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14. ABSTRACT
This project centers on creating a molecular framework of DCIS (ductal carcinoma in situ). DCIS is considered to be the precursor to Invasive Ductal Carcinoma (IDC), the most common form of breast cancer. IDC accounts for 80% of all breast cancers, predominantly affecting women aged 55 and older; however, at least a third of women with IDC are diagnosed before they reach 55. Not all patients with DCIS will develop IDC however, we are looking for ways to better predict those patients that need life-saving treatment, and separate these from those patients who are less at risk.

So far we have made over 1300 RNA libraries and 410 whole genome libraries and dissected material from 115 freshly frozen patient biopsies. The tissue included for RNA and DNA analysis DCIS, IDC, stroma adjacent to DCIS/IDC and normal tissue.

15. SUBJECT TERMS
DCIS, IDC, LCM, RNAseq, DNAseq, evolution

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A Molecular Framework for understanding DCIS

Award No. W81XWH-14-1-0110
Annual report year 3

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Introduction

This project centers on creating a molecular framework of DCIS (ductal carcinoma in situ). DCIS is considered to be the precursor to Invasive Ductal Carcinoma (IDC), the most common form of breast cancer. IDC accounts for 80% of all breast cancers, predominantly affecting women aged 55 and older; however, at least a third of women with IDC are diagnosed before they reach 55.

Utilizing a unique bank of frozen mammary biopsies, containing samples with DCIS alone, and a combination of DCIS and IDC, we have started to profile both DCIS and related tissue components. It is our aim to sample the ~300 biopsies, and compare both by RNA seq, and whole genome amplification, DCIS lesions, within, and between patients, and see how these may be correlated with IDC lesions. We also intend to look for changes in the stroma between those patients that present with IDC and those that do not. This work aims to identify characteristics that may be suggestive of a patients' likelihood of progressing from DCIS to IDC, with the purpose of reducing the need for over treatment for this disease.

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Keywords

Ductal carcinoma in situ, DCIS, Invasive ductal carcinoma, IDC, RNA, DNA, Copy number, Laser capture microscope, LCM

3.

Accomplishments

Aim 1. The evolution of DCIS.

Task 1. Sample collection and annotation

Annotation on the tissue bank is on going

Task 2. Sample choice from frozen bank.

We have received 146 samples from the frozen bank now and have processed 115 of these so far. These include pure DCIS and also mixed DCIS and IDC samples. We have selected samples that had 5 or more DCIS legions for this Aim as these will be more informative for looking at the evolution of DCIS. We are using both CNV profiles and SNPs (variants are called using the stromal tissue).

Task 3. Laser capture of frozen samples for characterization

From each of the 115 samples we have dissected material for DNA, however we have material from 18 patients for characterization (based on having 5 or more DCIS legions). We have selected DCIS legions, IDC regions, normal epithelium, where present, Athypical epithelium, Solid DCIS, papillary DCIS, benign epithelium, and stroma (as far away from DCIS or IDC regions as possible). The table below represents the distribution across patients, with a total of 214 legions including the normal and variants of epithelium.

Number of DCIS legions	Number of samples	Number of samples with IDC	Number of IDC legions per sample
5	4	2	4,4
6	7	3	8,2,4
7	6	3	5,7,5
8	1	0	
9	1	1	5
10	1	1	6
11	0	0	
12	0	0	
13	1	0	
Total	144	10	50

