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This paper attempts to envision the impact of human genome editing through 2033 and describe how the U.S. Army might exploit it in support of future manning efforts. To exploit the opportunity, the U.S. Army should collect, sequence, and analyze each individual Soldier and applicant's genome, augment currently employed manning heuristics, and employ genome editing of adult volunteers in limited circumstances. The Army must balance the risk of exploring and employing socially controversial and practically problematic human genome information and editing techniques with the opportunity to be the first mover in optimizing humans for future warfare.

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FUTURE WAR PAPER

A New Model Army: The Impact of Human Genome Editing on U.S. Army Manning

**SUBMITTED IN PARTIAL FULFILLMENT
OF THE REQUIREMENTS FOR THE DEGREE OF
MASTER OF OPERATIONAL STUDIES**

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THE OPINIONS AND CONCLUSIONS EXPRESSED HEREIN ARE THOSE OF THE INDIVIDUAL STUDENT AUTHOR AND DO NOT NECESSARILY REPRESENT THE VIEWS OF EITHER THE SCHOOL OF ADVANCED WARFIGHTING OR ANY OTHER GOVERNMENTAL AGENCY. REFERENCES TO THIS STUDY SHOULD INCLUDE THE FOREGOING STATEMENT.

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Preface

This paper attempts to envision the future impact of human genome editing over the next fifteen years and describe how the U.S. Army might exploit it in support of future manning efforts. I would like to acknowledge the help of my advisor, Dr. Kerry Fosher, for challenging my conclusions and helping me clarify and express my argument. Her guidance has been invaluable. Additionally, I would like to thank Dr. Renee Wegrzyn and Dr. Colby Stoddard of the Defense Advanced Research Projects Agency for providing insight into the nuts and bolts of gene editing. Thanks also to Major Danny Sanchez, Officer Mahvash Siddiqui, Dr. Patrick Rose, Lieutenant Colonel Jeffrey Bacon, and Ms. Christi Bayha for taking time to speak with me regarding their particular areas of expertise.

Glossary[1]

Deoxyribonucleic Acid (DNA) - DNA is the chemical name for the molecule that carries genetic instructions in all living things. The DNA molecule consists of two strands that wind around one another to form a shape known as a double helix. Each strand has a backbone made of alternating sugar (deoxyribose) and phosphate groups. Attached to each sugar is one of four bases--adenine (A), cytosine (C), guanine (G), and thymine (T). The two strands are held together by bonds between the bases; adenine bonds with thymine, and cytosine bonds with guanine. The sequence of the bases along the backbones serves as instructions for assembling protein and RNA molecules.

Epigenetics - Epigenetics is an emerging field of science that studies heritable changes caused by the activation and deactivation of genes without any change in the underlying DNA sequence of the organism. The word epigenetics is of Greek origin and literally means over and above (epi) the genome.

Exon - An exon is the portion of a gene that codes for amino acids. In the cells of plants and animals, most gene sequences are broken up by one or more DNA sequences called introns. The parts of the gene sequence that are expressed in the protein are called exons, because they are expressed, while the parts of the gene sequence that are not expressed in the protein are called introns, because they come in between--or interfere with--the exons.

Gene - The gene is the basic physical unit of inheritance. Genes are passed from parents to offspring and contain the information needed to specify traits. Genes are arranged, one after another, on structures called chromosomes. A chromosome contains a single, long DNA molecule, only a portion of which corresponds to a single gene. Humans have approximately 20,000 genes arranged on their chromosomes.

Genome - The genome is the entire set of genetic instructions found in a cell. In humans, the genome consists of 23 pairs of chromosomes, found in the nucleus, as well as a small chromosome found in the cells' mitochondria. Each set of 23 chromosomes contains approximately 3.1 billion bases of DNA sequence.

