REPORT DOCUMENTATION PAGE

Form Approved
OMB No. 0704-0188

The public reporting burden for this collection of information is estimated to average 1 hour per response, including the time for reviewing instructions, searching existing data sources, gathering and maintaining the data needed, and completing and reviewing the collection of information. Send comments regarding this burden estimate or any other aspect of this collection of information, including suggestions for reducing the burden, to the Department of Defense, Executive Service Directorate (0704-0188). Respondents should be aware that notwithstanding any other provision of law, no person shall be subject to any penalty for failing to comply with a collection of information if it does not display a currently valid OMB control number.

PLEASE DO NOT RETURN YOUR FORM TO THE ABOVE ORGANIZATION.

1. REPORT DATE *(DD-MM-YYYY)*	2. REPORT TYPE	3. DATES COVERED *(From - To)*
29/11/2018	Presentation	11/29-30/2018

4. TITLE AND SUBTITLE
Enabling Personalized Medicine Through Exome Sequencing in the U.S. Air Force

5a. CONTRACT NUMBER

5b. GRANT NUMBER

5c. PROGRAM ELEMENT NUMBER

6. AUTHOR(S)
Green, Robert C

5d. PROJECT NUMBER

5e. TASK NUMBER

5f. WORK UNIT NUMBER

7. PERFORMING ORGANIZATION NAME(S) AND ADDRESS(ES)
59th Clinical Investigations and Research Support
1100 Wilford Hall Loop, Bldg 4430
JBSA – Lackland, TX 78236-9908
210-292-7141

8. PERFORMING ORGANIZATION REPORT NUMBER
18225

9. SPONSORING/MONITORING AGENCY NAME(S) AND ADDRESS(ES)
59th Clinical Investigations and Research Support
1100 Wilford Hall Loop, Bldg 4430
JBSA – Lackland, TX 78236-9908
210-292-7141

10. SPONSOR/MONITOR'S ACRONYM(S)

11. SPONSOR/MONITOR'S REPORT NUMBER(S)

12. DISTRIBUTION/AVAILABILITY STATEMENT
Approved for public release. Distribution is unlimited.

13. SUPPLEMENTARY NOTES
Integrative and Collaborative Biomedical Research for the 21st Century, Fort Detrick Maryland, 29-30 November 2018

14. ABSTRACT

15. SUBJECT TERMS

16. SECURITY CLASSIFICATION OF:			17. LIMITATION OF ABSTRACT	18. NUMBER OF PAGES	19a. NAME OF RESPONSIBLE PERSON
a. REPORT	b. ABSTRACT	c. THIS PAGE			SSgt Toth
					19b. TELEPHONE NUMBER *(Include area code)* 210-292-7141

INSTRUCTIONS FOR COMPLETING SF 298

1. REPORT DATE. Full publication date, including day, month, if available. Must cite at least the year and be Year 2000 compliant, e.g. 30-06-1998; xx-06-1998; xx-xx-1998.

2. REPORT TYPE. State the type of report, such as final, technical, interim, memorandum, master's thesis, progress, quarterly, research, special, group study, etc.

3. DATES COVERED. Indicate the time during which the work was performed and the report was written, e.g., Jun 1997 - Jun 1998; 1-10 Jun 1996; May - Nov 1998; Nov 1998.

4. TITLE. Enter title and subtitle with volume number and part number, if applicable. On classified documents, enter the title classification in parentheses.

5a. CONTRACT NUMBER. Enter all contract numbers as they appear in the report, e.g. F33615-86-C-5169.

5b. GRANT NUMBER. Enter all grant numbers as they appear in the report, e.g. AFOSR-82-1234.

5c. PROGRAM ELEMENT NUMBER. Enter all program element numbers as they appear in the report, e.g. 61101A.

5d. PROJECT NUMBER. Enter all project numbers as they appear in the report, e.g. 1F665702D1257; ILIR.

5e. TASK NUMBER. Enter all task numbers as they appear in the report, e.g. 05; RF0330201; T4112.

5f. WORK UNIT NUMBER. Enter all work unit numbers as they appear in the report, e.g. 001; AFAPL30480105.

6. AUTHOR(S). Enter name(s) of person(s) responsible for writing the report, performing the research, or credited with the content of the report. The form of entry is the last name, first name, middle initial, and additional qualifiers separated by commas, e.g. Smith, Richard, J, Jr.

7. PERFORMING ORGANIZATION NAME(S) AND ADDRESS(ES). Self-explanatory.

8. PERFORMING ORGANIZATION REPORT NUMBER. Enter all unique alphanumeric report numbers assigned by the performing organization, e.g. BRL-1234; AFWL-TR-85-4017-Vol-21-PT-2.

9. SPONSORING/MONITORING AGENCY NAME(S) AND ADDRESS(ES). Enter the name and address of the organization(s) financially responsible for and monitoring the work.

10. SPONSOR/MONITOR'S ACRONYM(S). Enter, if available, e.g. BRL, ARDEC, NADC.

11. SPONSOR/MONITOR'S REPORT NUMBER(S). Enter report number as assigned by the sponsoring/ monitoring agency, if available, e.g. BRL-TR-829; -215.

12. DISTRIBUTION/AVAILABILITY STATEMENT. Use agency-mandated availability statements to indicate the public availability or distribution limitations of the report. If additional limitations/ restrictions or special markings are indicated, follow agency authorization procedures, e.g. RD/FRD, PROPIN, ITAR, etc. Include copyright information.

13. SUPPLEMENTARY NOTES. Enter information not included elsewhere such as: prepared in cooperation with; translation of; report supersedes; old edition number, etc.

14. ABSTRACT. A brief (approximately 200 words) factual summary of the most significant information.

15. SUBJECT TERMS. Key words or phrases identifying major concepts in the report.

16. SECURITY CLASSIFICATION. Enter security classification in accordance with security classification regulations, e.g. U, C, S, etc. If this form contains classified information, stamp classification level on the top and bottom of this page.

17. LIMITATION OF ABSTRACT. This block must be completed to assign a distribution limitation to the abstract. Enter UU (Unclassified Unlimited) or SAR (Same as Report). An entry in this block is necessary if the abstract is to be limited.

Enabling Personalized Medicine through Exome Sequencing in the U.S. Air Force

Robert C. Green, MD, MPH
Professor of Medicine, Harvard Medical School
@RobertCGreen

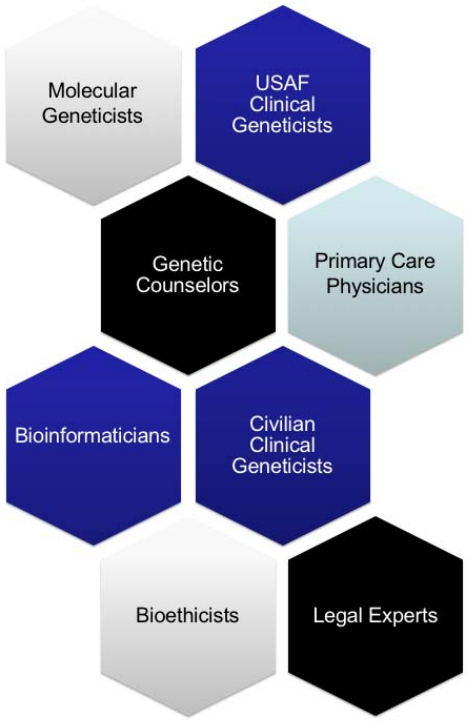
Director, Genomes2People Research Program
Brigham and Women's Hospital and Broad Institute

Dr. Green's Support and Disclosures

Research:	US National Institutes of Health US Department of Defense Broad Institute of MIT & Harvard Franca Sozzani Fund for Preventive Genomics
Advisory:	AIA, Applied Therapeutics, Helix, Ohana Biosciences, OptraHealth, Prudential, Verily, Veritas
Co-Founder:	Genome Medical – a company providing telegenetics expertise to patients, providers, employers and care systems
Disclaimer:	The views expressed are those of the author(s) and do not reflect the official views or policy of the Department of Defense or its Components. The voluntary, fully informed consent of the subjects used in this research was obtained as required by 32 CFR 219 and DODI 3216.02_AFI 40-402.

