicine Speaker America's Most Honored Doctors – Top 5% 2022	2019 2021 2022
BOARD CERTIFICATION American Board of Internal Medicine 2001-2011 2003-present (recertified in 2013) Medical Oncology **MEDICAL LICENSE** 2000-2005 State of Massachusetts State of Washington (MD00044089) 2004-present State of Montana (MED-PHYS-LIC-102493) 2021-present NPI #1043390016 **Diversity, Equity and Inclusion Activities:** Diverse Enrollment Institutional Review Board Subcommittee 2021-present Fred Hutchinson Cancer Research Consortium 2021-present Cancer Center Director's Task Force for DEI in Clinical Investigations Fred Hutchinson Cancer Research Consortium 2022 Asian American Cancer Disparities Webinar American Cancer Society **PROFESSIONAL ORGANIZATIONS** American Association of Cancer Research American Medical Association American Radium Society American Society of Clinical Oncology American Society of Internal Medicine American Urological Association Association of American Cancer Institutes **European Society of Medical Oncology Hoosier Cancer Research Network** Massachusetts Medical Society Society for Immunotherapy of Cancer Society of Urologic Oncology Southwest Oncology Group (SWOG) Washington State Medical Oncology Society **TEACHING RESPONSIBILITIES** Tutor, Basic Sciences, Microbiology and Biochemistry, School of Medicine, University of Washington 1997-1998 Adjunct Instructor, Health Sciences, Massachusetts College of Pharmacy 1999-2000 Adjunct Instructor, Health Sciences, Massachusetts School of Health Sciences 1999-2000 2004 Preceptor, Patient-Doctor II Course, Harvard Medical School Teaching of Fellows, Residents, and Medical Students, University of Washington 2004-present Research Mentor, American Cancer Society Medical Student Research Program, University of Washington (Student - Brian Rezvani) 2007 Preceptor, University of Washington School of Medicine (Students Andrew Stergachis, Michael Zhang, Gabriel Loeb, Erica Nees, and Qian Zhang) 2008-2011 Research Mentor (Students), University of Washington Brian B. Rezvani – Now thoracic surgeon 2007 Kevin F. Kuo – Now internal medicine faculty at Stanford University 2009-2013

Jason Flamiatos – Now Urologist	2011-2013
Daniel Lim – Current internal medicine resident at University of Washington	2017-present
Alex Carlson – Now internal medicine resident at University of Wisconsin	2018-2020
Olivia Do – Current pediatrics resident at University of Washington	2019-2021
Lorin Ferris – Current pediatrics resident at Inova L.J. Murphy Children's Hospita	l 2019-2021
Research Mentor (Fellows), Fred Hutchinson Cancer Research Center Oncology Fellow	rship
Junfeng Wang – Assistant Professor at University of Utah and Huntsman	
Cancer Institute (Division of Oncology, Department of Medicine)	2012
Swaminathan Murugappan – Now Executive Medical Director at Kite	2012
Heather H. Cheng – Now Associate Professor at University of Washington	2012-present
Jorge D. Ramos – Assistant Professor at University of Washington, now	
Medical Director at Seattle Genetics	2013-2017
Risa Wong – Now Assistant Professor at University of Pittsburgh	2019-2021
Rafee Talukder – Current hematology/oncology fellow	2021-present
Editorial Responsibilities	
Senior/Associate Editor	
Clinical Genitourinary Cancer	2016-2018
UroToday (Clinical Trials Portal)	2016-present
Clinical Cancer Research	2017-present
Editorial Board	
Clinical Genitourinary Cancer	2010-2018
Journal of Cancer Therapeutics and Research	2011-2017
Asian Journal of Andrology	2015-2018
Everyday Oncology	2016-2017

"Ad hoc" Reviewer

Annals of Oncology, Asian Journal of Urology, Bladder Cancer Journal, British Journal of Cancer, BMC Cancer, British Journal of Urology International, Cancer, Cancer Control Journal, Cancer Discovery, Clinical Cancer Research, Clinical Interventions in Aging, Clinical Medicine Insights: Oncology, Drugs, European Journal of Cancer, European Urology, Expert Opinions on Investigational Drugs, Expert Review of Anticancer Therapy, Investigational New Drugs, Journal of American Medical Association, Journal of Clinical Endocrinology and Metabolism, Journal of Clinical Investigation, Journal of Clinical Oncology, JCO Clinical Cancer Informatics, Journal of ImmunoTherapy of Cancer, Journal of the National Cancer Institute, Journal of the National Comprehensive Cancer Network, Journal of Nuclear Medicine, Journal of Oncotargets and Therapy, Journal of Urology, Lancet Oncology, New England Journal of Medicine, The Oncologist, Oncotarget, PLOS ONE, Proceedings of the National Academy of Sciences, The Prostate, Prostate Cancer and Prostatic Diseases, Up-to-Date: Genitourinary Oncology, Urologic Oncology, Urology

Grant and Funding Organization Reviews

Cancer Research United Kingdom, Department of Defense, National Cancer Institute, Prostate Cancer Charity, Prostate Cancer Foundation Challenge and Young Investigator Awards, PNW SPORE Pilot Projects, Solid Tumor Translational Research (STTR) Grant Program, V Foundation

NATIONAL RESPONSIBILITIES	
Reviewer, Department of Defense	2005
Prostate Cancer Translational Grant Study Section	
Steering Committee Member, Dasatinib Phase 3 Registration Study	2009-2013

	Imaging Committee, Prostate Cancer Working Group	2009-2012
	Co-Chair and Faculty, 2010 American Society of Clinical Oncology	2010
	Genitourinary Cancer (Prostate) Oral Abstract Session	
	Co-Chair, Quantitative Imaging Network (QIN) Outreach Working Group	2010
	Genitourinary Committee Member, SWOG	2010-present
	Co-Chair and Faculty, 2011 American Society of Clinical Oncology	2011
	Genitourinary Cancer (Non-Prostate) Oral Abstract Session	
	Advanced Prostate Cancer Chair (covering), SWOG Fall 2011 Group Meeting	2011
	Genitourinary Committee	
	SPORE Representative, National Cancer Institute	2012-2014
	Genitourinary Cancers Steering Committee	
	Steering Committee Member, PREDICT Biomarker Committee	2013-2016
	Special Clinical Expert, National Cancer Institute (Served 1 year of 2 nd 3-year term)	2014-2018
	Genitourinary Cancers Steering Committee	
	Advisory Member, Society of Urology Oncology (Clinical Trials Consortium, Inc.)	2015-present
	Board of Directors and the Prostate Organ Site Committee	
	Test Question Writer, American Society of Clinical Oncology and National Board of	2017-2019
	Medical Examiners	
	ASCO University Courses, ASCO-SEP Mock Exam, In-Training Exam	
	Member, American Society of Oncology Annual Meeting Education Committee	2017-2020
	Genitourinary (Nonprostate) Cancer	
	Member, Bone Metastasis Expert Panel	2017-2019
	American Radium Society	
	GU Prostate Cancer Committee Member, SWOG	2017-present
	Co-Chair (Medical Oncology), National Cancer Institute (3-year term renewed)	2018-present
	Prostate Cancer Task Force	
	Imaging Committee Member, SWOG	2018-present
	Member, Education Committee	2019-present
	Association of American Cancer Institutes	
	Member, Board of Governors, SWOG	2020-present
	Member, AACR Annual Meeting Clinical Trials Committee	2020-2022
	American Association for Cancer Research	
	Test Question Writer, American Society of Clinical Oncology Question Writing	2021-present
	Group for ASCO Self-Assessment Programs	
	Reviewer, National Cancer Institute	2021
	Cancer Clinical Investigator Team Leadership Award (CCITLA) Grant Reviewer	
	Co-Chair, American Society of Clinical Oncology	2021-present
	Germline and Somatic Genomic Testing for Advanced and Metastatic Prostate	Cancer
	Reviewer, National Cancer Institute Intramural Research Program	2021
	Molecular Imaging Branch	
	Member, Hoosier Cancer Research Network	2021-present
	Genitourinary Clincal Trial Working Group	
	Member, AACR Continuing Medical Education Committee	2022-present
	American Association for Cancer Research	
	Member, Imaging Committee	2022- present
	Prostate Cancer Working Group 4	
Loc	AL RESPONSIBILITIES	
	4th Floor Solutions Committee,	2004–2006
	Seattle Cancer Care Alliance	

Genitourinary Practice Committee	2004–2005
Recruitment and Community Outreach Core	2004–2005
Multicultural Affairs Advisory Board	2006–2007
University of Washington Department of Medicine Translational Research Task Force	2006–2008
University of Washington Translational Grant Committee	
Accreditation Council for Graduate Medical Education	2006–2017
University of Washington Medicine Residency Program	
Oncology and Hematology Fellowship Program Admissions Committee University of Washington / Fred Hutchinson Cancer Research Center	2006–present
Prostate Cancer Task Force	2007–2008
Washington Comprehensive Cancer Control Partnership	
Imaging Working Group	2007–2008
Prostate Specialized Programs of Research Excellence (SPORE)	
Quality Improvement/Safety Steering Committee	2007–2010
Seattle Cancer Care Alliance	
Medical Student Research Training Program Committee	2008-2016
University of Washington School of Medicine	
Medical Student Admissions Committee	1995-1998
University of Washington School of Medicine	2009-2016
Institute for Prostate Cancer Research Committee	2009-present
University of Washington	2010
Grant Reviewer	2010
INBRE-WSU Spokane Institute for Translational Health Sciences	2010 2017
Internal Medicine Residency Education Coordinator (Oncology)	2010-2017
Core Eaculty Designation Internal Medicine Residency	2010 procept
Liniversity of Washington	2010-present
	2012-present
Pacific Northwest Prostate Cancer SPORE	2012-present
Reviewer for the University of Washington	2013
American Cancer Society Summer Fellowshin in Clinical Cancer Research	2015
New Faculty Search Committee Member	2013-2015
University of Washington Pediatric Oncology and Seattle Children's Hospital	
Prostate Cancer Clinical Pathways	2013-2017
Seattle Cancer Care Alliance	
Scientific Review Committee, Sub-Committee B Member	2014
University of Washington / Fred Hutchinson Cancer Research Center Consortium	
Scientific Review Committee, Sub-Committee B Co-Chair	2015-2017
University of Washington / Fred Hutchinson Cancer Research Center Consortium	
New Radiochemistry Faculty Search Committee Member	2015-2018
University of Washington Department of Radiology	
New Faculty Search Committee Member	2016-2017
University of Washington Genitourinary Oncology	
Genitourinary Oncology Leadership Committee	2017-present
University of Washington / Fred Hutchinson Cancer Research Center Consortium	
Clinical Trials Process Improvement Oversight Committee Seattle Cancer Care Alliance	2017-present

External Performance Site Assessment Committee	2018
Fred Hutchinson Cancer Consortium	
Site Initiation Visit Escalation Policy Committee	2017-2018
Seattle Cancer Care Alliance	
New Faculty Search Committee, Director of Nuclear Medicine	2018-2019
Seattle Cancer Care Alliance	
Research Ethics Committee	2018-present
Fred Hutchinson Board of Trustees	
Institutional Review Board Chair Liason Committee	2018-present
Fred Hutchinson Cancer Research Consortium	
Compliance Sub-Committee, Clinical Research Services	2018-present
Fred Hutchinson Cancer Research Consortium	
Clinical Trial Oversight Committee, Clinical Research Services	2018-present
Fred Hutchinson Cancer Research Consortium	
Institutional Sponsored IND Oversight Committee, Clinical Research Services	2018-present
Fred Hutchinson Cancer Research Consortium	
NCI National Cancer Trials Network Leadership Committee	2020-present
Fred Hutchinson Cancer Research Consortium	
Adult Oncology Strategic Plan: Research Advisory Group	2021-present
Seattle Cancer Care Alliance/University of Washington Medicine/Fred	
Hutchinson Cancer Research Center	
New Faculty Search Committee, Director of Nuclear Medicine Theranostics	2021-present
Seattle Cancer Care Alliance	
Co-Chair, Faculty Advisory Committee, Clinical Trials Joint Steering Committee	2022-present
University of Washington and Fred Hutchinson Cancer Center	

PEER REVIEW FUNDING

- 1.
 Prostate Cancer Research Program Clinical Consortium Award.

 W81XWH-16-PCRP-CCRSA (Cheng)

 Grant amount:

 Source:
 Department of Defense

 Role:
 Co-site principal investigator (5% effort)

 Dates:
 01/01/07 09/29/27 (4 successful competitive renewals)
- Pacific Northwest Prostate Cancer SPORE Core D (Clinical)
 P50 CA097186 (Nelson/Core D Yu and Gore)
 Grant amount: (this funding cycle)
 Source: Pacific Northwest Prostate Cancer SPORE
 Role: Clinical Core Leader for clinical trials and biospecimen acquisition
 Dates: 9/17/13 08/31/23 (2 successful competitive renewals)

Cancer Consortium Support Grant P30 CA015704 (Gilliland) / Clinical Research Support (Yu) Grant amount: Role: Medical Director, Clinical Research Support Office Dates: 01/01/97 – 12/31/24

Lead Academic Participating Site (LAPS) Grant
 UG1 CA233328 (Yu)
 Grant Amount:
 Source: NIH/NCI
 Role: Site co-Principal Investigator
 Dates: 03/06/19 - 02/28/25

PEER REVIEW FUNDING: COMPLETED

1.	Pilot Project - Pos	sitron Emission Tomography Imaging of Bone in Patients with Metastatic
	Prostate Cancer - A	A Pilot Study Evaluating Treatment Response.
	5 P30 CA015704 (H	Hartwell) / Pilot (Yu)
	Grant amount:	
	Source:	NIH/NCI Cancer Center Support Grant
	Role:	Concept development and overall principal investigator
	Dates:	10/01/05 – 12/31/07

 Pilot Project - Positron Emission Tomography Imaging of Bone in Patients with Metastatic Prostate Cancer.
 P50 CA97186 (Lange) / Pilot (Yu)

PSUCASTIOU (Lange)	/ Fliot (fu)
Grant amount:	
Source:	Pacific Northwest Prostate Cancer SPORE
Role:	Concept development and overall principal investigator
Dates:	01/01/07 – 12/31/07

3. A randomized phase II study of OGX-011 in combination with docetaxel and prednisone or docetaxel and prednisone alone in patients with metastatic hormone-refractory prostate cancer.

Grant amount:	
Source:	National Cancer Institute of Canada (Cooperative Group Trial)
Role:	Site Principal Investigator
Dates:	11/01/05 – 09/30/09

4. Phase 2 randomized trial of gemcitabine and cisplatin with or without Cetuximab in patients with urothelial carcinoma.

Grant amount:	
Source:	National Comprehensive Cancer Network (Cooperative Group Trial)
Role:	Site principal investigator
Dates:	01/15/09 - 03/04/11

 Phase 2, multicenter evaluation of ¹⁸F-fluoride PET as a pharmacodynamic biomarker for Dasatinib, a SRC kinase inhibitor, in men with castration-resistant prostate cancer and bone metastases (ACRIN 6687).
 Grant amount:

Source:	American College of Radiology Imaging Network (ACRIN)
	(Cooperative Group Trial)
Role:	Concept development, multicenter study chair, and overall principal investigator (20% effort)
Dates:	07/01/09 – 06/30/12

6. Genitourinary Oncology Clinical Trials Core.

Infrastructure Support Proposal (PI: Yu)Grant amount:Source:Institute of Prostate Cancer ResearchRole:Core DirectorDates:11/19/12 – 11/18/13

7. A randomized phase 2 study of combined androgen deprivation versus combined androgen deprivation with Cixutumumab (IMC-A12) for patients with new hormone-sensitive metastatic prostate cancer (SWOG 0925).

Grant amount:

Source:	Southwest Oncology Group (SWOG) (Cooperative Group Trial) and
	Imclone Pharmaceuticals
Role:	Concept development, multicenter study chair, and overall principal
	investigator

- Dates: 06/01/11-05/31/14
- 8. Advanced PET/CT imaging for improving clinical trials.
 1U01 CA148131 (Kinahan)
 Grant amount:
 Source: National Institute of Health
 Role: Leader of prostate cancer imaging trials (5% effort)
 Dates: 04/16/10 04/15/15
- Biomarkers of response to treatment with XL184.
 Creativity Award (Co-PIs: Knudsen, Yu)
 Grant amount:
 Source: Prostate Cancer Foundation
 Role: Concept development and leader of PET imaging effort
 Dates: 05/23/12 08/22/16 (no cost extension)
- A Phase II Study of MAOA Inhibitor Plus Docetaxel in Patients Currently Receiving and Progressing on Docetaxel Therapy. Grant amount:

Source:	Wayne D. Kuni and Joan E. Kuni Foundation (subcontract award from
	Oregon Health Sciences University)
Role:	Site principal investigator
Dates:	12/01/12 – 05/31/17

- A phase 2 study of recombinant glycosylated human interleukin-7 (CYT107) after completion of standard FDA approved therapy with sipuleucel-T for patients with asymptomatic or minimally symptomatic metastatic castration-resistant prostate cancer. Grant amount:
 Source: Cancer Immunotherapy Trials Network Role: Site principal investigator for lead site
 - Dates: 02/04/15 02/03/18
- A pilot study of TIL therapy generation for urothelial bladder cancer. Bezos family Immunotherapy Pilot Award (Yu) Grant amount: Source: Bezos family Immunotherapy Initiative

Role:	Concept development and principal investigator
Dates:	07/01/15 – 06/30/18 (no cost extension)

13. INTense Exercise foR surVivAL among men with Metastatic Castrate-Resistant Prostate Cancer (INTERVAL – MCRPC): A multicenter, randomized, controlled, phase III study Grant amount: Source: Movember GAP4 Role: Site principal investigator 10/05/16 - 10/04/21

PHARMACEUTICAL FUNDING: INVESTIGATOR INITIATED

Dates:

Biologic tissue effect of Grant amount:	of sipuleucel-T on metastatic castration-resistant prostate cancer.
Source:	Dendreon
Role:	Concept development and overall principal investigator
Dates:	01/27/15 – 04/14/23
	Biologic tissue effect Grant amount: Source: Role: Dates:

- 2. A randomized phase II study of atezolizumab plus recombinant human IL-7 (CYT107) in patients with locally advanced or metastatic urothelial carcinoma. Grant amount: Genentech, Inc. and NCI Cancer Immunotherapy Trials Network Source: Role: Concept development and overall national principal investigator Dates: 06/28/19 - 09/30/23
- The impact of DNA repair pathway alterations identified by circulating tumor DNA on 3. sensitivity to Radium-223 in bone metastatic castration-resistant prostate cancer. Grant amount: Source: Bayer HealthCare Pharmaceuticals, Inc. Role: Concept development and overall national principal investigator 01/09/20 - 09/08/24 Dates:
- 4. Fluciclovine (FACBC) PET/CT site-directed therapy of oligometastatic prostate cancer (FLU-BLAST-PC trial) Grant amount: Source: Blue Earth

Role:	Concept development and overall principal investigator
Dates:	02/07/20 – 02/06/24

5. A randomized phase II study of atezolizumab plus recombinant human IL-7 (CYT107) in patients with locally advanced or metastatic urothelial carcinoma. Grant amount: (supplemental funding agreement) Revimmune, Inc. and NCI Cancer Immunotherapy Trials Network Source: Concept development and overall national principal investigator Role: Dates: 03/31/20 - 09/30/23

PHARMACEUTICAL FUNDING: INVESTIGATOR INITIATED: COMPLETED

A phase II study of BAY 43-9006 (Sorafenib) prior to prostatectomy in patients with high-risk 1. localized prostate cancerGrant amount:

Source:	Bayer Pharmaceuticals, Corp.
Role:	Concept development and overall principal investigator
Dates:	07/01/06 – 06/31/11

A randomized phase II study of docetaxel + / - ZD6474 (Zactima) in metastatic transitional cell carcinoma.
 Grant amount:
 Source: Astrazeneca Pharmaceuticals, LP (subcontract award from Dana-Farber Cancer Institute)

Role:	Site principal investigator
Dates:	05/31/07 – 03/14/12

3. A phase II trial of genomic guided therapy with dasatinib or nilutamide in metastatic castration-resistant prostate cancer.

Grant amount:	
Source:	Bristol-Myers Squibb (subcontract award from Duke University)
Role:	Site principal investigator with input into concept development
Dates:	05/12/09 – 12/31/12

 Phase 2, multicenter evaluation of 18F-fluoride PET as a pharmacodynamic biomarker for Dasatinib, a SRC kinase inhibitor, in men with castration-resistant prostate cancer and bone metastases.

Grant amount:	
Source:	Bristol Myers Squibb Co.
Role:	Concept development, multicenter study chair, and overall principal investigator
Dates:	06/01/10 - 06/30/13

5. A randomized phase II study of OGX-427 (a second-generation antisense oligonucleotide to Heat Shock Protein-27) in patients with castration resistant prostate cancer who have not previously received chemotherapy for metastatic disease.

Grant amo	unt:
Sourco	

Source:	OncoGeneX Techologies, Inc.
Role:	Site principal investigator
Dates:	11/08/11 – 08/25/15

A Phase II Study of BKM120 in Men with Metastatic Castration-Resistant Prostate Cancer.
 Grant amount:
 Source: Novartis (subcontract award from Duke University)

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Role:	Site principal investigator
Dates:	07/12/13 - 09/29/15

 Retrospective analysis of clinical benefit from radium-223 in castrate resistant prostate cancer Grant amount: Source: Bayer via University of Michigan

Source.	Dayer via Oniversity Of Michigan
Role:	Senior and site principal investigator
Dates:	05/08/15 – 05/17/17

8. PET/CT for assessment of systemic treatment response and direction of metastatic biopsy for molecular characterization of metastatic castration resistant prostate cancer

Grant amount:	
Source:	Bayer
Role:	Concept development and overall principal investigator
Dates:	11/03/15 - 04/30/18

 A phase 2 study of recombinant glycosylated human interleukin-7 (CYT107) after completion of standard FDA approved therapy with sipuleucel-T for patients with asymptomatic or minimally symptomatic metastatic castration-resistant prostate cancer.

or arre arrive arres	
Sources:	Dendreon
Role:	Site principal investigator for lead site
Dates:	09/01/14 - 08/31/18

PHARMACEUTICAL INITIATED FUNDING

- Phase 1b/II trial of pembrolizumab (MK-3475) combination therapies in metastatic castration-resistant prostate cancer (KEYNOTE-365). Grant amount: Source: Merck Sharp &Dohme Corp. Role: Concept and protocol co-developed with Merck and Overall Principal Investigator for international trial
 Dates: 01/13/17 – 12/31/23
- 2. A phase 1b, multicenter, two-part, open label study of DS-8201A, an anti-human epidermal growth factor receptor-2 (HER2)-antibody drug conjugate in combination with nivolumab, an anti PD-1 antibody for subjects with HER2-expressing advanced breast and urothelial cancer.

Grant amount.	
Source:	Daiichi Sankyo
Role:	Site principal investigator
Dates:	01/07/19-03/31/23

3. A phase 1, open-label, non-randomized, safety, tolerability, and pharmacokinetic study of TAS3681 in patients with metastatic castration-resistant prostate cancer.

Taiho
Site principal investigator
09/12/19 – 05/31/24

4. An open-label, randomized, controlled phase 3 study of enfortumab vedotin in combination with pembrolizumab with or without chemotherapy, versus chemotherapy alone in previously untreated locally advanced or metastatic urothelial cancer.

Grant amount:	
Source:	Seattle Genetics, Inc.
Role:	Site principal investigator
Dates:	12/10/19 - 04/30/25

A phase 1b/2 study of ibrutinib combination therapy in selected advanced gastrointestinal and genitourinary tumors.
 Grant amount:
 Source: Pharmacyclics, Inc.
 Role: Site principal investigator

Dates: 01/06/20 - 09/25/24

6. A phase 3, randomized open-label study of pembrolizumab (MK-3475) plus olaparib versus abiraterone acetate or enzalutamide in participants with metastatic castration-resistant prostate cancer (mCRPC) who are unselected for homologous recombination repair. Grant amount:

Source:	Merck Sharp & Dohme Corp.
Role:	Site and overall international principal
Dates:	investigator 01/17/20 – 05/31/24

- 7. DAROL: Darolutamide observational study in nonmetastatic castration-resistant prostate cancer patients.
 Grant amount:
 Source: Bayer AG
 Role: Site and overall international principal investigator
 Dates: 05/27/20 10/14/24
- A multicenter, randomized, controlled phase 2 study: Efficacy and safety of ¹³¹I-1095 radiotherapy in combination with enzalutamide in metastatic castration-resistant prostate cancer patients who are ¹⁸F-DCFPyL prostate-specific membrane antigen-avid, chemotherapy-naïve, and progressed on abiraterone (ARROW).
 Grant amount:
 Source: Progenics Pharmaceuticals, Inc.
 Role: Site and overall international principal investigator
 - Dates: 06/03/20 05/31/24
- 9. A phase 2 basket study of Tucatinib in combination with trastuzumab in subjects with previously treated, locally-advanced unresectable or metastatic solid tumors driven by HER2 alterations.

Grant amount:	
Source:	Seagen, Inc.
Role:	Site and overall international principal investigator
Dates:	02/24/21-01/31/26

10. A phase 2 trial of SRF617 in combination with AB928 (Etrumadenant) and AB122 (Zimberelimab) in patients with metastatic castration resistant prostate cancer. Grant amount:
 Source: Surface Oncology, Inc.
 Role: Site and overall principal investigator
 Dates: 05/17/22 - 01/31/27

PHARMACEUTICAL INITIATED FUNDING: COMPLETED

1. A Phase II multicenter evaluation of the safety and efficacy of Tocosol paclitaxel (s-8184 paclitaxel injectable emulsion) in patients with metastatic or locally advanced unresectable transitional cell carcinoma of the urothelium.

Grant amount:

Source:	Sonus Pharmaceuticals, Inc.
Role:	Site principal investigator
Dates:	12/15/04 - 12/15/08

 A phase II multi-center open-label study of YM155 in subjects with hormone-refractory prostate cancer previously treated with at least one prior chemotherapy regimen. Grant amount:

Source:	Astellas Pharma US, Inc.
Role:	Site principal investigator
Dates:	09/01/07 – 04/30/09

 Phase II Study of Dasatinib for Androgen-Deprived Progressive Prostate Cancer. Grant amount:
 Source: Bristol Myers Squibb Co.
 Polo: Overall principal investigator.

Role:	Overall principal investigator
Dates:	05/01/07 - 04/01/10

 A phase 1 study evaluating a second-generation antisense oligonucleotide (OGX-427) that inhibits heat shock protein 27 (HSP27).
 Grant amount:

Grant anount.	
Source:	OncoGeneX Technologies, Inc.
Role:	Site principal investigator
Dates:	05/17/07 - 04/30/11

5. A phase III randomized placebo-controlled double-blind study to assess the efficacy and safety of once-daily orally administered ZD4054 10 mg in non-metastatic hormone-resistant prostate cancer patients.

Grant amount:	
Source:	AstraZeneca Pharmaceuticals, LP
Role:	Site principal investigator
Dates:	04/01/08-03/31/11

6. A phase III randomized double-blind placebo-controlled study of abiraterone acetate (CB7630) plus prednisone in patients with metastatic castration-resistant prostate cancer who have failed docetaxel-based chemotherapy.

Grant amount:	
Source:	Cougar Biotechnology
Role	Site principal investiga

Role:	Site principal investigator
Dates:	10/1/08 - 09/30/11

7. A randomized double-blind phase III trial comparing docetaxel combined with dasatinib to docetaxel combined with placebo in castration-resistant prostate cancer. Grant amount:

Bristol-Myers Squibb Co.
Steering committee member and site principal investigator
06/15/09 - 06/14/14

8. A phase 3, randomized, double-blind, placebo-controlled study of abiraterone acetate (CB7630) plus prednisone in asymptomatic or mildly symptomatic patients with metastatic castration-resistant prostate cancer.