Genotype - A genotype is an individual's collection of genes. The term also can refer to the two alleles inherited for a particular gene. The genotype is expressed when the information encoded in the genes' DNA is used to make protein and RNA molecules. The expression of the genotype contributes to the individual's observable traits, called the phenotype

Germ Line - A germ line is the sex cells (eggs and sperm) that are used by sexually reproducing organisms to pass on genes from generation to generation. Egg and sperm cells are called germ cells, in contrast to the other cells of the body that are called somatic cells.

Mitochondrial DNA - Mitochondrial DNA is the small circular chromosome found inside mitochondria. The mitochondria are organelles found in cells that are the sites of energy production. The mitochondria, and thus mitochondrial DNA, are passed from mother to offspring.

Phenotype – A phenotype is an individual's observable traits, such as height, eye color, and blood type. The genetic contribution to the phenotype is called the genotype. Some traits are largely determined by the genotype, while other traits are largely determined by environmental factors.

Ribonucleic Acid (RNA) - Ribonucleic acid (RNA) is a molecule similar to DNA. Unlike DNA, RNA is single-stranded. An RNA strand has a backbone made of alternating sugar (ribose) and phosphate groups. Attached to each sugar is one of four bases--adenine (A), uracil (U), cytosine (C), or guanine (G). Different types of RNA exist in the cell: messenger RNA (mRNA), ribosomal RNA (rRNA), and transfer RNA (tRNA). More recently, some small RNAs have been found to be involved in regulating gene expression.

Somatic Cell - A somatic cell is any cell of the body except sperm and egg cells. Somatic cells are diploid, meaning that they contain two sets of chromosomes, one inherited from each parent. Mutations in somatic cells can affect the individual, but they are not passed on to offspring.

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[1] Definitions taken from National Human Genome Research Institute, "Talking Glossary of Genetic Terms," accessed October 15, 2018, https://www.genome.gov/glossary/index.cfm.

Anticipating the increasing complexity of future warfare, the U.S. Army established a vision in 2014 for achieving advantage over adversaries by exploiting the human dimension. Superior personnel and organizations would exploit human advantages allowing the Army to achieve a position of advantage relative to adversarial forces. The accompanying strategy described the initial phase of achieving this vision as, "optimiz[ing] the human performance of every Soldier and Army Civilian in the Total Force."[2] With such an optimally manned organization, the Army would proceed to build cohesive teams comfortable operating in the anticipated complexity of future operating environments. Further emphasizing the criticality of the human dimension, the December 2018 Army Operating Concept highlighted the foundational importance of superior personnel to the future success of the Army. In certain terms, General Stephen Townsend, Commander of U.S. Army Training and Doctrine Command noted, "this concept is about warfighting and its centerpiece is the American Soldier."[3] Clearly, optimally manning the Army undergirds future Army success.

Though initially appearing wishful, a collection of technologies maturing concurrently over the next few decades may help fulfill the bold vision described in U.S. Army future concepts. Gene sequencing and editing technologies appear poised to enable increasingly precise understanding of an individual's genetic information while permitting limited manipulation of those attributes. If so, the maturation of gene editing technologies will allow the U.S. Army to embrace greater precision in making manning decisions, ultimately resulting in more optimal combinations of Soldiers and teams. To exploit this opportunity, the U.S. Army should collect, sequence, and analyze each individual Soldier and applicant's genome, augment currently employed manning heuristics, and employ genome editing of adult volunteers in limited circumstances.

The Prospect of Human Genome Editing

Today it is practical to map an individual's genetic information. An individual's genome can be mapped cheaply, swiftly, and accurately permitting a precise measurement of an individual's genotype. The cost to sequence a human genome has plummeted from more than $100 million in 2001 to around $1,500 per instance in 2015.[4] Likewise, the speed of sequencing an individual genome has increased fantastically from requiring more than a decade to less than a day.[5] Accuracy in sequencing has not suffered greatly in the push for speed and affordability, providing low error rates when a mix of techniques are used.[6] Obtaining accurate un-interpreted genetic data is growing increasingly practicable.