The MilSeq Project: A Military-Academic Collaboration

Carrie L. Blout, MS, CGC
Ruth Brenner, MD, Lt Col, USAF
Kurt D. Christensen, PhD, MPH
Mauricio DeCastro, MD, Maj, USAF
Cubby Gardner, PhD, Maj, USAF
Robert C. Green, MD, MPH
Jacqueline Killian, PhD, Lt Col, USAF
Joel B. Krier, MD, MMSc
Matthew Lebo, PhD
Amy L. McGuire, JD, PhD
Megan D. Maxwell, MS, LCGC
Maxwell J. Mehlman, JD
Debra Neimeyer, PhD, CIV, USAF*
Efthimios Parasidis, JD, MBioethics
Stacey Pereira, PhD
Jill O. Robinson, MA
Jason L. Vassy, MD, MPH, SM
Jameson Voss, MD, MPH, Maj, USAF

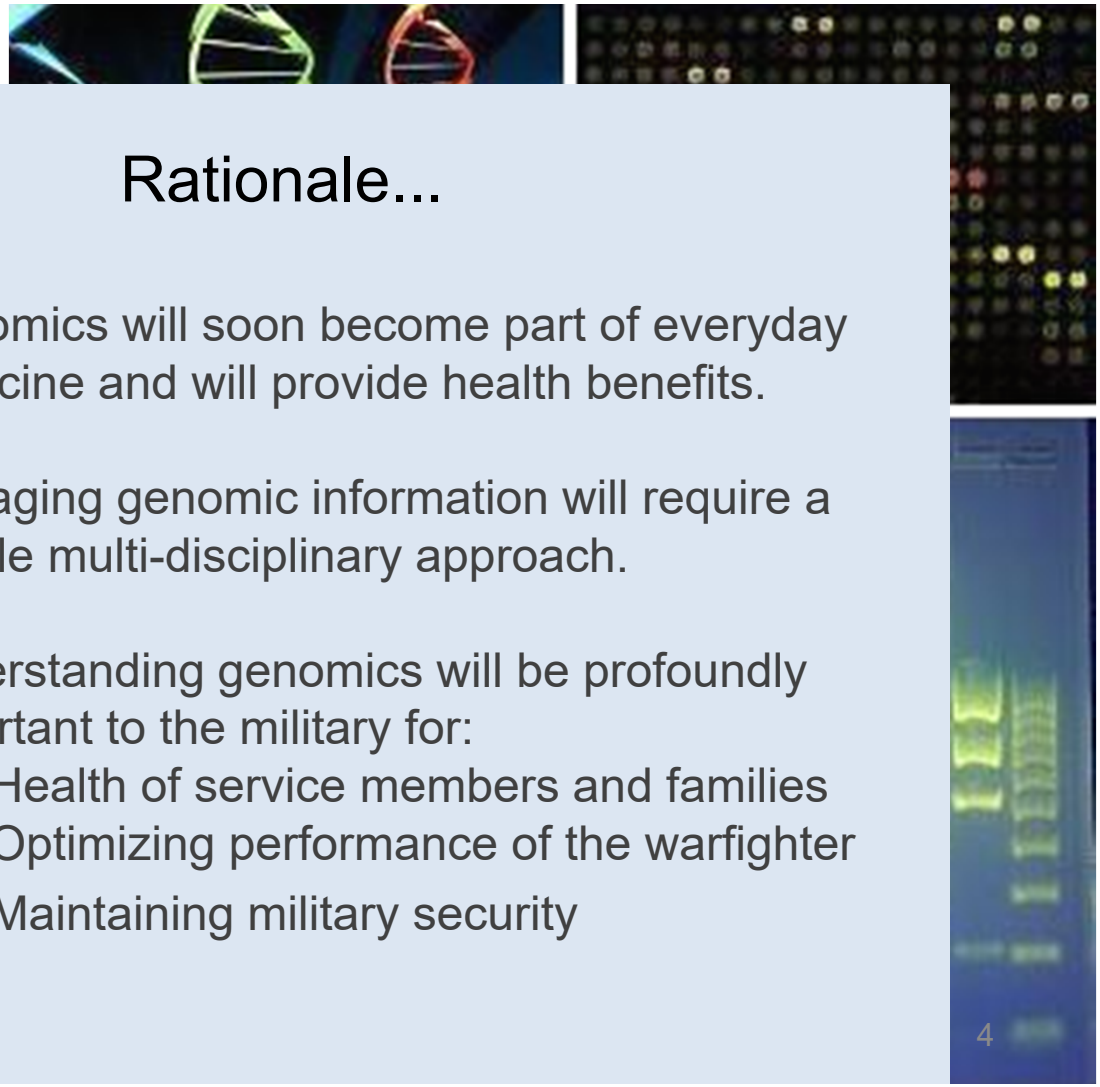


Rationale...

1. Genomics will soon become part of everyday medicine and will provide health benefits.

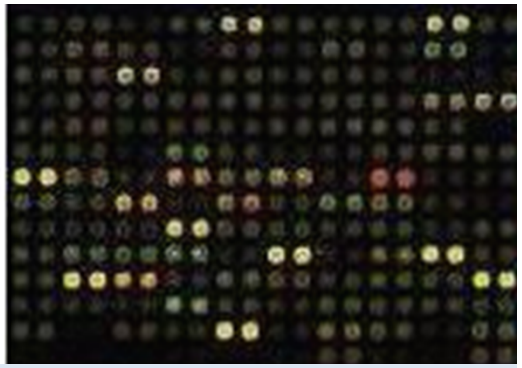
2. Managing genomic information will require a nimble multi-disciplinary approach.

3. Understanding genomics will be profoundly important to the military for:
   a. Health of service members and families
   b. Optimizing performance of the warfighter
   c. Maintaining military security

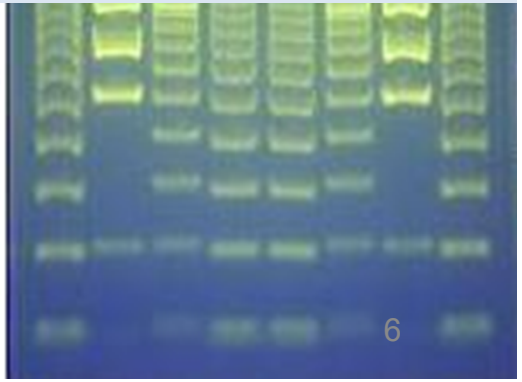


The MilSeq Project

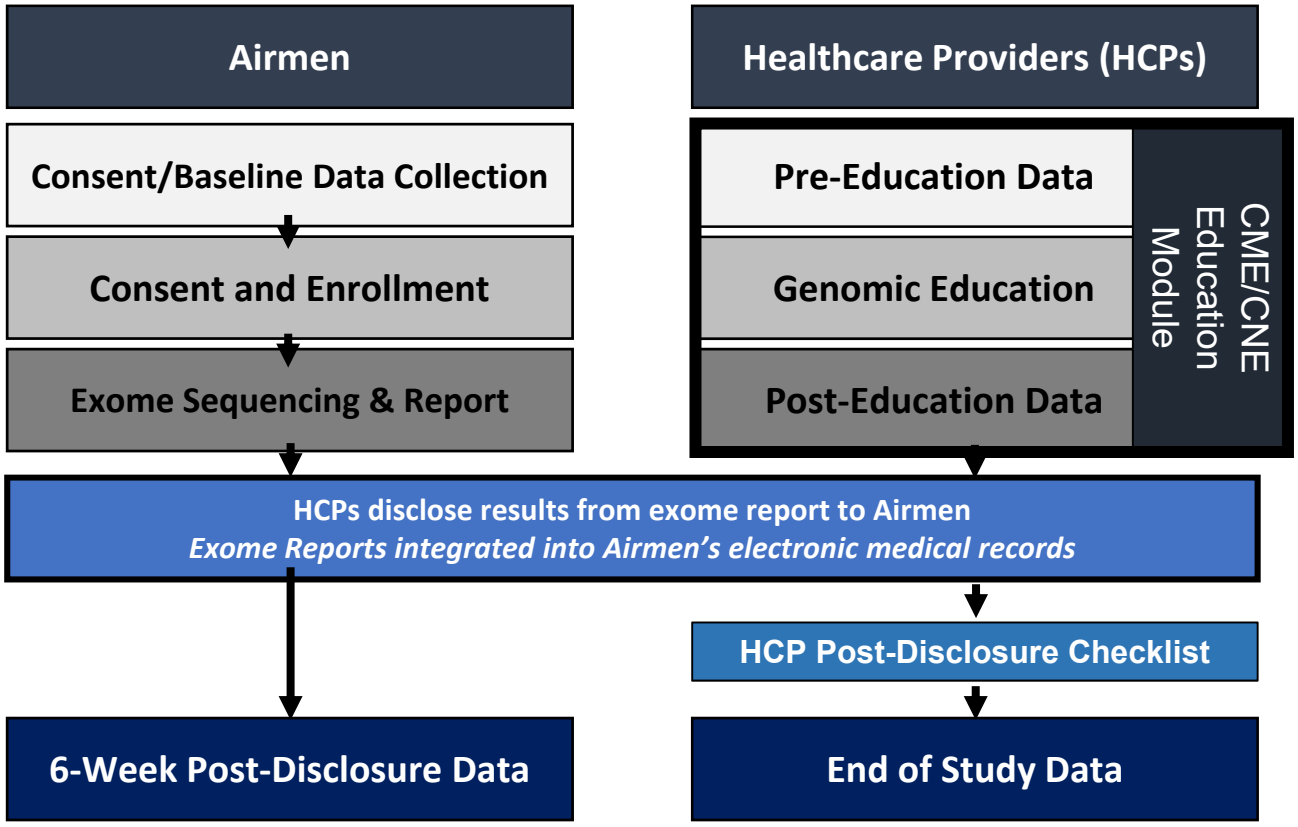
- Initially funded by the United States Air Force (USAF) through Air Force Medical Support Agency (FA8650-17-2-6704)
- Continuation funding through 59th Medical Wing (Joint Base San Antonio-Lackland Air Force Base) and 711th Human Performance Wing (Wright-Patterson Air Force Base)
- Goal is to pilot the implementation of sequencing in day-to-day medicine (consent, sample collection, sequencing, interpretation, report generation, report disclosure, follow up care)
  - Recruit 75 active-duty Airmen and 12 USAF healthcare providers at Lackland to participate in a pilot trial of implementing genomic medicine in the USAF
  - Assess short term medical, behavioral and economic impact
  - Examine the special circumstances associated with implementation of genomic medicine within the active duty military