Grant amount: Source: (

Site principal investigator

Dates: 06/15/09 – 03/16/15

- 9. A phase II, open-label, single-arm trial evaluating KX2-391 in patients with bone-metastatic, castration-resistant prostate cancer who have not received prior chemotherapy. Grant amount:
 Source: Kinex Pharmaceuticals
 Role: Site principal investigator and assistance with protocol development
 Dates: 05/05/10 12/19/12
- 10. A randomized, open-label, phase 2 trial examining the sequencing of sipuleucel-T and androgen deprivation therapy in men with non-metastatic prostate cancer and a rising prostate specific antigen after primary therapy.

Grant annount.	
Source:	Dendreon
Role:	Site principal investigator
Dates:	11/04/11 - 11/03/15

11. A randomized, double-blind phase 2 study comparing gemcitabine and cisplatin in combination with OGX-427 or placebo in patients with advanced transitional cell carcinoma. Grant amount:

Source:	OncoGeneX Technologies, Inc.
Role:	Site principal investigator
Dates:	02/14/12 - 11/03/15

 Open label study of the effect of GTx-758 on serum PSA and free testosterone levels in men with castration resistant prostate cancer and maintained on androgen deprivation therapy. Grant amount:

Source:	GTx, Inc.
Role:	Overall principal investigator and assistance with protocol development
Dates:	02/16/12 – 02/27/12

13. An open-label, multicenter, randomized phase 2 study evaluating the safety and efficacy of docetaxel in combination with IMC-1121B or IMC-18F1 or without investigational therapy as second line therapy in patients with metastatic transitional cell carcinoma. Grant amount:

Source:	Imclone Systems, Inc.
Role:	Site principal investigator
Dates:	05/08/12 – 01/14/15

14. Phase II, open label study of the effect of GTx-758 as secondary hormonal therapy on serum PSA and serum free testosterone levels in men with metastatic castration resistant prostate cancer maintained on androgen deprivation therapy.

Grant amount:	
Source:	GTx, Inc.
Role:	Overall principal investigator
Dates:	12/20/12 - 09/30/15

A phase II, multicenter, single-arm study of MPDL3280A in patients with locally advanced or metastatic urothelial bladder cancer.
 Grant amount:
 Source: Genentech/Roche

Role:	Site principal investigator
Dates:	08/21/14 - 08/20/16

 A phase 3, randomized, double-blind, placebo-controlled study of ramucirumab plus docetaxel vs. placebo plus docetaxel in patients with locally advanced or unresectable or metastatic urothelial carcinoma who progressed on or after platinum-based therapy.
 Grant amount:

Grant amount.	
Source:	Eli Lilly and Company
Role:	Site principal investigator
Dates:	06/21/16 - 07/31/17

17. A multicenter, single-arm, open-label, post-marketing safety study to evaluate the risk of seizure among subjects with metastatic castration-resistant prostate cancer treated with enzalutamide who are at potential increased risk of seizure.

Grant amount:	
Source:	Astellas, Inc.
Role:	Site principal investigator
Dates:	09/12/14 – 09/11/17

 A phase I study of the safety and pharmacokinetics of escalating doses of AGS15E given as monotherapy in subjects with metastatic urothelial cancer.

Grant amount:	
Source:	Agensys Inc.
Role:	Site principal investigator
Dates:	03/12/14 – 12/31/17

19. A phase II clinical trial of pembrolizumab (MK-3475) in subjects with advanced/unresectable or metastatic urothelial cancer.

Grant amount:

Source:	Merck Sharp & Dohme Corp.
Role:	Site principal investigator
Dates:	03/22/16 - 03/21/18

20. A phase 2 study of TGF-inhibition (Vactosertib) with Anti-PD-L1 (Durvalumab) in patients with advanced or recurrent urothelial carcinoma failing to achieve response with checkpoint inhibition.

Grant amount:	
Source:	MedPacto
Role:	Site principal investigator
Dates:	09/01/20 - 01/04/21

21. A single-arm, open-label, multicenter study of enfortumab vedotin (ASG-22CE) for treatment of patients with locally advanced or metastatic urothelial cancer who previously received immune checkpoint inhibitor therapy.

Grant amount.	
Source:	Seattle Genetics, Inc.
Role:	Steering committee member and Site principal investigator
Dates:	10/13/17 – 08/31/22

22. A phase 3 randomized, controlled clinical trial of pembrolizumab with or without platinumbased combination chemotherapy vs. chemotherapy in subjects with advanced or metastatic urothelial carcinoma.

Grant amount:

Source:	Merck Sharp & Dohme Corp.
Role:	Site principal investigator
Dates:	11/16/16 – 11/15/22

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- 2. <u>Yu EY</u>. Editor's Note Evan Yu introduces Clinical Trials Portal. Uro-Today. On-line, December 15, 2016.
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- 4. <u>Yu EY</u>. Non-metastatic castration-resistant prostate cancer, a disease state misnomer that is a seriously unmet therapeutic need. Uro-Today. On-line, March 14, 2017.
- 5. <u>Yu EY</u>. From the Desk of Evan Yu: PD-1 or PD-L1 inhibition for front-line metastatic urothelial cancer. Uro-Today. On-line, April 11, 2017.
- 6. <u>Yu EY</u>. From the Desk of Evan Yu: No...the ball game is not over...adjuvant trials of PD-1 and PD-L1 antibodies in urothelial carcinoma must go on! Uro-Today. On-line, May 18, 2017.
- 7. <u>Yu EY</u>. From the Desk of Evan Yu: What should I do with my new metastatic clear cell renal carcinoma patients? Uro-Today. On-line, June 8, 2017.
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- 9. <u>Yu EY</u>. From the Desk of Evan Yu: Does PD-1/PD-L1 inhibition really work in prostate cancer? Uro-Today. On-line, August 14, 2017.
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- 129. Makrakis D, Roudier M, Wang Y, Vakar-Lopez F, Garcia J, Dash A, Lin DW, Schade G, Mostaghel EA, Cheng HH, Schweizer MT, Holt SK, Gore JL, <u>Yu EY</u>, Lam HM, Wright JL, Montgomery B. A phase 1/2 study of rapamycin and cisplatin/gemcitabine for treatment of patients with muscle-invasive bladder cancer. Abstract PD10-06. *J Urol* Vol. 207, No. 5S:e185. Poster presentation at American Urological Association 2022 Annual Meeting, New Orleans, LA, May 2022.
- 130. Noonavath M, Mun K, Marquardt P, Fintelmann FJ, O'Malley R, Holt SK, Dwyer E, Maldonado R, Diamantopoulos L, Makrakis D, Laidlaw G, Schade GR, Lin DW, Wright JL, Gore JL. Associations between skeletal muscle gauge and survival following radical cystectomy for bladder cancer: A novel assessment of muscle mass and quality. Abstract MP56-06. *J Urol* Vol. 207, No. 5S:e973. Poster presentation at American Urological Association 2022 Annual Meeting, New Orleans, LA, May 2022.
- Garcia J, Vakar-Lopez F, Roudier M, Grivas P, <u>Yu EY</u>, Cheng HH, Schweizer MT, Haffner M, Lee JK, Corey E, Montgomery B, Hsieh AC, Wright JL, Lam HM. Urothelial cancer rapid autopsy program: Biospecimens and patient-derived preclinical models. Abstract MP06-05. *J Urol* Vol. 207, No. 5S:e78. Poster presentation at American Urological Association 2022 Annual Meeting, New Orleans, LA, May 2022.
- 132. <u>Yu EY</u>, Pieczonka CM, Armstrong AJ, Suzuki H, Bailen JL, Murphy DG, Lebret T, Luz M, Thiery-Vuillemin A, Ortiz JA, Khan J, Briganti A. DARolutamide Observational (DAROL) study in

patients with nonmetastatic castration-resistant prostate cancer. *J Clin Oncol* 40, 2022 (suppl 16; abstr e17029).

- 133. Gulhane A, Talukder R, Dash A, Ellis WJ, Schade G, Chen JJ, Weg ES, Cheng HH, Grivas P, Hawley J, Lee JK, Montgomery RB, Nelson PS, Schweizer MT, Yezefski TY, <u>Yu EY</u>, Lin DW, Cheng DL. Clinical impact of PSMA PET in patients with biochemically recurrent prostate cancer after locoregional definitive therapy. *J Clin Oncol* 40, 2022 (suppl 16; abstr e17009).
- 134. Sokolova A, Gulati R, Cheng HH, Beer TM, Graff JN, Amador M, Toulouse A, Taylor K, Bailey S, Smith S, Tabatabaei S, Sinit R, Slottke R, Vuky J, Yezefski T, Grivas P, <u>Yu EY</u>, Schweizer MT. Durvalumab and Olaparib for the treatment of prostate cancer in men predicted to have a high neoantigen load. *J Clin Oncol* 40, 2022 (suppl 16; abstr TPS5099). Poster presentation at ASCO Annual Meeting, Chicago, IL, Jun. 2022.
- 135. Wong RL, Cheng HH, Fann JR, Hnida J, Chakoian M, Schenker Y, <u>Yu EY</u>, Gore JL. Longitudinal screening for depression and anxiety in prostate cancer and association with disease and treatment factors. *J Clin Oncol* 40, 2022 (suppl 16; abstr 5023). Poster presentation at ASCO Annual Meeting, Chicago, IL, Jun. 2022.
- 136. Gulhane A, Talukder R, Wu ZJ, Lin DW, Dash A, Ellis WJ, Nyame YA, Schade G, Wright JL, Apisarnthanarax S, Chen J, Liao JL, Wallner K, Weg ES, Cheng HH, Grivas P, Hawley J, Hsieh AC, Lee JK, Montgomery B, Nelson PS, Schweizer MT, Yezefski T, Yu EY, Cheng DL. [⁶⁸Ga]-PSMA-11 can clarify equivocal lesions on conventional imaging and change management decisions among men with previously treated prostate cancer. Poster presentation at Society of Nuclear Medicine and Molecular Imaging Annual Meeting, Vancouver, BC, Jun. 2022.
- 137. Yu EY, Park SH, Goh JC, Shin SJ, Mehra N, McDermott R, Sala Gonzalez N, Fong P, Greil R, Retz M, Sade JP, Huang YH, Begbie SD, Rey F, Kramer G, Suzuki H, Zhang J, Kim J, Poehlein C, Antonarakis ES. Pembrolizumab plus Olaparib vs. abiraterone or enzalutamide for patients with previously treated metastatic castration-resistant prostate cancer: Randomized open-label phase 3 KEYLYNK-010 study. Oral presentation at ESMO Congress 2022, Paris, France, Sept 2022.
- 138. Kramer G, de Bono J, Joshua AM, Shore ND, Zhu P, Poehlein CH, Schloss C, <u>Yu EY</u>. Phase 1b/2 study of pembrolizumab plus Lenvatinib, vibostolimab, or platinum-based chemotherapy for adenocarcinoma metastatic castration-resistant prostate cancer or neuroendocrine metastatic prostate cancer: KEYNOTE-365 cohorts E-I. Poster presentation at ESMO Congress 2022, Paris, France, Sept 2022.
- 139. Linch MD, Ferrario C, Stoeckle M, Laguerre B, Arranz J, Todenhofer T, Fong P, Piulats JM, Berry W, Emmenegger U, Mourey L, Mar N, Appleman L, Joshua AM, Conter H, Li XT, Schloss C, Poehlein C, de Bono JS, <u>Yu EY</u>. Two year follow-up of KEYNOTE-365 Cohort D: Pembrolizumab plus abiraterone acetate and prednisone in patients with chemotherapy-naïve metastatic castration-resistant prostate cancer. Poster presentation at ESMO Congress 2022, Paris, France, Sept 2022.
- 140. Galsky MD, O'Donnell PH, Burgess E, Van der Heijden M, Krieger L, Necchi A, <u>Yu EY</u>, Matsubara N, Campbell MT, Gadde S, Aragon-Ching JB, Koshkin VS, Zhang W, Sokolowski K, Powles T. Phase 2 clinical study evaluating the efficacy and safety of distamab vedotin with or without

pembrolizumab in patients with HER2-expressing urothelial carcinoma (RC48G001, TIP). Poster presentation at 2022 Society for Immunotherapy of Cancer at Boston, MA, Nov. 2022.

INVITED TALKS AND LECTURES

UNIVERSITY/LOCAL CONFERENCES

- Program in Prostate Cancer Research/SPORE: "Retroviral RNA interference: systems development, biologic discoveries with telomerase, and future applications." Fred Hutchinson Cancer Research Center, Seattle, WA. March 4, 2004.
- Jobson Education: "Hormone refractory prostate cancer: Early vs. late vs. asymptomatic" Seattle, WA. June 24, 2005.
- Hematology/Oncology Fellows' Lecture Series: "Bladder cancer: Clinical implications." Fred Hutchinson Cancer Research Center, Seattle, WA. October 21, 2005.
- Resident Teaching Conference: "A case-based approach to managing metastatic bone disease." University of Washington, Seattle, WA. October 25, 2005.
- Seattle Cancer Care Alliance Physician Educational Outreach Program: "Hormone-refractory prostate cancer; the medical oncologist's perspective." Mount Vernon, WA. October 25, 2005.
- Breast and Prostate Program Bone Metastases Retreat: "Response to treatment in patients with metastatic prostate cancer: using PET scans as a surrogate marker for bone-dominant disease." Fred Hutchinson Cancer Research Center, Seattle, WA. November 14, 2005.
- Puget Sound Oncology Consortium's Annual Highlights of ASCO meeting: "Genitourinary Oncology ASCO 2006: review of prostate, bladder and testicular cancer." Seattle, WA. June 29, 2006.
- 6th Annual Pacific Northwest Prostate Cancer Conference: "A rising PSA after local therapy...implications and utility of PSA kinetics." Seattle, WA. September 16, 2006.
- Nuclear Medicine Internal Advisory Board: "Metabolic Imaging in prostate cancer the future with PET." University of Washington, Seattle, WA. September 25, 2006.
- Program in Prostate Cancer Research/SPORE: "PET measures response to therapy in prostate cancer." University of Washington, Seattle, WA. November 2, 2006.
- North Star Lodge: "New concepts in genitourinary oncology." Yakima, WA. November 9, 2006.
- Nuclear Medicine External Advisory Board: "Metabolic imaging of prostate cancer as a biomarker of treatment response." University of Washington, Seattle, WA. November 30, 2006.
- Asian Senior Concerns Foundation: "Bladder cancer the basics." Bellevue, WA. January 20, 2007.
- Asian Senior Concerns Foundation: "Prostate cancer PSA screening, treatments, and public concerns." Bellevue, WA. January 20, 2007.
- Virginia Mason Medical Center: "Mediastinal germ cell tumors." Seattle, WA. February 1, 2007.
- Hematology/Oncology Fellows' Lecture Series: "Bladder cancer: the need for new knowledge." Fred Hutchinson Cancer Research Center, Seattle, WA. March 2, 2007.
- A&P Lecture: "Imaging biomarkers in prostate cancer: the potential impact of tumor metabolism on clinical trials and drug development." University of Washington, Seattle, WA. March 6, 2007.
- Pacific Northwest SPORE: "Positron emission tomography imaging of bone in patients with metastatic prostate cancer." Fred Hutchinson/University of Washington Cancer Center Support Grant, Seattle, WA. May 21, 2007.
- Patient Power Radio Show: "Prostate, bladder, and testicular cancer update: ASCO 2007." Seattle, WA. June 10, 2007.

- Puget Sound Oncology Consortium Annual Highlights of ASCO meeting: "ASCO 2007 prostate cancer review." Seattle, WA. June 28, 2007.
- Emerging Trends in Oncology: "Update in prostate cancer, ASCO review." Seattle, WA. June 30, 2007.
- Patient Power Radio Show: "Prostate cancer: who to treat and when." Seattle, WA. July 11, 2007.
- American College of Physicians, Seattle Internal Medicine Board Review Course: "Solid tumor oncology cases." Seattle, WA. July 13, 2007.
- University of Washington Internal Medicine Residents' Educational Lecture Series: "Prostate cancer A chronic disease." University of Washington, Seattle, WA. October 31, 2007.
- Oncology Grand Rounds: "A case of urothelial carcinoma of the bladder with leukemoid reaction: was GCSF playing a negative role?" Fred Hutchinson Research Center, Seattle, WA. November 6, 2007.
- Hematology/Oncology Fellows' Lecture Series: "Germ cell tumors/testicular cancer what you really need to know." Fred Hutchinson Cancer Research Center, Seattle, WA. November 16, 2007.
- Program in Prostate Cancer Research/SPORE: "Positron emission tomography imaging of bone in patients with metastatic prostate cancer." Fred Hutchinson Cancer Research Center, Seattle, WA. March 6, 2008.
- Gilda's Club: "Advanced prostate cancer: an update on hormones, chemotherapy, and clinical trials." Seattle, WA. March 29, 2008.
- Hematology/Oncology Fellows' Lecture Series: "Bladder cancer: An unmet need." Fred Hutchinson Cancer Research Center, Seattle, WA. May 2, 2008.
- Patient Power Radio Show: "Prostate cancer biomarkers." Seattle, WA. May 7, 2008.
- 8th Annual Pacific Northwest Prostate Cancer Conference: "When is PSA useful? Why it may not always be reliable?" Fred Hutchinson Cancer Research Center. September 27, 2008.
- Seattle Cancer Care Alliance Network Physician Educational Outreach Program Multicare Tacoma: "Bladder cancer an unmet need." Tacoma, WA. September 30, 2008.
- Program in Prostate Cancer Research/SPORE: "Bone health for men with prostate cancer." Fred Hutchinson Cancer Research Center, Seattle, WA. November 6, 2008.
- Hematology/Oncology Educational Lecture Series: "Germ cell tumors/testicular cancer a boards exam favorite." Fred Hutchinson Cancer Research Center, Seattle, WA. April 3, 2009.
- University of Washington CME Current Concepts in Drug Therapy: "Primary care issues for patients with prostate cancer undergoing androgen deprivation therapy." Seattle, WA. May 8, 2009.
- Seattle Cancer Care Alliance Scientific Lunch: "Drug development for prostate cancer rebounding well from tough times." Seattle Cancer Care Alliance, Seattle, WA. June 11, 2009.
- Radiation Oncology Residents' Educational Lecture Series: "PSA kinetics to drive decision making for men with prostate cancer." University of Washington, Seattle, WA. June 18, 2009.
- Pacific Northwest SPORE Retreat: "PET imaging as a prostate cancer bone biomarker." University of British Columbia, Vancouver, BC. July 10, 2009.
- American College of Physicians, Seattle Internal Medicine Board Review Course: "Solid tumor oncology cases." Seattle, WA. July 17, 2009.
- Scripps 6th Annual Oncology Update: "ASCO review of prostate cancer." Seattle, WA. July 25, 2009.
- Hematology/Oncology Fellows' Lecture Series: "Bladder cancer: is it our turn yet?" Fred Hutchinson Cancer Research Center, Seattle, WA. August 21, 2009.
- Virginia Mason Community Journal Review: "Androgen deprivation therapy induced estrogen deficiency side effects." Seattle, WA. October 13, 2009.
- Seattle Cancer Care Alliance Network Physician Educational Outreach Program Skagit Valley and Olympic Medical Centers: "Upcoming new drugs for prostate cancer therapy." Mt. Vernon, WA. October 15, 2009.
- Center for Biomedical Continuing Education: "Bone health across the cancer continuum: Updates and insight to an evolving story." Seattle, WA. January 28, 2010.
- Oncology Grand Rounds: "Prostate cancer and broken bones? Only from sticks and stones..." Fred Hutchinson Cancer Research Center, Seattle, WA. March 9, 2010.
- Hematology/Oncology Fellow's Lecture Series: "Germ cell tumors/testicular cancer hitting the ball out of the park." Fred Hutchinson Cancer Research Center, Seattle, WA. March 26, 2010.
- 13th Annual Advanced Prostate Brachytherapy Conference: "Managing androgen deprivation therapy associated side effects." Seattle Prostate Institute, Seattle, WA. May 14, 2010.
- American College of Physicians, Seattle Internal Medicine Board Review Course: "Solid tumor oncology cases." Seattle, WA. July 23, 2010.
- Scripps 7th Annual Oncology Update: "Prostate cancer update: New therapies for castrationresistant disease." Seattle, WA. August 14, 2010.
- Patient Power Radio Show: "New treatments for prostate cancer." Seattle, WA. August 27, 2010.
- University of Washington Comprehensive Oncology Review: "Bladder cancer keeping in the loop." Seattle, WA. October 2, 2010.
- University of Washington Comprehensive Oncology Review: "Germ cell tumors/testicular cancer keeping an eye on the ball." Seattle, WA. October 3, 2010.
- Sanofi-Aventis Roundtable Program: "Cabazitaxel: A new option for metastatic hormonerefractory prostate cancer following a docetaxel containing regimen." Seattle, WA. October 7, 2010.
- 10th Annual Pacific Northwest Prostate Cancer Conference: "Protecting bone for prostate cancer patients." Fred Hutchinson Cancer Research Center, Seattle, WA. October 9, 2010.
- Multicare Tacoma: "Cabazitaxel: A new option for metastatic hormone-refractory prostate cancer following a docetaxel containing regimen." Tacoma, WA. November 16, 2010.
- Hematology/Oncology Fellows' Lecture Series: "Bladder cancer: getting in the loop." Fred Hutchinson Cancer Research Center, Seattle, WA. November 19, 2010.
- Science over Lunch: "Rapidly changing paradigms in prostate cancer new FDA approvals and local contributions." Fred Hutchinson Cancer Research Center, Seattle, WA. March 10, 2011.
- Hematology/Oncology Educational Lecture Series: "Germ cell tumors/testicular cancer." Fred Hutchinson Cancer Research Center, Seattle, WA. March 11, 2011.
- Pacific Northwest Prostate Cancer SPORE: "Metabolic imaging and biomarkers to monitor treatment response of castration-resistant prostate cancer." Fred Hutchinson Cancer Research Center, Seattle, WA. March 28, 2011.
- Nuclear Medicine U01 Meeting: "Discerning Cabozantinib (XL184) biology with ¹¹C-acetate and ¹⁸F-fluoride PET/CT imaging." Seattle Cancer Care Alliance, Seattle, WA. April 12, 2011.
- Scripps 8th Annual Oncology Update: "Genitourinary cancer update." Seattle, WA. August 13, 2011.
- University of Washington Comprehensive Oncology Review (2nd Annual): "Germ cell tumors/testicular cancer." Seattle, WA. September 18, 2011.
- University of Washington Comprehensive Oncology Review (2nd Annual): "Genitourinary Cancer Cases Question and Answer Session." Seattle, WA. September 18, 2011.
- Hematology/Oncology Fellows' Lecture Series: "Bladder cancer: updates and local research endeavors." Fred Hutchinson Cancer Research Center, Seattle, WA. October 28, 2011.
- Hematology/Oncology Fellows' Solid Tumor Conference: "Prostate cancer: local research efforts." Seattle Cancer Care Alliance, Seattle, WA. October 28, 2011.

- Program in Prostate Cancer Research/SPORE: "Hormone-sensitive prostate cancer updates on recent and ongoing clinical trials." Fred Hutchinson Cancer Research Center, Seattle, WA. November 3, 2011.
- Uganda Cancer Institute: "Cases from Kampala prostate cancer case conference." Fred Hutchinson Cancer Research Center, Seattle, WA. June 14, 2012.
- University of Washington Comprehensive Oncology Review (3rd Annual): "Germ cell tumors/testicular cancer." Seattle, WA. September 23, 2012.
- Hematology/Oncology Fellows' Lecture Series: "Germ cell tumors/testicular cancer." Fred Hutchinson Cancer Research Center, Seattle, WA. October 12, 2012.
- Updates in Oncology and Blood/Marrow Transplantation A Spotlight on Seattle Cancer Care Alliance: "Research advancements for castration-resistant prostate cancer." Seattle, WA. October 15, 2012.
- Hematology/Oncology Fellows' Lecture Series: "Bladder cancer: the next big thing in genitourinary oncology." Fred Hutchinson Cancer Research Center, Seattle, WA. November 2, 2012.
- Program in Prostate Cancer Research/SPORE: "Prostate cancer bone biomarkers: clinical trial tool or ready for prime time in the clinic?" Fred Hutchinson Cancer Research Center, Seattle, WA. March 7, 2013.
- Institute for Prostate Cancer Research 2013 Symposium Breakthroughs in prostate cancer research: "Imaging advanced prostate cancer beyond finding the tumor." Fred Hutchinson Cancer Research Center, Seattle, WA. March 17, 2013.
- Uganda Cancer Institute: "Cases from Kampala prostate cancer case conference." Fred Hutchinson Cancer Research Center, Seattle, WA. July 11, 2013.
- Pacific Northwest Cancer SPORE Retreat 2013: "Identification of molecular characteristics of prostate cancer with ¹¹C-acetate and ¹⁸F-FDG PET/CT-directed rapid autopsy." Fred Hutchinson Cancer Research Center, Seattle, WA. July 12, 2013.
- Seattle Cancer Care Alliance Network Physician Educational Outreach Program Multicare Tacoma: "Recent and future therapeutic advancements for metastatic castration-resistant prostate cancer." Tacoma, WA. July 19, 2013.
- Medical Oncology Faculty Sections Meeting: "Fellowship Updates 2013." Seattle Cancer Care Alliance, Seattle, WA. August 1, 2013.
- Hematology/Oncology Educational Lecture Series: "Germ cell tumors/testicular cancer." Fred Hutchinson Cancer Research Center, Seattle, WA. September 13, 2013.
- University of Washington Comprehensive Oncology Review (4th Annual): "Germ cell tumors/testicular cancer." Seattle, WA. October 1, 2013.
- The Everett Clinic: "Cancer immunotherapy fundamental concepts and emerging role." Everett, WA. October 1, 2013.
- Pacific Northwest SPORE Advocacy Meeting: "Sequencing of novel secondary hormonal therapies in metastatic castration-resistant prostate cancer." Fred Hutchinson Cancer Research Center, Seattle, WA. December 12, 2013.
- Program in Prostate Cancer Research/SPORE: "A review of PET imaging for prostate cancer: past, present and future." Fred Hutchinson Cancer Research Center, Seattle, WA. March 27, 2014.
- Institute for Prostate Cancer Research 2014 Symposium Breakthroughs in prostate cancer research: "Imaging prostate cancer present and future." Fred Hutchinson Cancer Research Center, Seattle, WA. April 12, 2014.
- Multicare Tacoma: "Overcoming cancer immunoevasion: the role of immunotherapy." Tacoma, WA. April 17, 2014.

- Seattle Cancer Care Alliance Network Physician Educational Outreach Program: "Role of immunotherapy for bladder cancer – a focus on the PDL1/PD1 axis." Bellevue, WA. June 25, 2014.
- Pacific NorthWest Prostate Cancer SPORE Retreat: "Clinical Core D." Fred Hutchinson Cancer Research Center, Seattle, WA. July 21, 2014.
- Hematology/Oncology Fellows' Lecture Series: "Germ cell tumors/testicular cancer." Fred Hutchinson Cancer Research Center, Seattle, WA. September 5, 2014.
- Seattle Cancer Care Alliance Network Physician Educational Outreach Program Skagit Valley Medical Center: "The promise of immunotherapy for bladder cancer." Mt. Vernon, WA. September 17, 2014.
- Seattle Cancer Care Alliance Network Physician Educational Outreach Program Bend Memorial Clinic: "The promise of immunotherapy for bladder cancer." Bend, OR. September 25, 2014.
- University of Washington Comprehensive Oncology Review (5th Annual): "Germ cell tumors/testicular cancer." Seattle, WA. September 27, 2014.
- Seattle Cancer Care Alliance Network Physician Educational Outreach Program Bozeman Deaconess Cancer Center: "Hot topics for prostate and bladder cancer." Bozeman, MT. October 14, 2014.
- Program in Prostate Cancer Research/SPORE: "Clinical experience with insulin-like growth factor receptor I (IGF-IR) inhibition in prostate cancer." Fred Hutchinson Cancer Research Center, Seattle, WA. October 30, 2014.
- Body Imaging Radiology Section Lecture Series: "Challenges in imaging of genitourinary malignancies." University of Washington Medical Center, Seattle, WA. November 12, 2014.
- Seattle Cancer Care Alliance Network Physician Educational Outreach Program Spokane Valley Cancer Center: "The promise of immunotherapy for bladder cancer." Spokane, WA. November 13, 2014.
- Hematology/Oncology Fellows' Lecture Series: "Bladder cancer: a rapidly growing research arena." Fred Hutchinson Cancer Research Center, Seattle, WA. December 19, 2014.
- Oncology Grand Rounds: "Prostate cancer from the medical oncologist perspective...it's not all about castration-resistant disease." Fred Hutchinson Cancer Research Center, Seattle, WA. December 23, 2014.
- Us Too: "Timing and sequencing of therapeutic agents in metastatic prostate cancer." Greenwood Senior Center, Seattle, WA. March 25, 2015.
- Seattle Cancer Care Alliance Network Physician Educational Outreach Program Tri Cities Cancer Center: "Metastatic prostate cancer therapeutic sequencing, combination and trials." Kennewick, WA. April 23, 2015.
- Seattle Cancer Care Alliance Network Physician Educational Outreach Program The Vancouver Clinic: "Key therapeutic questions in metastatic prostate cancer." Vancouver, WA. May 5, 2015.
- Scripps 12th Annual Oncology Update: "Genitourinary cancer update." Seattle, WA. August 15, 2015.
- Flash Rounds: "Seven tips to developing a clinical research career." Fred Hutchinson Cancer Research Center. Seattle, WA. September 4, 2015.
- Genentech Educational Presentation: "Current challenges in managing bladder cancer." Seattle, WA. October 22, 2015.
- Hematology/Oncology Fellows' Lecture Series: "Germ cell tumors/testicular cancer." Fred Hutchinson Cancer Research Center. Seattle, WA. October 23, 2015.
- Fred Hutch Clinical Oncology Grand Rounds: "PET imaging in prostate cancer: Will it ever be more than a research tool?" Fred Hutchinson Cancer Research Center. Seattle, WA. January 12, 2016.