Complementarily, maturing gene editing technologies are improving understanding of what that genetic information means. An individual's phenotype represents a complex interaction between an individual's microbiome, epigenetic factors, physical environment, social environment, and genotype.[7] Put simply, a human's attributes result from genetic information and environmental factors. A person is neither all nature nor all nurture, but a complex interaction of both. Historically, the inability to differentiate causal factors has limited the understanding of genetic influence on an individual's phenotype. However, current gene editing techniques can precisely break apart deoxyribonucleic acid (DNA) strands to permit the addition, deletion, suppression, or expression of portions of DNA. As a result, researchers can precisely affect a specific gene and observe the resulting change in a living organism, clarifying some aspects of the influence of genotype on the resulting phenotype. Additionally, current techniques permit the targeting and isolation of epigenetic factors, further differentiating causality.[8]

Beyond mapping and understanding, gene editing technologies could permit selective presentation of human genetic attributes. This process has become routine with crop plants to

change their taste, appearance, drought resistance, disease resistance, or pest resistance.[9] Similarly, numerous animal experiments have demonstrated the technological possibility. Researchers used gene editing to produce pigs with more muscle, less fat, and better ability to manage body temperature in 2017.[10] Likewise, mice have been enhanced to improve cognitive function.[11] Medical research employing gene editing techniques on humans are underway and show promise. As of 2016, hundreds of early-stage gene therapy trials had begun and some had progressed to human trials.[12] Such research includes therapies addressing cystic fibrosis, sickle cell anemia, HIV, and some cancers.[13] The first attempts at modifying human genetic information and resulting individual attributes are already occurring. The techniques being perfected today for therapeutic causes could be reoriented to enhance humans tomorrow.

The development of the CRISPR editing technique has further accelerated the development of genetic understanding and ability to selectively edit living organisms. Taken from the natural process some bacteria use to fight off viral invasions, the Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR) system simplified programming of editing efforts over earlier gene editing techniques.[14] The U.S. National Academy of Sciences summarized CRISPR as a, "simpler, faster, and cheaper relative to earlier methods and . . . highly efficient."[15] For example, synthetization of the necessary compounds using the older Zinc Finger Nuclease technique cost $5,000. It costs a mere $30 using the CRISPR technique.[16] As a result, the technique has greatly increased the tempo of experimentation, thereby increasing the rate at which genetic understanding is improved.[17]

As with any infant technology, practical barriers to human gene editing beyond lack of genetic understanding exist. A number of factors including cellular efficiency in repairing damage, target site location, and the presence of specific ribonucleic acids (RNA) limit the

efficacy of gene editing. The largest practical hindrance appears to be delivery as physical, viral, and non-viral delivery vectors have shown mixed results.[18] Additionally, current gene editing techniques tend to edit off-target, outside of the desired area, possibly causing genetic damage or cancers. One 2018 study of CRISPR found off-target edits further afield from the target site than previously suspected and including some edits with pathogenic qualities.[19] Researchers continue to refine technologies to address these shortfalls. For example, the Defense Advanced Research Projects Agency is pursuing a program called Safe Genes to prevent unsafe gene editing activities including the prevention of off-target effects.[20] However, these practical limitations currently bound the efficacy and safety of gene editing technology.

Still, the greatest limiting factors are likely to be social and ethical as the desirability of human genome editing remains unsettled. Polling of American views demonstrates support for therapeutic use of gene editing while use for enhancement faces significant opposition.[21] The line between therapy and enhancement is ill defined and subject to varying interpretations and applications of national and international laws and norms. Further, the definitions of terms such as "natural" and "normal", subjective in themselves, may frame interpretations of what constitutes appropriate policy.[22] Sharply contested and deeply held beliefs regarding life, identity, and liberty are likely to compete as gene editing technology approaches maturation. In sum, therapeutic gene editing is likely to prosper under commonly accepted American regulations and norms that govern the development of medicines while the path for its use in enhancement remains unclear.[23]