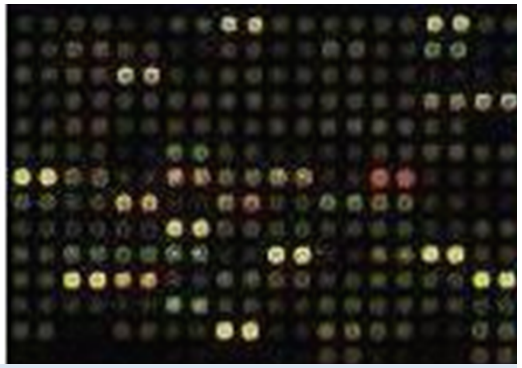



Experimental Design

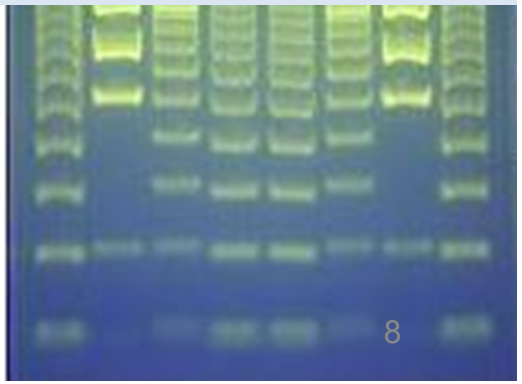



The MilSeq Project Protocol



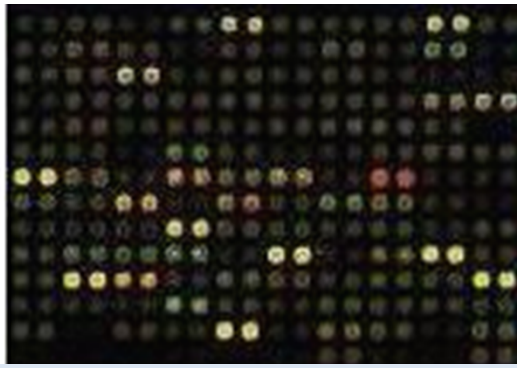


Safety of Participants

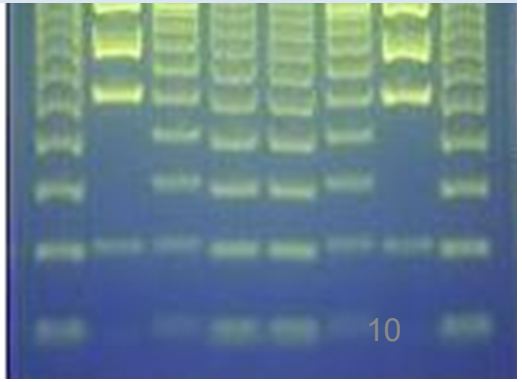


Risk Mitigation in the MilSeq Project

- IRB approved with robust consent process.
- Optional recruitment without coercive messaging.
- Entire sequencing/interpretation process is CLIA/CAP certified and positives confirmed before disclosure.
- Genetic counselor onsite with additional 24-7 availability of experts.
- Patient-HCP disclosures taped and transcribed to be reviewed by study personnel.



Study Recruitment



Recruitment Methods

- Brochure
- Base newsletter
- Facebook posting
- Direct coordinator approach

Calling Active Duty Airmen to Participate in the MilSeq Project, a Study of Genomic Sequencing

What is the MilSeq Project?

The MilSeq Project is a clinical research study funded by the US Air Force designed to explore how genomic sequencing can be used in the practice of medicine.

What is the purpose of the study?

Genomic sequencing may soon be available to almost everyone. The purpose of this study is to explore how military health care providers (HCPs) and active service Airmen feel about genomic sequencing information and ultimately how they use this information in healthcare.

Who may participate?

We are enrolling healthy active duty Air Force members and military health care providers.

What will happen in this study?

Interested Active duty Air Force members are invited to participate in a baseline survey asking about their thoughts about genomic sequencing. At the end of the survey, they will be asked about their interest in participating in a study where they may have the opportunity to have whole exome sequencing, a type of genomic sequencing.

Survey

-Complete a survey to tell us your opinions and feelings about genomic sequencing and how you think this type of info might impact your medical care.

-In the survey we will ask if you are interested in learning more about another part of our study that may allow you to have whole exome sequencing.

▼

Follow-up

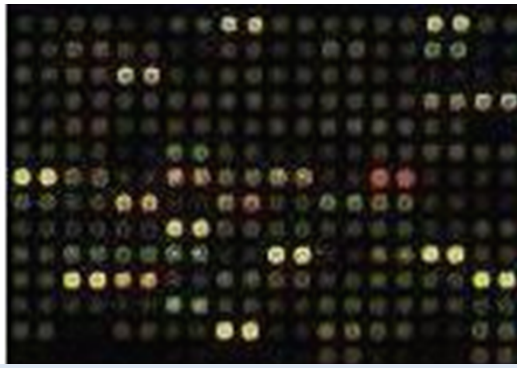
If you tell us you are interested in learning more about the sequencing study, our study Genetic Counselor will call or email you to provide additional information.

If you are not interested, your participation ends with the survey.

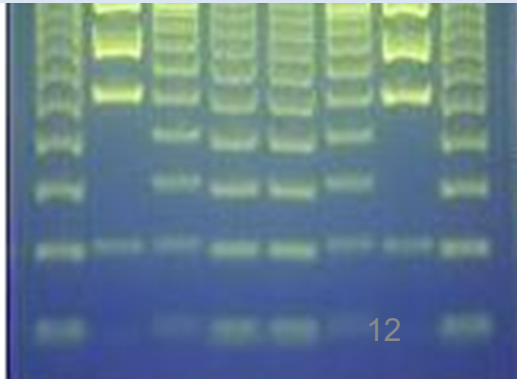
▼

To Participate Use this Link: https://is.gd/milseq

To learn more please contact: **Megan Maxwell** Genetic Counselor at (210) 292-7556

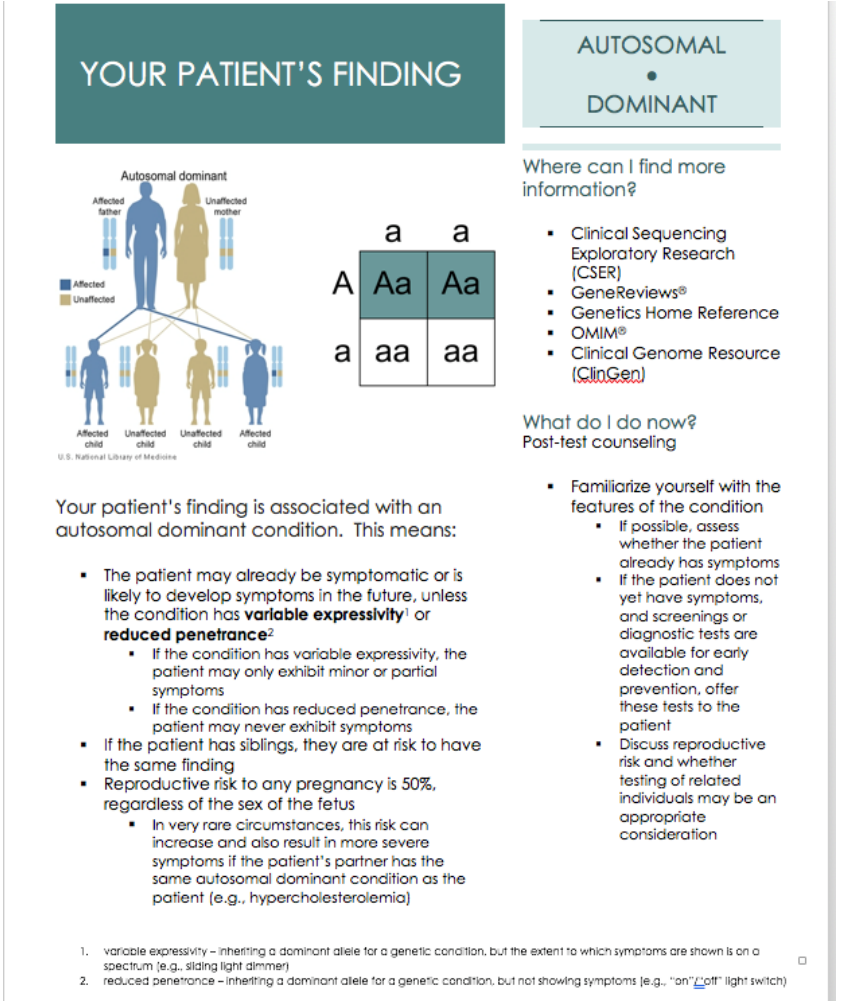


Health Care Provider Preparation



HCP Education and Support

- 3-hour, military-specific didactic lecture from a genetic counselor
- Inheritance ACTion Sheets (4)