- Seattle Cancer Care Alliance Network Physician Educational Outreach Program Bozeman Deaconess Cancer Center: "Urothelial carcinoma – Life after platinum." Bozeman, MT. May 20, 2016.
- Pacific NorthWest Prostate Cancer SPORE Retreat: "Clinical Core D." Fred Hutchinson Cancer Research Center, Seattle, WA. July 25, 2016.
- Genitourinary Oncology Staff Education Sessions: "ASCO 2016 prostate and bladder cancer updates." Seattle Cancer Care Alliance, Seattle, WA. August 11, 2016.
- Society for Immunotherapy of Cancer's (SITC) Advances in Cancer Immunotherapy Washington Program: "Immunotherapy for genitourinary cancers." Seattle, WA. August 19, 2016.
- Remedica Medical Education and Publishing CME Lecture to Seattle Cancer Care Alliance Advanced Practice Providers: "P3 – Patient selection and Practice in Prostate cancer." Seattle, WA. November 21, 2016.
- Providence Regional Medical Center: "P3 Patient selection and Practice in Prostate cancer." Everett, WA. December 8, 2016.
- Remedica Medical Education and Publishing CME Lecture to Fred Hutchinson Cancer Research Center Hematology/Oncology Fellows: "P3 – Patient selection and Practice in Prostate cancer." Seattle, WA. December 14, 2016.
- Seattle Cancer Care Alliance Educational Lecture: "Emerging immunotherapies and systemic therapies for metastatic urothelial carcinoma." Seatac, WA. March 1, 2017.
- 2016 6th Annual Institute of Prostate Cancer Research Symposium: "PET imaging in prostate cancer: Finding local recurrences and management of oligometastatic disease." Fred Hutchinson Cancer Research Center, Seattle, WA. March 18, 2017.
- Pacific NorthWest Prostate Cancer SPORE Retreat: "Clinical Core D." Fred Hutchinson Cancer Research Center, Seattle, WA. July 24, 2017.
- Seattle Genetics Lecture Series: "The evolving urothelial carcinoma landscape." Bothell, WA. August 4, 2017.
- University of Washington Comprehensive Hematology and Oncology Review (8th Annual): "Prostate cancer board review." Seattle, WA. September 25, 2017.
- Clinical Research Division: "Informed consent elements documentation." Fred Hutchinson Cancer Research Center, Seattle, WA. November 13, 2017.
- Medical Oncology Sections Meeting: "Informed consent elements documentation." Seattle Cancer Care Alliance, Seattle, WA. December 7, 2017.
- University of Washington Medicine Grand Rounds: "Clinical research in prostate cancer." University of Washington School of Medicine, Seattle, WA. January 11, 2018.
- Clinical Research Services, Fred Hutchinson Cancer Research Consortium: "Prostate cancer overview and impactful clinical research." Fred Hutchinson Cancer Research Center, Seattle, WA. January 11, 2018.
- Solid Tumor Conference, Fred Hutchinson Hematology-Oncology Fellowship Program: "GU boards review for fellows Key points to remember." Fred Hutchinson Cancer Research Center, Seattle, WA. April 27, 2018.
- Institute for Prostate Cancer Research 2018 Symposium Breakthroughs in prostate cancer research: "Prostate Cancer Tumor Board." Fred Hutchinson Cancer Research Center, Seattle, WA. April 28, 2018.
- External Advisory Board Meeting, Fred Hutchinson/University of Washington Cancer Consortium: "Clinical Protocol and Data Management." Fred Hutchinson Cancer Research Center, Seattle, WA. June 15, 2018.
- Oncology Grand Rounds: "Treatment intensification for castration-sensitive prostate cancer and management of oligometastatic disease." Fred Hutchinson Cancer Research Center, Seattle, WA. June 19, 2018.

- University of Washington Comprehensive Hematology and Oncology Review (9th Annual): "Prostate cancer board review." Seattle, WA. September 15, 2018.
- Genitourinary Oncology Staff Education Sessions: "Prostate cancer overview clinical and research impact." Seattle Cancer Care Alliance, Seattle, WA. February 7, 2019.
- External Advisory Board Meeting, Fred Hutchinson/University of Washington Cancer Consortium: "Clinical Protocol and Data Management." Fred Hutchinson Cancer Research Center, Seattle, WA. March 8, 2019.
- Institute for Prostate Cancer Research 2019 Symposium Breakthroughs in prostate cancer research: "Imaging in prostate cancer state of the field." Fred Hutchinson Cancer Research Center, Seattle, WA. May 11, 2019.
- Program in Prostate Cancer Research/SPORE: "Implications of next generation PET imaging in prostate cancer." Fred Hutchinson Cancer Research Center, Seattle, WA. May 16, 2019.
- NCI Cancer Center Support Grant Site Visit: "Clinical drotocol and data management." Fred Hutchinson Cancer Research Center, Seattle, WA. May 29, 2019.
- 7th Annual International Conferences on Advances in Hematology and Oncology: "Bladder cancer updates from ASCO 2019." Seattle, WA. June 30, 2019.
- Seattle (Bellevue) UsToo: "Prostate cancer disease states and treatments." Bellevue, WA. July 15, 2019.
- Seattle (Bellevue) UsToo: "Next generation PET imaging in prostate cancer." Bellevue, WA. July 15, 2019.
- Medical Oncology Sections Meeting: "Genitourinary Medical Oncology (GUMO) research interests and updates." Seattle Cancer Care Alliance, Seattle, WA. August 1, 2019.
- Genitourinary Oncology Staff Education Sessions: "Immunotherapy for genitourinary cancers." Seattle Cancer Care Alliance, Seattle, WA. October 10, 2019.
- Institute of Prostate Cancer Research Development Lecture: "Proving the impact of next generation PET imaging in prostate cancer." Fred Hutchinson Cancer Research Center, Seattle, WA. October 17, 2019.
- Seattle Cancer Care Alliance NeuroEndocrine Tumor Board: "Iobenguane ¹³¹I for the treatment of advanced neuroendocrine tumors that are norepinephrine transporter avid on imaging, in a multicenter, open-label phase 2 basket trial (FORESIGHT)." Seattle Cancer Care Alliance, Seattle, WA. December 20, 2019.
- Seattle UsToo: "The future impact of next generation PET imaging in prostate cancer." Seattle, WA. January 22, 2020.
- GU Medical Oncology Research Staff: "Recent updates in the last year for advanced prostate cancer." Fred Hutchinson Cancer Research Center, Seattle, WA. January 23, 2020.
- Curio Science Community Opinions in Prostate Cancer: "Current and emerging therapies for practice with metastatic castration-sensitive prostate cancer." Seattle, WA. March 5, 2020.
- Medical Oncology Sections Meeting: "Clinical research updates Learning from feedback on our competitive renewals and upcoming process improvments." Seattle Cancer Care Alliance, Seattle, WA. April 2, 2020.
- Lead Academic Performance Site National Clinical Trials Network Leadership Meeting: "NCTN Leadership Team introduction." Seattle Cancer Care Alliance, Seattle, WA. September 2, 2020.
- Medical Oncology Sections Meeting: "Clinical trials startup process improvements." Seattle Cancer Care Alliance, Seattle, WA. September 3, 2020.
- Genitourinary Leadership Committee Meeting: "Clinical trials startup process improvements specific to Genitourinary Oncology." Seattle Cancer Care Alliance, Seattle, WA. October 20, 2020.

- Clinical Research Division Faculty Meeting: "Clinical trials startup process improvements specific to CRD." Fred Hutchinson Cancer Research Center, Seattle, WA. November 2, 2020.
- Curio Science Opinions in Bladder Cancer: "Treatment of metastatic urothelial cancer in the post-platinum, post-immunotherapy setting." Seattle, WA by Virtual Meeting. November 11, 2020.
- Institutional Perspectives in Cancer presented by OncLive: "Increasing awareness of nonmetastatic (M0) castration-resistant prostate cancer." Seattle, WA by Virtual Meeting. November 24, 2020.
- University of Washington Clinical Research Director Meeting: "Clinical trial start-up process improvements and challenges." Seattle, WA by Virtual Meeting. February 1, 2021.
- Seattle Cancer Care Alliance Board of Directors' Enrichment Series: "Paving the path forward with next generation PET imaging in prostate cancer." Seattle, WA by Virtual Meeting. February 22, 2021.
- Program in Prostate Cancer Research/SPORE: "Antibody drug conjugates in bladder cancer reaching new targets." Fred Hutchinson Cancer Research Center, Seattle, WA. February 25, 2021.
- National Cancer Trials Network Leadership Committee Meeting: "Bi-annual Spring Meeting." Fred Hutchinson Cancer Research Center, Seattle, WA. March 26, 2021.
- University of Washington Clinical Research Director Meeting: "Race and ethnicity clinical trial accrual data." Seattle Cancer Care Alliance, Seattle, WA. May 3, 2021.
- Fred Hutchinson Cancer Research Consortium Institutional Review Board Diverse Enrollment Subcommittee: "Race and ethnicity clinical trial accrual data." Fred Hutchinson Cancer Research Center, Seattle, WA. May 14, 2021.
- Genitourinary Oncology Leadership Meeting: "Race and ethnicity clinical trial accrual data." Seattle Cancer Care Alliance, Seattle, WA. May 18, 2021.
- Fred Hutchinson Cancer Consortium Executive Committee: "Race and ethnicity clinical trial accrual data." Seattle Cancer Care Alliance, Seattle, WA. June 1, 2021.
- Institute for Prostate Cancer Research (IPCR) 2021 Symposium Advanced prostate cancer: "PSMA-targeted therapy – The next big thing?" Fred Hutchinson Cancer Research Center, Seattle, WA. June 5, 2021.
- Targeted Oncology and HRA: "Case-based round table meeting on castration resistant prostate cancer." Virtual Meeting, Washington. June 15, 2021.
- 2021 Seattle Cancer Care Alliance Genitourinary Oncology Retreat: "Next generation imaging." Seattle, WA. June 17, 2021.
- 2021 Seattle Cancer Care Alliance Genitourinary Oncology Retreat: "Expanding research in the community NCTN pilot." Seattle, WA. June 17, 2021.
- Seattle UsToo: "PSMA-targeted theranostics for prostate cancer." Virtual Meeting, Seattle, WA. July 28, 2021.
- Medical Oncology Sections Meeting: "Race and ethnicity clinical trial accrual data." Seattle Cancer Care Alliance, Seattle, WA. September 2, 2021.
- External Advisory Board Meeting, Fred Hutchinson/University of Washington Cancer Consortium: "Clinical Protocol and Data Management." Fred Hutchinson Cancer Research Center, Seattle, WA. September 27, 2021.
- National Cancer Trials Network Leadership Committee Meeting: "Bi-annual Virtual Fall Meeting." Fred Hutchinson Cancer Research Center, Seattle, WA. October 1, 2021.
- University of Washington and Fred Hutchinson Cancer Research Center Assistant Professors' Meeting: "Consortium trial startup and clinical trial process improvement." Fred Hutchinson Cancer Research Center, Seattle, WA. February 8, 2022.

- University of Washington and Fred Hutchinson Cancer Research Center Associate Professors' Meeting: "Consortium trial startup and clinical trial process improvement." Fred Hutchinson Cancer Research Center, Seattle, WA. March 1, 2022.
- University of Washington Internal Medicine Residency Program: "How to think about the PSA test and prostate cancer screening." March 18, 2022.
- External Advisory Board Meeting, Fred Hutchinson/University of Washington Cancer Consortium: "Clinical Research Overview and Clinical Protocol and Data Management." Fred Hutchinson Cancer Research Center, Seattle, WA. May 26, 2022.
- Curio Science Community Opinions Opinions in Bladder Cancer, An Interactive Local Workshop: "Post-platinum or post immunotherapy, and subsequent therapy for locally advanced/metastatic urothelial carcinoma." Seattle, WA. August 31, 2022.
- Medical Oncology Sections Meeting: "Ongoing Genitourinary Medical Oncology (GUMO) clinical/translational research highlights." Fred Hutchinson Cancer Center, Seattle, WA. November 3, 2022.
- Fred Hutchinson Cancer Center Strategic Planning Meeting: "Clinical research updates from the lab to the bedside" Fred Hutchinson Cancer Center, Seattle, WA. November 4, 2022.
- Aptitude Health Live CASES: "Management of metastatic hormone sensitive prostate cancer." Seattle, WA. November 19, 2022.
- Aptitude Health Live CASES: "Management of metastatic castration resist prostate cancer." Seattle, WA. November 19, 2022.
- Aptitude Health Live CASES: "First-line therapy for advanced urothelial carcinoma." Seattle, WA. November 19, 2022.
- Aptitude Health Live CASES: "Second-line and subsequent management of advanced urothelial carcinoma." Seattle, WA. November 19, 2022.

INVITED SPEAKER NATIONAL/INTERNATIONAL

- Genentech, Inc.: "Retroviral RNA interference: systems development and biologic discoveries with telomerase." San Francisco, CA. April 6, 2004.
- Stanford University Medical Center: "Retroviral RNA interference: systems development and biologic discoveries with telomerase." Stanford, CA. April 27, 2004.
- University of California Davis School of Medicine: "Retroviral RNA interference: systems development and biologic discoveries with telomerase." Sacramento, CA. April 30, 2004.
- 8th Annual Western Hawaii Cancer Symposium: "Clinical implications of angiogenesis in solid tumor oncology." Kona, HI. September 10, 2005.
- Novartis Oncology: "Current issues in the treatment of bone metastases." Reno, NV. February 20, 2007.
- Novartis Oncology: "Treatment of solid tumor bone metastases with bisphosphonates." Anchorage, AK. June 13, 2007.
- Southwest Oncology Group Fall GU Committee Meeting: "Tissue inhibitor of metalloproteinase-1 (TIMP-1) as a prognostic and predictive biomarker for men receiving chemotherapy for hormone-refractory prostate cancer." Huntington Beach, CA. October 4, 2007.
- American Urologic Association Northeastern Section: "Emerging role of selective estrogen receptor modulators in prostate cancer." Santa Ana Pueblo, NM. September 20, 2008.
- American Urologic Association New England Section: "Emerging role of selective estrogen receptor modulators in prostate cancer." Rio Grande, Puerto Rico. September 26, 2008.
- Prostate Cancer Foundation Scientific Symposium: "Prostate cancer bone metastasis biomarkers." Lake Tahoe, NV. October 16, 2008.

- Southwest Oncology Group Spring GU Committee Meeting: "A phase 2 study of combined androgen deprivation and IMC-A12 for patients with new hormone-sensitive metastatic prostate cancer." San Francisco, CA. April 23, 2009.
- 12th Annual Western Hawaii Cancer Symposium: "Translational oncology in clinical practice." Kona, HI. September 4, 2009.
- Prostate Cancer Research Institute (PCRI) 2009 Prostate Cancer Conference: "Reducing side effects of testosterone deprivation." Los Angeles, CA. September 12, 2009.
- Southwest Oncology Group Fall GU Committee Meeting: "A randomized phase 2 study of combined androgen deprivation versus combined androgen deprivation and IMC-A12 for patients with new hormone-sensitive metastatic prostate cancer." Chicago, IL. October 24, 2009.
- Second Annual Roche Diagnostics Bone Metastatic Cancer Advisory Board: "Prognostic markers for metastatic bone disease in prostate cancer." Arlington, VA. October 29, 2009.
- Prostate Cancer Clinical Trials Consortium Annual Review: "Using metabolic imaging to assess response to therapy in prostate cancer bone metastases." Vienna, VA. November 18, 2009.
- Prostate Cancer Educational Council: "Beyond screening and diagnosis utility of prostate specific antigen by disease state." Content Development Working Group Moderator. Philadelphia, PA. November 20, 2009.
- 10th Annual Meeting of the Society of Urologic Oncology: "Androgen deprivation therapy induced estrogen deficiency side effects." Bethesda, MD. December 4, 2009.
- Center for Biomedical Continuing Education: "Bone health across the cancer continuum: Updates and insight to an evolving story." Chicago, IL. February 9, 2010.
- Billings Clinic Tumor Board: "Bone health across the cancer continuum: Updates and insight to an evolving story." Billings, MT. March 30, 2010.
- Center for Biomedical Continuing Education: "Bone health across the cancer continuum: Updates and insight to an evolving story." New York, NY. April 8, 2010.
- Southwest Oncology Group Spring GU Committee Meeting: "A randomized phase 2 study of combined androgen deprivation versus combined androgen deprivation and IMC-A12 for patients with new hormone-sensitive metastatic prostate cancer." San Francisco, CA. April 18, 2010.
- Mercy Regional Medical Center Grand Rounds: "Bone health across the cancer continuum: Updates and insight to an evolving story." Durango, CO. April 20, 2010.
- Sparrow Professional Building Grand Rounds: "Bone health across the cancer continuum: Updates and insight to an evolving story." Lansing, MI. April 30, 2010.
- Education Session, Evolving Standards of Care in Metastatic Castration-resistant Prostate Cancer: "Bone directed therapy for prostate cancer: present standards and potential new options." 2010 American Society of Clinical Oncology, Chicago, IL. June 7, 2010.
- University of Texas Southwestern Combined Modality Conference: "Boning up with prostate cancer." Dallas, TX. July 2, 2010.
- Wayne State University / Karmanos Cancer Institute Prostate Cancer Working Group Conference: "Bone health in prostate cancer: The basics and some propaganda." Detroit, MI. August 20, 2010.
- 13th Annual Western Hawaii Cancer Symposium: "Emerging new therapies for metastatic castration resistant prostate cancer." Kona, HI. September 4, 2010.
- South Texas Institute of Cancer: "Clinical debates in castration-refractory prostate cancer." Corpus Christi, TX. September 7, 2010.
- Texas Hematology/Oncology: "Clinical debates in castration-refractory prostate cancer." McKinney, TX. September 9, 2010.

- Prostate Cancer Foundation Scientific Symposium: "Imaging prostate cancer bone metastases with sodium fluoride (NaF) PET." Washington, DC. September 16, 2010.
- City of Hope Oncology Grand Rounds: "Clinical decision making in castration-resistant prostate cancer." Duarte, CA. October 5, 2010.
- Mount Clemens Regional Medical Center Oncology Grand Rounds: "Clinical debates in castration-refractory prostate cancer." Mount Clemens, MI. October 13, 2010.
- Great Falls Clinic Cancer Center: "Clinical debates in castration-refractory prostate cancer." Great Falls, MT. October 14, 2010.
- Southwest Oncology Group Fall GU Committee Meeting: "A randomized phase 2 study of combined androgen deprivation versus combined androgen deprivation and Cixutumumab (IMC-A12) for patients with new hormone-sensitive metastatic prostate cancer." Chicago, IL. October 23, 2010.
- Mercy Hospital: "Clinical debates in castration-refractory prostate cancer." Bakersfield, CA. November 3, 2010.
- University of California San Diego Hematology/Oncology Grand Rounds: "Prostate Cancer: Honing in on the bones." San Diego, CA. January 14, 2011.
- Southwest Oncology Group Spring GU Committee Meeting: "A randomized phase 2 study of combined androgen deprivation versus combined androgen deprivation and Cixutumumab (IMC-A12) for patients with new hormone-sensitive metastatic prostate cancer." San Francisco, CA. April 16, 2011.
- Providence Alaska Medical Center: "Advances in castration-resistant prostate cancer." Anchorage, AK. April 27, 2011.
- Bristol-Myers Squibb ASCO Dasatinib Investigator Initiated Trial Meeting: "Determining pharmacodynamic effects of Dasatinib on bone with ¹⁸F-fluoride PET imaging in men with castration resistant prostate cancer." Chicago, IL. June 4, 2011.
- Millennium Pharmaceuticals, Inc. Prostate Cancer Update Educational Program: "Hormonesensitive prostate cancer – recent updates and ongoing trials." Cambridge, MA. October 4, 2011.
- SWOG Fall GU Committee Meeting: "A randomized phase 2 study of combined androgen deprivation versus combined androgen deprivation and Cixutumumab (IMC-A12) for patients with new hormone-sensitive metastatic prostate cancer." San Antonio, TX. October 15, 2011.
- OncoGeneX OGX-427-02 Bladder Cancer Phase 2 Investigator Meeting: "A phase 1 trial of OGX-427, a 2-methoxyethyl antisense oligonucleotide against Heat Shock Protein 27." Scottsdale, AZ. November 5, 2011.
- Yale Cancer Center NP Conference: "Prostate cancer: It's all about the bones." New Haven, CT. November 18, 2011.
- 2012 Genitourinary Cancers Symposium, General Session II: Castrate Resistant Prostate Cancer

 Treatment Sequencing and Implementation: "Novel targets, agents, and trials." San Francisco, CA. February 2, 2012.
- 2012 Genitourinary Cancers Symposium, General Session II: Castrate Resistant Prostate Cancer – Treatment Sequencing and Implementation: "Case study and panel discussion." San Francisco, CA. February 2, 2012.
- Prostate Cancer Skeletal Metastasis Workshop, Combined P01 Meeting: "Imaging response to therapy in prostate cancer bone metastases PET as a biomarker." Ann Arbor, MI. April 12, 2012.
- SWOG Spring GU Committee Meeting: "A randomized phase 2 study of combined androgen deprivation versus combined androgen deprivation and Cixutumumab (IMC-A12) for patients with new hormone-sensitive metastatic prostate cancer." San Francisco, CA. April 14, 2012.

- Astellas Pharma Medical Science Liaison Education Lecture: "The dynamic treatment landscape for castration-resistant prostate cancer." Internet lecture. May 4, 2012.
- Vanderbilt University: "Dem bones, dem bones, dem prostate cancer bones." Nashville, TN. May 17, 2012.
- Genitourinary (Prostate) Cancer Poster Discussion Session: "Sex, Drugs, and Bones." 2012 American Society of Clinical Oncology, Chicago, IL. June 4, 2012.
- Dendreon Advisory Meeting: "The oncologist's perspective of Provenge for patients with asymptomatic/minimally symptomatic metastatic castrate-resistant prostate cancer." San Diego, CA. June 15, 2012.
- Dendreon Oncology Summit Advisory Board: "Provenge and the evolving treatment landscape for advanced prostate cancer." San Francisco, CA. June 23, 2012.
- Dendreon Oncology Summit Advisory Board: "Sequencing metastatic castration-resistant prostate cancer treatments of the future." San Francisco, CA. June 23, 2012.
- University of California Davis 13th Annual Advances in Oncology 2012: "New therapeutic options in advanced castration-resistant prostate cancer." Sacramento, CA. September 22, 2012.
- SWOG Fall Prostate Cancer Organ Site Meeting: "A randomized phase 2-3 trial of intermittent androgen deprivation therapy using Enzalutamide with a GnRH agonist versus Bicalutamide with a GnRH agonist in patients with non-metastatic castration-sensitive prostate cancer." Chicago, IL. October 19 and 20, 2012.
- SWOG Fall GU Committee Meeting: "A randomized phase 2 study of combined androgen deprivation versus combined androgen deprivation and Cixutumumab (IMC-A12) for patients with new hormone-sensitive metastatic prostate cancer." Chicago, IL. October 20, 2012.
- South Texas Comprehensive Cancer Center: "Optimizing care for patients with advanced prostate cancer: evolving targets and emerging treatment paradigms." Corpus Christi, TX. December 4, 2012.
- Hoag Memorial Hospital Oncology Grand Rounds: "Optimizing care for patients with advanced prostate cancer: evolving targets and emerging treatment paradigms." Newport Beach, CA. February 28, 2013.
- Dendreon Oncology Advisory Board Meeting: "Sipuleucel-T and its use in community-based oncology practices." Washington, DC. April 18, 2013.
- SWOG Spring GU Committee Meeting: "A randomized phase 2 study of combined androgen deprivation versus combined androgen deprivation and Cixutumumab (IMC-A12) for patients with new hormone-sensitive metastatic prostate cancer." San Francisco, CA. May 2, 2013.
- Medivation Preclinical ASCO Advisory Board Meeting: "The role of SRC in prostate cancer are there still potential clinical implications?" Chicago, IL. May 30, 2013.
- Dendreon Medical Oncologist Advisory Board: "Early detection of metastatic castrationresistant prostate cancer." Chicago, IL. May 31, 2013.
- Dendreon Medical Oncologist Advisory Board: "Metastatic castration-resistant prostate cancer, a changing landscape." Chicago, IL. May 31, 2013.
- Genitourinary (Prostate) Cancer Poster Discussion Session: "Prognosis and predication of outcomes in castration-resistant prostate cancer." 2013 American Society of Clinical Oncology, Chicago, IL. June 1, 2013.
- Janssen Post-ASCO Educational Update Meeting: "Updates on metastatic castration-resistant prostate cancer studies from ASCO 2013." Chicago, IL. June 4, 2013.
- Dendreon: "Cancer immunotherapy fundamental concepts and emerging role." Las Vegas, NV. July 25, 2013.
- Challenging Cases in Oncology powered by Xcenda: "Case 6 Advanced prostate cancer prognosis and treatment." Las Vegas, NV. July 27, 2013.