Exploiting Human Gene Editing

The Army can take advantage of the development of gene sequencing and editing technologies in pursuing a more optimally manned force. Already, the Army can embrace the

capability to map each individual Soldier's genome through genome sequencing. Spurred by the research potential of gene editing technologies, the Army will likely gain greater understanding of the genetic and non-genetic factors that influence a Soldier's attributes. Finally, as the onward march of technological advancement overcomes practical and safety limitations, slowly and unevenly, the Army may gain a limited ability to influence a Soldier's genetic attributes via direct genome editing. To take advantage of this opportunity, the Army will need to adjust some manning actions and metrics.

Collect, Sequence, and Analyze Individual Genomes

First, the Army should collect, sequence, and analyze all Soldiers' and applicants' genomes to exploit the maturation of gene editing technologies. Currently, the Department of Defense (DOD) maintains a repository of DNA samples from all service members and deployed civilians for the purpose of conclusively identifying remains.[24] Additionally, DOD permits the collection of DNA in support of certain criminal investigations.[25] In both instances, the collected genetic information enables a simplistic comparison of samples. The military does not undertake further analysis of DNA collected.

Sequencing individual genomes would provide insight into the genetic factors influencing each Soldier and applicant. As individuals represent a unique combination of genetic and environmental factors, any precise assessment of the individual would first have to establish what those factors are. Collecting, sequencing, and analyzing each individual would provide a foundational component within a larger assessment of the individual. Thus, to gain any benefit from the maturation of gene editing technology, the Army will need to request exemption from or directly encourage the Department of Defense to change its policy to accommodate collection, sequencing, and analysis of individual genomes.

Building the collection of individual genomes into a database with cross referenceable medical history would help the Army build the understanding necessary to employ genetic information in manning decisions. Developing tools to assess the impact of genetic information on manning decisions is currently problematic due to the low level of genetic understanding. Even as this understanding expands, researchers will struggle due to the overwhelming size and complexity of the human genome. Extending to over six billion bits of information, it is difficult to know where in the genome to explore. Further, as many human traits rely on the interaction of multiple areas of the genome, looking only in one area provides the researcher a distorted view of human genetics. A large database of many genomes would provide sufficient data richness to correlate genetic information with possible medical issues. As one review of the potential for big data in healthcare learning describes it, "the strength of big data is finding associations . . . not focused on causal inference, but rather on correlation or on identifying patterns amid complex data."[26] The Army's large database of genomes would enable data analytics to highlight counterintuitive or unforeseen correlations, empowering further targeted research.

Similar projects are already underway, but at a much smaller scale. A database of 60,706 individuals containing only a portion of each individual's genetic information, is credited with helping researchers identify 183 genes that are not as susceptible to mutation as previously thought and more than 3,000 that are more vulnerable than previously believed.[27] In the United Kingdom, the National Health Service is building a database of 100,000 genomes to, "create a better understanding of the causes of disease" by comparing patient records with their sequenced genomes.[28] By correlating connections across the genome researchers can better target their research, increasing the probability of making important findings.

The size of the Army genome database would provide additional advantages. An Army database would dwarf any other database constructed. With over one million service members across the total force and an annual applicant pool of between 60,000 and 80,000, the Army could rapidly build the largest database of genomes in the world. Pairing the individual genomes with medical records would further genetic understanding and permit researchers to build better predictive analytic tools. Further, the size of the database would help eliminate statistical biases. Recently, researchers identified significant differences between the genomes of individuals of African descent and the reference genome developed by the Human Genome Project. About ten percent of the African derived genomic information was missing from the reference genome.[29] Such dramatic variances emanating from small data sets could lead to dramatic misunderstandings and bad manning decisions. Thus, the size of an Army database would help ensure more robust data informed conclusions.