YOUR PATIENT'S FINDING

AUTOSOMAL • DOMINANT

	a	a
A	Aa	Aa
a	aa	aa

Your patient's finding is associated with an autosomal dominant condition. This means:

- The patient may already be symptomatic or is likely to develop symptoms in the future, unless the condition has **variable expressivity**[1] or **reduced penetrance**[2]
  - If the condition has variable expressivity, the patient may only exhibit minor or partial symptoms
  - If the condition has reduced penetrance, the patient may never exhibit symptoms
- If the patient has siblings, they are at risk to have the same finding
- Reproductive risk to any pregnancy is 50%, regardless of the sex of the fetus
  - In very rare circumstances, this risk can increase and also result in more severe symptoms if the patient's partner has the same autosomal dominant condition as the patient (e.g., hypercholesterolemia)

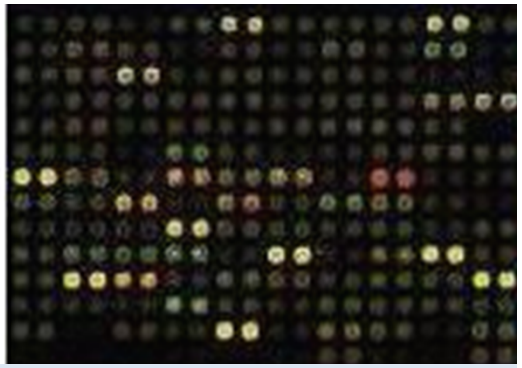
Where can I find more information?

- Clinical Sequencing Exploratory Research (CSER)
- GeneReviews®
- Genetics Home Reference
- OMIM®
- Clinical Genome Resource (ClinGen)

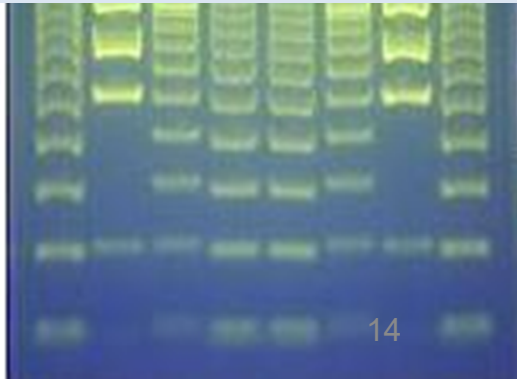
What do I do now?
Post-test counseling

- Familiarize yourself with the features of the condition
  - If possible, assess whether the patient already has symptoms
  - If the patient does not yet have symptoms, and screenings or diagnostic tests are available for early detection and prevention, offer these tests to the patient
  - Discuss reproductive risk and whether testing of related individuals may be an appropriate consideration

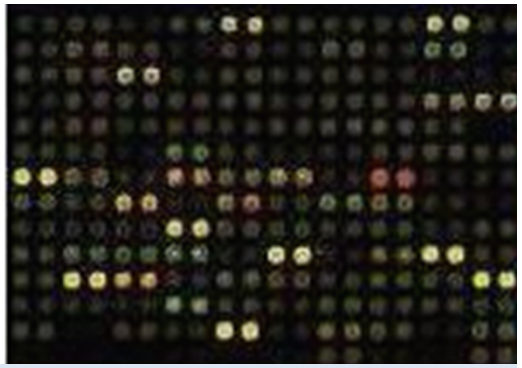
1. variable expressivity – inheriting a dominant allele for a genetic condition, but the extent to which symptoms are shown is on a spectrum (e.g., sliding light dimmer)
2. reduced penetrance – inheriting a dominant allele for a genetic condition, but not showing symptoms (e.g., "on"/"off" light switch)



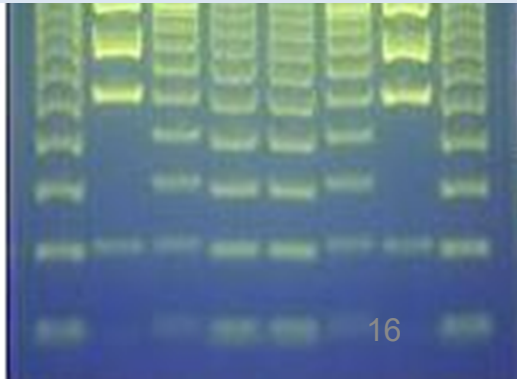
Exome Sequencing



Exome Sequencing at Partners Healthcare Laboratory for Molecular Medicine



How Many Genes Were Analyzed?



All (~ 5000) known monogenic (Mendelian) genes

Dominant (e.g. *BRCA1, MLH1, MYH7, KCNQ1, RYR1*)

Recessive (e.g. *CFTR, HBB*)

All (~ 5000) known monogenic (Mendelian) genes

Dominant (e.g. *BRCA1*, *MLH1*, *MYH7*, *KCNQ1*, *RYR1*)

Recessive (e.g. *CFTR*, *HBB*)

Selected (9) genes with risk alleles (e.g. *APOE*, *F5*)

All (~ 5000) known monogenic (Mendelian) genes

Dominant (e.g. *BRCA1, MLH1, MYH7, KCNQ1, RYR1*)

Recessive (e.g. *CFTR, HBB*)

Selected (9) genes with risk alleles (e.g. *APOE, F5*)

Selected pharmacogenomic variants (~ 60 medications)

All (~ 5000) known monogenic (Mendelian) genes

Dominant (e.g. *BRCA1, MLH1, MYH7, KCNQ1, RYR1*)

Recessive (e.g. *CFTR, HBB*)

Selected (9) genes with risk alleles (e.g. *APOE, F5*)

Selected pharmacogenomic variants (~ 60 medications)

Genetic determinants of (~ 333) RBC/platelet antigens

All (~ 5000) known monogenic (Mendelian) genes

Dominant (e.g. *BRCA1, MLH1, MYH7, KCNQ1, RYR1*)

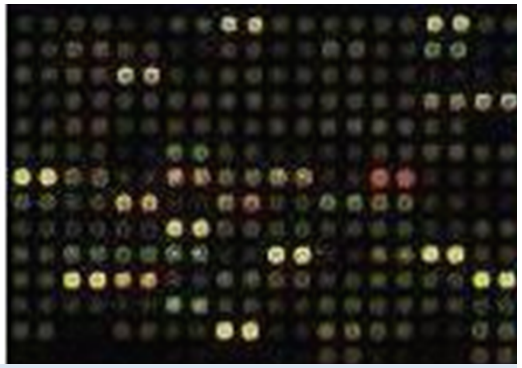
Recessive (e.g. *CFTR, HBB*)

Selected (9) genes with risk alleles (e.g. *APOE, F5*)

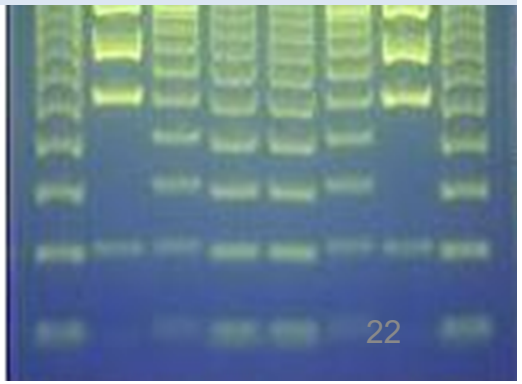
Selected pharmacogenomic variants (~ 60 medications)