- Challenging Cases in Oncology powered by Xcenda: "Prostate cancer debrief." Las Vegas, NV. July 27, 2013.
- Compass Oncology 2013 Comprehensive Cancer Network: "Integration of novel management strategies for castrate-resistant prostate cancer." Portland, OR. September 19, 2013.
- Abilene Regional Medical Center 2013 Comprehensive Cancer Network: "Integration of novel management strategies for castrate-resistant prostate cancer." Abilene, TX. September 24, 2013.
- Mercy Medical Center 2013 Comprehensive Cancer Network: "Integration of novel management strategies for castrate-resistant prostate cancer." Canton, OH. October 4, 2013.
- SWOG Fall Prostate Cancer Organ Site Meeting: "A randomized phase 2-3 trial of intermittent androgen deprivation therapy using Enzalutamide with a GnRH agonist versus a GnRH agonist alone in patients with non-metastatic castration-sensitive prostate cancer." Chicago, IL. October 11, 2013.
- SWOG Fall GU Committee Meeting: "A randomized phase 2 study of combined androgen deprivation versus combined androgen deprivation and Cixutumumab (IMC-A12) for patients with new hormone-sensitive metastatic prostate cancer." Chicago, IL. October 11, 2013.
- Myriad Genetics and Laboratories: "Prostate cancer/Prolaris medical oncology advisory board meeting." Salt Lake City, UT. October 19, 2013.
- 18th Brazilian Oncology Conference: "Post-ADT phase 3 clinical evidence: Efficacy of abiraterone acetate." Brasilia, Brazil. October 23, 2013.
- Janssen Dinner Launch: "Metastatic castration-resistant prostate cancer cases." Brasilia, Brazil. October 24, 2013.
- Chemotherapy Foundation Symposium: "Novel PET imaging in prostate cancer." New York City, NY. November 8, 2013.
- St. Lukes Mountain States Tumor Institute 2013 Comprehensive Cancer Network: "Integration of novel management strategies for castrate-resistant prostate cancer." Boise, ID. November 13, 2013.
- Bergan Mercy Medical Center 2013 Comprehensive Cancer Network: "Integration of novel management strategies for castrate-resistant prostate cancer." Omaha, NE. November 20, 2013.
- Medivation Incorporated: "A randomized phase 2-3 trial of intermittent androgen deprivation therapy using enzalutamide with a GnRH agonist versus a GnRH agonist alone in patients with non-metastatic castration-sensitive prostate cancer." San Francisco, CA. November 22, 2013.
- Elsevier Urology Round Table: "Measuring immune response in men with metastatic castrationresistant prostate cancer." Washington, DC. December 7, 2013.
- Dendreon: "Cancer immunotherapy fundamental concepts and emerging role." Santa Barbara, CA. December 19, 2013.
- Hoag Memorial Hospital Oncology Grand Rounds: "Integration of novel management strategies for castrate-resistant prostate cancer." Newport Beach, CA. January 23, 2014.
- Dendreon Medical Oncologist Advisory Board: "Cancer immunotherapy fundamental concepts and emerging role." Santa Barbara, CA. February 6, 2014.
- Dendreon: "Cancer immunotherapy fundamental concepts and emerging role." Honolulu, HI. February 19, 2014.
- 7th Annual IntraSPORE Prostate Cancer Program Retreat: "Prostate cancer and the clinical sciences where are we and what we need to do?" Fort Lauderdale, FL. March 17, 2014.
- St. Lukes Mountain States Tumor Institute: "Overcoming cancer immunoevasion: the role of immunotherapy." Boise, ID. April 3, 2014.
- Dendreon: "Overcoming cancer immunoevasion: the role of immunotherapy." Billings, MT. April 22, 2014.

- SWOG Spring GU Organ Site Working Group Meeting: "A randomized phase 2 study of combined androgen deprivation versus combined androgen deprivation and Cixutumumab (IMC-A12) for patients with new hormone-sensitive metastatic prostate cancer." San Francisco, CA. May 1, 2014.
- Dendreon Junior Faculty ASCO Advisory Meeting: "A new era of immunotherapy in treating prostate cancer." Chicago, IL. May 29, 2014.
- Janssen Post-ASCO 2014 Educational Update Meeting: "Developments in initial treatment approaches for advanced prostate cancer." Chicago, IL. June 3, 2014.
- Dendreon Sales Training Workshop: "Health care provider training for clinical proficiency." Atlanta, GA. June 18, 2014.
- Enzalutamide Medical Advisory Board: "Current clinical practice landscape incorporating ASCO 2014 data and upcoming key clinical trials in prostate cancer." New York, NY. July 26, 2014.
- Best of ASCO 2014: "Prostate cancer 2014 Progress! Not progression." Seattle, WA. August 23, 2014.
- Meet the Expert for Zytiga a community forum: "The metastatic castration-resistant prostate cancer treatment paradigm: more choices, more questions." Yokohama, Japan. August 27, 2014.
- 52nd Annual Meeting of Japanese Society of Clinical Oncology: "The metastatic castrationresistant prostate cancer treatment paradigm: more choices, more questions." Yokohama, Japan. August 28, 2014.
- Meet the Expert for Castration-Resistant Prostate Cancer an academician forum: "The metastatic castration-resistant prostate cancer treatment paradigm: more choices, more questions." Yokohama, Japan. August 29, 2014.
- Challenging Cases in Prostate Cancer powered by Xcenda: "The metastatic castration-resistant prostate cancer smorgasbord." Las Vegas, NV. September 19, 2014.
- Regional Summit on Practical and Emerging Agents in Prostate Cancer: "Immunotherapy approaches to prostate cancer." New York, NY. October 4, 2014.
- 15th Annual Meeting of the Society of Urologic Oncology: "Prostate cancer sequencing prior to chemotherapy." Bethesda, MA. December 5, 2014.
- University of Chicago: "Immunotherapy for genitourinary malignancies." Chicago, IL. December 18, 2014.
- Elmhurst Memorial Clinic: "Overcoming cancer immunoevasion: the role of immunotherapy." Elmhurst, IL. December 18, 2014.
- Tolmar Advisory Council Meeting: "Maximal castration for advanced prostate cancer? Correlations between testosterone levels and outcomes." San Diego, CA. January 9, 2015.
- Regional Summit on Practical and Emerging Agents in Prostate Cancer: "Sipuleucel-T: Current status and optimal patient selection." Dallas, TX. January 17, 2015.
- Rocky Mountain Cancer Center Boulder: "Overcoming cancer immunoevasion: the role of immunotherapy." Boulder, CO. February 5, 2015.
- Dendreon: "Overcoming cancer immunoevasion: the role of immunotherapy." Denver, CO. February 5, 2015.
- The Urology Center of Colorado: "Immunotherapy for bladder cancer." Denver, CO. February 6, 2015.
- 2015 Genitourinary Cancers Symposium, General Session II: Evolving role of multimodality treatment in low volume hormone-sensitive metastatic disease: "Selection of systemic therapy: Chemotherapy and androgen axis agents." Orlando, FL. February 26, 2015.
- PeerView Live CME: Clinical challenges in castration-resistant prostate cancer How to choose the right treatment for the right patient at the right time: "Current and future directions with hormone therapy in prostate cancer." Orlando, FL. February 27, 2015.

- University of Texas Houston: "Overcoming cancer immunoevasion: the role of immunotherapy." Houston, TX. March 16, 2015.
- University of Arizona Oncology Grand Rounds: "Clinical research in prostate cancer exploring the castration-sensitive disease state." Tucson, AZ. March 27, 2015.
- Genentech Bladder Cancer Steering Committee: "Urothelial bladder cancer disease states education." Dallas, TX. April 17, 2015.
- Dendreon Advisory Meeting Integrating Leading-Edge Data Into Prostate Cancer Treatment and Research: "Impact of recent data on treatment considerations in prostate cancer: Resistance to androgen-targeted agents." Chicago, IL. May 28, 2015.
- Dendreon Advisory Meeting Integrating Leading-Edge Data Into Prostate Cancer Treatment and Research: "Antigen spread following sipuleucel-T treatment." Chicago, IL. May 28, 2015.
- Peerview Live CME Applying the Latest Evidence to Treatment Decisions in CRPC: Real Cases, Difficult Choices – You Make the Call: "Management options for previously treated metastatic CRPC: Latest data and considerations." Chicago, IL. May 29, 2015.
- Urologic Oncology Summit: "Castration-resistant prostate cancer: Biology and definitions." Panama City, Panama. June 27, 2015.
- Urologic Oncology Summit: "An overview of non-metastatic (M0) castration-resistant prostate cancer." Panama City, Panama. June 27, 2015.
- Urologic Oncology Summit: "Placing the evidence together in metastatic castration-resistant prostate cancer: Sequencing, combination?" Panama City, Panama. June 27, 2015.
- Urologic Oncology Summit: "Panel discussion: Special clinical scenarios for advanced prostate cancer." Panama City, Panama. June 27, 2015.
- Urologic Oncology Summit: "Role of docetaxel in the management of castration-sensitive prostate cancer." Panama City, Panama. June 27, 2015.
- 6th International Pacrim Breast and Prostate Cancer Meeting: PET imaging in prostate cancer: Research tool of standard clinical practice?" Stevenson, WA. July 21, 2015.
- Enzalutamide Medical Advisory Board: "ASCO 2015 data review." New York, NY. July 31, 2015.
- 3rd Annual International Conferences on Advances in Hematology and Oncology: "Metastatic prostate cancer Management in the era of novel agents." Coeur d'Alene, ID. August 29, 2015.
- Genentech Educational Presentation: "The PD-L1 pathway in cancer immune evasion." Portland, OR. November 10, 2015.
- Janssen West Community Oncology Advisory Board Meeting: "Data review of abiraterone and enzalutamide, clinical sequencing and future directions in prostate cancer." Los Angeles, CA. November 11, 2015.
- 16th Annual Meeting of the Society of Urologic Oncology: "Clinical implications of genomics in treating prostate cancer." Washington, DC. December 3, 2015.
- Merck Genitourinary Oncology Global Advisory Board Meeting: "Current treatment options for metastatic castration-resistant prostate cancer and potential role for checkpoint inhibitors in the future." Barcelona, Spain. January 29, 2016.
- Merck Genitourinary Oncology Global Advisory Board Meeting: "Update on checkpoint inhibitor data in bladder cancer." Barcelona, Spain. January 29, 2016.
- Genentech Educational Presentation: "The PD-L1 pathway in cancer immune evasion." Irvine, CA. March 10, 2016.
- Genentech Educational Presentation: "The PD-L1 pathway in cancer immune evasion." Anchorage, AK. March 16, 2016.
- Genentech Educational Presentation: "The PD-L1 pathway in cancer immune evasion." Phoenix, AZ. March 24, 2016.

- Florida Society of Clinical Oncology (FLASCO) Spring Session: "Sequencing agents in metastatic prostate cancer." Kissimmee, FL. April 9, 2016.
- Seattle Cancer Care Alliance 1st Comprehensive Cancer Update: "Treatment decision making for patients with metastatic prostate cancer." Honolulu, HI. April 16, 2016.
- Seattle Cancer Care Alliance 1st Comprehensive Cancer Update: "Bladder cancer Major advancements coming soon." Honolulu, HI. April 16, 2016.
- Seattle Cancer Care Alliance 1st Comprehensive Cancer Update: "Testicular cancer Winning the ball game." Honolulu, HI. April 16, 2016.
- Bayer West Area Meeting: "Metastatic castration-resistant prostate cancer overview." Phoenix, AZ. April 28, 2016.
- Genentech Educational Presentation: "The PD-L1 pathway in cancer immune evasion." Oxnard, CA. May 24, 2016.
- Bayer Corporation: "Post-ASCO 2016 Point of View." Global Webex. June 23, 2016.
- 4th Annual Canadian Urological Association and Canadian Urologic Oncology Group Multidisciplinary Meeting: "The promise of checkpoint inhibitors in urothelial cancer." Vancouver, BC, Canada. June 25, 2016.
- Janssen Medical Oncology Advisory Board: "Janssen oncology clinical development program in genitourinary malignancies." Chicago, IL. July 14, 2016.
- Genentech Lung and Urothelial Cancer Advisory Board: "Atezolizumab in urothelial cancer." Seattle, WA. July 16, 2016.
- Best of ASCO 2016: "Genitourinary (Non-prostate) Cancer." San Diego, CA. August 13, 2016.
- 4th Annual International Conferences on Advances in Hematology and Oncology: "Choices and decisions in metastatic prostate cancer." Coeur d'Alene, ID. August 14, 2016.
- American Urological Association Advanced Prostate Cancer: Managing the Spectrum of Disease Symposium: "Comorbidities and side effect profiles: Considerations for various castration-resistant prostate cancer therapeutic strategies." Chicago, IL. September 24, 2016.
- Merck KEYNOTE-365 Investigator Meeting: "Metastatic castration-resistant prostate cancer overview, current treatment and future directions." Baltimore, MD. October 20, 2016.
- 3rd Annual Summit on Genitourinary Malignancies: "Identifying prostate cancer patients for immunotherapy approaches." New York, NY. October 23, 2016.
- prIME Oncology, 2nd Annual West Cancer Center Oncology Conference, Collaboration for the Future Cure Precision Medicine and Immuno-Oncology: "Immunotherapy in genitourinary cancers: The new frontier." Memphis, TN. November 18, 2016.
- 17th Annual Meeting of the Society of Urologic Oncology: "Immunotherapy for prostate cancer: What is the way forward?" San Antonio, TX. December 2, 2016.
- American Urological Association Advanced Prostate Cancer: Managing the Spectrum of Disease Symposium: "Comorbidities and side effect profiles: Considerations for various castration-resistant prostate cancer therapeutic strategies." Washington, DC. December 10, 2016.
- Society of Government Service Urologists 2017 Kimbrough Urological Seminar: "Considerations for the symptomatic metastatic castration resistant prostate cancer patient: Beyond Abiraterone and Enzalutamide." San Diego, CA. January 14, 2017.
- Annenberg Center for Health Sciences CME: Experts in Residence "Bridging the gap from knowledge to practice in castration-resistant prostate cancer." Cancer Treatment Centers of America, Zion, IL. January 27, 2017.
- St. Lukes Mountain States Tumor Institute Remedica Medical Education and Publishing CME: "P3 – Patient selection and Practice in Prostate cancer." Boise, ID. February 7, 2017.

- Targeted Oncology Case-Based Peer Perspectives: "Immunotherapy in advanced bladder cancer." Orlando, FL. February 24, 2017.
- Annenberg Center for Health Sciences CME: Experts in Residence "Bridging the gap from knowledge to practice in castration-resistant prostate cancer." Beaumont Hospital, Royal Oak, MI. March 7, 2017.
- Annenberg Center for Health Sciences CME: Experts in Residence "Bridging the gap from knowledge to practice in castration-resistant prostate cancer." Summerlin Hospital, Las Vegas, NV. March 14, 2017.
- Bayer Pharmaceuticals Meet the Professor: "Overview of data related to sequential use of novel hormonal therapies in metastatic castration-resistant prostate cancer." Hanover, NJ. March 24, 2017.
- Hawaii Pacific Health Remedica Medical Education and Publishing CME: "P3 Patient selection and Practice in Prostate cancer." Honolulu, HI. April 10, 2017.
- SWOG Spring GU Organ Site Working Group Meeting: "Combination immune-oncology therapeutics in metastatic castration-resistant prostate cancer." San Francisco, CA. April 28, 2017.
- American Urological Association 2017 Castration-Resistant Prostate Cancer Live Forum for Residents & Fellows: "Role of chemotherapy for metastatic castration-resistant prostate cancer." Boston, MA. May 11, 2017.
- PROSPECT 2017 Symposium Keynote Presentation: "What's hot in advanced prostate cancer today?" Melbourne, Australia. May 19, 2017.
- PROSPECT 2017 Symposium Diagnosis, Staging and Management of Locally Advanced Prostate Cancer: "Advances in imaging and implications for treatment of oligometastatic disease." Melbourne, Australia. May 20, 2017.
- PROSPECT 2017 Symposium Sequencing in Advanced Prostate Cancer Current Therapies: "Therapeutic sequencing in metastatic castration-resistant prostate cancer." Melbourne, Australia. May 20, 2017.
- PROSPECT 2017 Symposium Rapid Fire Multidisciplinary Cases: "Case sequencing in metastatic castration-resistant prostate cancer." Melbourne, Australia. May 20, 2017.
- PROSPECT 2017 Symposium A Look to the Future Personalised and Supportive Care in Advanced Prostate Cancer: "High-risk non-metastatic (M0) castration-resistant prostate cancer an evolving landscape." Melbourne, Australia. May 20, 2017.
- Denali Oncology Group's 34th Educational Program Oncology in the Last Frontier: "Comorbidities and side effects and their effect on how we use therapeutic agents for advanced prostate cancer." Barrow, AK. June 24, 2017.
- Denali Oncology Group's 34th Educational Program Oncology in the Last Frontier: "Considerations with next generation sequencing results and precision medicine in prostate cancer." Barrow, AK. June 24, 2017.
- Bozeman Health Remedica Medical Education and Publishing CME: "P3 Patient selection and Practice in Prostate cancer." Bozeman, MT. July 6, 2017.
- 5th Annual International Conferences on Advances in Hematology and Oncology: "Metastatic prostate cancer: How to sequence newer agents." Coeur d'Alene, ID. August 12, 2017.
- 18th Future Directions in Urology Symposium: "Updates on use of radiopharmaceuticals in prostate cancer clinical trials." Colorado Springs, CO. August 22, 2017.
- American Urological Association 2017 Castration-Resistant Prostate Cancer Live Forum for Residents & Fellows: "Role of chemotherapy for metastatic prostate cancer." Dallas, TX. September 9, 2017.
- American Urological Association Practical Management of Metastatic Prostate Cancer: Guidelines and Beyond: "Comorbidities and side effect profiles: Considerations for various

castration-resistant prostate cancer therapeutic strategies." Dallas, TX. September 10, 2017.

- American Urological Association Practical Management of Metastatic Prostate Cancer: Guidelines and Beyond: "Future directions in systemic therapy for prostate cancer." Dallas, TX. September 10, 2017.
- University of Utah/Huntsman Cancer Institute Remedica Medical Education and Publishing CME: "P3 – Patient selection and Practice in Prostate cancer." Salt Lake City, UT. September 28, 2017.
- Urological Oncology Committee of Taiwan Urological Association Preceptorship: "Novel therapies for the management of advanced prostate cancer." Taipei, Taiwan. October 14, 2017.
- Bayer Taiwan and Southeast Asia Advisory Meeting: "Real life experience with Radium-223 and new clinical evidence." Taipei, Taiwan. October 15, 2017.
- Bayer Taiwan and Southeast Asia Advisory Meeting: "Insights from evaluation criteria to treatment outcomes of Radium-223." Taipei, Taiwan. October 15, 2017.
- American Urological Association 2017 Castration-Resistant Prostate Cancer Live Forum for Residents & Fellows: "Role of chemotherapy for metastatic prostate cancer." Los Angeles, CA. October 28, 2017.
- American Urological Association Practical Management of Metastatic Prostate Cancer: Guidelines and Beyond: "Comorbidities and side effect profiles: Considerations for various castration-resistant prostate cancer therapeutic strategies." Los Angeles, CA. October 29, 2017.
- American Urological Association Practical Management of Metastatic Prostate Cancer: Guidelines and Beyond: "Future directions in systemic therapy for prostate cancer." Los Angelese, CA. October 29, 2017.
- Cancer Immunotherapy Trials Network Annual Meeting: "A randomized phase 2 study of atezolizumab plus recombinant human IL-7 (CYT107) in patients with locally advanced or metastatic urothelial carcinoma." National Harbor, MD. November 9, 2017.
- Remedica Medical Education and Publishing CME: "P3 Patient selection and Practice in Prostate cancer." Summerlin Hospital, Las Vegas, NV. November 27, 2017.
- Purdue University PeerView CME: "Candid conversations in prostate cancer: State of the science and implications for improving patient care and outcomes." VA Southern Nevada Health Care System, Las Vegas, NV. December 19, 2017.
- Annenberg Center for Health Sciences CME: "Optimizing patient outcomes in castrationresistant prostate cancer: Moving urologists from knowledge to action." Holy Cross Hospital (Sinai Health System), Chicago, IL. February 28, 2018.
- Merck/MSD Prostate Cancer Global Advisory Board: "PARP inhibition and DNA repair deficiency in metastatic castration-resistant prostate cancer." San Francisco, CA. May 17, 2018.
- Society for Basic Urology Research (SBUR)/Suociety of Urologic Oncology (SUO) Joint Meeting at the American Urological Association Annual Meeting: "Treatment of cisplatin-ineligible muscle-invasive bladder cancer patients." San Francisco, CA. May 19, 2018.
- Onclive 2018 State of the Science: Genitourinary Cancers: "Treatment intensification for castration-sensitive prostate cancer." Salt Lake City, UT. May 24, 2018.
- Huntsman Cancer Institute Genitourinary Oncology Symposium: "Future of immuno-oncology in prostate cancer." Huntsman Cancer Institute/University of Utah, Salt Lake City, UT. May 25, 2018.
- Peerview Live CME Newest Advances and Strategies in Prostate Cancer Science and Stories on the Evolving Treatment Landscape and Implications for Patient Cancer: "DNA repair deficiency and implications for men with prostate cancer." Chicago, IL. June 1, 2018.

- Education Session, Role of Precision Therapy in the Treatment of Advanced Urothelial Cancer: "Targeted therapies in advanced urothelial cancer." 2018 American Society of Clinical Oncology, Chicago, IL. June 4, 2018.
- Annenberg Center for Health Sciences CME: "Optimizing patient outcomes in castrationresistant prostate cancer: Moving urologists from knowledge to action." North Side Hospital, Atlanta, GA. June 14, 2018.
- 6th Annual International Conferences on Advances in Hematology and Oncology: "Prostate cancer: Optimizing the use of newer agents." Coeur d'Alene, ID. August 5, 2018.
- 19th Future Directions in Urology Symposium: "Next generation anti-androgen therapies." Colorado Springs, CO. August 13, 2018.
- 19th Future Directions in Urology Symposium: "Next generation advanced and endocrine refractory prostate cancer." Colorado Springs, CO. August 14, 2018.
- Prostate Cancer Research Institute (PCRI) 2018 Prostate Cancer Patient Conference: "Pills, immune boosters & radiopharmaceuticals for prostate cancer treatment: Who, Where, When, How and Now?!" Los Angeles, CA. September 8, 2018.
- Singapore Urological Association: "Targeted alpha therapy in metastatic castration-resistant prostate cancer: Dawn or Dusk" Singapore. September 25, 2018.
- Asia-Pacific Metastatic Castration-Resistant Prostate Cancer Expert Exchange Summit: "Optimizing survival in metastatic castration-resistant prostate cancer: Radium-223 and its place in treatment plans: Clinician's perspective." National Cancer Center, Singapore. September 26, 2018.
- National University Hospital: "Targeted alpha therapy in metastatic castration-resistant prostate cancer: Dawn or Dusk" Singapore. September 27, 2018.
- Prostate Cancer Academy: "Role of androgen receptor blockers in advanced prostate cancer." Los Angeles, CA. October 13, 2018.
- Prostate Cancer Academy: "Role of chemotherapy and radiopharmaceuticals in the management and treatment of advanced prostate cancer." Los Angeles, CA. October 13, 2018.
- ESMO Satellite Symposium Checkpoint inhibition in the treatment of cancer: Building the new standard of care across multiple solid tumors: "Checkpoint inhibition for the treatment of genitourinary cancers." Munich, Germany. October 19, 2018.
- Cancer Immunotherapy Trials Network Annual Meeting: "A randomized phase 2 study of atezolizumab plus recombinant human IL-7 (CYT107) in patients with locally advanced or metastatic urothelial carcinoma." Washington, DC. November 7, 2018.
- Windsor Regional Cancer Centre: "Integrating immune-oncology within the current treatment of advanced urothelial carcinoma." Windsor, ON, Canada. November 13, 2018.
- Ottowa Dinner Round: "Integrating immune-oncology within the current treatment of advanced urothelial carcinoma." Ottowa, ON, Canada. November 13, 2018.
- Juravinski Cancer Centre Grand Rounds: "Integrating immune-oncology within the current treatment of advanced urothelial carcinoma." Hamilton, ON, Canada. November 14, 2018.
- Sherbrooke Dinner Rounds: "Integrating immune-oncology within the current treatment of advanced urothelial carcinoma." Montreal, QC, Canada. November 14, 2018.
- Princess Margaret Cancer Centre Grand Rounds: "Integrating immune-oncology within the current treatment of advanced urothelial carcinoma." Toronto, ON, Canada. November 15, 2018.
- Greater Toronto Area Dinner Rounds: "Integrating immune-oncology within the current treatment of advanced urothelial carcinoma." Etobicoke, ON, Canada. November 15, 2018.

- Radium-223 dichloride Oncology Hospital Advisory Board: Management and unmet needs in metastatic castration-resistant prostate cancer: Radium-223 new clinical trials data. Dallas, TX. December 8, 2018.
- Peerview Live CME Unraveling the Complexities of Prostate Cancer Management Focus on Therapeutic Decisions for Early-Stage Disease and the Implications for Later-Stage Disease: "Androgen-targeting therapy in nonmetastatic (M0) castration-resistant prostate cancer." San Francisco, CA. February 15, 2019.
- 44th Annual UCLA State of the Art Urology Conference: "Late breaking news treatment of oligometastatic prostate cancer." Marina Del Rey, CA. March 9, 2019.
- 44th Annual UCLA State of the Art Urology Conference: "Pragmatic sequencing therapy for castrate resistant prostate cancer." Marina Del Rey, CA. March 9, 2019.
- 44th Annual UCLA State of the Art Urology Conference: "Making the immune system work for the urologist." Marina Del Rey, CA. March 9, 2019.
- Enfortumab Vedotin Community Advisory Board: "Metastatic urothelial cancer community patient profile." Dallas, TX. March 15, 2019.
- Enfortumab Vedotin Community Advisory Board: "Potential future treatment options for metastatic urothelial carcinoma." Dallas, TX. March 15, 2019.
- Food & Drug Administration Mini-Symposium on Pathologic Complete Response in Bladder Cancer: "Clinical restaging in muscle-invasive bladder cancer How do we do it and what does it mean?" Silver Spring, MD. March 27, 2019.
- Annenberg Center for Health Sciences CME: "Optimizing patient outcomes in castrationresistant prostate cancer: Moving urologists from knowledge to action." Eisenhower Medical Center, Rancho Mirage, CA. March 28, 2019.
- Bayer Pharmaceuticals Meet the Professor: "Earlier use of novel hormones for advanced prostate cancer and impact on the metastatic castration-resistant prostate cancer population." Hanover, NJ. April 4, 2019.
- Merck Pharmaceuticals Prostate Program Phase III Studies Investigator Meeting Series: "KEYNOTE-365 Cohort A: Pembrolizumab plus olaparib in docetaxel-pretreated patients with metastatic castrate-resistant prostate cancer." Jersey City, NJ. April 12, 2019.
- American Urological Association 2019 Evolving Role of the Urologist in Metastatic and Castration Resistant Prostate Cancer: A Guidelines and Case-Based Discussion: "Role of chemotherapy, treatment sequencing and future approaches." Chicago, IL. May 2, 2019.
- Peerview Live CME New Concepts in Prostate Cancer What Oncologists Need to Know to Optimize Patient Outcomes: "Non-metastatic castration resistant prostate cancer." Chicago, IL. June 1, 2019.
- Education Session Genitourinary (Non-prostate) Cancer Formidable Scenarios in Urothelial and Variant Cancers of the Urinary Tract: "Cisplatin-ineligible patients with urothelial carcinoma – medical oncology perspective." 2019 American Society of Clinical Oncology Annual Meeting. Chicago, IL. June 2, 2019.
- Washington State Urology Association Annual Conference: "Unraveling the complex treatment landscape of prostate cancer Guidance for delivering evidence-based, patient-centered care." Leavenworth, WA. June 22, 2019.
- ASCO Direct Highlights 2019 Official Annual Meeting Review: "Genitourinary cancers The advances continue." New York, NY. July 19, 2019.
- FDA Bladder Cancer Advocacy Network Workshop: "Clinical restaging in muscle-invasive bladder cancer How do we do it and what does it mean?" Washington, DC. August 8, 2019.
- Clovis Prostate Cancer Clinical Immersion: "Biochemically-recurrent prostate cancer and implifcations of next generation PET imaging." Boulder, CO. August 27, 2019.