Augment Current Manning Heuristics

Second, the Army should develop and deploy individualized genetic predictive models to further exploit the maturation of gene sequencing and editing technology. In much the same way that actuaries make educated guesses on the risk to insure a life or property based on statistical data of historical events, the Army could augment its current manning heuristics to provide a more nuanced assessment of the suitability of an applicant for service. Ultimately, this would give the Army something akin to a personalized genetic risk rating for each applicant. The Army could then make more precise manning decisions.

Currently, the Army employs a paradigm of sufficiency in assessing applicants, establishing a minimum acceptable baseline for individuals across nine dimensions: age, citizenship, education, aptitude, medical fitness, physical fitness, dependency status,

character/conduct, and drug/alcohol abuse.[30] Providing some optimization, the Army varies minimum standards for certain military occupational specialty requirements to better match personnel. For example, occupational physical assessment test scores restrict those individuals least physically capable from entering more rigorous specialties. The nine dimensions currently employed provide a comprehensive but static picture of an individual. Of the assessable dimensions, medical fitness, physical fitness, age, mental aptitude, and character represent dynamic qualities. As they can change over time, these dimensions represent areas in which greater precision is desirable.

Sequencing individual genomes to proactively identify potential medical issues would enable predictive medical screening to augment current measures focused on current health reporting and medical history. Today, over 3,000 gene variations have been linked to disease expression in humans.[31] A full analysis of an applicant's genome would permit the Army to deny service or apply preventative therapies to those most likely to develop complicating medical issues. Already, the use of limited genetic testing to identify disease potential pre-symptomatically has become standard practice in certain contexts. For example, all U.S. states require limited genetic testing of newborns for genetic disorders, though states have not standardized specific testing requirements.[32] Newborns are tested for more than 30 treatable diseases within the first week of life to permit early diagnosis and treatment.[33] With newborns, blanket genetic screening enables early medical intervention. For the Army, a similar policy would enable greater selectivity in manning or employment of more aggressive prophylactic measures. The result would be fewer medical issues and greater individual readiness.

Algorithms developed to help the Army understand the medical risk of a particular individual developing a condition preventing successful completion of service would require

nuance and frequent review. Genetic understanding develops over time, but researchers frequently double back on what was previously thought to be known. For example, researchers have linked variations in the BRCA1 and BRCA2 genes to elevated risk of breast, ovarian, and other cancers.[34] However, this does not mean that all individuals with these variations end up having cancer. Thus, manning decisions employing a genetic component of medical risk should consider the probability and severity of a possible outcome, while shying away from dichotomous if-then decision making.

As with medical fitness assessments, the Army could utilize genetic understanding to augment physical fitness measurements that currently provide insight into a single point of time. The Army Occupational Physical Assessment Test and the Army Physical Fitness Test provide snapshots of physical ability at the time of the test and under the conditions of the testing site. This produces a simple measurement that determines whether an individual possesses sufficient physical fitness to perform a range of combat duties. However, it provides no information regarding the possible progression or regression of individual physical ability. Thus, as the Army tries to build teams of optimized individuals, it does so with static measurements of a dynamic quality.

Physical ability is partly the result of an individual's genetic makeup. A recent estimate placed the role of genetics in physical ability at between thirty and eighty percent of an individual's ability.[35] Though physical ability emerges from the interaction of many genes, around 150 genes have been linked to specific aspects of athletic ability.[36] Additionally, some genes appear to limit physical ability under certain environmental conditions. For example, variations of a gene designated CASQ1 could lead to poor physical performance in hot environments culminating in heat injury.[37]

Clearly, much of the genetic influence on physical ability remains poorly understood. However, as understanding of genetic influence continues to grow under the relentless exploration of gene editing research, the picture of the relative influence of genetics and environment on individual physical ability should become clearer. The Army could then augment its single point physical assessments with genetic assessments that frame an individual's possible physical limits. Estimating an upper limit to an individual's speed, power, and endurance could be quite useful in developing optimal teams. Further, greater understanding of the environmental conditions that would bound a Soldier's physical abilities would help in making more precise manning decisions. As with medical fitness, algorithms employed to help assess changes in physical fitness over time and environment should involve the same care taken to prevent oversimplification and imprecise assertions.