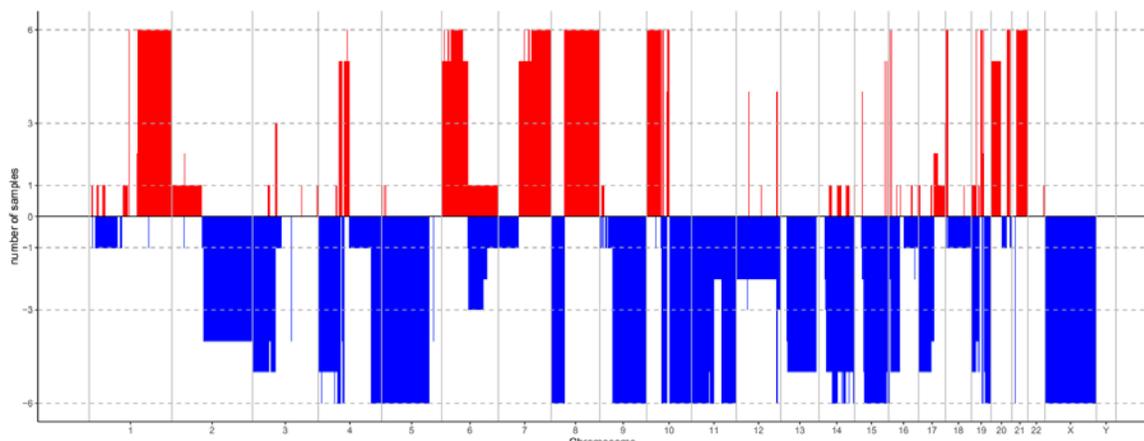
Task 4. Exome capture and sequencing

We initiated work on this using the Nextera Exome Capture kit, however on the couple of samples we used, this did not prove successful, as there was a very low distribution of probes represented. Having investigated the costs and what is needed to get deep enough coverage for accurately calling CNVs and SNVs, we decided to make use of the X10 sequencing machine at the NYGC and do whole genome sequencing instead. A trial run with this demonstrated that the Whole Genome Sequencing kit that we were using (and other kits on the market) was only compatible with sequencing machines after the DNA had been sheared (resulting in removal of end primers). This was not efficient with sequencing on the X10, as reads are generally longer and shearing would result in very short reads. We therefore established a new protocol, where by we enzymatically chewed the primers off the ends of DNA strands after amplification with the WGA kit, this then allowed us to attach the primers for sequencing (this was somehow hindered without removal of the WGA primers). This pipeline proved very effective and in addition to the 18 patients we selected for the evolution study, we have also sequenced an additional 40 patients, making a total of 59 patients. This amounts to 410 DNA X10 libraries, comprising of 81 IDC, 201 DCIS, 69 stroma and the remainder of normal epithelium, atypia and benign epithelium.