- Clovis Prostate Cancer Clinical Immersion: "Advanced prostate cancer and treatment sequencing." Boulder, CO. August 27, 2019.
- Clovis Prostate Cancer Clinical Immersion: "Prostate cancer biology, mechanisms of castrationresistance and drug-resistance." Boulder, CO. August 27, 2019.
- Prostate Cancer Academy: "Role of androgen receptor blockers in advanced prostate cancer." Los Angeles, CA. September 21, 2019.
- Prostate Cancer Academy: "Role of chemotherapy and radiopharmaceuticals in the management and treatment of advanced prostate cancer." Los Angeles, CA. September 21, 2019.
- GU Connect Face to Face Meeting at ESMO 2019: "GU Connect educational focus and priorities 2020." Barcelona, Spain. September 28, 2019.
- Janssen Advisory Board 2019 Meeting: "Current approach and treatment patterns in metastatic castration sensitive prostate cancer." San Francisco, CA. October 12, 2019.
- Targeted Oncology and HRA: "Case-based perspectives in prostate cancer." Orlando, FL. November 14, 2019.
- Sanofi Genzyme Key Opinion Leader Expert Seminar: "Future treatment options for advanced prostate cancer." Webex. November 21, 2019.
- Bayer Oncology Advisory Board: "Cognitive impairment: Impact in prostate cancer." San Diego, CA. November 23, 2019.
- Bayer Oncology Advisory Board: "Non-metastatic castration-resistant prostate cancer: Definitions and deciding to treat." San Diego, CA. November 23, 2019.
- American Urological Association / Society of Urologic Oncology 2019 Evolving Role of the Urologist in Metastatic and Castration Resistant Prostate Cancer: A Guidelines and Case-Based Discussion: "Role of chemotherapy, treatment sequencing and future approaches." Washington, DC. December 3, 2019.
- Merck Pharmaceuticals Prostate Scientific Input Engagement: "KEYNOTE-365 Cohort A, B, C ASCO GU 2019 – 1st data release." San Francisco, CA. February 12, 2020.
- Peerview Live CME Mapping the Pathways to Better Patient Outcomes in Prostate Cancer: Personal Insights and Guidance from the Patient Casebook: "Emerging novel strategies in metastatic prostate cancer." San Francisco, CA. February 14, 2020.
- Institute of Molecular Medicine and Biomedical Research Optimal Treatment of Prostate Cancer (converted to Virtual Meeting): "Treatment of metastatic castration-resistant prostate cancer." Athens, Greece. March 13, 2020.
- Institute of Molecular Medicine and Biomedical Research Optimal Treatment of Urothelial Cancer (converted to Virtual Meeting): "Treatment of locally advanced unresectable and metastatic disease." Athens, Greece. March 13, 2020.
- Prostate Cancer Research Institute (PCRI) 2020 Prostate Cancer Patient Conference Mid Year Update (converted to Virtual Meeting): "Updates in advanced prostate cancer." Los Angeles, CA. March 28, 2020.
- Targeted Oncology: "Case based peer perspectives in prostate cancer." Virtual Meeting. May 7, 2020.
- Peerview Live CME: "How I think, How I treat Learning to navigate the modern prostate cancer landscape." Virtual Meeting. June 9, 2020.
- Medscape Oncology CME: "Managing a patient with BCG-Unresponsive non-muscle-invasive bladder cancer." Virtual Meeting. June 10, 2020.
- West Coast Bayer Community Advisory Board: "Understanding the perceptions and practices shaping community oncologists' use of radium-223 dichloride." Virtual Meeting. June 18, 2020.

- Advanced Accelerator Applications Advanced Prostate Cancer Virtual Advisory Board: "Harnessing phenotypes in precision medicine and advanced prostate cancer." Virtual Meeting. June 19, 2020.
- Advanced Accelerator Applications Advanced Prostate Cancer Virtual Advisory Board: "Overview of targeted radioligand therapy and ¹⁷⁷Lu-PSMA-617 clinical trials." Virtual Meeting. June 19, 2020.
- Section of Hematology/Oncology Special Seminar: "The future of advanced prostate cancer curing patients with genotypic and phenotypic precision." University of Chicago by Virtual Meeting. July 17, 2020.
- 2020 UroGPO Virtual Uro-Onc Symposium Implications for Independent Urologists: "2020 Prostate cancer updates." Virtual Meeting. July 24, 2020.
- American Urological Association Summer Course Webinar Series What's new in the management of hormone naïve and castrate resistant prostate cancer: "Metastatic castration-resistant prostate cancer." Virtual Meeting. August 25, 2020.
- Curio Science Opinions in Prostate Cancer: "Metastatic castration-sensitive prostate cancer: Current treatment landscape and use of PARP inhibitors." Virtual Meeting. August 25, 2020.
- Prostate Cancer Academy: "The evolving role of novel hormonal therapy agents in advanced prostate cancer." Atlanta, GA by Virtual Meeting. October 3, 2020.
- Prostate Cancer Academy: "Optimizing the use of chemotherapy and introducing radiopharmaceuticals into our treatment paradigm for advanced prostate cancer." Atlanta, GA by Virtual Meeting. October 3, 2020.
- Curio Science Opinions in Prostate Cancer: "Metastatic castration-sensitive prostate cancer: Current treatment landscape and use of PARP inhibitors." Dallas, TX by Virtual Meeting. October 27, 2020.
- Bayer Advisory Board: "Current approaches to managing metastatic castration-sensitive prostate cancer." Virtual Meeting. October 29, 2020.
- GU Connect Prostate Cancer Virtual MasterClass: "Non metastatic castration resistant prostate cancer." Plenary session, Virtual Meeting. November 7, 2020.
- GU Connect Prostate Cancer Virtual MasterClass: "A case-based journey through the treatment of castration-sensitive and castration-resistant prostate cancer." Virtual Meeting. November 7, 2020.
- GU Connect Prostate Cancer Virtual MasterClass: "Delivering integrated care with a multidisciplinary team from theory to reality and the future vision." Virtual Meeting. November 7, 2020.
- Exelixis Prostate Cancer Virtual Advisory Board: "Prostate cancer current and evolving treatment landscape and practice patterns." Virtual Meeting. December 1, 2020.
- 21st Annual Meeting of the Society of Urologic Oncology: "Evaluating novel therapies and strategies – A look at the changing treatment landscape for metastatic castration-resistant prostate cancer an implications for patient care." Dallas, TX by Virtual Meeting. December 4, 2020
- Curio Science Opinions in Bladder Cancer: "Treatment of metastatic urothelial cancer in the post-platinum, post-immunotherapy setting." Atlanta, GA by Virtual Meeting. December 8, 2020.
- Taiwan Urological Association: "Positioning radium-223 in the metastatic castration-resistant prostate cancer treatment paradigm." Taipei, Taiwan. December 22, 2020.
- 2021 UroGPO Virtual Uro-Onc Symposium Implications for Independent Urologists: "2021 Prostate cancer updates." Virtual Meeting. March 25, 2021.
- Targeted Oncology and HRA: "Case-based perspectives on prostate cancer." Portland, OR. March 25, 2021.

- Rocky Mountain Urological Society Peerview Live CME: "Understanding the evolving treatment landscape in prostate cancer – How to leverage the latest advances and strategies." Denver, CO. April 9, 2021.
- IntrinsiQ Emerging Perspectives in Prostate Cancer Focus Group: "M0 castration-resistant prostate cancer." Virtual Meeting. April 10, 2021.
- Mid Atlantic American Urological Association Mondays Peerview Live CME: "Understanding the evolving treatment landscape in prostate cancer How to leverage the latest advances and strategies." Virtual Meeting. April 12, 2021.
- Curio Science Community Opinions Opinions in Bladder Cancer, An Interactive Local Workshop: "Post platinum or post immunotherapy treatment for locally advanced/metastatic urothelial carcinoma." Virtual Meeting for San Francisco, Los Angeles, and Palm Desert, CA. April 22, 2021.
- Curio Science Community Opinions Opinions in Bladder Cancer, An Interactive Local Workshop: "Subsequent therapy for locally advanced/metastatic urothelial carcinoma." Virtual Meeting for San Francisco, Los Angeles, and Palm Desert, CA. April 22, 2021.
- Targeted Oncology and HRA: "Case-based round table meeting on prostate cancer." Virtual Meeting, Northwest United States. April 29, 2021.
- IntrinsiQ Emerging Perspectives in Prostate Cancer Focus Group: "M0 castration-resistant prostate cancer." Virtual Meeting. May 1, 2021.
- Curio Science Community Opinions Opinions in Bladder Cancer, An Interactive Local Workshop: "Subsequent therapy for locally advanced/metastatic urothelial carcinoma." Virtual Meeting for Kentucky and Tennessee. May 25, 2021.
- Education Session Genitourinary Cancer Kidney and Bladder: "Optimizing Urothelial Cancer Management From Organ-Confined to Metastastic Disease." 2021 American Society of Clinical Oncology Annual Virtual Meeting. Chicago, IL. June 4, 2021.
- Translational Medicine Speaker Series Montana WWAMI Program: "Forward and reverse translation in oncology: Lessons learned from a career in prostate cancer." Montana State University, Bozeman, MT. June 11, 2021.
- Merck Global Prostate Cancer Post-ASCO Expert Input Forum: "ASCO and GU ASCO 2021 key updates PSMA theranostics." Virtual Meeting. June 24, 2021.
- Amgen Incorporated Monthly Grand Rounds: "That's hot! Inflaming prostate cancer." Virtual Grand Rounds Meeting. June 24, 2021.
- Genitourinary Cancer Virtual Symposium Urothelial cancer: "Real world clinical outcomes of FGFR targeted treatment in metastatic urothelial carcinoma." Taiwan Urological Association, Virtual Meeting, Taiwan. July 24, 2021.
- Advanced Accelerator Applications: "Precision medicine in advanced prostate cancer: A phenotypic approach." Advanced Prostate Cancer Virtual Advisory Board. August 13, 2021.
- Curio Science Community Opinions Opinions in Bladder Cancer, An Interactive Local Workshop: "Post platinum or post immunotherapy treatment for locally advanced/metastatic urothelial carcinoma." Virtual Meeting for Iowa and Minnesota. September 7, 2021.
- American Urological Association 2021 What's new in the management of hormone naïve and castrate resistant prostate cancer: "Metastatic castration-resistant prostate cancer." Virtual Meeting. September 12, 2021.
- American Urological Association 2021 Live from AUA 2021: "Highlights in advanced prostate cancer." Virtual Meeting. September 12, 2021.
- Bayer United States Medical Affairs Prostate Cancer Virtual Advisory Board: "Optimizing prostate cancer diagnostics biomarker testing." Virtual Meeting. September 28, 2021.

- Onclive Institutional Perspectives in Cancer: Renal Cell Carcinoma and Bladder Cancer: "Second and later-line treatment of metastatic urothelial carcinoma." Virtual Meeting. September 30, 2021.
- Curio Science Community Opinions Opinions in Bladder Cancer, An Interactive Local Workshop: "Post platinum or post immunotherapy treatment and adverse events for locally advanced/metastatic urothelial carcinoma." Virtual Meeting for Denver, CO. October 5, 2021.
- Curio Science Community Opinions Opinions in Bladder Cancer, An Interactive Local Workshop: "Post platinum or post immunotherapy treatment, subsequent therapy, and adverse events for locally advanced/metastatic urothelial carcinoma." Virtual Meeting for, California. October 27, 2021.
- Curio Science Community Opinions Opinions in Bladder Cancer, An Interactive Local Workshop: "Post platinum or post immunotherapy treatment, subsequent therapy, and adverse events for locally advanced/metastatic urothelial carcinoma." Virtual Meeting for, Portland, OR. November 18, 2021.
- 29th Annual Perspectives in Urology Point Counterpoint: "PSMA Theranostics ¹⁷⁷Lu-PSMA-617 recent data and considerations." Coronado Island, San Diego, CA. November 20, 2021.
- 25th Annual Southwest Prostate Cancer Symposium: "Immunotherapy in metastatic prostate cancer." Scottsdale, AZ. December 11, 2021.
- Oncternal Therapeutics R&D Day: "Metastatic castration-resistant prostate cancer: Present and Future." Virtual Meeting to San Diego, CA. January 25, 2022.
- 2022 Genitourinary Cancers Symposium: Primary Track Urothelial Carcinoma: "Demystifying next-generation sequencing in urothelial carcinoma: A case-based approach." San Francisco, CA. February 18, 2022.
- Bayer ARASENS Data Advisory Board: "Current approaches to managing metastatic hormonesensitive prostate cancer and ARASENS data and planning." Seattle, WA. March 12, 2022.
- Curio Science Community Opinions Opinions in Bladder Cancer, An Interactive Local Workshop: "Post platinum or post immunotherapy treatment, subsequent therapy, and adverse events for locally advanced/metastatic urothelial carcinoma." Virtual Meeting for Pacific Northwest. March 17, 2022.
- SWOG Spring GU Committee Meeting: "SWOG 2210: Targeted neoadjuvant treatment for patients with localized prostate cancer and germline DNA repair deficiency." Seattle, WA. April 9, 2022.
- Curio Science Community Opinions Opinions in Bladder Cancer, An Interactive Local Workshop: "Adjuvant, front-line, post platinum or post immunotherapy, and subsequent therapy for locally advanced/metastatic urothelial carcinoma." Virtual Meeting for Portland, OR. May 26, 2022.
- Prostate Cancer Academy: "ASCO-GU/AUA/ASCO: Advanced prostate cancer highlights." Chicago, IL. June 17, 2022.
- Prostate Cancer Academy: "Metastatic hormone sensitive prostate cancer: Is monotherapy still an option? Case studies." Chicago, IL. June 17, 2022.
- Prostate Cancer Academy: "Beyond first-line novel hormonal therapy: considerations for optimizing treatment sequence." Chicago, IL. June 17, 2022.
- ASCO Direct Highlights: 2022 Official Annual Meeting Review: "Prostate cancer." Seattle, WA. June 18, 2022.
- IntrinsiQ Virtual Emerging Perspectives in Metastatic Hormone Sensitive Prostate Cancer Focus Group: "Metastatic hormone sensitive prostate cancer." Virtual Meeting. June 25, 2022.
- ASCO Direct Highlights: 2022 Official Annual Meeting Review: "Prostate cancer." Las Vegas, NV. July 17, 2022.

- Curio Science Community Opinions Opinions in Bladder Cancer, An Interactive Local Workshop: "Post-platinum or post immunotherapy, and subsequent therapy for locally advanced/metastatic urothelial carcinoma." San Francisco, CA. July 20, 2022.
- Curio Science Community Opinions Opinions in Bladder Cancer, An Interactive Local Workshop: "Post-platinum or post immunotherapy, and subsequent therapy for locally advanced/metastatic urothelial carcinoma." Las Vegas, NV. July 28, 2022.
- Curio Science Community Opinions Opinions in Bladder Cancer, An Interactive Local Workshop: "Adjuvant therapy for muscle-invasive urothelial cancer and front-line therapy for locally advanced/metastatic urothelial carcinoma." San Diego, CA. August 11, 2022.
- IntrinsiQ Virtual Emerging Perspectives in Metastatic Hormone Sensitive Prostate Cancer Focus Group: "Metastatic hormone sensitive prostate cancer." Virtual Meeting. September 17, 2022.
- Targeted Oncology and HRA Case-Based Round Table Meetings: "Later line therapy for metastastic castration-resistant prostate cancer." Virtual Meeting for Arizona. September 19, 2022.
- IntrinsiQ Virtual Challenging Cases: "Treatment of metastatic urothelial carcinoma." Virtual Meeting. September 17, 2022.
- Florida Cancer Specialists Retreat with Dr. Neil Love: "Oprimal integration of antibody drug conjugates and targeted treatment in metastatic urothelial bladder cancer." Orlando, FL. October 22, 2022.
- Merck, Sharpe, and Dohme Advisory Meeting: "Neuroendocrine determination in prostate cancer." Virtual meeting. November 14, 2022.
- Curio Science Community Opinions Opinions in Bladder Cancer, An Interactive Local Workshop: "Post-platinum or post immunotherapy, and subsequent therapy for locally advanced/metastatic urothelial carcinoma." San Antonio, TX. November 17, 2022.
- Targeted Oncology and HRA Case-Based Round Table Meetings: "Therapeutic sequencing for metastastic castration-resistant prostate cancer." Virtual Meeting for California, Oregon & Washington. November 22, 2022.
- IntrinsiQ Virtual Challenging Cases: "Treatment of metastatic urothelial carcinoma." Virtual Meeting. December 13, 2022.

Michael Schweizer, MD

1. Personal Data:

2.	Education:		
	2004 - 2008	<i>Temple University School of Medicine</i> , Philadelphia, PA Doctor of Medicine, May 2008	
	1999 – 2004	University of Delaware, Newark, DE Bachelor of Chemical Engineering, May 2004	
3.	Postgraduate Training:		
	2011 - 2014	Medical Oncology Fellowship, The Sidney Kimmel Comprehensive Cancer Center, Johns Hopkins University, Baltimore, MD	
	2008 - 2011	Internal Medicine Residency, The University of Chicago, Chicago, IL	
4.	Faculty Positions Held:		
	2014 – Present	Assistant Professor Internal Medicine, Division of Medical Oncology, <i>The University of Washington</i> , Seattle, WA	
	2014 - 2019	Assistant Professor, Clinical Research Division, Fred Hutchinson Cancer Center, Seattle, WA	
	2019 – Present	Associate Professor, Clinical Research Division, Fred Hutchinson Cancer Center, Seattle, WA	
	2020 – Present	Associate Professor Internal Medicine, Division of Medical Oncology, <i>The University of Washington</i> , Seattle, WA	
5.	Hospital Positions Held:		
	2014 - Present	Attending Physician, University of Washington Medical Center, Seattle, WA	
	2014 - Present	Attending Physician, Fred Hutchinson Cancer Center, Seattle, WA	
6.	Honors:		
	2015 2015 2014 – 2020 2013-2014 Inducted 2008 Inducted 2003 1999 – 2004	Department of Defense Physician Research Training Award Prostate Cancer Foundation Young Investigator Award NIH Loan Repayment Program Award Recipient Chief Fellow, Medical Oncology, Johns Hopkins University Alpha Omega Alpha Medical Honor Society OXE Chemical Engineering Honor Society The University of Delaware Dean's List	

7. Board Certification:

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2013 - 2023 2011 - 2021	Medical Oncology Board Certification Internal Medicine Board Certification			
Current License(s) to Practice:				
2014 – present	Washington State Medical License: MD60473280			
Professional Organizations:				
2012 – present 2012 – 2013 2014 – Present	American Society of Clinical Oncology, Member ID: 166489 American Association for Cancer Research, Member ID: 274966 Southwest Oncology Group, Genitourinary Oncology Committee			
Teaching Responsibilities:				
2015 – present	Precept oncology fellows in clinic approximately one $\frac{1}{2}$ day per week and attend on the inpatient oncology teaching service			
2015 – present	Lecture every 6-12 months at the Prostate Cancer SPORE Lecture Series			
2016 - 2021	Mentor to Laura Graham MD, Currently faculty in the Division of Oncology at the University of Colorado			
2016 - 2019	Small group leader, UW School of Medicine: Blood and Cancer Course			
2016 – present	MED 505: First year medical student preceptorship elective (2-4 students per year)			
2016 - 2020	Precept urology residents in clinic approximately one ½ day per month			
2016 – present	Lecture every 12 months at Department of Medicine Core Teaching Conference Series			
2016 – present	Lecture every 12 months at Fellow's Lecture Series			
Editorial Responsibilities:				
2014 – Present 2020 – Present 2022 – Present	Editorial Board: <i>Medical Oncology</i> Associate Editor: <i>Frontiers in Oncology</i> Editorial Board: <i>The Prostate</i>			

12. Special National Responsibilities:

2014 – 2018, 2020 Grant and Funding Organization Reviews: Department of Defense Prostate Cancer Research Program

13. Special Local Responsibilities: University and hospital committees.

2015 - 2019	SPORE Pilot Grant Review
2017 – present	Member, UW/FHCRC Cancer Consortium Scientific Review Committee

2017 – present	Leader, Fred Hutchinson Cancer Center, Prostate Cancer Clinical Pathway Team
2017 – 2022	Member, Scientific Review Committee, Fred Hutch / University of Washington Cancer Consortium
2022 – present	Chair, Scientific Review Committee, Fred Hutch / University of Washington Cancer Consortium
2022 – present	Clinical Research Director, Genitourinary Oncology, Fred Hutch / University of Washington Cancer Consortium

14. Research Support

Ongoing Research Support:

Industry Sponsored TrialSchweizer (PI)10/14/16 – 06/30/22Protocol WO29636: A Phase III, Open-Label, Multicenter, Randomized Study of Atezolizumab vs.Observation as Adjuvant Therapy in Patients with High-Risk Muscle-Invasive Urothelial Carcinomaafter Surgical Resection

The major goal of this trial is to evaluate the efficacy and safety of adjuvant treatment with atezolizumab compared with observation in patients with muscle-invasive urothelial carcinoma who are at high risk for recurrence following resection. Role: Site PI

Industry Sponsored TrialSchweizer (PI)07/27/18 – 04/30/23A Phase 1b Safety and Tolerability Study of ZEN003694 in Combination with Enzalutamide or
Abiraterone in Patients with Metastatic Castration-Resistant Prostate Cancer07/27/18 – 04/30/23The major goal of this study is to determine the safety, tolerability, and maximum tolerated dose of
ZEN003694 in combination with enzalutamide or apalutamide or with abiraterone.
criteria 2007
Role: Site PI07/27/18 – 04/30/23

Investigator Initiated Trial Schweizer (PI) 08/01/18 – 03/31/23 Bipolar Androgen Therapy Plus Olaparib in Patient with Castration-Resistant Prostate Cancer The major goal of this study is to determine whether treating prostate cancer patients with bipolar androgen therapy plus olaparib will result in high response rates, particularly in patients with DNA damage repair deficiencies. Role: PI

 Industry Sponsored Trial
 (Schweizer PI)
 03/19/19 - 05/01/24

 A Phase 1, First-in-Human, Dose Escalation Study of JNJ-63898081, in Subjects with Advanced

 Stage Solid Tumors

The major goal of this study is to determine whether JNJ-63898081 will direct the body's immune cells to kill the malignant cells overexpressing prostate-specific membrane antigen (PSMA). Role: Site PI

Investigator Initiated Trial(Schweizer PI)07/25/19 - 06/30/24Erdafitinib plus Abiraterone Acetate or Enzalutamide in Double Negative Prostate CancerThe major goal of this study is to determine the objective tumor response rate in subjects with
measurable lesions as defined by RECIST v1.1 criteria in mCRPC patients with a DNPC molecular
phenotype receiving either enzalutamide or abiraterone acetate in combination with erdafitinib.
Role: PI

Industry Sponsored Trial(Schweizer PI)01/09/20 - 01/31/25A Phase 3 Randomized, Double-Blind Study of Nivolumab or Placebo in Combination with
Docetaxel, in Men with Metastatic Castration-resistant Prostate Cancer (CheckMate 7DX:
CHECKpoint pathway and nivoluMAB clinical Trial Evaluation 7DX) (CA2097DX)The current study aims to demonstrate that treatment with docetaxel in combination with nivolumab
will be efficacious in participants with mCRPC. Additional objectives of the study include
characterization of safety and tolerability, as well as pharmacokinetics, potential predictive
biomarkers, and changes in patient reported outcomes for quality of life assessments.
Role: Site PI

Industry Sponsored Trial(Schweizer PI)02/28/20 - 01/31/25CART-PSMA-TGF β RDN-02: A Phase 1 Open-Label, Multi-Center Study of PSMA TargetedGenetically Modified Chimeric Antigen Receptor T Cells in Patients with Metastatic CastrationResistant Prostate Cancer

The major goal of this trial is to establish the safety of PSMA targeted CAR T-cell therapy in men with metastatic castration-resistant prostate cancer. This study also seeks to determine if there is preliminary evidence for clinical efficacy and explore potential biomarkers associated with response/resistance.

Role: Site PI

Industry Sponsored Trial(Schweizer PI)03/23/20 - 02/28/25A Phase 3, Randomized, Double-blind Trial of Pembrolizumab (MK-3475) Plus Enzalutamide PlusADT Versus Placebo Plus Enzalutamide Plus ADT in Participants With Metastatic Hormone-
Sensitive Prostate Cancer (mHSPC) (KEYNOTE-991)

The major goal is to look at Pembrolizumab (MK-3475) Plus Enzalutamide Plus ADT Versus Placebo Plus Enzalutamide Plus ADT in Participants With Metastatic Hormone-Sensitive Prostate Cancer.

Role: Site PI

Investigator Initiated Trial (Schweizer PI) 05/15/20 – 02/28/25 Durvalumab (MEDI4736) and Olaparib (AZD2281) for treatment of biochemically recurrent prostate cancer in men predicted to have a high neoantigen load: a pilot study The major goal of this study is to evaluate the efficacy of durvalumab plus olaparib in genomic subgroups of prostate cancer expected to be sensitive to immunotherapy. Role: PI

Industry Sponsored Trial(Schweizer PI)08/10/20 - 08/31/25A Phase I Study Exploring the Safety, Tolerability, Pharmacokinetics, and Pharmacodynamics ofINCB099280 in Participants With Select Advanced Solid TumorsMajor Goals: To determine the safety, tolerability of INCB099280 (oral PDL1 inhibitor).Role: Site PI

Industry Sponsored Trial(Schweizer PI)01/25/21 - 02/11/26PSMAfore: A phase III, Open-label, Multi-Center, Randomized Study Comparing 177Lu-PSMA-617vs. a Change of androgen receptor-directed therapy in the Treatment of Taxane Naïve Men withProgressive Metastatic Castrate Resistant Prostate CancerMajor Goals: To evaluate whether treatment with 177Lu-PSMA-617 improves the time toradiographic progression by PCWG3-modified RECIST v1.1 or death in participants with progressivePSMA-positive mCRPC compared to participants treated with androgen receptor-directed therapy.Role: Site PI

Investigator Initiated Trial(Schweizer PI)03/05/21 - 4/30/25ATTAMAGE-A1.1: Phase I/II study of Autologous CD8+ and CD4+ Transgenic T cells expressing

high affinity MAGE-A1-specific T-Cell Receptor (TCR) combined with Atezolizumab in patients with metastatic MAGE-A1 expressing cancer

Major Goals: To evaluate the safety and tolerability of FH-MagIC TCR-R and to assess preliminary clinical activity

Role: PI

Industry Sponsored Trial (Schweizer PI) 07/28/21 – 08/31/26 *A Phase 2 Multiple-Dose, Multiple-Arm, Parallel Assignment Study to Evaluate the Safety, Tolerability, and Preliminary Efficacy of XmAb20717 Alone or in Combination with Chemotherapy or Targeted Therapies in Selected Subjects with Metastatic Castration-Resistant Prostate Cancer* Major Goals: The major goal of this study is to determine the safety and tolerability of XmAb20717 (dual CTLA4/PD1 bispecific antibody) as monotherapy and in combination for subjects with metastatic castration-resistant prostate cancer (mCRPC) who have progressed after treatment with at least 2 prior lines of therapy Role: Site PI

Industry Sponsored Trial(Schweizer PI)10/13/21 – 08/31/26Randomized Phase 2b Study of ZEN003694 in Combination with Enzalutamide versus EnzalutamideMonotherapy in Patients with Metastatic Castration-Resistant Prostate CancerMajor Goals: To assess the effect of ZEN003694 in combination with enzalutamide versus singleagent enzalutamide on radiographic progression-free survival (rPFS) in patients with metastaticcastration-resistant prostate cancer (mCPRC)Role: Site PI

Investigator Initiated Trial(Schweizer PI)8/17/21 - 4/30/26Olaparib in Prostate Cancer Patients With Evidence of Homologous Recombination Deficiency As
Assessed Using an Integrated Genomic Signature

Major Goals: Determine the percent of patients achieving a \geq 50% reduction in PSA (PSA50 response) following at least 12 weeks of treatment with olaparib 300mg twice daily in men with metastatic castration-resistant prostate cancer (mCRPC) who are iHRD+ and who have progressed on a second-generation hormonal agent (e.g. abiraterone or enzalutamide). Role: PI

Recently Completed Research:

W81XWH-16-1-0484Schweizer (PI)09/30/16 - 09/29/21Pharmacologic Dose Testosterone to Treat Castration-Resistant Prostate Cancer: Mechanisms of
Action and Drivers of ResponseThe major goal of this project is to determining germ-line and somatic features that are predictive of
response to Supra-Physiological Testosterone (SPT) and evaluate the mechanisms of action underlying
the observed clinical effects of SPT.
Role: PI

Investigator Initiated TrialSchweizer (PI)04/12/17 - 04/30/21A Phase 2 Study of ARN-509 in Active Surveillance Patients04/12/17 - 04/30/21The major goal of this study is to determine if a 90-day course of ARN-509 will lead to a negative
repeat prostate biopsy in active surveillance patients.04/12/17 - 04/30/21Role: PI04/12/17 - 04/30/21

Investigator Initiated TrialMcNeel (PI)01/30/17 - 01/29/21A Phase I Study of a DNA Vaccine Encoding Androgen Receptor Ligand-Binding Domain (AR LBD),With or Without Granulocyte Macrophage Colony-Stimulating Factor Adjuvant, in Patients WithMetastatic Prostate Cancer

The major goal of this study is to determine if a vaccine called pTVG-AR can enhance patients' immune response against prostate cancer. Role: Site PI

W81XWH-14-2-0189 Denmeade (PI) 01/01/15 – 03/29/20 A Randomized Phase II Study Comparing Bipolar Androgen Therapy vs. Enzalutamide in Asymptomatic Men with Castration Resistant Metastatic Prostate Cancer: The TRANSFORMER Trial The major goal of this study is to determine if treatment with supraphysiologic testosterone will improve radiographic progression free survival compared to enzalutamide in men with metastatic castrate-resistant prostate cancer post-treatment with abiraterone. Role: Site PI

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Book chapters.