Likewise, using age as a metric to determine suitability of applicants bears augmentation. The Army uses age as a shorthand for mental and physical development and thereafter, decline. However, using age as a metric in manning is imprecise as aging does not affect all persons equally. A recent estimate asserted that environmental factors exert the largest influence on an individual's longevity with only twenty-five percent determined by an individual's genotype.[38] Thus, while aging is a complex event, specific genomic and mitochondrial DNA influence longevity. Just as some genetic diseases severely undercut longevity, other gene variations influence extended lifespans.[39] An individual's genome matters in how age affects her.

As understanding of the influence of genetic factors on aging grows, it will become possible to better balance age, skill, and experience in manning decisions. An augmented age metric could highlight genetic probabilities influencing the acceptance of an older candidate or the exclusion of a younger candidate. As environment appears to play the largest role, the

impact of using genetic information to augment age-based metrics would be milder than for augmenting medical or physical fitness evaluations. Still, as highly skilled individuals tend to cluster in higher age groups, a more predictive metric for understanding individual aging would provide a clear advantage.

Augmenting aptitude assessments would prove desirable but is likely to prove more problematic than medical fitness, physical fitness, or aging assessments. As with the Army's physical heuristics, an individual's score on the Armed Forces Qualification Test and proof of educational attainment, such as completion of secondary schooling, represent static and backward looking measurements of an individual's mental aptitude. They therefore appear to provide little in the way of predicting future abilities.

While there likely is a genetic component to intelligence, its influence on intelligence is difficult to discern. A recent estimate concluded that up to fifty percent of an individual's potential intellect emanates from genotype.[40] A number of other studies show no specific genes that explain differences in intelligence.[41] Both findings cannot be correct, but resolution is likely to come more slowly than answers regarding physical ability or medical vulnerability. Unlike the emergence of physical ability, the emergence of intelligence is more poorly understood and more difficult to study. How exactly the biomechanical processes of the brain relate to learning, reasoning, solving problems, communicating, or remembering is unclear. In *Brainwashed: The Seductive Appeal of Mindless Neuroscience*, the authors argue convincingly that science has not developed sufficiently convincing models to explain individual variations in how the brain operates or how the nonphysical mind functions.[42] Further, measuring intelligence is more difficult than measuring physical changes. As many generations of genetically altered mice may give us a clear picture into how particular genes influence physical characteristics, they will

provide much less compelling evidence as to how gene variations impact intelligence. Simply put, studying the genetic impact on aptitude is more difficult. Thus, until genetic understanding and theories of cognition improve substantively, augmentation of current measures for aptitude are unlikely to be useful. Given that educational attainment and testing already demonstrates a high correlation to individual intelligence, current manning heuristics appear as good as possible for the foreseeable future.[43]

Augmenting metrics of character may prove even more problematic. *DODI 1304.26 Qualification Standards for Enlistment, Appointment, and Induction*, the guiding document for assessment of all applicants to military service states the purpose of evaluating individual character of applicants, "is to minimize entrance of persons who are likely to become disciplinary cases, security risks, or who are likely to disrupt good order, morale, and discipline."[44] To do so, the Army employs criminal record checks, drug and alcohol screening, and security clearance checks to assess an individual's personal history and current status. Again, these would appear to be backwards looking when prediction is the specific quality mandated by the DOD instruction.