Genetic determinants of (~ 333) RBC/platelet antigens

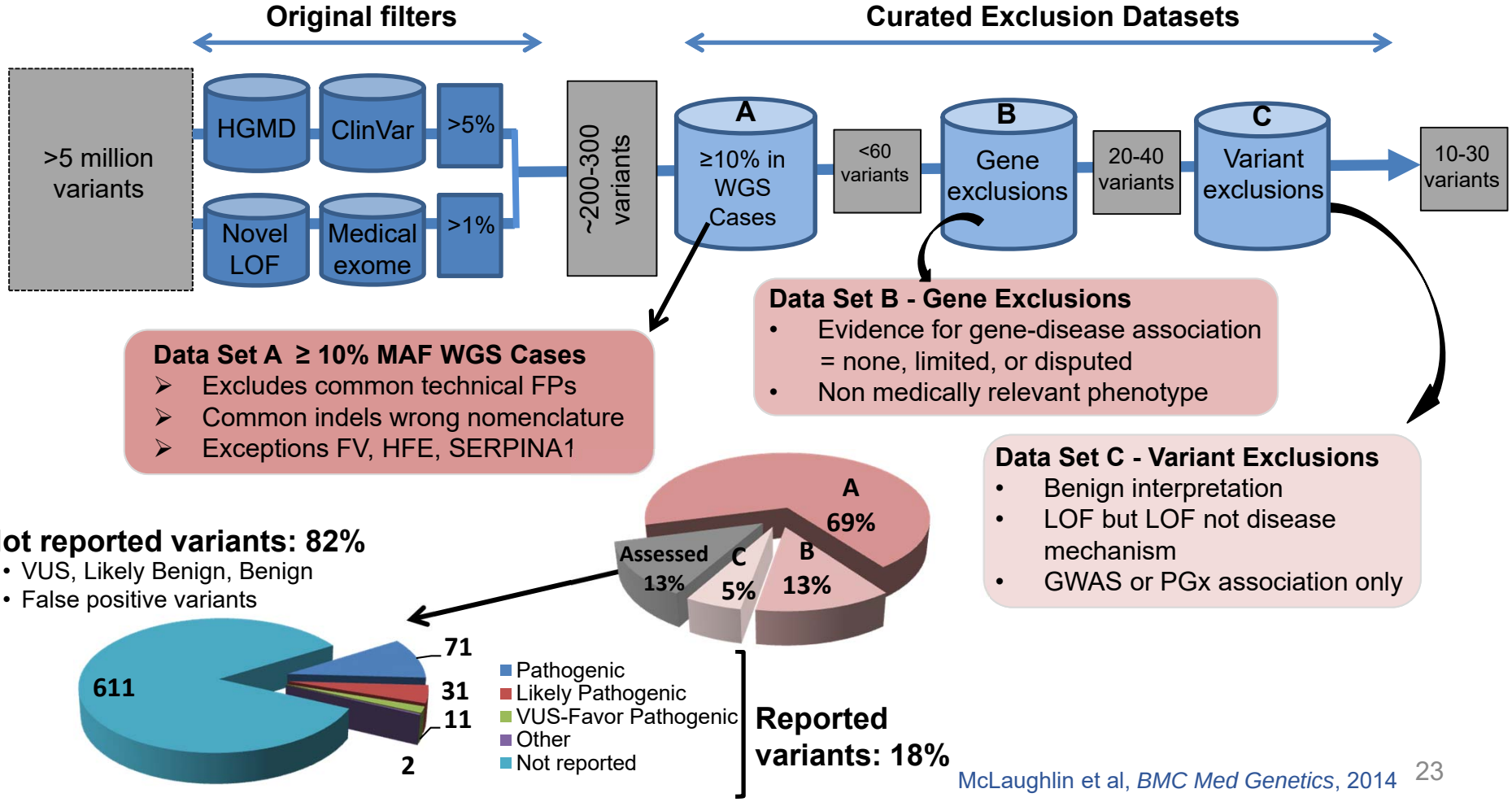
~~**Polygenic Risk Scores**~~



Variant Classification



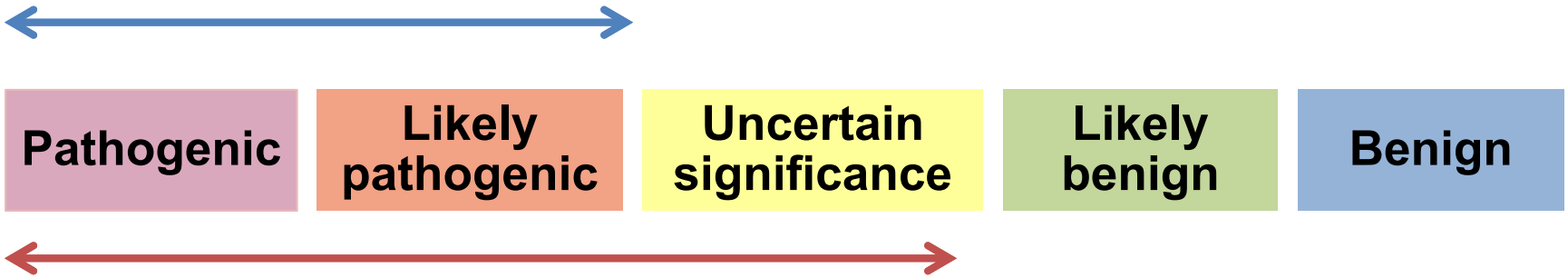
MilSeq Exome Filtering Approach



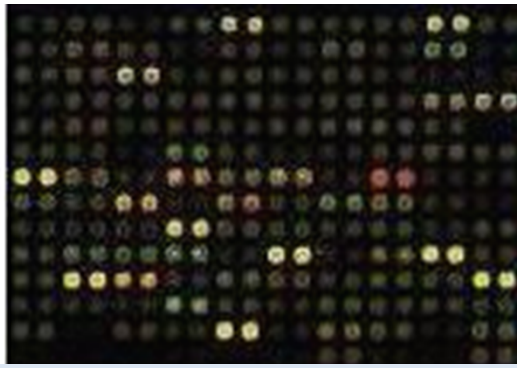
McLaughlin et al, *BMC Med Genetics*, 2014

ACMG Criteria for Variant Pathogenicity and Inclusion in MilSeq Reports

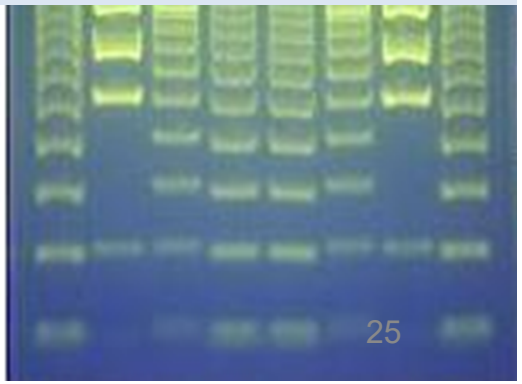
MilSeq Exome Sequencing Report



Standard Indication-Based Genetic Testing Reports



Report Design



MilSeq Project Exome Report

- Monogenic (dom) risks
- Monogenic (rec) carrier status
- Disease-associated risk alleles
- Pharmacogenomic variants
- Blood serology (not shown)

RESULT: VARIANTS OF CLINICAL SIGNIFICANCE IDENTIFIED
One variant conferring carrier status and one variant with disease-associated risks were identified

RESULT SUMMARY

Sequencing of this individual's exome did NOT identify variants with strong evidence to cause a highly penetrant disorder, but identified one variant associated with an increased risk of disease. In addition, sequencing identified carrier status for one variant that may impact disease risk in future children or other family members, depending on the carrier status of the partner(s). All results are summarized on page 1 with further details provided on subsequent pages.

INTERPRETATION SUMMARY

A. MONOGENIC DISEASE RISK VARIANTS

This test did NOT identify variants with strong evidence to cause a highly penetrant disorder.

B. CARRIER STATUS VARIANTS

This test identified carrier status for one recessive disorder. **In the heterozygous state, this variant is not known to play a role in disease, since pathogenic variants in both copies of the *X* gene are necessary to cause disease.**

Being a carrier of this variant does NOT put this individual at risk for disease, but it may impact disease risk in future children, depending on the carrier status of this individual's future partner(s).

Please note, we cannot conclusively rule out a pathogenic variant on the other copy of the gene given test and analysis limitations.

Disease, Inheritance	Gene Transcript	Variant	Allele state	Classification	Penetrance	Carrier Phenotype
Adenylosuccinate lyase deficiency, Autosomal recessive	*ADSL* NM_000026.2	c.1277G>A p.Arg426His	Heterozygous	Pathogenic	High	None reported

C. DISEASE-ASSOCIATED RISK ALLELES

This test identified one variant associated with an increased risk of developing clinical manifestations. Please see below and subsequent pages for more detailed variant information.

Disease, Inheritance	Gene Transcript	Variant	Allele state	Classification	Relative Risk
Pulmonary Fibrosis	*MUC5B* NM_002458.2	c.-3133G>T	Heterozygous	Established Risk Allele	3.7

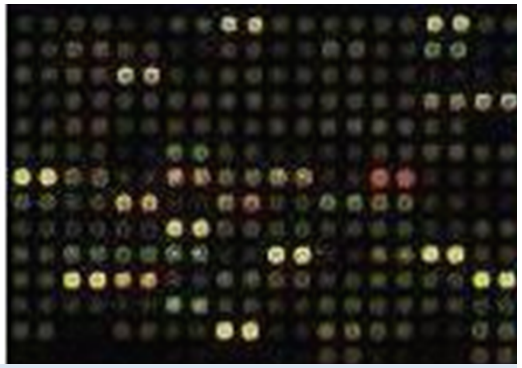
D. PHARMACOGENOMIC ASSOCIATIONS

This test identified the following pharmacogenomic associations with a potential change in management. Additional pharmacogenomic associations can be found on subsequent pages.