1. Schweizer MT, Montgomery RB. Sequencing Therapies in Metastatic Castration Resistant Prostate Cancer. In: Balaji K, ed. Castration Resistant Prostate Cancer: Springer Science; 2015.

Published books, videos, software, etc.

N/A

Other publications (e.g., in non-refereed journals and letters to the editor).

Abstracts

- Schweizer, M.T., Penkov, K.D., Tolcher, A.W., Choudhury, A.D., Doronin, V., Aljumaily, R., Calvo, E., Frank, R.C., Hamm, J.T., Moreno Garcia, V., Vorobyev, V., Billotte, S., Bowler, T., Chen, J., Lin, T., Liu, L., Maity, A., Sharma, S. & Johnson, M.L. Phase I trial of PF-06821497, a potent and selective inhibitor of enhancer of zeste homolog 2 (EZH2), in follicular lymphoma (FL), small cell lung cancer (SCLC) and castration-resistant prostate cancer (CRPC). in *ESMO Congress*, Paris, France.
- Schweizer MT, Gulati R, Yezefski T, Cheng HH, Sievers C, Dumpit R, Alexander K, McDonald N, Lai M, Nega K, Hammond J, Grivas P, Hsieh A, Montgomery B, Nelson PS, Yu EY. Bipolar Androgen Therapy (BAT) plus Olaparib in Men with Metastatic Castration-resistant Prostate Cancer (mCRPC). Poster presented at: 2021 ESMO Annual Meeting. Virtual.
- 3. Schweizer MT, True L, Ellis W, Schade G, Montgomery RB, Goyal S, Nega K, Pienta K, Nelson P, Lin D, Wright J. Resetting the Active Surveillance Clock: Apalutamide in Lower Risk Prostate Cancer. Oral Presentation at: 2020 Society of Urologic Oncology Annual Meeting. Virtual
- 4. Graham L, Reder N, Gulati R, Grivas P, Wright J, Yu E, Hou W, Nega K, Yezefski T, Montgomery RB, Mostaghel E, Ellis W, True L, Lin DW, Nelson P, Schweizer MT. Targeting Backdoor Androgen Synthesis Through AKR1C3 Inhibition: A Presurgical Hormonal Ablative Neoadjuvant Trial in High Risk Localized Prostate Cancer (PC). Poster presented at: 2019 ASCO Annual Meeting, Chicago, IL.
- Schweizer MT, Haugk K, Cheng H, Dumpit R, Nelson PS, Montgomery RB, Plymate SR, Yu EY. Challenges in Enrolling to Metastatic Castration-Resistant Prostate Cancer (mCRPC) Studies that Require Androgen Receptor Splice Variant (AR-V) Positivity. Poster presented at: 2017 Genitourinary Cancers Symposium, Orlando, FL
- 6. Schweizer MT, Wang H, Luber B, et al. Bipolar Androgen Therapy (BAT) in Men with Hormone Sensitive (HS) Prostate Cancer (PC). Poster presented at: 2016 Genitourinary Cancers Symposium, San Francisco, CA.
- 7. Schweizer MT, Antonarakis ES, Wang H, et al. A Pilot Study of Parenteral Testosterone and Oral Etoposide in Men with Castrate-Resistant Prostate Cancer. Poster presented at: 2014 ASCO Annual Meeting, Chicago, IL.
- 8. Schweizer MT, Antonarakis ES, Wang H, et al. A Pilot Study of Parenteral Testosterone and Oral Etoposide in Men with Castrate-Resistant Prostate Cancer. Poster presented at: 2014 ASCO Genitourinary Cancers Symposium, San Francisco, CA.
- 9. Schweizer MT, Zhou XC, Wang H, et al. The Effect of Prior Abiraterone Treatment on Subsequent Response to Docetaxel in Men with Metastatic Castrate-Resistant Prostate Cancer (CRPC). Poster presented at: 2014 ASCO Genitourinary Cancers Symposium, San Francisco, CA.
- Schweizer MT, Huang P, Sternberg CN, De Wit R, Ecstein-Fraisse EB, Kattan MW, Kibel AS, Eisenberger, MA. Prospective evaluation of testosterone (T) recovery and PSA relapse following 18 months of androgen deprivation (ADT) after prostatectomy (RP): Results from the TAX-3501 trial. J Clin Oncol 31, 2013 (suppl; abstr 5023). Poster discussion presented at: 2013 ASCO Annual Meeting, Chicago, IL.

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- Schweizer MT, Bardia A, Blackford A, Lin J, Armstrong AJ, King A, Rudek MA, Yegnasubramanian A, Carducci MA. A Prostate Cancer Clinical Trials Consortium Trial of Disulfiram (D) in Men with Non-metastatic Recurrent Prostate Cancer (PCa). J Clin Oncol 31, 2013 (suppl 6; abstr 219). Poster presented at: 2013 ASCO Genitourinary Cancers Symposium, Orlando, FL.
- 12. Schweizer MT, Zhou XC, Wang H, Yang T, Shaukat F, Eisenberger MA, Antonarakis ES. Metastasis-Free Survival (MFS) is Associated with Overall Survival (OS) in Men with PSA-Recurrent Prostate Cancer Treated with Deferred Androgen Deprivation Therapy. J Clin Oncol 31, 2013 (suppl 6; abstr 109). Poster presented at: 2013 ASCO Genitourinary Cancers Symposium, Orlando, FL.
- Schweizer MT, Zhang Y, Kunnavakkam R, Karrison R, Le Beau MM, Larson RA. Detection of combinations of cytogenetic abnormalities in chronic lymphocytic leukemia (CLL) by fluorescent in situ hybridization (FISH) probes. J Clin Oncol 28:15s, 2010 (suppl; abstr 6591). Poster presented at: 2010 ASCO Annual Meeting, Chicago, IL.
- 16. Other:

2022	Speaker, Comprehensive UW Medicine Hematology & Oncology Review Course, <i>Prostate Cancer</i> , Seattle, WA. September, 2022.
2022	Speaker, 2022 ASCO Annual Meeting, Innovative Immune Approaches in Prostate Cancer: A Case-Based Review of CAR T, T cell Engagers, and Next-Generation Agents, Chicago, IL. June 6, 2022
2021	Speaker, 21 st Annual Pacific NW Prostate Cancer Conference, <i>Changing Landscape of Metastatic Prostate Cancer</i> , Virtual. October 2, 2021
2021	Speaker, Comprehensive UW Medicine Hematology & Oncology Review Course, <i>Prostate Cancer</i> , Virtual. June, 2021.
2021	Speaker, Society for Immunotherapy of Cancer: Advances in Cancer Immunotherapy, <i>Immunotherapy for the Treatment of Genitourinary Malignancies</i> , Virtual. April 2, 2021.
2020	Speaker, Society of Urologic Oncology Annual Meeting, <i>Resetting the Active Surveillance Clock: Apalutamide in Lower Risk Prostate Cancer</i> , virtual meeting. December 3, 2020
2020	Speaker, Medscape CME, Immune Checkpoint and PARP Inhibitors in Prostate Cancer, virtual. December 2020
2020	Speaker, Opinions in Genitourinary Malignancies Global Summit, <i>Great Debates in GU Malignancies</i> , virtual. September 28, 2020
2020	Speaker, Opinions in Prostate Cancer: An Interactive Workshop, <i>Genomic Testing and Interpretation</i> , virtual. August 25, 2020
2020	Speaker, Community Opinions in Prostate Cancer, <i>Patient and Disease Characteristics that Influence Treatment Selection in mCSPC</i> , Seattle, WA. March 3, 2020

2019	Speaker, 26 th Annual Prostate Cancer Foundation Scientific Retreat. <i>FGFR-inhibition</i> <i>in Double Negative Prostate Cancer: Rationale and Future Directions,</i> Carlsbad, CA. October 25, 2019
2019	Speaker, 5 th Annual Men's Health Update. <i>Prostate Cancer: A Lifelong Disease</i> , Seattle, WA. August 23, 2019
2019	Speaker, Gordon's Research Conference: Hormone-dependent Cancers. <i>Targeting Prostate Cancer Drug Resistance</i> , Newry, ME. August 7, 2019
2019	Keynote Speaker, Brotman Baty Institute for Precision Medicine: Cell-free DNA Symposium, <i>Applications of cfDNA in Prostate Cancer</i> , Seattle, WA. April 17, 2019.
2019	Speaker, UWMC Chief of Medicine Conference, Germ Cell Tumors/Testicular Cancer, Seattle, WA. March 19, 2019
2019	Speaker, Selected Topics in Hematology / Oncology Fellow's Lecture Series, Bladder Cancer, Seattle, WA. March 15, 2019
2019	Speaker, Nuclear Medicine Topical Conference, <i>Prostate Cancer 101</i> , Seattle, WA. March 12, 2019.
2019	Speaker, Prostate Cancer SPORE Seminar, <i>Targeting Backdoor Androgen Synthesis vis AKR1C3 Inhibition</i> , Seattle, WA. February 28, 2019
2019	Speaker, Skagit Valley Hospital, Emerging Therapies in Cancer: New Treatments for Prostate Cancer, Mt Vernon, WA. February 27, 2019
2019	Speaker, VA Puget Sound Health Care System, <i>Oncologic Emergencies</i> , Seattle, WA. February 26, 2019.
2018	Speaker, Cancer Immunotherapy Trial Network Meeting, <i>CDK12 Mutation as a Biomarker for Response to Immune Checkpoint Blockade</i> , Washington, D.C. November 7, 2018.
2018	Speaker, Society for Immunotherapy of Cancer: Advances in Cancer Immunotherapy, <i>Immunotherapy for the Treatment of Genitourinary Malignancies</i> , Seattle, WA. November 3, 2018.
2018	Speaker, Fred Hutchinson Cancer Research Center Grand Rounds, <i>Targeting Prostate Cancer Drug Resistance</i> , Seattle, WA. October 2, 2018.
2018	Speaker, Society of Utah Medical Oncologists, Urothelial Carcinoma: Updates and Future Directions, Park City, UT. September 22, 2018.
2018	Speaker, Prostate Cancer SPORE Seminar, <i>PNW Prostate Cancer Clinical Trials Overview: UW/SCCA</i> , Seattle, WA. September 6, 2018
2018	Speaker, Comprehensive UW Medicine Hematology & Oncology Review Course, Systemic Therapy In The Treatment of Bladder Cancer, Seattle, WA. September 15, 2018.

2018	Speaker, Fellow Research Flash Rounds, <i>Translational Prostate Cancer Research</i> , Seattle, WA. July 31, 2018.
2018	Speaker, University of Utah: Huntsman Cancer Institute Genitourinary Oncology Symposium, <i>MSI-high Prostate Cancer: Finding the Needle in the Haystack</i> , Salt Lake City UT. May 25, 2018
2018	Speaker, University of Utah: Huntsman Cancer Institute Translational Oncology Seminar, <i>High-dose Testosterone Therapy for Prostate Cancer: Biomarkers and Combination Strategies</i> , Salt Lake City UT. May 24, 2018.
2018	Speaker, Institute for Prostate Cancer Research Symposium, <i>Improving Survival with Combination Therapy</i> , Seattle, WA. April 28, 2018.
2018	Speaker, City of Hope: Special Lecture, <i>Prostate Cancer: Histologic Subtypes and Molecular Correlates</i> , Duarte, CA. January 18, 2018.
2017	Speaker, CCSG Retreat, <i>State of Research: Clinical Trials</i> , Seattle, WA. November 9, 2017.
2017	Speaker, Everett Clinic, <i>Evolving Options for GU Cancers</i> , Everett, WA. November 6, 2017
2017	Speaker, Selected Topics in Hematology / Oncology Fellow's Lecture Series, <i>Systemic Therapy in the Treatment of Bladder Cancer</i> , Seattle, WA. October 20, 2017.
2017	Speaker, Prostate Cancer Clinical Trials Consortium, <i>High-dose Testosterone Plus PARP Inhibition in mCRPC</i> , teleconferenced nationally. August 29, 2017.
2017	Speaker, Comprehensive UW Medicine Hematology & Oncology Review Course, <i>Systemic Therapy in The Treatment of Bladder Cancer</i> , Seattle, WA. September 25, 2017.
2017	Speaker, SWOG GU Organ Site Meeting: Prostate Organ Site, <i>Bipolar Androgen Therapy for Metastatic Castration-Resistant Prostate Cancer</i> , San Francisco, CA. April 28, 2017.
2017	Speaker, Prostate Cancer Clinical Trials Consortium, <i>Durvalumab in MSI-high CRPC</i> , teleconferenced nationally. April 20, 2017.
2017	Speaker, Institute for Prostate Cancer Research Symposium, <i>Liquid Tumor Biopsies</i> to Guide Precision Medicine. Seattle, WA. March 18, 2017.
2017	Speaker, Fred Hutchinson Cancer Research Center Grand Rounds, <i>High-dose Testosterone to Treat Prostate Cancer</i> , Seattle, WA. January 31, 2017.
2016	Speaker, Selected Topics in Hematology / Oncology Fellow's Lecture Series, <i>Systemic Therapy in the Treatment of Bladder Cancer</i> , Seattle, WA. December 30, 2016.
2016	Speaker, Department of Medicine Core Teaching Conference, Prostate Cancer: Screening and Beyond, Seattle, WA. October 17, 2016.

2016	Speaker, Prostate Cancer SPORE Seminar, <i>Immunotherapy in Hypermutated Prostate Cancers</i> , Seattle, WA. September 29, 2016.
2016	Speaker, Comprehensive UW Medicine Hematology & Oncology Review Course, <i>Systemic Therapy in The Treatment of Bladder Cancer</i> , Seattle, WA. September 24, 2016.
2016	Speaker, Prostate Cancer SPORE Seminar, A Phase I Study of Niclosamide in Combination with Enzalutamide in Men with Androgen Receptor Splice Variant Positive Castration- Resistant Prostate Cancer, Seattle, WA. July 28, 2016.
2016	Speaker, Institute for Prostate Cancer Research Symposium, <i>Cancer Immunology</i> 101, Seattle, WA. April 30, 2016.
2015	Speaker, Comprehensive UW Medicine Hematology & Oncology Review Course, Systemic Therapy in The Treatment of Bladder Cancer, Seattle, WA. September 27, 2015
2015	Speaker, Comprehensive UW Medicine Hematology & Oncology Review Course, Germ Cell Tumors/Testicular Cancer, Seattle, WA. September 27, 2015
2015	Speaker, Coffey-Holden Prostate Cancer Academy Meeting, <i>Moving Chemotherapy Earlier in the Disease Process</i> , La Jolla, CA. June 26, 2015.
2015	Speaker, Institute for Prostate Cancer Research Symposium, <i>Testosterone Therapy: Science, Rationale and Caution</i> , Seattle, WA. April 11, 2015.
2015	Speaker, Prostate Cancer SPORE Seminar, Old Drugs, New Tricks: Repurposing Approved Drugs to Treat Prostate Cancer, Seattle, WA. February 5, 2015.
2014	Speaker, Annual Multi-Institutional Prostate Cancer Program Retreat, A Pilot Study of Supraphysiologic Testosterone and Oral Etoposide in Men with Castrate-Resistant Prostate Cancer, Fort Lauderdale, FL. March 17, 2014.

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 Schweizer, M.T., Penkov, K.D., Tolcher, A.W., Choudhury, A.D., Doronin, V., Aljumaily, R., Calvo, E., Frank, R.C., Hamm, J.T., Moreno Garcia, V., Vorobyev, V., Billotte, S., Bowler, T., Chen, J., Lin, T., Liu, L., Maity, A., Sharma, S. & Johnson, M.L. Phase I trial of PF-06821497, a potent and selective inhibitor of enhancer of zeste homolog 2 (EZH2), in follicular lymphoma (FL), small cell lung cancer (SCLC) and castration-resistant prostate cancer (CRPC). in *ESMO Congress* (Paris, France).

CURRICULUM VITAE

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EDUCATION Undergraduate Bryn Mawr College Bryn Mawr, Pennsylvania	1970-1971
Clark University Worcester, Massachusetts	1972-1975
Medical University of Massachusetts Worcester, Massachusetts	1975-1979
Post Graduate Internal Medicine Residency Mayo Graduate School of Medicine Rochester, Minnesota	1979-1982
Hematology/Oncology Fellowship University of Washington Seattle, Washington	1982-1984
AACR/ASCO Clinical Trials Graduate Workshop Vail, Colorado	1998
ASCO Leadership Seminar Alexandria, Virginia	2011
FACULTY APPOINTMENTS Acting Instructor, Department of Medicine School of Medicine, University of Washington	1984-1988
Acting Assistant Professor, Department of Medicine School of Medicine, University of Washington	1988-1989
Associate in Clinical Research Fred Hutchinson Cancer Research Center	1988-2008
Assistant Professor, Department of Medicine School of Medicine, University of Washington	1989-1997
Associate Professor, Department of Medicine School of Medicine, University of Washington	1997-2008
Adjunct Associate Professor, Department of Urology School of Medicine, University of Washington	1997-1999
Associate Professor, Department of Urology School of Medicine, University of Washington	1999-2008
Professor, Department of Medicine School of Medicine, University of Washington	2008-present

	Professor, Department of Urology School of Medicine, University of Washington	2008-present
	Member, Clinical Research Division Fred Hutchinson Cancer Research Center	2008-present
	Affiliate Member, Dept of Urologic Sciences University of British Columbia	2013-present
	Medical Director, Prostate Cancer Supportive Care Program Vancouver Prostate Centre, Vancouver General Hospital	2013-present
TRAIN	IEES (last 5 vears)	
	Jennifer Bossio. PhD	2015-present
	Lindsav Hedden. PhD	2015-present
	Evandro Bezerra, MD	2017-present
	Sarah Weller, MSc Candidate	2017-present
HONC	RS AND AWARDS	
	National Honor Society	1969
	Phi Beta Kappa	1975
	Lange Award, Outstanding Medical Student	1979
	American Medical Writers Association	2005
	America's Top Doctors List	2005 – present
	Alpha Omega Alpha	2007
	Fellow, American College of Physicians	2008
	Prostate Cancer Challenge Award	2011
	Forbes Distinguished Alumni Award, Bancroft School	2015
	Top Cancer Doctors Award, Newsweek	2015
	National Association of Professional Women, VIP Woman of the Year	2015-2016
BOAR	D CERTIFICATION	
	American Board of Internal Medicine	1982
	Medical Oncology	1985
MEDI	CAL LICENSES	
	Minnesota	1979-1982
	Washington	1982-present
	California	2010-present
PROFE	SSIONAL ORGANIZATIONS	
	American Association for Cancer Research	1992-present
	American Society of Clinical Oncology	1985-present
	Puget Sound Oncology Consortium	1994-2015
	American Society of Hematology	1994-present
	American Urological Association	1997-present
	Society of Women in Urology	1996-present
	Southwest Oncology Group	1985-present
	The Society of Urologic Oncology	2002-present
	European Society for Medical Oncology	2013-present
	Washington State Medical Association	1985-present
	Washington State Medical Oncology Society	1999-present
	Washington State Prostate Cancer Coalition	2002-present

EDITORIAL BOARDS

American Cancer Society Clinical Care for Prostatic Disease Clinical Genitourinary Cancer Clinical Prostate Cancer Journal of Clinical Oncology

NATIONAL RESPONSIBILITIES

Amer	ican Society of Clinical Oncology (ASCO)	2003-2005
	Scientific Program Committee ASCO Prostate Cancer Symposium	2003-2005
	American College of Padiology Appropriateness Criteria Papel Member	2005-2008
	Ad Hoc ASCO Prostate Cancer Guideline Peview Panel	2005-2008
	Au Hoc ASCO Prostate Califer Guideline Review Parler	2000
	Candidate for ASCO Nominating Committee	2008 2011
	Cancer Education Committee – Genitourinary Cancer Track	2008-2011
	Candidate for Nominating Committee	2014
	Member, Continuing Education Committee	2015-present
	Chair, Continuing Education Ccommittee	2017-2018
Amer	ican Urological Association (AUA)	
	Treatment of Localized Prostate Cancer Consensus Committee	2001
	External peer reviewer for Localized Prostate Cancer Treatment Guidelines	2016
Amer	ican Association of Cancer Research (AACR)	
	Scientific Program Committee, 2018 AACR Annual Meeting	2017-2018
Societ	ty of Urologic Opcology (SUO)	2003
JUCIE	Consensus Panel on Hormone Refractory Prostate Cancer	2005
	consensus Parlei on Hormone Renactory Prostate Cancer	
South	west Oncology Group (SWOG)	1002
	Oncology Discipline Chair, Genitourinary Committee	1993-present
	Endpoints Review Committee, Prostate Cancer Prevention Trial	1998-2004
Specia	alized Program of Research Excellence in Prostate Cancer (SPORE)	
	Pacific Northwest PC SPORE Clinical Core Director	2002-2012
	Co-chair, InterSPORE Clinical Trials Concept Review Committee	2002-2005
Natio	nal Comprehensive Cancer Network (NCCN)	
	Member, Prostate Cancer Guidelines Panel	2010-present
	NCCN/VA CRPC Curriculum Development Committee	2015
	Panel Member, Value Pathways Task Force	2018-
Natio	nal Cancer Institute (NCI)	
Natio	Member SyOOI Drug Development Task Force	2008-2015
	Weinber, skede brug bevelopment rusk i oree	2000 2010
Prosta	ate Cancer Working Group (PCWG)	2001 2004
	PSA Working Group	2001-2004
	PCWG 2	2004-2008
	PCWG 3	2011-2016
Prosta	ate Cancer Foundation (PCF)	
	Standing Review Committee	2010-present
	PCF-Canada ASAP 2012	2012
	PCF-Australia/Movember MRTA-3 review panel member	2012
	PCE-Capada/Movember Transformational Science Award reviewer	2017

Eastern Cooperative Oncology Group Reverse Site Visit	2003
American Joint Committee on Cancer Genitourinary Task Force	2005-2007
West Hawaii Cancer Symposium Co-Chair and Co-organizer	2000-present
Treatment and the Focal Lesion Paradigm Consensus Panel	2005 2006
Member, International Task Force on Prostate Cancer	2005-2006
International Bisphosphonate Summit Meeting Chair and Organizer	2002
UpToDate in Oncology: Peer Review Board	2005-2006
INDEPENDENT DATA SAFETY MONITORING BOARDS	
Member, 2 Millenium phase 3 trials	2010-2014
Member, SOTIO phase 3 trial	2014-present
Member, Alliance Foundation Trials (AFT)	2016-present
Member, Movember GAP 4 (INTERVAL)	2016-present
Chair, Advantagene phase 3 trial	2016-present
SCIENTIFIC STEERING COMMITTEES	
Cell Genesys GVAX Steering Committee, global PI for VITAL 1 phase 3	2008-2009
Cougar Biotech (Abiraterone Acetate) Steering Committee	2008-2010
AstraZeneca (ENTHUSE/zibotentan) Steering Committee, global PI for phase 3	2008-2012
Medivation (STRIVE) Steering Committee	2010-2015
Dendreon (PROCEED Registry) Steering Committee	2010-present
Teva (OGX-011 Custirsen) Steering Committee, global co-PI with Chi and de Bono	2011-2016
Bayer Xofigo (REASSURE Registry) Steering Committee	2011-present
Bayer RA 223 Phase 3 Steering Committee, global co-PI with Matthew Smith	2013-present
MorphoSys (MOR209) Steering Committee	2011-present
Ferring (PRONOUNCE) Steering Committee	2015-present
Pfizer talazoparib phase 2 Steering Committee	2016-present
Clovis (TRITON) Steering Committee	2016-present
Pfizer Talazoparib Steering Committee	2017-presnet
SCIENTIFIC ADVISORY BOARDS since 2010	
Amgen (XGEVA denosumab) Advisory Board	2008-2011
Medivation (PREVAIL) Advisory Board	2010-2014
Bristol-Myers Squibb (IDEA) Advisory Board	2011
Genentech Prostate/Bladder Advisory Board	2011
Orion (ODM-201) Advisory Board	2012
Novartis – Prostate Cancer Advisory Board	2012
Dendreon Sequencing Therapy Advisory Board	2012
Veridex Steering Committee	2012-2013
Dendreon Data Mining/PDAAC	2013
Johnson & Johnson Cellsearch Advisory Board	2013
AbbVie – Lupron Advisory Board	2013
Ferring – Firmagon Intermittent Therapy	2013
BHR – Estragel Advisory Board	2014
Astellas (XTANDI) Advisory Board	2014-2016
Astellas Global Medical Atfairs Advisory Board	2015

Churchill Prostate Cancer Advisory Board Emergent (STRIVE/TERRAIN) Advisory Board Blue Earth Diagnostics Advisory Board Dendreon Advisory Board Endocyte Advisory Board Asana BioSciences Advisory Board Orion Advisory Board	2015 2015-2016 2015-present 2016 2016-present 2016-present 2017-present
LOCAL RESPONSIBILITIES	
State of Washington	
American Cancer Society, Northwest Chapter Washington State Prostate Cancer Coalition Task Force	1998-2002 2002-present
University of Washington/Fred Hutchinson	
Institute for Prostate Cancer Research Committee	1999-2014
Sponsored Programs/Human Subjects Faculty Advisory Committee	2004-2006
Research Trials Office Oversight Committee	2002-2006
University of Washington Search Committees:	
Associate Director of Clinical Research Division	2002-2005
Phase I Clinical Trials Director of Medical Oncology	2006-2007
Renal/Melanoma Faculty	2007-2008
Lung and Head and Neck Faculty	2008-2010
Seattle Cancer Care Alliance	
Joint Oncology Planning Committee, GU Patient-Care Subcommittee	1999-2001
Space Planning Committee	2008-2010
SCCA Strategic Planning Committee	2008-2009
Eastside Prostate Cancer Support Group	1997-present
Bellevue Rotary Club	1997
American Cancer Society, Northwest Chapter, Prostate Cancer Task Force	1998-2006
Northwest Hospital Prostate Cancer Support Group	1998
Northwest Prostate Cancer Foundation	2000
Washington State Prostate Cancer Coalition	2002-present
Tacoma Prostate Cancer Support Group	2006
UsTOO in Seattle	2010-present

INVITED TALKS AND LECTURES SINCE 2012

UNIVERSITY/LOCAL

- 1. Fred Hutchinson Cancer Research Center's 2nd Symposium on Cancer Survivorship for Clinicians: Monitoring and Managing the Side Effects of Adrogen Deprivation Therapy for Prostate Cancer. Seattle, WA. February 2012.
- 2. "New approaches to androgen deprivation therapy", Virginia Mason GU Tumor Board, Virginia Mason Medical Center. Seattle, October 2012.
- 3. 12th Annual Pacific Northwest Prostate Cancer Conference, Seattle, WA. October 2012.
- 4. "Immunotherapy for Prostate Cancer", IPCR Symposium, Fred Hutchinson Cancer Research Center, Seattle, March 2013.
- 5. "Beyond hormonal therapy", PNW Prostate Cancer SPORE Retreat, Seattle, July 2013.

- 6. 13th Annual Pacific Northwest Prostate Cancer Conference, Seattle, September 2013.
- 7. PNW Prostate Cancer SPORE Retreat, Seattle, July 2014.
- 8. 14th Annual Pacific Northwest Prostate Cancer Conference, Seattle, September 2014.
- 9. "New Treatments on the Horizon" 15th Annual Pacific Northwest Prostate Cancer Conference, Seattle, September 2015.
- 10. "Androgen deprivation therapy and cardiovascular risk: What's the real story?" Fred Hutchinson Cancer Research Center, Grand Rounds, Seattle, April, 2016.
- 11. "Hormone therapy and cardiovascular risk: What do we know?" 16th Annual Pacific Northwest Prostate Cancer Conference, Seattle, September, 2016.