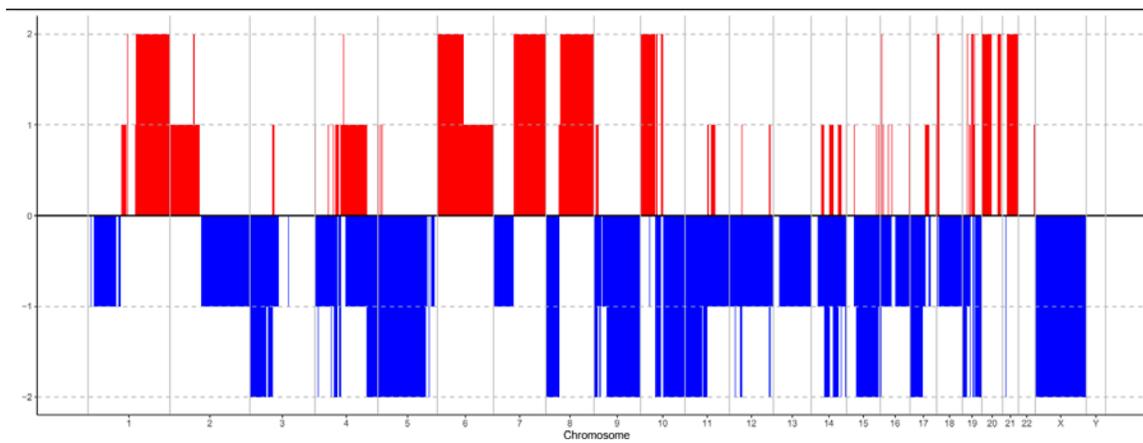
Task 5. Analyze Exome capture data

The final submission of libraries for X10 sequencing is still being processed however all 410 libraries should have been processed within a week or two. We run a few quality control analyses on the samples once they have gone through a standard pipeline (this is done by the NYGC). Concordance analysis looks for any discrepancies between a "normal" sample and its paired "tumor" sample. Pairs generally have over 90% concordance, however this analysis has proved useful as it identified a misread tube label and thus allows us to correct such errors. Where samples have a low concordance that can not be corrected easily (ie. We have no other way to identify a mis labeled sample) they are unfortunately put to one side for the time being. We also run analyses for "contamination" this could be from the tissue, or from other samples in the library prep. It is likely that the lower the quality or quantity then the higher the effects of any contamination are likely to be. Samples with very low coverage are also put to one side. After removing samples with low concordance, low contamination and low sequencing coverage we currently have data from 17 patients and 165 libraries (We are still waiting on analysis on an additional ~100 samples and ~37 patients).

Initial analysis on CNV data has been carried out on 11 patients thus far and shows that there are both similarities and differences to be seen between DCIS lesions within the same patient. An example for one patient is below. The plot shows CNVs that are located among the 6 DCIS samples from this patient. You can see that some are shared by all 6 samples (sample number on the Y axis, chromosome number along the X axis) and some are unique to just one or two samples.

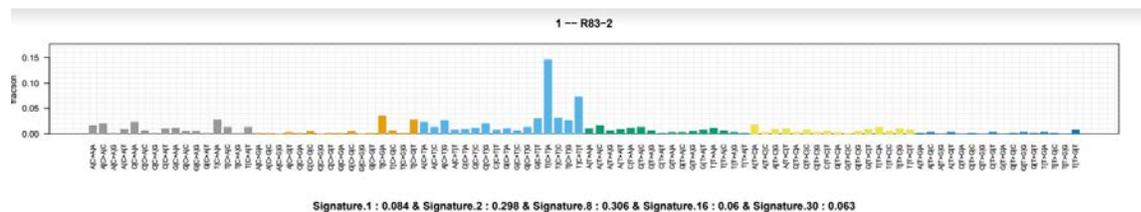


The plot below shows the CNVs that are shared or unique between the DCIS and the IDC of this same patient. The X axis represents a shared region (1 is the CNV is located in only a dcis sample, or just an IDC sample, 2 is that the cnv is found in both an IDC sample and a dcis sample).



We are currently working on constructing phylogenetic trees using the program LICHEE, using the SNVs. The trees are fairly complex so we are working on creating a simpler/ singular tree using only regions of 2N as determined by the CNV profiles. We have also worked out a confidence cut off for the SNVs based on the number of reads per SNV and the VAF number. We have made this fairly stringent to minimize “noise”.

In addition to this we have carried out work on the mutational signatures of these samples to look for characteristic signature patterns. We have found so far a couple of patients with the APOBEC signature, see figure below.



Further, more indepth analysis will be carried out on the phylogeny of the DCIS and IDC legions and if there are any associations between the differences we see in the DNA data and the differences we see in the RNA data. This is being carried out together with the bioinformaticians at the NYGC and we will seek further analysis from groups here at Cambridge who specialize in tumor evolution.

Aim 2. A transcriptional landscape of early breast cancer.

Task 6. Sample choice from frozen bank.

- choose samples for pure DCIS and DCIS with microinvasion/IDC

Task 7. Laser capture of frozen samples for characterization

We have received 146 samples from the frozen bank now and have processed 115 of these so far. For each sample the following regions are annotated by Joe (the pathologist) and dissected in triplicate for RNA: DCIS, IDC, normal epithelium, Athypical epithelium, Solid DCIS, papillary DCIS, benign epithelium, areas of high immune infiltration, stroma adjacent to DCIS, stroma adjacent to IDC and stroma away (as far away from DCIS or IDC regions as possible). This has provided over 6300 legions. This Task is still on going.

Task 8. RNAseq library construction

Approximately 1300 RNA seq libraries have been sequenced. Currently we have been focusing on DCIS and IDC and normal and other epithelium and are prioritizing these for sequencing now. This task is still on going.