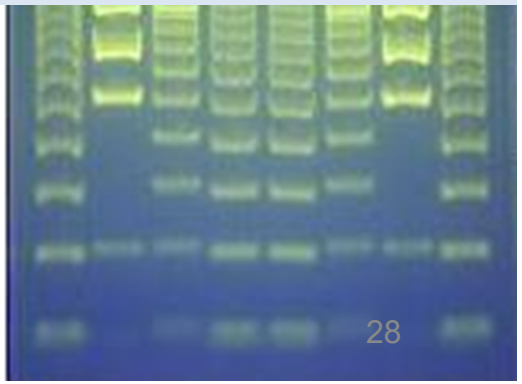
Drug	Gene Transcript	Variant(s)	Genotype	Risk and dosing information
Clopidogrel	*CYP2C19* NM_000769.1	c.[-806C(;)681G(;)636G]; c.[-806C(;)681G>A (;)636G]	*1/*2	Decreased response to clopidogrel
Digoxin	*ABCB1* NM_000927.4	c.3435T>C p.Ile1145Ile	TT	Decreased metabolism and increased serum concentration of digoxin


Results


PRIORITY
MAIL



Recruitment Progress to Date



Patient-Participants

93 completed Phase I (baseline survey)

↓

75 consented and enrolled

↓

51 results disclosed and integrated into EMR
24 pending result disclosure

Provider-Participants

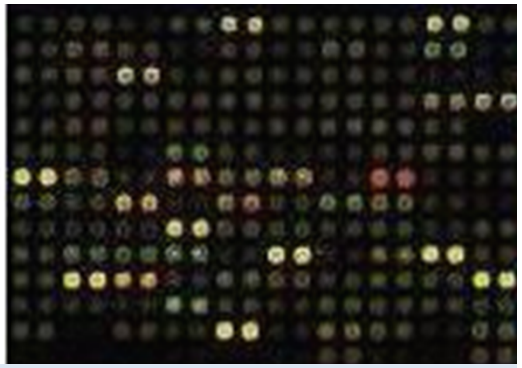
12 HCPs: 5 staff physicians, 5 resident physicians, 2 NPs

↓

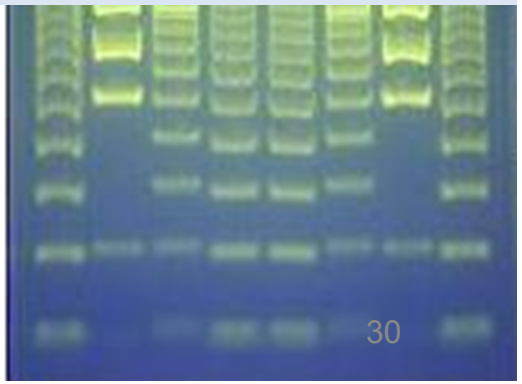
12 consented, received education, and completed pre/post-education surveys

↓

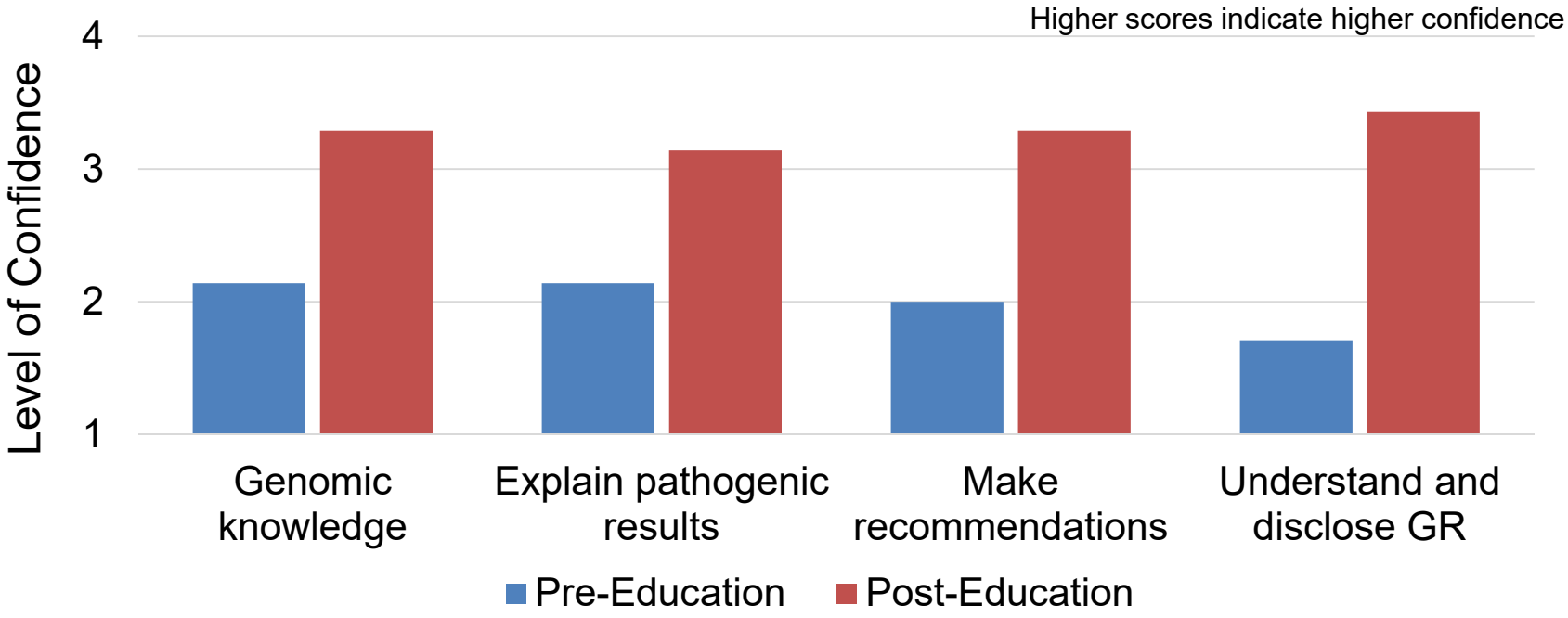
All HCP-participants have disclosed at least 1 result

Health Care Provider Education

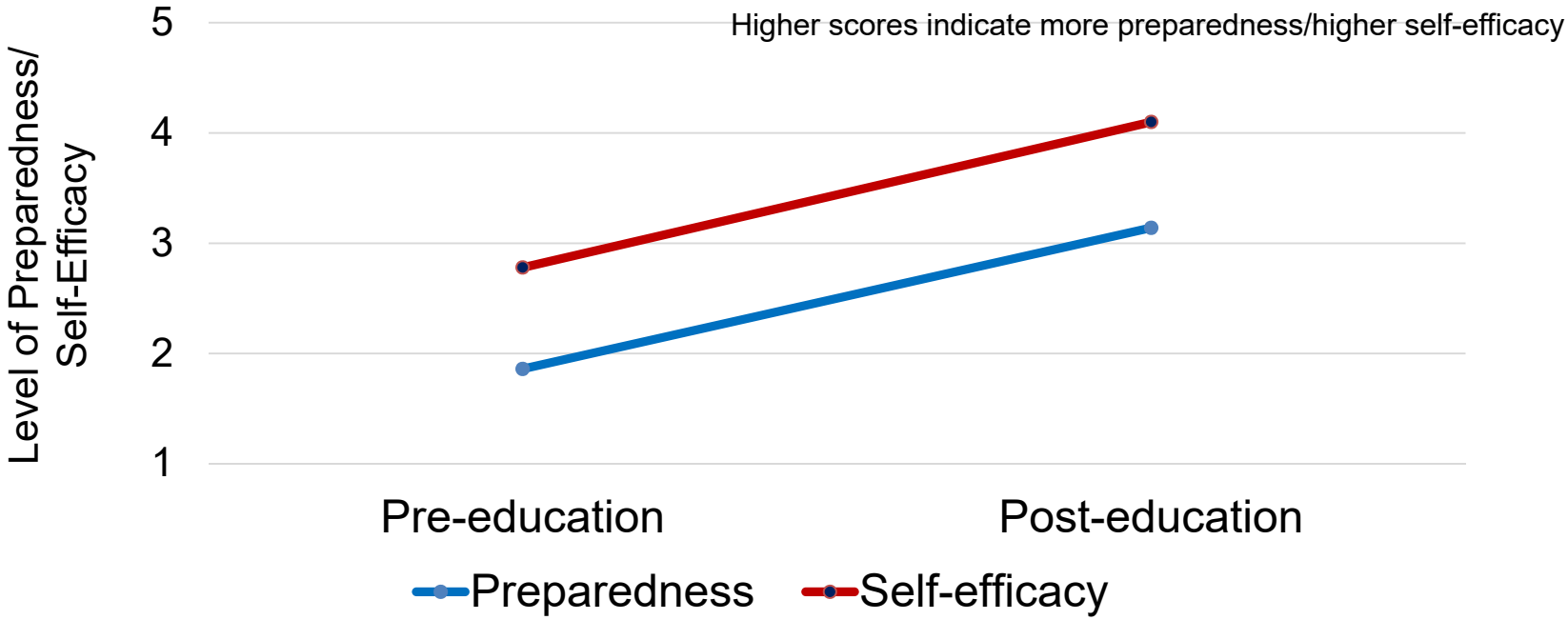



Healthcare Provider Confidence Pre- vs. Post-Education

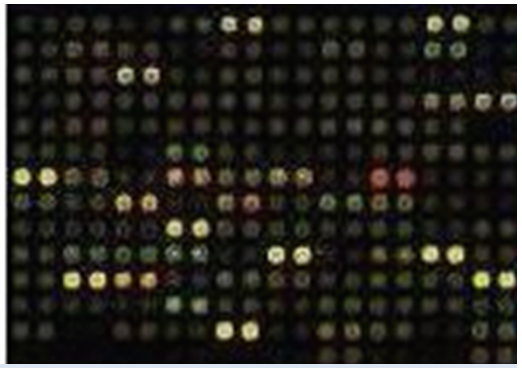


HCP's reported significantly higher feelings of confidence in each domain after attending the education session (all $p<0.05$).