NATIONAL/INTERNATIONAL

- 1. ASCO GU Satellite Symposium. "Sequencing of New and Emerging Agents in mCRPC." San Francisco, CA. February 2012.
- 2. Fresenius Kabi AG, FORCE Meeting: The Evolving Treatment Paradigm for Castration Resistant Prostate Cancer. "Advances in supportive care for cancer management." Ho Chi Minh City, Vietnam. February 2012.
- 3. Fresenius Kabi AG, FORCE Meeting: Monitoring and Managing the Side Effects of Androgen Deprivation Therapy for Prostate Cancer. "Management of PSA Recurrent." Ho Chi Minh City, Vietnam. February 2012.
- 4. Clinical Care Options Satellite Symposium. "Metastatic prostate cancer case: Skeletal related events". ASCO Annual Meeting. Chicago, IL. June 2012.
- Chinese Society of Clinical Oncology. "Optimal hormonal therapy for metastatic prostate Cancer" and "Current standard of practice after ASCO 2012: the evolving treatment paradigm prostate cancer". Best of ASCO China, Nanjing, China. July 2012.
- Best of ASCO Satellite Symposium: Pathways to Progress in Castration-Resistant Prostate Cancer and Renal Cell Carcinoma: Practical Guidance for Clinicians. "Androgens still matter in castration resistant prostate cancer: targeting androgen signaling beyond castration resistance." San Diego, CA. August 2012.
- 7. 15th Annual West Hawaii Cancer Symposium. "Health Care Reform and Clinical Trials." Kailua-Kona, HI. September 2012.
- 8. MD Anderson Cancer Center Comprehensive Board Review Course. "Prostate Cancer 2012" Houston, TX. September 2012.
- 9. "Novel immunotherapeutic approaches in metastatic castration resistant prostate cancer". GU ASCO Satellite Symposium: Castration-Resistant Prostate Cancer, Important Questions, Encouraging Answers. Orlando, FL. February 2013.
- 10. "Leveraging the immune system in prostate cancer". GU ASCO Satellite Symposium: Research to Practice Symposium: A Live Investigator Think Tank. Orlando, FL. February 2013.
- 11. Gold Journal (*Urology*) Roundtable Resource Center. "Immunotherapy in clinical practice." Chicago, IL. February 2013. Urology on line <u>http://education.goldjournal.net/path.php?1396:0:Media:title:bxvcs</u>
- "Latrogenic side effects of androgen deprivation therapy: a practical clinical approach" and "Systemic management of CRPC, Panel discussion". Issues and Controversies in Prostate Care 2013: Review of prostate cancer clinical trials. Whistler, BC. March 2013.
- 13. ASCO Satellite Symposium: The Team Quiz Challenge: Bone Modifying Agents in the Treatment of Cancer. Program Director. "Metabolic and skeletal complication of androgram deprivation therapy." Chicago, IL. June 2013.
- 14. ASCO Satellite Symposium: Modern management of metastatic castration-resistant prostate cancer in 2013 and beyond: navigating the successes, hurdles, and practicalities. "Immunotherapy for Advanced Prostate Cancer: Current status and future potential." Chicago, IL. June 2013.
- 15. ASCO Education Session, Androgen Deprivation Therapy for Prostate Cancer. "Metabolic and skeletal complications of androgen deprivation therapy." Chicago, IL. June 2013.

- 16. "Intermittent androgen deprivation: Recommendations." NCCN Prostate Cancer Panel meeting. Philadelphia, PA. June 2013.
- 17. "Prostate cancer 2013: a case based review", 23rd Annual Mayo Clinic Hematology Oncology Reviews, Amelia Island, FL. August 2013.
- "New Treatment Options for Metastatic Prostate Cancer", 16th Annual West Hawaii Cancer Symposium, Kailua-Kona, HI. September 2013.
- 19. "Holistic Approach to PCa Therapy: A Multidisciplinary Opportunity." Chair, AbbVie Advisory Board. Vancouver, BC. September 2013.
- "Overall survival benefit with Radium-223: Pre and post docetaxel." and "Novel immunotherapeutic approaches in Prostate Cancer." 1st International State-of-the-Art Uro-Oncology Conference on Prostate and Kidney Cancers, EUOG, Amsterdam, Netherlands. September 2013.
- 21. "Identifying common molecular features of ERG positive tumors in primary and castration-resistant prostate cancer", Annual Prostate Cancer Foundation Retreat, National Harbor MD. October 2013.
- 22. "Real-world experience with Sipuleucel-T in metastatic castration-resistant prostate cancer (mCRPC) patients (pts) >80 years-old: data from PROCEED", Western AUA Conference, Monterey CA. November 2013.
- 23. "Use of intermittent androgen deprivation therapy based on mathematical modeling of PSA and other parameters", Mathematical Modeling Workshop, Institute of Industrial Science, University of Tokyo Japan. December 2013.
- "Non-hormone Therapy for Metastatic Castration-Resistant Prostate Cancer: Chemotherapy, Bone-Targeted Treatments and Others", Scripps 34th Annual Conference of Clinical Hematology & Oncology, San Diego CA. February 2014.
- 25. "Advancing the Standard of Cancer Care: New Developments in the Treatment of Hormone Refractory Prostate Cancer", NCCN Annual Meeting, Fort Lauderdale, Florida. March 2014.
- 26. "Radium-223 for the treatment of metastatic castration resistant prostate cancer." ERA-223 Investigator Meeting. San Diego, CA. April 2014.
- 27. "On the Shoulders of Giants Prostate Cancer Therapy: How Did We Get Here and Where Are We Going" Topic: Immunotherapy for Prostate Cancer, ASCO Annual Meeting, Chicago. May 2014.
- 28. "New developments in the treatment of metastatic castration resistant prostate cancer." And "The evolving role of chemotherapy for metastatic castration resistant prostate cancer." Mexican Urologic Oncology Society Annual Meeting. Acapulco, Mexico. July 2014.
- 29. MD Anderson Cancer Center Comprehensive Board Review Course. "Prostate Cancer 2014" Houston, TX. September 2014.
- 30. "Effect of prior abiraterone or enzalutamide on sipuleucel-T manufacture in PROEED Registray patients." Western Section AUA Meeting. Maui, Hl. October 2014.
- 31. Movember Foundation Revolutionary Team 3 Award Grant Review. Panel member. Sydney Australia. November 2014.
- 32. "Prostate Cancer, a glance at the near future." 1st International Geriatric Oncology Meeting. Rome, Italy. December 2014.
- 33. "Advanced Prostate Cancer: using Sip-T first in mCRPC", Dendreon National Sales Meeting, Santa Barbara, CA. January 2015.
- 34. ASCO CME Committee meeting. Alexandria, VA. February 2015.
- 35. "Novel Therapies: Radiopharmaceuticals for Castration-Resistant Prostate Cancer", New York GU, 8th Annual Interdisciplinary Congress, New York, NY. March 2015.
- 36. Panelist for the OncLive TV Peer Exchange Channel. Expert Panel Discussion: "Management of mCRPC; A Practical Review of Guideline Updates and Case Study Perspectives" (video). New Orleans, LA. May, 2015

- 37. "STRIVE, A Multicenter Phase 2 Study of Enzalutamide versus Bicalutamide in Men with Nonmetastatic or Metastatic Castration-Resistant Prostate Cancer." AUA Annual Meeting, Plenary Session. New Orleans, LA. May 2015.
- 38. ASCO Post Interviewer. ASCO Annual Meeting, Chicago, IL. June 2015
- 39. "Advances in hormonal therapy for prostate cancer over the last five years." Regional Summit on Practical and Emerging Trends in Genitourinary Malignancies, San Francisco, CA. June 2015.
- 40. "Implementation of the Prostate Cancer Supportive Care Program, A Comprehensive Approach for Men with Prostate Cancer and Their Partners." Multinational Association of Supportive Care in Cancer Annual Meeting. Copenhagen, Denmark. June 2015.
- 41. "Radium 223 Benefit in Castration Resistant Prostate Cancer", 33rd National Congress in Oncology, Mexican Society of Oncology. Cancun, Mexico. October 2015.
- 42. "Changing landscape in early castration-resistant prostate cancer." Astellas Advisory Board Meeting. Budapest, Hungary. November 2015.
- 43. FDA "Type A" Meeting (Churchill Pharma). Silver Spring, MD. November 2015.
- 44. "Androgen Deprivation Therapy: What's the real story about cardiovascular risk?", Provincial Tumour Group Meeting. Vancouver, Canada. November 2015.
- 45. Movember Prostate Cancer Outcomes: Global Initiative to Compare and Reduce Variation. Delegate. Culver City, CA. December 2015.
- 46. "Analysis of the PROCEED registry by baseline prostate-specific antigen (PSA) quartiles: Preliminary analysis of realworld sipuleucel-T (sip-T) use." Poster presentation. ASCO-GU Symposium. San Francisco, CA. January 2016.
- 47. Session 7: Testicular Cancer. Session Monitor. ASCU-GU Symposium. San Francisco, CA. January 2016.
- 48. "Successful implementation of a disease-specific survivorship program for men with prostate cancer (PC) and their partners." Poster presentation. 2016 Cancer Survivorsip Symposium: Advancing Care and Research. San Francisco, CA. January 2016.
- 49. "Utilization of sexual health and pelvic floor physiotherapy services in Vancouver's Prostate Cancer Supportive Care (PCSC) Program. 2016 Cancer Survivorship Symposium: Advancing Care and Research. San Francisco, CA. January 2016.
- 50. "Management of metastatic prostate cancer." Mayo Clinic: Clinical and Multidisciplinary Hematology and Oncology 2016 13th Annual Review. Scottsdale, AZ. January 2016.
- 51. ASCO CME Subcommittee Meeting. Alexandria, VA. February 2016.
- 52. "Integrating immunotherapy in the management of metastatic castration resistant prostate cancer." And "Challenging Case Debates." New York GU, 9th Annual Interdisciplinary Congress, New York, NY. March 2016.
- 53. "Prostate Cancer: A Discussion of the Latest Developments to Change Care in the Oncology Clinic." Program Director: Optimizing the Treatment of Advanced Prostate Cancer: Expert Review of the Latest Data and Guideline Recommendations. CCO/ NCCN Satellite Symposium at ASCO. Chicago, IL. June 2016.
- 54. "Utilization of sexual health and pelvic floor physiotherapy services in Vancouver's Prostate Cancer Support Care Program." Poster presentation. ASCO Annual Meeting. Chicago, IL. June 2016.
- 55. Prostate Cancer Co-chair. 2nd RIMOG New and Emerging Therapeutic Options in Geriatric Oncology Meeting. Florence, Italy. July 2016.
- 56. "Arv-7 Story and clinical implications." 17th Asia-Pacific Prostate Cancer Conference. Melbourne, Australia. August/September, 2016.
- 57. "ADT and Cardiovascular Risk." 17th Asia-Pacific Prostate Cancer Conference. Melbourne, Australia. August/September, 2016.
- 58. "Successful Implementation of a Prostate Cancer Survivorship Program." 17th Asia-Pacific Prostate Cancer Conference. Melbourne, Australia. August/September, 2016.

- 59. "Pain and the Prostate Cancer Patient." 17th Asia-Pacific Prostate Cancer Conference. Melbourne, Australia. August/September, 2016.
- 60. MD Anderson Cancer Center Comprehensive Board Review Course. "Prostate Cancer 2016" Houston, TX. September 2016.
- 61. Module 2: "Sequence and Selection of Secondary Hormonal Therapy, Immunotherapy and Cytotoxic Therapy for Patients with mCRPC", Research to Practice Satellite Symposium Cases from the Community: Clinical Investigators Provide their Perspectives on Emerging Research and Actual Patients with Advanced Prostate Cancer. Orlando, FL. February, 2017.
- 62. "The changing landscape of metastatic castration-resistant prostate cancer." Genentech Grand Rounds. San Francisco, CA. February 2017.
- 63. "Updagte of On-going phase 3 trials in metastatic hormone sensitive prostate cancer." 2nd Advanced Prostate Cancer Consensus Conference (APCCC). St. Gallen, Switzerland. March, 2017.
- 64. "Isotope therapy and PARP inhibitors for advanced prostate cancer." and "Case debates: best practices." New York GU, 10th Annual Interdisciplinary Congress, New York, NY. March 2017.
- 65. "Best practices for the management of metastatic castration-resistant prostate cancer across the disease continuum." Practicing Clinicians Exchange (PCE) Symposium. Anaheim, CA. March 2017.
- 66. "Personalized sequencing in castration-resistant prostate cancer." PER Medical Crossfire Symposia. Chicago, IL. June 2017.
- 67. "The changing treatment landscape for metastatic castration-resistant prostate cancer" and "Considerations for sequencing of therapy for metastatic castration resistant prostate cancer." Japanese Society of Medical Oncology. Kobe, Japan. June 2017.
- 68. "The changing landscape of metastatic prostate cancer over the last 20 years." West Hawaii Cancer Symposium. Kona, HI. September 2017.
- 69. MD Anderson Cancer Center Comprehensive Board Review Course. "Prostate Cancer" Houston, TX. September 2017.
- 70. "Updates in Prostate Cancer: New Cancer Drugs." Seventh Annual Prostate Cancer Advocacy Symposium: A National Summit. Detroit, MI. September 2017.
- 71. "Treatment decisions in a new therapeutic landscape in men with mCRPC." Thai Society of Clinical Oncology Symposium. Bangkok, Thailand. November 2017.
- 72. "Focus on Safety Issues of Newer Hormonal Therapies." prIME Oncology CME-certified Symposium: Hormonal Therapy in Prostate Cancer: Improving Clinical Outcomes in Metastatic and Non-Metastatic Disease. San Francisco, CA. February 2018.
- 73. "Early Use of Systemic Therapy: Abiraterone Versus Docetaxel for Hormone-Sensitive Prostate Cancer." New York GU: 11th Annual Interdisciplinary Prostate Cancer Congress and Other Genitourinary Malignancies. New York, NY. March 2018.
- 74. "Prostate Cancer Disparities: Focus on African American Men." American Association for Cancer Research (AACR) Annual Meeting 2018. Chicago, IL. April 2018.
- 75. "Role of Data Monitoring Committees in Complicated Trials." Society for Clinical Trials (SCT) Annual Meeting. Portland, OR. May, 2018.
- 76. "Balancing Toxicities, and Therapeutics Perspective." 2018 ASCO Annual Meeting Session: Metastatic Prostate Cancer Tumor Board: Optimizing Patient Selection and Treatment. Chicago, IL. June 2018.
- 77. "Off Protocol Treatment of Oligometastatic Hormone Sensitive or CRPC Disease with SRRT." Asia-Pacific Prostate Cancer Conference (APPCC). Brisbane, Australia. August 2018.
- 78. "Implementation of an Electronic Patient Reported Outcome System in the Prostate Clinic at the Vancouver Prostate Centre." Asia-Pacific Prostate Cancer Conference (APPCC). Brisbane, Australia. August 2018.

- 79. "Hormone Sensitive Metastatic Disease: Treatment Options." Asia-Pacific Prostate Cancer Conference (APPCC). Brisbane, Australia. August 2018.
- 80. "New Options in MO CRPC Who (if anybody) needs treatment." Asia-Pacific Prostate Cancer Conference (APPCC). Brisbane, Australia. August 2018.
- 81. "Current Data & Takeaways: Radium-223's Role as a Life-Prolonging Agent." ESMO 2018 Industry Satellite Symposium. Munich, Germany. October 2018.
- 82. "To Screen or Not to Screen That is the Question." The University of Massachusetts Medical School Grand Rounds. Worcester, MA. October 2018.
- 83. "Biologic Rationale for Next-Generation AR Inhibitors." Global Summit on Genitourinary Malignancies. Banff, Canada. November 2018.

PEER-REVIEWED PUBLICATIONS

- 1. Tallman MS, McGuffin RW, <u>Higano CS</u>, Starkebaum G, Collins SJ, Johnston H, Singer JW, Perry DJ, Kunath A. Bone marrow transplantation in a patient with myelodysplasia associated with diffuse eosinophilic fascitis. *Am J Hematol*. 1987 24(1):93-99.
- 2. Abdel-Nabi HH, Schwartz AN, <u>Higano CS</u>, Wechter DG, Unger MW. Colorectal carcinoma: Detection with indium-111 anticarcinoembryonic-antigen monoclonal antibody ZCE-025. *Radiology*. 1987 164(3):617-621.
- 3. Livingston RB, Griffin BR, <u>Higano CS</u>, Laramore GE, Rivkin SE, Goldberg RS, Schulman SF. Combined treatment with chemotherapy and neutron irradiation for limited non-small cell lung cancer: A Southwest Oncology Group Study. *J Clin Oncol.* 1987 5(11):1716-1724.
- 4. Mortimer JE, <u>Higano CS</u>. Continuous infusion 5-fluorouracil and folinic acid in disseminated colorectal cancer. *Cancer Invest.* 1988 6(2):129-132.
- 5. Tallman MS, Nemunaitis JJ, McGuire TR, Yee GC, Hughes TE, Almgren JD, Appelbaum FR, <u>Higano CS</u>, McGuffin RW, Singer JW, Thomas ED. Comparison of two intravenous cyclosporine infusion schedules in marrow transplant recipients. *Transplantation.* 1988 45(4):810-813.
- 6. McGuire TR, Tallman MS, Yee GC, Nemunaitis JJ, <u>Higano CS</u>, McGuffin RW, Singer JW. Influence of infustion duration on the efficacy and toxicity of intravenous cyclosporine in bone marrow transplant patients. *Transplant Proc.* 1988 20(3 Suppl 3):501-504.
- 7. Russell KJ, Boileau MA, Ireton RC, <u>Higano CS</u>, Collins C, Koh WJ, Griffin BR, Chapman WH, Griffin TW. Transitional cell carcinoma of the urinary bladder: histologic clearance with combined 5-FU chemotherapy and radiation therapy. Preliminary results of a bladder-preservation study. *Radiology*. 1988 167(3):845-848.
- 8. Griffin BR, Livingston RB, Stewart GR, <u>Higano CS</u>, Russell KJ, Griffin TW, Laramore GE. Prophylactic cranial irradiation for limited non-small cell lung cancer. *Cancer.* 1988 62(1):36-39.
- 9. Collins C, <u>Higano CS</u>, Livingston RB, Griffin BR, Keppen MD, Miller TP. Cyclophosphamide, vincristine, cisplatin, VP-16 and radiation therapy in extensive small-cell lung cancer. A Southwest Oncology Group study. *Cancer Chemother Pharmacol.* 1989 24(2):128-132.
- 10. <u>Higano CS</u>, Livingston RB. Oral dipyridamole and methotrexate in human solid tumors: a toxicity trial. *Cancer Chemother Pharmacol.* 1989 23(4):259-262.
- Jacobson AF, Cerqueira MD, Breitz HB, Whitley MA, <u>Higano CS</u>. Pleuroperitoneal communication associated with malignant ascites. A potential cause for new pleural effusion suggestive of pulmonary embolism. *Clin Nucl Med*. 1990 May; 15(5):317-320.
- 12. Bianco JA, <u>Higano CS</u>, Singer JW, Appelbaum FR, McDonald GB. The somatostatin analog octreotide in the management of the secretory diarrhea of the acute intestinal graft-versus-host disease in a patient after bone marrow transplantation. *Transplantation*. 1990 49(6):1194-1195.

- 13. <u>Higano CS</u>, Brixey M, Bryant EM, Durnam DM, Doney K, Sullivan KM, Singer JW. Durable complete remission of acute nonlymphocytic leukemia associated with discontinuation of immunosuppression following relapse after allogeneic bone marrow transplantation: A case report of a graft-versus-leukemia effect. *Transplantation*. 1990 50(1):175-177.
- 14. Bianco JA, Pepe MS, <u>Higano CS</u>, Appelbaum FR, McDonald GB, Singer JW. Prevalence of clinically relevant bacteremia following upper gastrointestinal endoscopy in bone marrow transplant recipients. *Am J Med.* 1990 89(2):134-136.
- 15. Russell KJ, Boileau MA, <u>Higano CS</u>, Collins C, Russell AH, Koh WJ, Cole SB, Chapman WH, Griffin TW. Combined 5fluorouracil and irradiation for transitional cell carcinoma of the urinary bladder. *Int J Radiat Oncol Biol Phys.* 1990 19(3):693-699.
- 16. Abdel-Nabi HH, Schwartz AN, Wechter DG, <u>Higano CS</u>, Ortman-Nabi JA, Unger MW. Scintigraphic detection of gastric and pancreatic carcinomas with In-111 ZCE 025 monoclonal antibody. *World J Surg.* 1991 15(1):122-127.
- 17. Nemunaitis J, Buckner CD, Appelbaum FR, <u>Higano CS</u>, Mori M, Bianco J, Epstein C, Lipani J, Hansen J, Storb R, et al. Phase I/II trial of recombinant human granulocyte-macrophage colony-stimulating factor following allogeneic bone marrow transplantation. *Blood.* 1991 77(9):2065-2071.
- 18. <u>Higano CS</u>, Crowley J, Livingston RB, Goodwin JW, Barlogie B, Stuckey WJ. A weekly cisplatin-based induction regimen for extensive non-small cell lung cancer. A Southwest Oncology Group study. *Cancer.* 1991 67(10):2439-2442.
- Nemunaitis J, Meyers JD, Buckner CD, Shannon-Dorcy K, Mori M, Shulman H, Bianco JA, <u>Higano CS</u>, Groves E, Storb R, Hansen J, Appelbaum FR, Singer JW. Phase I trial of recombinant human macrophage colony-stimulating factor in patients with invasive fungal infections. *Blood.* 1991 78(4):907-913.
- 20. <u>Higano CS</u>, Goodman P, Craig JB, Kish JA, Rivkin SE, Wolf M, Crawford ED. Phase II evaluation of amonafide in renal cell carcinoma. A Southwest Oncology Group study. *Invest New Drugs*. 1991 9(4):361-363.
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HIGANO SUPPORT

GRANTS - Current

PCF Challenge Award (Febbo/Higano)

Prostate Cancer Foundation

09/01/2011 - 07/31/2019

Howard R Soule, PhD | 1250 Fourth St | Santa Monica, CA 90401

A Pilot Study of the Effects of Cabozantinib (XL184) on Bone Turnover and the Microenvironment in Men with Non-Metastatic and Metastatic Castration-Resistant Prostate Cancer

The primary goal is to assess the impact of cabozantinib on markers of bone turnover and microenvironment in men with no evidence of bone metastases.

Role: Co-PI

W81XH-16-PCRP-CCRSA (Higano)

DOD Prostate Cancer Research Program

USA Med Research Acq Activity I Dana Herndon I 820 Chandler St

Fort Detrick, MD 21702-5014

Prostate Cancer Clinical Trials Consortium – Member Site

The Department of Defense provides funding for infrastructure to participate as a clinical site in the Prostate Cancer Clinical Trials Consortium.

Role: Clinical Site PI

D2017-1893 Movember Discovery Grant (Brotto)

Prostate Cancer Canada

Stuart Edmonds | 2 Lombard St 3rd Flr | Toronto, ON M5C 1M1

Innovations in the treatment of sexual dysfunction and couple intimacy after prostate cancer: A randomized trial of mindfulness versus cognitive behavioural therapy.

09/30/2017 - 09/29/2020

01/01/2017 - 06/30/2019

Role: Co-PI

GRANTS - Pending

CCSG Early Phase Clinical Research Support Grant (Higano)

Seattle Translational Tumor Research (NCI P30 CA015704-41)

Heidi Tham | 1100 Fairview Ave N | Seattle, WA 98109

Mechanisms of Metabolic and Hormone Action on Plaque Formation in Brain and Carotid Vessels in Men Undergoing Androgen Deprivation Therapy

The primary goal is to measure the impact of androgen deprivation on metabolic, brain and cardiovascular endpoints. Role: PI

CLINICAL TRIAL CONTRACTS - Current

Protocol # MDV3100-03 (Higano)

Medivation, Inc.

Alicia Tyson | 201 Spear St, 3rd fl | San Francisco, CA 94105

PREVAIL: A Multinational Phase 3, Randomized, Double-Blind, Placebo-Controlled Efficacy and Safety Study of Oral MDV3100 in Chemotherapy-Naïve Patients with Progressive Metastatic Prostate Cancer who have Failed Androgen Deprivation Therapy.

The primary goals are to determine the benefit of MDV3100 as compared to placebo as assessed by overall survival, and to determine the benefit of MDV3100 as compared to placebo as assessed by radiographic progression-free survival (rPFS).

Role: Site PI

Protocol # MDV3100-09 (Higano)

Medivation, Inc

Lynn Bui, MD | 525 Market St, 36th fl | San Francisco, CA 94105

STRIVE: A Mulitcenter Phase 2, Randomized, Double-Blind, Efficacy and Safety Study of Enzalutamide vs. Bicalutamide in Men with Prostate Cancer Who Have Failed Primary Androgen Deprivation Therapy

The primary goal is to determine the benefit of enzalutamide (formerly MDV3100) as compared to bicalutamide as assessed by progression-free survival (PFS).

Role: Site PI

Protocol # ARN-509-002 (Higano)

Aragon Pharmaceuticals, Inc

Rich Heyman | 12780 El Camino Real #301 | San Diego, CA 92130

The Role of Highly Selective Androgen Receptor (AR) Targeted Therapy in Men with Biochemically Relapsed Hormone Sensitive Prostate Cancer

The primary goals are to compare the mean change in QOL as measured by total FACT-P score after 12 months of therapy with ARN-509 monotherapy compared with LHRHa monotherapy in men with BCR, and; to compare the mean change in QOL as measured by total FACT-P score after 12 months of therapy of ARN-509 + LHRHa vs. LHRHa monotherapy in men with BCR.

Role: Site PI

Protocol # D4620C00001 (Higano)

AstraZeneca AB

1800 Concord Pike | Wilmington, DE 19850

A Phase I, Open-label, Multicentre Study to Assess the Safety, Tolerability, Pharmacokinetics and Preliminary Anti-tumor Activity of Ascending Doses of AZD8186 in Patients with Advanced Castrate-resistant Prostate Cancer (CRPC), Squamous Non-Small Cell Lung Cancer (sqNSCLC), Triple Negative Breast Cancer (TNBC) and Patients with Known PTEN-deficient Advanced Solid Malignancies, with Expansion to Assess the Pharmacodynamic Activity of AZD8186 within Prospectivelyvalidated PTEN-deficient Tumors

02/15/2013 - 12/31/2018

11/06/2012 - 10/31/2018



11/00/2012 - 10/31/2018

02/15/2011 - 09/30/2018

The primary goal is to investigate the safety and tolerability of AZD8186 when given orally to patients with advanced castrate-resistant prostate cancer (CRPC), squamous non-small cell lung cancer (NSCLC) and triple negative breast

cancer (TNBC) and known PTEN-deficient advanced solid malignancies. Role: Site PI

Protocol # ARN-509-003 (Higano)

Aragon Pharmaceuticals, Inc

Rich Heyman | 12780 El Camino Real #301 | San Diego, CA 92130

A Multicenter Randomized, Double-Blind, Placebo-Controlled, Phase III Study of ARN-509 in Men with Non-Metastatic (M0) Castration-Resistant Prostate Cancer

The primary goal is to demonstrate superiority in the metastasis-free survival (MFS) of men with high risk NM-CRPC treated with ARN-509 versus placebo.

Role: Site PI

Protocol # 15396 (Higano)

Bayer Health Care Montville, NJ

A phase III randomized, double-blind, placebo-controlled trial of Radium-223 dichloride in combination with abiraterone acetate and prednisone/ prednisone in the treatment of asymptomatic or mildly symptomatic chemotherapy-naïve subjects with bone predominant metastatic castration-resistant prostate cancer (CRPC)

The primary goal is to compare, in subjects with asymptomatic or mildly symptomatic chemotherapy-naïve bone predominant metastatic castration-resistant prostate cancer, the clinical benefit of radium-223 dichloride versus placebo in combination with abiraterone and prednisone/prednisolone.