Though augmenting behavioral heuristics with predictive genetic tools would be desirable, it is likely to be unfruitful. A recent estimate asserted that genetic influence explained between thirty-nine and fifty-eight percent of an individual's personality.[45] Potentially, then, a deeper understanding of genetics could augment the backward-looking measures the Army uses today. However, possession of particular personality traits does not determine behavior in a particular situation. Further, appropriate behavior is context dependent. Acting violently can be immensely desirable in combat situations and completely unacceptable in most others. Some behavioral characteristics simply resist explanation. The Army would incur great risk in

reducing the X factor of leadership to a genetic formula.[46] Even more so than with mental aptitude, researchers have much to prove regarding links between particular genotypes and particular behaviors.

Clearly, the extent to which augmenting manning heuristics with predictive genetic models is tied to the level of genetic understanding at any particular point in time. The Army will have to strike a balance between allowing genetic knowledge to advance and employing it to make more nuanced manning decisions. If successful, the Army can make more optimal manning decisions, having a more nuanced view of the Soldier beyond that produced by static assessments currently used. Manning with the assistance of predictive models based on genetic understanding would allow the Army to better understand the risk blindly incurred today.

Financially, genetic assessment of medical suitability, physical ability, and age would prove highly desirable. Greater selectivity in health screening alone would reduce the cost of attrition as more entrants would complete their terms of service. The Government Accountability Office estimated each enlisted Soldier cost the Army around $75,000 to recruit, screen, and train between 2005 and 2015.[47] Between 2010 and 2015, Army attrition from all causes approached seventeen percent in the first two years of service.[48] Put another way, nearly one in five Soldiers failed to complete the minimum term of service. The resulting bill amounted to around $1.1 billion in unplanned personnel costs for individuals who did not complete the minimum term of service.[49] In some areas, preventative genetic screening may already be financially favorable. One study concluded that conducting limited genetic testing on service applicants to detect certain cardio-pulmonary irregularities would already be cost-effective.[50]

Additionally, employing predictive models will improve the ethics of choosing to serve as risk could be more properly understood. Currently, the induction and employment of

individuals with genetic vulnerabilities to the conditions of military service remains ethically sound only to the extent that such information is unknowable. Some element of risk will remain unknowable as it will remain impossible to predict all of the conditions of military service. However, some conditions are predictable. For example, many Army duty positions involve routine exposure to petroleum, oils, and lubricants. With greater understanding of the interaction of genotype and environment, the individual and service may make more informed decisions regarding known exposures. Employing this ability might take the form of proactively restricting duty of otherwise completely healthy Soldiers in the same manner that pregnant Soldiers are routinely restricted from motor pool duties to prevent toxic exposure to their babies. It might take the form of denying service to those deemed otherwise fully healthy. It also places the applicant in a better position to understand the risks she incurs in accepting service. The resulting more informed decisions would be more ethically sound for all concerned.

Conservatively Employ Genome Editing

Third, the army should take advantage of gene editing technologies by permitting limited genome editing of adult volunteers. Doing so would permit the Army to grow the pool of potential candidates. Such a move would align the Army's actions with national values and sidestep most, but not all, of the ethical conundrums associated with gene editing. However, the associated risk of individual injury or death and consequential loss of trust in the Army by the people of the United States requires severe limits be placed on the eventual employment of gene editing.

Dangerously, the pool of qualified applicants for service appears to be declining. The quantity of Americans meeting minimum standards and demonstrating willingness to serve bounds the Army's ability to be selective in personnel decisions. A 2013 study of seventeen to

twenty-three year-olds, the age group most likely to enter military service, found only twenty-nine percent met all minimum standards. A mere thirteen percent met all standards and would score above the thirtieth percentile on the Armed Forces Qualification Test.[51] As the pool of sufficiently qualified individuals diminishes, the Army's ability to optimize manning and resulting performance also diminishes.