Task 9. Analyze RNAseq datasets

Thus far we have analyzed 1200 DCIS, IDC, benign/normal epithelium and stroma away libraries. For quality control samples with a Gene Assignment of $< 15\%$ with % of Uniquely mapped reads < 20 , are removed from the group analysis.

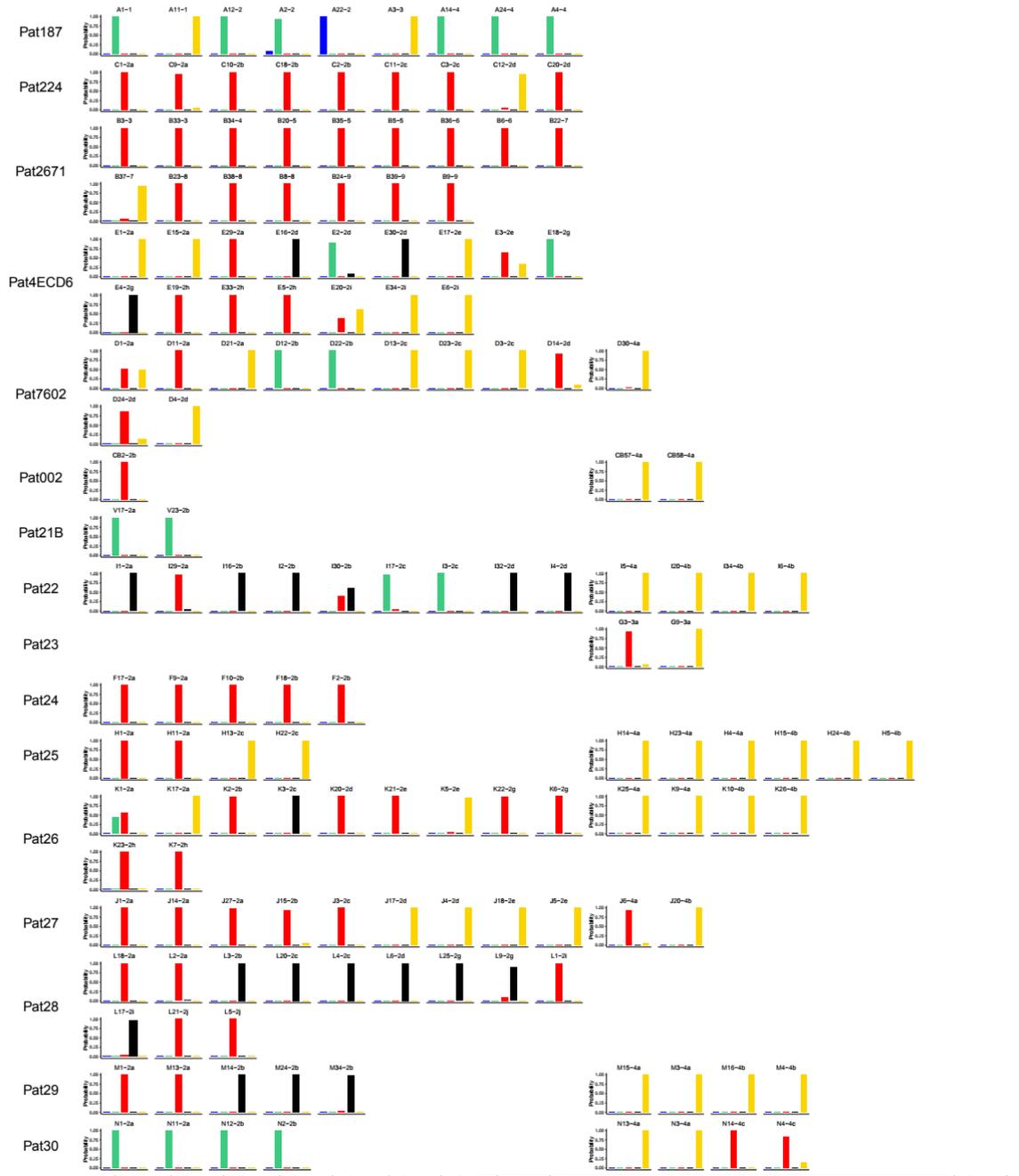
We have carried out subtype analysis on the DCIS and IDC samples that we have data for using both the PAM50 and the AIMS methods. We have decided to use the output for the AIMS method rather than the PAM50, as we have found that the subtype profiles tend to change depending on which samples you add to the group. For the Aims method, this does not happen and each subtype is classified based only on the data for that sample.