Role: Global PI/Site PI

Protocol # 16544 (Higano)

Bayer Health Care Montville, NJ

- A Randomized Open-Label Phase IIa Study Evaluating the Efficacy and Safety of Radium-223 Dichloride in Combination with Abiraterone Acetate or Enzalutamide in Subjects with Castration Resistant Prostate Cancer (CRPC) who have Bone Metastases
- The primary goal is to describe radiological progression free survival (rPFS) in subjects treated with radium-223 dichloride 50 kBq/kg administered every 4 weeks; radium-223 dichloride 50 kBq/kg administered every 4 weeks together with abiraterone acetate 1000 mg orally daily plus prednisone orally twice daily (bid); or radium-223 dichloride 50 kBq/kg administered every 4 weeks together with enzalutamide 160 mg orally daily.

Role: Site PI

Protocol # 401 (Higano)

Emergent BioSolutions Seattle, WA

A Phase 1 Study of ES414 in Patients with Metastatic Castration-Resistant Prostate Cancer

The primary goal is to identify the maximum tolerated dose and determine clinical activity of ES414 in patients with mCRPC that have not received prior chemotherapy.

Role: Site PI

Protocol # 16913 (Higano)

Bayer Health Care

Kelly Peters I Katnar Health, LLC I 11960 Westline Industrial Dr, Ste 180 I St. Louis, MO 63149

REASSURE – Radium-223 alpha Emitter Agent in Safety Study in mCRPC population for long-term evaluation

The primary goal is to assess the incidence of second primary malignancies among patients with metastatic Castration Resistant Prostate Cancer (mCRPC) receiving Radium-223 in routine clinical practice.

Role: Site PI

Protocol # B7791001 (Higano) Pfizer

Celestia S. Higano, MD, FACP Curriculum Vitae - Continued, page 53

04/18/2016 - 04/30/2019

12/18/2014 - 12/31/2019

09/17/2014 - 09/16/2019

01/12/2014 - 12/31/2018

<u>12/03/201</u>4 - 03/01/2019

03/16/2016 - 02/29/2024

Megan Shannon I 235 East 42nd Street I New York, NY 10017

- A Phase 1 Study to Evaluate the Safety, Pharmacokinetics and Pharmacodynamics of Escalating Doses of a Vaccine-based Immunotherapy Regimen (VBIR) for Prostate Cancer (PF-06753512)
- The primary goal is to assess safety and tolerability of increasing dose levels of the prostate cancer vaccine-based immunotherapy regimen (PrCa VBIR) components.

Role: Site PI

Protocol # B030013 (Higano)

Hoffman LaRoche

Prasanna Bhende I Covance I 206 Carnegie Center I Princeton, NJ 08540

- A Phase IB, Open-Label Study of the Safety and Tolerability of Atezolizumab in Comination with Radium-223 Dichloride in Patients with Castrate-Resistant Prostate Cancer Who Have Progressed Following Treatment with an Androgen Pathway Inhibitor
- The primary goals are to assess the safety and tolerability of atezolizumab when given in combination with radium-223 dichloride in patients with mCRPC and to identify a recommended treatment schedule.

Protocol # 9785-CL-0123 (Higano)

Astellas Pharma Global Development, Inc

Courtney Paul (INC Research) | 4800 Falls of Neuse Rd, Suite 600 | Raleigh, NC 27609

- A Phase 2 Open-label Extension Study for Subjects With Prostate Cancer Who Previously Participated in an Enzalutamide Clinical Study
- The primary goal of the study is to provide access to continued treatment for subjects who are currently participating in an enzalutamide clinical study, sponsored by Astellas or Medivation, for their prostate cancer and who are continuing to derive clinical benefit based on the assessment of the investigator.

CLINICAL TRIAL CONTRACTS - Pending

Protocol # CO-338-063 (Higano)

Clovis Oncology, Inc

Anthony Golsorkhi, MD | Clovis Oncology | San Francisco, CA

- TRITON3: A Multicenter, Randomized, Open-label Phase 3 Study of Rucaparib versus Physician's Choice of Therapy for Patients with Metastatic Castration-resistant Prostate Cancer Associated with Homologous Recombination Deficiency
- The primary goal of the study is to assess the efficacy of rucaparib versus physician's choice of treatment based on radiographic progression free survival (rPFS0 in mCRPC patients with HRD who progressed on prior AR-directed therapy and have not yet received chemotherapy in the castration-resistant setting.

Protocol # MDV3800-06 (Higano)

Medivation, Inc

Rena Ullum (Quintiles) | 4820 Emperor Blvd, Q Plaza Room 895E | Durham, NC 27703

- A Phase 2, Open-label, 2-Arm, Response Rate Study of Talazoparib in Men with DNA Repair Defects and Metastatic
 - Castration-Resistant Prostate Cancer who Previously Received Taxane-Based Chemotherapy and Progressed on at Least 1 Novel Hormonal Agent (Enzalutamide and/or Abiraterone Acetate/Prednisone)
- The primary goal of the study is to evaluate efficacy, as measured by best objective response rate (ORR).

Protocol # 000108 (Higano)

Ferring Pharmaceuticals

Ashley Underhill (IQVIA) | 4820 Emperor Blvd, Q Plaza Room 895E | Durham, NC 27703

- A Multi-Center, Randomized, Assessor-Blind, Controlled Trial Conparing the Occurrence of Major Adverse Cardiovascular Events (MACEs) in Patients with Prostate Cancer and Cardiovascular Disease Receiving Degarelix (GnRH Receptor Antagonist) or Leuprolide (GnRH Receptor Agonist)
- The primary goal of the study is to assess the effect of a GnRH receptor antagonist on the risk of occurrents of MACEs as compared to GnRH receptor agonist in patients with prostate cancer and cardiovascular disease.

Protocol # 18-150 (Higano)

Memorial Sloan Kettering Cancer Center/Bayer Pharmaceuticals Melanie Chen (MSKCC) | 1275 York Ave | New York, NY 10065

03/16/2017-03/15/2022

03/20/2017 - 05/31/2022

Phase III Trial of Docetaxel vs. Docetaxel and Radium-223 for Metastatic Castration-Resistant Prostate Cancer (mCRPC).

The primary goal of the study is to compare overall survival for subjects treated with docetaxel versus subjects treated with docetaxel plus radium-223.

Protocol # eFT508-0009 (Higano)

eFFECTOR Therapeutics

Angela White (Medpace) | 5375 Medpace Way | Cincinnati, OH 45240

A Phase 2 Non-randomized Open-label Study Examining the Effect of eFT508 in Patients with Advanced Castrate-resistant Prostate Cancer (CRPC).

The primary goal of the study is to assess the anti-tumor response of eFT508 in advanced CRPC.

GRANTS - Prior

W81XWH-09-1-0144 (Higano)

DOD Prostate Cancer Research Program

USA Med Research Acg Activity

Dana Herndon | 820 Chandler St | Fort Detrick, MD 21702-5014

Prostate Cancer Clinical Trials Consortium - Member Site

The Department of Defense provides funding for infrastructure to participate as a clinical site in the Prostate Cancer Clinical Trials Consortium.

Role: Clinical Site PI

W81XWH-BAA-11-1 (Basch)

UNC-Chapel Hill (DoD flow through)

Mark Kramer | 450 West Drive, CB 7295 | Chapel Hill, NC 27599

DOD Prostate Cancer Research Program: Observational Longitudinal Study of Pain in Men with Metastatic Castrate-**Resistant Prostate Cancer**

The primary goal is to estimate the proportion of pain palliation responders and the proportion experiencing pain progression as measured by items from the Brief Pain Inventory (BPI) among patients with metastatic castrate-resistant prostate cancer starting systemic therapy. Role: Site PI

W81XWH-09-1-0144 (Higano)

DOD Prostate Cancer Research Program

USA Med Research Acq Activity | Dana Herndon | 820 Chandler St

Fort Detrick, MD 21702-5014

Prostate Cancer Clinical Trials Consortium - Member Site

The Department of Defense provides funding for infrastructure to participate as a clinical site in the Prostate Cancer Clinical Trials Consortium.

Role: Clinical Site PI

U19 AT-006028-03 (Standish)

Bastyr/UW Oncomycology Research Center

Bastyr University | Marie Kirkman | 14500 Juanita Dr NE, Room 459 | Seattle, WA 98028-4966 Project 2 (Higano/Wenner):

Enhancing innate immunity by combining PSK with docetaxel in prostate cancer

The primary goal of this phase 1 study is to establish the MTD of PSK alone and in combination with docetaxel and to study the immune effects of each alone and in combination.

Role: Project 2 Co-PI

R01 CA 120933 (Cherrier)

NIH/NCI

Assessment of Cognitive and Mood Effects from ADT in Men with Prostate Cancer The primary goal of this project is to assess the affects of androgen deprivation therapy on mood, information processing, and quality of life

08/07/2007-5/31/2013

04/01/2009-12/31/2014

Celestia S. Higano, MD, FACP Curriculum Vitae - Continued, page 55

11/06/2013 - 2/28/2017

09/29/2010-08/31/2013

12/25/2014 - 09/29/2017

Role: Co-Investigator

P50 CA 097186-06 (Nelson)

Fred Hutchinson Cancer Research Center (NIH/NCI flow through) Jill Lauson | 1100 Fairview Ave N | Seattle, WA 98109 Pacific Northwest Prostate Cancer SPORE Clinical Core D (Higano)

The major goals of this project are to design and execute clinical trials relevant to SPORE projects, to support and enhance the CAISIS clinical data repository, and to support and engage the SPORE Advocacy Committee in SPORE activities in the Pacific Northwest.

Role: Director Clinical Core D

P50 CA 097186 (Lange)

NIH/NCI

Pacific Northwest Prostate Cancer Specialized Program of Research Excellence (SPORE)

The main goal of this project is to understand the molecular biology of prostate cancer through all stages of its progression. Focus will be on analyzing gene and protein expression in the entire spectrum of prostate tumors, from those clinically localized and slow-growing to those advance and highly aggressive. The major goals of Core E are to establish a unified database to serve as a clinical data repository, design and execute clinical trials relevant to SPORE projects, and to support and engage the SPORE Advocacy Committee in SPORE activities in the Pacific Northwest.

Role: Co-investigator and Director Clinical Core E (Higano)

CLINICAL TRIAL CONTRACTS - Prior

Protocol # S-3100-1-01 (Higano)

Medivation, Inc.

Herb Waddell | 55 Hawthorne Street | San Francisco, CA 94105

- A Phase I Open-Label Dose-Escalation Safety and Pharmacokinetic Study of MDV3100 in Patients with Castration-Resistant **Prostate Cancer**
- The primary goal is to determine the safety and tolerability profile of MDV3100, including the dose-limiting toxicities (DLTs), and the maximum tolerated dose (MTD; if possible) when administered orally to subjects with castrationresistant prostate cancer.

Role: Site PI

Protocol # P10-3 (Higano)

Dendreon Corporation

Mark Frohlich, MD/Chief Medical Officer | 1301 2nd Ave, Ste 3200 | Seattle, WA 98101

A Registry of Sipuleucel-T Therapy in Men with Advanced Prostate Cancer

The primary goal is to further quantify the risk of cerebrovascular events (CVEs) following sipuleucel-T therapy for all subjects.

Role: Site PI, Member Steering Committee

Protocol # DST4964g (Higano)

Genentech, Inc

Daniel Maslyar | 1 DNA Way | South San Francisco, CA 94080

A Phase I, Open-Label Study of the Safety and Pharmacokinetics of Escalating Doses of DSTP3086S in Patients with Metastatic Castration-Resistant Prostate Cancer.

The primary goals are to evaluate the safety and tolerability of every-3-week administration and of weekly administration of DSTP3086S to patients with CRPC, and; to determine the maximum tolerated dose (MTD) and dose-limiting toxicities (DLTs) of every-3-week administration and of weekly administration of DSTP3086S to patients with CRPC, and; to identify the recommended Phase II dose of every-3-week administration and of weekly administration of DSTP3086S (at or below the MTD) in patients with CRPC.

Role: Site PI

Celestia S. Higano, MD, FACP Curriculum Vitae - Continued, page 56

06/27/2007-05/31/2018

06/01/2012 - 03/31/2017

04/25/2012 - 07/31/2017





09/01/02-08/31/07

Protocol # BC1-10 (Higano)

Algeta ASA

Kari Lyseng | Kjelsaveien 172 A | NO 0411 Oslo | NORWAY

A Phase I/IIa Study of Safety and Efficacy of Alpharadin with Docetaxel in Patients with Bone Metastases from Castration-**Resistant Prostate Cancer**

The primary goals are to establish a recommended dose of Alpharadin to be used with docetaxel, and; to investigate safety and explore efficacy of the recommended dose of Alpharadin used with the standard treatment regimen of docetaxel in patients with bone metastases from castration resistant prostate cancer, and; to evaluate the feasibility of patient self-reporting of pain intensity and analgesic use via an interactive voice response (IVR) system.

Role: Site PI, member phase 1 working group

Protocol # P07-2 (Higano)

Dendreon Corporation

Jovine Umail | 1301 Second Ave, Ste 3200 | Seattle, WA 98101

A Randomized, Multicenter, Single Blind Study in Men with Metastatic Androgen Independent Prostate Cancer to Evaluate Sipuleucel-T Manufactured with Different Concentrations of PA2024 Antigen

The primary goal is to compare the cumulative CD54 upregulation ratio between each of the cohorts. Role: Site PI

Protocol # ARN-509-001 (Higano)

Aragon Pharmaceuticals, Inc

Rich Heyman | 12780 El Camino Real #301 | San Diego, CA 92130

An Open-Label, Phase 1/2 Safety, Pharmacokinetic, and Proof-of-Concept Study of ARN-509 in Patients with Progressive Metastatic Castration-Resistant Prostate Cancer

The primary goal of Phase 1 is to assess the safety of ARN-509 in patients with progressive advanced castration-resistant prostate cancer (CRPC), and determine the maximum tolerated dose (MTD) and/or recommended Phase 2 dose (RP2D) of ARN-509 that leads to a dose limiting toxicity (DLT) in a maximum of 30% of patients.

The primary goal of Phase 2 is to determine PSA response at 12 weeks according to PCWG2 criteria. Role: Site PI

Protocol # XRP6258-CABAZL06056 (Higano)

Sanofi US Services Inc

Debra Dawson | 55 Corporate Drive | Bridgewater, NJ 08807

Phase II Trial to Evaluate Benefit of Early Switch from First-Line Docetaxel/Prednisone to Cabazitaxel/Prednisone and the Opposite Sequence, Exploring Molecular Markers and Mechanisms of Taxane Resistance in Men with Metastatic Castration-Resistant Prostate Cancer (mCRPC) Who Have Not Received Prior Chemotherapy

The primary goal is to explore the benefit of an early switch from docetaxel/prednisone to cabazitaxel/ prednisone in men with mCRPC who do not achieve _30% prostate-specific antigen (PSA) decline from baseline by cycle 4 with the initial docetaxel treatment (in comparison with historical control of patients who were treated with docetaxel and did not switch).

Role: Site PI

Protocol # P11-4 (Higano)

Dendreon Corporation Mark Frohlich, MD/Chief Medical Officer | 1301 2nd Ave, Ste 3200 | Seattle, WA 98101 Immune Monitoring Protocol in Men with Prostate Cancer Enrolled in a Clinical Trial of Sipuleucel-T The primary goal is to evaluate the immune response induced by sipuleuceI-T. Role: Site PI

Protocol # C14009 (Higano)

Millennium Pharmaceuticals, Inc.

Laurie LoBue | 40 Landsdowne Street | Cambridge, MA 02139

A Randomized Phase 2 Study of Docetaxel/Prednisone with or without MLN8237, a Novel Aurora A Kinase Inhibitor, in Patients with Castration-Resistant Prostate Cancer Preceded by a Phase 1 Dose-Escalation

08/18/2010 - 03/31/2015

<u>1</u>2/23/2013 - 01/29/2016

11/01/2011 - 01/28/2016

09/10/2010 - 05/31/2016

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09/06/2012 - 04/14/2015

07/30/2012 - 09/30/2016

The primary goals are to assess the safety and tolerability of MLN8237 administered in patients with solid tumors, including patients with CRPC who are eligible to receive treatment with docetaxel and to determine the recommended dose and

schedule of the combination regimen of MLN8237 and docetaxel applicable to future development in phase 2 studies. Role: Site PI

Protocol # OGX-011-11 (Higano)

Teva Pharmaceutical Industries

Shawn T Conahan, PhD | 425 Privet Road | PO Box 1005 | Horsham, PA 19044-8005

A Randomized Phase 3 Study Comparing Standard First-Line Docetaxel/Prednisone to Docetaxel/Prednisone in Combination with Custirsen (OGX-011) in Men with Metastatic Castrate Resistant Prostate Cancer

The primary goal is to ascertain whether the survival time distribution for patients randomized to the investigational arm is consistent with longer survival as compared to patients randomized to the control arm.

Role: International Co-PI

Protocol # OGX-11-11 CTC (Higano)

Teva Pharmaceutical Industries, Ltd

Finance Manager – R&D Division | Industrial Zone, Kiryat Nordau | Netanya | ISRAEL Enumeration of Circulating Tumour Cells in Patients Enrolled in Protocol OGX-011-11

The primary goals are to enumerate CTC5 at baseline and cycle 2 and 4 in CRPC patients enrolled to Study Protocol OGX-

O11-11, and; to demonstrate that the addition of OGX-O1 1 increases the frequency and magnitude of CTC count falls, and; to confirm that CTC count falls associate with overall survival benefit meeting criteria for surrogacy. Role: Site PI

Protocol #XL 184-203 (Higano)

Exelixis, Inc.

Pamela A Simonton | 170 Harbor Way | PO Box 511 | South San Francisco, CA 94083-0511

A Randomized Discontinuation Study of XL 184 Subjects with Advanced Solid Tumors The primary goal is to evaluate the efficacy of cabozantinib (XL184) in subjects with advanced solid tumors Role: Site PI

Protocol # OGX-011-11SP (Higano)

Teva Pharmaceutical Industries, Ltd

Shawn T Conahan, PhD | 425 Privet Road | PO Box 1005 | Horsha, PA 19044-8005

Pharmacokinetic and Cardiac Monitoring Study Supplement to Protocol OGX-011-11: A Randomized Phase 3 Study Comparing Standard First-Line Docetaxel/Prednisone to Docetaxel/Prednisone in Combination with Custirsen (OGX-011) in Men with Metastatic Castrate Resistant Prostate Cancer

The primary goals are to determine if custirsen alone or if co-administered with docetaxel alters ECG intervals and morphology with special emphasis on changes in the QTcF interval duration, and; to explore if co-administration of docetaxel and custirsen alters the pharmacokinetics of custirsen, and; to explore if co-administration of docetaxel and custirsen alters the pharmacokinetics of docetaxel, and; to explore the urinary metabolites of custirsen. Role: Site PI

Protocol # OGX-011-10 (Higano)

OncoGenex Technologies

Scott Cormack | 400-1001 West Broadway | Vancouver, BC V6H 4B1 | CANADA

- A Randomized, Placebo-Controlled, Double-Blind, Phase 3 Study Evaluating the Clinical Benefit of Adding Custirsen to Docetaxel Retreatment/Prednisone as an Option for Second-Line Therapy in Men with Castrate Resistant Prostate Cancer.
- The primary goal is to ascertain whether the investigational arm has a greater proportion of patients with durable pain palliation as compared to the control arm.

Role: Site PI

Protocol # CC 055511 (Higano)

University of California San Francisco Alice Chin | 1600 Divisadero St, Box 1770 | San Francisco, CA 94115 06/18/2008 - 12/31/2012

05/06/2011 - 05/06/2014

04/16/2012 - 04/15/2013

11/01/2010 - 04/04/2013

08/04/2011 - 12/31/2014

01/19/2012 - 11/3/2014

A Randomized Phase II Study of Intermittent Chemotherapy or Intermittent Chemotherapy with Maintenance GM-CSF in Patients with Previously Untreated Metastatic Hormone Refractory Prostate Cancer

The primary goal is to determine time to disease progression while receiving chemotherapy (i.e. time to chemotherapy resistance) for both arms (intermittent docetaxel/prednisone with or without maintenance GM-CSF).

Role: Site Pl

Protocol # CURC/CUOG AVIAS-0601 (Higano)

Canadian Urology Research Consortium

Patty Djan | Sunnybrook and Women's College Health Sciences Centre | 2075 Bayview Avenue, Ste A3 04 | Toronto, ON M4N 3M5 | CANADA

Multicentre, Double-Blind Study Ccomparing 0.5mg Dutasteride vs Placebo Daily in Men Receiving Intermittent Androgen Ablation Therapy for Prostate Cancer

The primary goal is to assess the effect of therapy with repeat oral once daily dosing of dutasteride 0.5mg on the length of the off treatment interval in men receiving intermittent androgen ablation therapy for localized prostate cancer. Role: Site PI

Protocol # CRPC2 (Higano)

Medivation, Inc.

Contract Administration | 201 Spear St, 3rd fl | San Francisco, CA 94105

A Multinational Phase 3, Randomized, Double-Blind, Placebo-Controlled Efficacy and Safety Study of Oral MDV3100 in Patients with Progressive Castration-Resistant Prostate Cancer Previously Treated with Docetaxel-Based Chemotherapy The primary goal is to determine the benefit of MDV3100 as compared to placebo as assessed by overall survival. Role: Site PI

Protocol # IMCL CP13-0603 (Higano)

ImClone Systems, Inc.

John Blanchette | 33 ImClone Dr | Branchburg, NJ 08876

Phase II Single Arm, Open-Label Study of IMC-A12 in Asymptomatic, Chemotherapy-Naïve Patients with Metastatic Androgen-Independent Prostate Cancer.

The primary goals are to determine the composite time to disease progression for chemotherapy-naive patients with asymptomatic, metastatic and rogen-independent prostate cancer (AIPC) treated with IMC-A12 every other week, and; to determine the safety and pharmacokinetic profile of IMC-A12 administered at a dose of 20 mg/kg every 3 weeks in chemotherapy-naive patients with asymptomatic, metastatic AIPC.

Role: Site PI

Protocol #IMCL CP18-0601A (Higano)

ImClone Systems, Inc.

Clinical Affairs Department | 33 ImClone Dr | Branchburg, NJ 08876

A Phase 2, Multicenter, Randomized Study of IMC-A12 or IMC-1121B plus Mitoxantrone and Prednisone in Metastatic Androgen-Independent Prostate Cancer Following Disease Progression on Docetaxel-Based Chemotherapy

The primary goal is to determine a composite progression-free survival (PFS) associated with the treatment regimen in each arm of the study.

Role: Site PI

Protocol # CMCS110A2101 (Higano)

Novartis

Wanda Ruiz, PhD | 59 Route 10 | East Hanover, NJ 07936-1080

A Phase I/II Open-Label Study to Assess the Safety, Tolerability, Pharmacokinetics and Pharmacodynamics of MCS110 in Patients with Prostate Cancer and Bone Metastases

The primary goal of the dose escalation phase is to determine the maximum-tolerated dose (MTD) or optimal biological dose (OBD) and to characterize dose limiting toxicity (DLT) of escalating doses of MCS110 administered as an IV infusion every 2 weeks on a 28-day cycle in patients with asymptomatic castrate-resistant prostate cancer with bone metastases who have not received any bisphosphonates in the 12 months prior to enrollment.

The primary goal of the dose expansion phase is to assess the effect of MCS110 administered as an IV infusion every 2 weeks on a 28-day cycle on bone resorption marker uNTx in patients with asymptomatic castrate-resistant prostate cancer with bone metastases who have not received any bisphosphonates in the 12 months prior to enrollment.

07/19/2007 - 06/30/2012

12/04/2008 - 06/17/2012

12/16/09 - 8/30/2012



04/05/2007 - 11/30/2012

Role: Site PI

Protocol # IMCL CP13-0501 (Higano)

ImClone Systems, Inc

Tom Perone | 33 ImClone Dr | Branchburg, NJ 08876

with Advanced Solid Tumors

antibody IMC-A12 administered weekly in patients with advanced solid tumors who no longer respond to standard therapy or for whom no standard therapy is available.

Protocol # AURA-6202-007 (Higano)

Nerviano Medical Sciences

Elma Ravizza | Viale Pasteur 10 | 20014 Nerviano (MI) | ITALY

A Phase II Study of PHA-739358 in Patients with Metastatic Hormone Refractory Prostate Cancer

- The primary goal is to assess the antitumor activity of PHA-739358 administered as IV infusion according to two different dose schedules in metastatic HRPC patients progressing on standard, docetaxel-based, 1st-line chemotherapy for HRPC
 - based on PSA response rate and to select the best dose schedule for further investigation.

Role: Site PI

Protocol # AMG 102-20070611 (Higano)

Amgen, Inc

Maria Earle | One Amgen Center Drive, MS 28-1-A | Thousand Oaks, CA 91320

- A Phase 1b/2 Study to Assess the Safety and Efficacy of AMG 102 in Combination with Mitoxantrone and Prednisone in Subjects with Previously Treated Castrate Resistant Prostate Cancer
- The primary goal is to identify safe dose levels of AMG 102, up to 15 mg/kg Q3W, to combine with mitoxantrone and prednisone (MP).

Role: Site PI

Protocol # MDX010-21 (Higano)

Medarex, Inc

Project Manager | 519 Route 173 West | Bloomsbury, NJ 08804

- A Phase I/II, Open-Label, Dose-Escalation Study of MDX-010 Administered Every 3 Weeks for 4 Doses in Patients with Metastatic Hormone-Refractory Prostate Cancer
- The primary goal is to determine the safety profile of escalating doses of MDX-010 (hereafter referred to as ipilimumab) with and without a single dose of focal radiotherapy administered every 3 weeks up to 4 times to patients with metastatic hormone-refractory prostate cancer (HRPC).

Role: Site PI

Protocol # D9902 (Higano)

Dendreon

Mark Frohlich, MD/Chief Medical Officer | 1301 2nd Ave, Ste 3200 | Seattle, WA 98101

- A Randomized, Double Blind, Placebo Controlled Phase 3 Trial of Immunotherapy with Autologous Antigen Presenting Cells Loaded With PA2024 (Provenge[®], APC8015) in Asymptomatic Subjects With Gleason Sum ≤ 7, Metastatic, Androgen Independent Prostatic Adenocarcinomas
- The primary goal is to assess the safety and efficacy of sipuleucel-T in prolonging survival of men with metastatic androgen independent prostate cancer.

Role: Site PI

Protocol # G-0029 (Higano)

Cell Genesys

Karen Peterson | 500 Forbes Blvd | South San Francisco, CA 94080

A Phase III Randomized, Open-Label Study of CG1940 and CG8711 Versus Docetaxel and Prednisone in Patients with Metastatic Hormone-Refractory Prostate Cancer who are Chemotherapy-Naïve

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10/01/2003 - 09/30/2010

11/01/2008 - 10/31/2011

02/01/2006 - 02/01/2011

02/01/2008 - 12/31/2011

A Phase 1 Study of Weekly Anti-Insulin-Like Growth Factor-1 Receptor (IGF-IR) Monoclonal Antibody IMC-A12 in Patients

The primary goal is to establish the safety profile and maximum tolerated dose (MTD) of the anti-IGF-IR monoclonal

Role: Site PI

08/19/2005 - 12/31/2011

08/15/2005 - 08/31/2010

The primary goal is to compare the duration of survival between the two treatment arms. Role: Site PI

Protocol # APL-B-011-02 (Higano)

03/01/2006 - 02/28/2010

PharmaMar

Clementina Martinez | Avda. De los Reyes, 1 | Pol. Ind. La Mina-Norte | 28770-Colmenar Viejo | Madrid, Spain A Phase II, Multicenter, Open-Label, Clinical and Pharmacokinetic Study of Aplidin[®] as a 3-hour IV Infusion Every 2 Weeks, in Relapsing or Refractory Patients with Androgen-Independent Prostate Adenocarcinoma

The primary goal is to assess the anti-tumor activity of Aplidin[®] given intravenously over 3-hours every 2 weeks, in patients with castrate metastatic adenocarcinoma of the prostate that have relapsed or progressed after two previous lines of systemic therapy, considering biological agents or chemotherapy as systemic therapy and taking into account that patients must have received prior docetaxel-based chemotherapy.

Role: Site PI