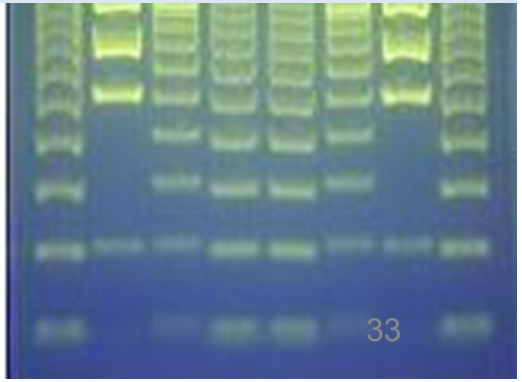
HCP Preparedness & Self-Efficacy Pre- vs. Post-Education



HCP's reported significantly higher feelings of preparedness (scale 1-4, p=0.037) and self-efficacy (scale 1-5, p=0.018) after attending the education session.

Cohort Description and Baseline Data

Patient-Participant Demographics

Airmen Demographics	
Characteristic – N (%) unless otherwise noted	N=93
Age (n=87)	
Mean in years (SD)	33.75 (±8.25)
Gender (n=93)	
Male	48 (51.6%)
Female	45 (48.4%)
Race/Ethnicity (n=93)	
Hispanic or Latino	17 (18.3%)
Non-Hispanic White	61 (65.6%)
Non-Hispanic Other*	13 (13.9%)
Prefer Not to Answer	2 (2.2%)
Education (n=93)	
Did not graduate from college	36 (38.7%)
College graduate or higher	57 (61.3%)
Annual Household Income (n=93)	
≤ $99,999	64 (68.8%)
≥ $100,000	29 (31.2%)

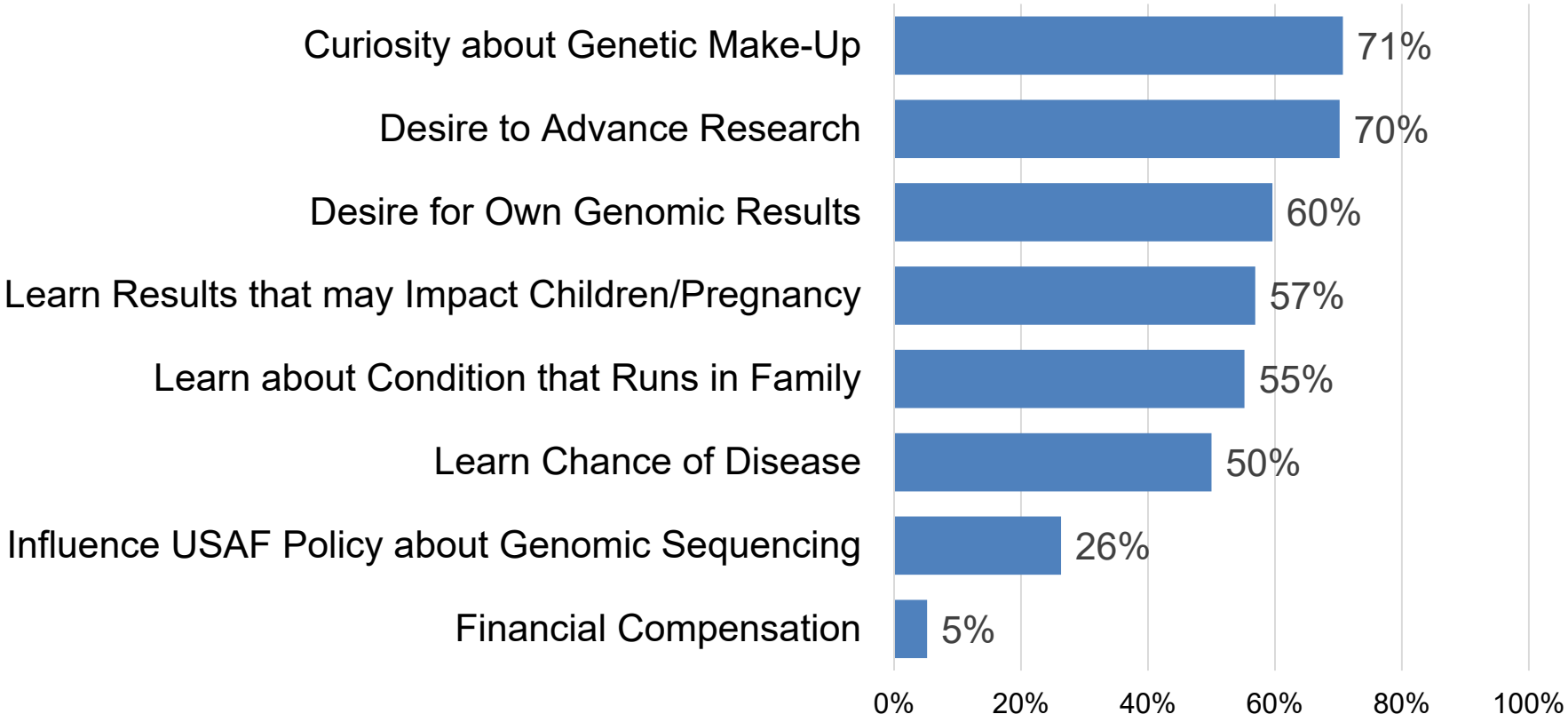
* Non-Hispanic Other includes African American, Asian, and Other

Healthcare Provider Demographics

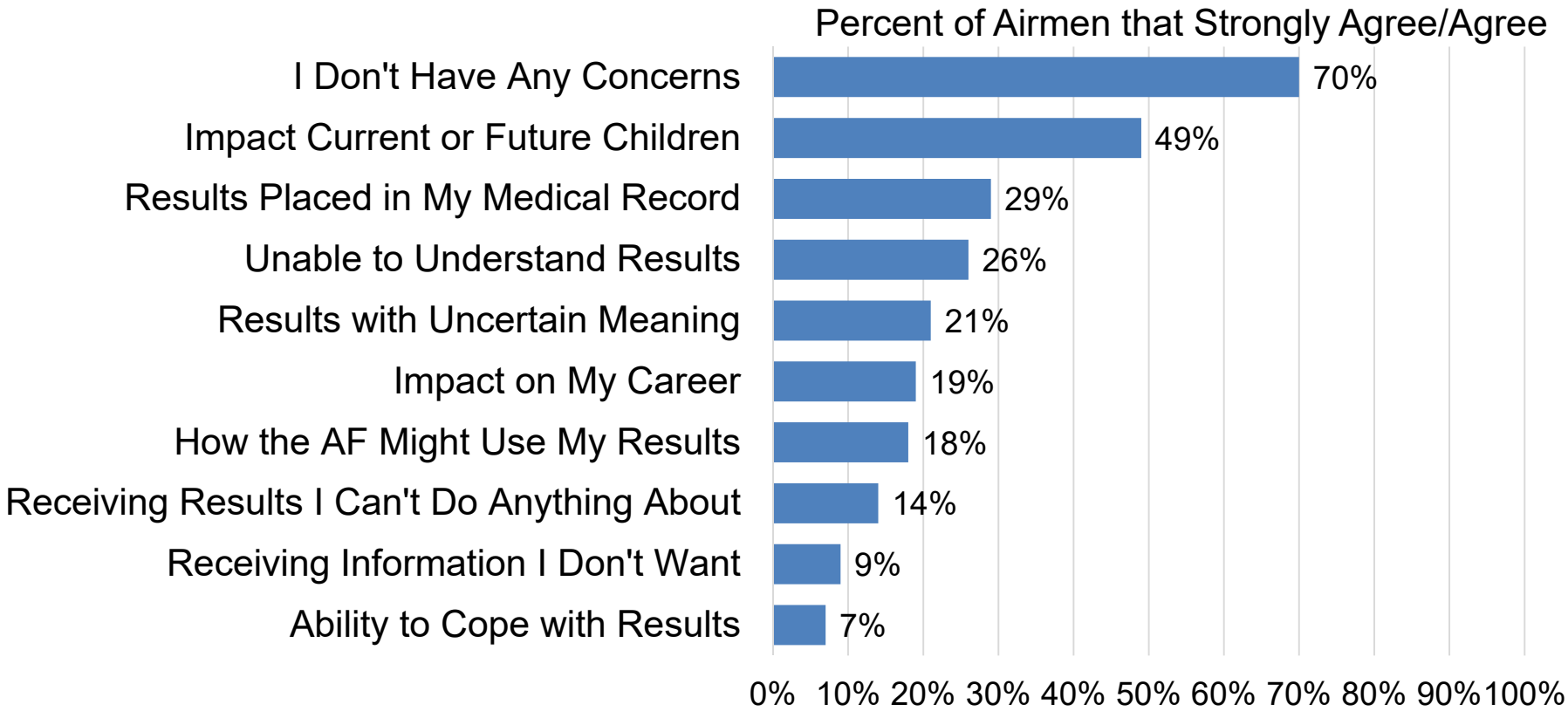
Health Care Provider Demographics	
Characteristic – N (%) unless otherwise noted	N=12
Age (n=11)	
Mean in years (SD)	39 (±9.25)
Gender (n=12)	
Male	8 (66.7%)
Female	4 (33.3%)
Race/Ethnicity (n=12)	
Hispanic or Latino	0 (0%)
Non-Hispanic White	6 (50%)
Non-Hispanic Other*	6 (50%)
Years in Practice (n=12)	
1-10	10 (83.4%)
21-30	2 (16.6%)
Genetics Training (n=12)	
No	11 (91.7%)
Yes	1 (8.3%)

* Non-Hispanic Other includes African American and Asian

Airmen's Motivations to Participate in a Genomic Sequencing Project



Airmen's Concerns about Participating in a Genomic Sequencing Project



Monogenic Disease Risk: 58 Exome Reports

- 4 participants (6.8%) with autosomal dominant findings
  - Familial hypercholesterolemia
    - Male, self-reported high cholesterol first diagnosed at 20 years of age
    - Cholesterol level of 300 on most recent lipid panel (2013)
    - Prescribed CRESTOR®* as a result of this finding
  - Dehydrated hereditary stomatocytosis I
    - Male, normal CBC, splenectomy contraindicated for affecteds
  - Familial exudative vitreoretinopathy
    - Female, no visual symptoms reported
  - Nonsyndromic hearing loss
    - Female, no hearing impairment reported

*The views of AstraZeneca are not necessarily the official views of, or endorsed by, the U.S. Government, the Department of Defense, or the Department of the Air Force. No Federal endorsement of AstraZeneca is intended.