Limited gene editing could be employed to help grow the pool of qualified applicants. Though unsafe at this stage, the potential of genetic therapies is frequently hailed as the future of precision healthcare. For example, problems with eyesight represent a leading cause of medical service disqualification. Disorders involving eyesight eliminated sixteen percent of applicants in 2015, representing the largest reason for disqualification.[52] Still, understanding of eyesight has leapt ahead over the past quarter century and it appears to be a good candidate for further exploration through gene editing research.[53] In the short term, this research will point to drug and other noninvasive therapies to correct eyesight disorders. Longer term, directly editing responsible genes could be employed to correct disorders, growing the pool of qualified applicants.

Similarly, obesity is proving to be a top concern. As humans across the planet become more sedentary, physical ability appears to be declining and commensurate weight gain appears to be increasing. Ten percent of the youths in a 2013 study would be disqualified from service based on obesity standards alone.[54] While the rise of obesity is environmentally caused, susceptibility to obesity is partly genetic. In 2015 researchers discovered a single gene variation that appears to predispose individuals to obesity.[55] Though editing a single gene is unlikely to resolve the larger issue, editing could reduce individual susceptibility to excessive body weight

gain. As with eyesight, gene editing offers an avenue to growing the population of minimally qualified personnel.

Still, in comparison to sequencing and augmenting manning heuristics, actually editing humans appears to be the least practical and most radical option. Though some gene editing therapies have progressed to clinical trials, approval for use is unlikely to occur for many years. One study concluded that the median length of time for a drug to go from conception to receiving FDA approval was thirty-six years. The median time from clinical trial to approval was eight years.[56] Further, though CRISPR appears to be pushing genetic understanding exponentially, the technologies enabling delivery are advancing more linearly. Thus, it is probable that researchers will have an understanding of genetic influence long in advance of being able to effectively manipulate that influence.

While gene editing would also be a more radical step, the degree of radicality could be moderated. Editing would have to be voluntarily accepted. As desirable as health improvements through genetic editing could be, they would not be medically necessary in most cases. Thus a mandatory policy would be out of line with current medical ethics and national values that cherish individual liberty. Further, editing would have to avoid seeking human enhancement beyond a baseline of human capability. Though the line between enhancement and therapy will shift with cultural mores over time, improving an individual to meet minimum necessary standards as opposed to shooting for optimal standards places the Army in a better ethical position to meet any criticism. Additionally, germline editing should be avoided. The editing of heritable traits impacts future generations with unforeseen consequences for those individuals and the larger society. Recently, a researcher astounded the world by claiming to have edited embryos that were brought to term.[57] The overwhelming pushback he received from nearly all

societal segments should serve warning to the Army if it even appears to be "designing" future Soldiers through editing of children. As with sequencing every Soldier's and applicant's genome and augmenting manning heuristics, the Army will need to find balance in how it embraces the ability to edit adult volunteers.

Conclusion

When the Wright brothers took to the air the risk was fairly clear: plummeting to the earth and death. Some of the risks to embracing genetic understanding and gene editing to improve Army manning are clear. Building a database of genomes presents risks to information security, privacy, equality, and fairness under the law. Gene editing of adult humans will inevitably cause injury or death as assuredly as flying involves crashes. Other risks are not so clear. Employing genetic understanding to augment traditional personnel selection heuristics may replace good thinking with bad science or induce social biases into fair selection processes. One wonders if 5'5" tall and 112-pound Audie Murphy would be permitted to serve in an Army rigorously employing manning policies here described. Further, gene editing might cause a public backlash and loss of faith in the Army as an institution of the American people.

Alternatively, Army leadership must consider the risks of not pursuing the opportunity presented. The Army has pinned its hopes for future success on the quality of the American Soldier. The human in the uniform will provide the position of advantage sought in the next conflict. Thus, to forego exploitation of advances in genetic understanding and gene editing technology is to cede battlefield advantage.

Embracing gene editing advances warrants careful consideration from scientific, medical, legal, ethical, and social perspectives before, during, and after implementation. As the Wright brothers failed frequently before finding a successful combination, the first incorporation of gene

editing into Army manning will not work well. However, it may be the necessary first step on the road to precision manning and future battlefield success.

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