Below is a table showing some patients so far and the subtype profile

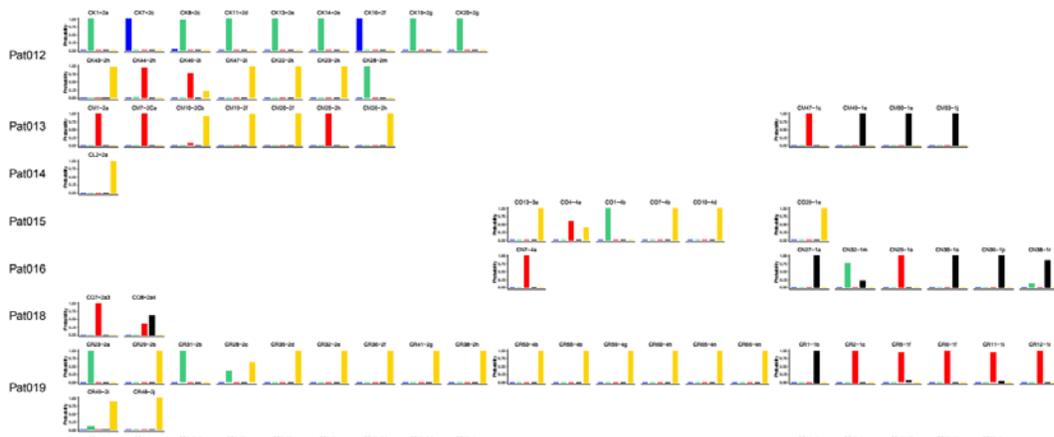
Subtype
 ■ Basal
 ■ Her2
 ■ LumA
 ■ LumB
 ■ Normal

DCIS

Epi



We have found that the subtype of the IDC can be different from the same patient's DCIS lesions, as show below.



We are doing some preliminary differential analysis on the RNA seq using different groups as defined by both the subtyping and the DNA data.

Opportunities for training and professional development

Nothing to report (not intended for training)

Results disseminated to communities of interest

Nothing to report

4. Impact

Nothing to report

5. Changes / problems

Nothing to report

6. Products

Nothing to report

7. Participants & other collaborating organizations

Individuals worked on the project

Name : Greg Hannon
 Project Role: Initiating PI – contributed to project design and liaising with bioinformatics team
 Nearest person month worked: 1 CM (10% x 8 months)
 Funding support: CR-UK and Royal society

Name : Clare Rebbeck

Project Role: Co-PI – contributed to project design, staining strategy, dissecting with the LCM, RNA and DNA library preparation and liaising with Bioinformatics team and pathologist.

Nearest person month worked: 7 CM (75% X 9 months – (3 months maternity))

Name : Jian Xian

Project Role: senior research assistant - contributed to dissecting with the LCM and RNA and DNA library preparation

Nearest person month worked: 12 CM

Funding support: CR-U

Name : Laurence de Torrente

Project Role: Post doc – bioinformatition

Nearest person month worked: 12 CM

Funding support: salaried via the NYGC subaward.

Change in active support since last report

Nothing to report (this is the first reporting period)

Other organizations involved as partners

Duke university – collaboration to provide tissue samples and clinical annotation; as detailed in the grant application.

New York Genome Center – Collaboration with the bioinformatics team to analysis the data; As detailed in the grant application