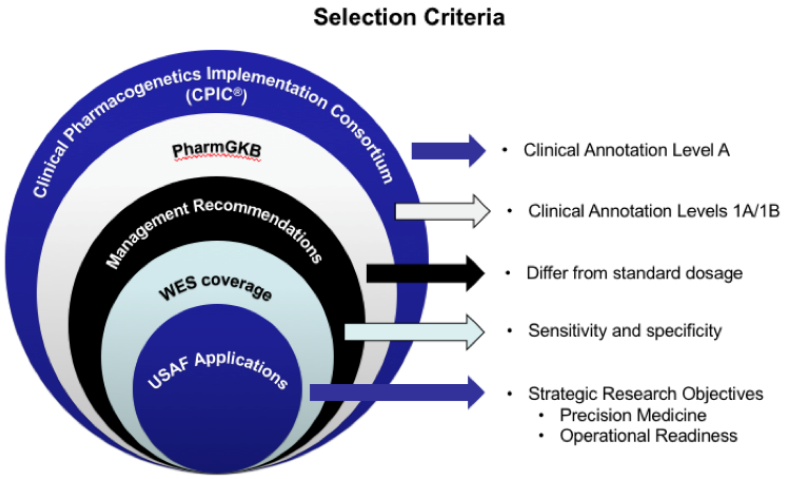
Carrier Status Variants: 58 Exome Reports

- 50 participants (86%) identified as carriers
  - Range: 0-6 per report; average: 2 per report
- Repeated findings:
  - Hereditary hemochromatosis: n=17
  - Stargardt disease: n=5
  - Primary ciliary dyskinesia: n=4
  - Thrombocytopenia with absent radius syndrome: n=4
  - Nonsyndromic autosomal recessive hearing loss: n=3

Carrier Status Variants: 58 Exome Reports 13 Possible Manifesting Heterozygotes!

- Congenital hypothyroidism: n=2
- Cystinuria: n=2
- Fanconi anemia: n=1
- Hypogonadotropic hypogonadism: n=1
- Myotonia congenita: n=1
- Nijmegen breakage syndrome: n=1
- Pseudocholinesterase deficiency: n=3
- Rippling muscle disease: n=1
- Sickle cell: n=1

All Participants have at Least One Atypical Pharmacogenomic Variants



PGx Panel Classifications & USAF Applications

Analgesic*	Anticoagulant	Anesthetic	Anticonvulsant	Psychiatric*
• Combat casualty care • Chronic pain management for combat-related disability • Musculoskeletal training injury	• Combat casualty care • Prophylaxis for post-amputation deep vein thrombosis	• Combat casualty care • Continuum of care for subsequent surgical interventions	• Combat casualty care • Traumatic brain injury	• Post traumatic stress disorder • Combat-related depression and anxiety • Sleep disturbances

**CYP2D6* variants are salient for informing pain management and mental health treatments in the USAF. WES may not be reliable for the detection of *CYP2D6* whole-gene duplications (decreased sensitivity). Therefore, supplemental CNV analysis is performed for inclusion in the MilSeq Project PGx panel.

Lessons from the MilSeq Study

- Multi-disciplinary team has demonstrated that sequencing can be integrated into the practice of military medicine
- Substantial number of Airmen interested in sequencing and are not deterred by thorough informed consent process.
- Participants are not distressed, even for positive findings.
- High motivation to learn about their own health (personal and reproductive)
- HCPs do not initially rate themselves as prepared but the 3-hour education module modestly improves their self-perceived level of preparedness
- Surprising amount of information pertinent to operational readiness (disease risk, performance vulnerabilities, pharmacogenomics, rapid and accurate typing for blood transfusion)

MilSeq Project Publications

npj | Genomic Medicine

www.nature.com/npjgenmed
All rights reserved 2056-7944/16

PERSPECTIVE OPEN

Genomic medicine in the military

Mauricio De Castro[1], Leslie G Biesecker[2], Clesson Turner[3], Ruth Brenner[4], Catherine Witkop[4], Maxwell Mehlman[5,6], Chris Bradburne[7] and Robert C Green[8]

Molecular Genetics & Genomic Medicine

Open Access

INVITED COMMENTARY

Military genomics: a perspective on the successes and challenges of genomic medicine in the Armed Services

Mauricio J. De Castro[1] & Clesson E. Turner[2]

[1]United States Air Force Medical Genetics Center, 81st Medical Group, Keesler AFB, Mississippi 39534
[2]Division of Genetics, Department of Pediatrics, Walter Reed National Military Medical Center, Bethesda, Maryland 20889

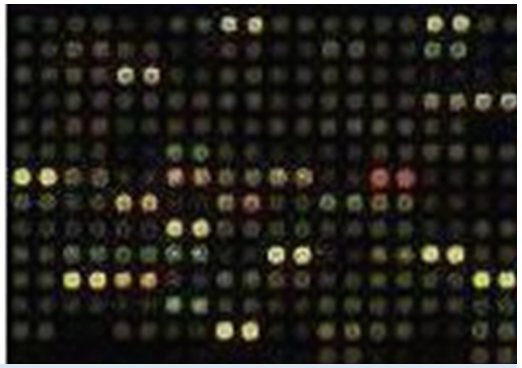
MilSeq Project Scientific Conference Presentations

2017

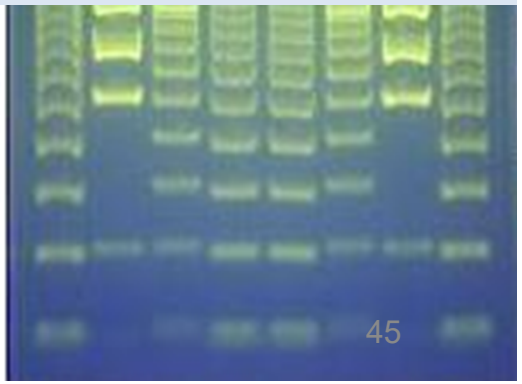
- Military Operational and Readiness Precision Medicine
- American Society of Human Genetics

2018

- Law and the Biosciences
- American Society of Law, Medicine and Ethics
- American College of Medical Genetics and Genomics
- Military Health System Research Symposium
- American Society for Bioethics and Humanities
- American Society of Human Genetics
- National Society for Genetic Counselors
- US Army Center for Environmental Health Research Science
- Integrative and Collaborative Biomedical Research



Future Potential



Potential Benefit to Warfighter

- Health and morale of warfighters and their families
- Identification of rare donors for blood transfusions
- Awareness of increased occupational risks
- Leveraging of genetic advantages
- Countermeasures for security vulnerabilities

The MilSeq Project – Future Potential

- Evaluate scalability by expanding the number of active duty military in MilSeq Project
  - Improve overall health of service members and families
  - Tailor warfighter performance with genetic/physiological strengths
  - Identify rare blood donors and recipients for transfusion
- Utilize existing DNA repositories and create DHA biobanks to improve knowledge base
- Contribute to ongoing security discussions

Thank you !

Carrie L. Blout, MS, CGC
Ruth Brenner, MD, Lt Col, USAF
Kurt D. Christensen, PhD, MPH
Mauricio DeCastro, MD, Maj, USAF
Cubby Gardner, PhD, Maj, USAF
Robert C. Green, MD, MPH
Jacqueline Killian, PhD, Lt Col, USAF
Joel B. Krier, MD, MMSc
Matthew Lebo, PhD
Amy L. McGuire, JD, PhD
Megan D. Maxwell, MS, LCGC
Maxwell J. Mehlman, JD
Debra Neimeyer, PhD, CIV, USAF
Efthimios Parasidis, JD, MBioethics
Stacey Pereira, PhD
Jill O. Robinson, MA
Jason L. Vassy, MD, MPH, SM
Jameson Voss, MD, MPH, Maj, USAF

Clifton Dalgard, PhD, USUHS
Lydia Hellwig, ScM, CGC
Luis Rohena, MD, Maj, US Army
Clesson Turner, MD, Lt Col, US Army

Jacqueline Killian, PhD, Lt Col, USAF: jacqueline.m.killian.mil@mail.mil
Robert Green, MD, MPH: rcgreen@bwh.harvard.edu
Megan Maxwell, MS, LCGC: mdmaxwell@bwh.harvard.edu