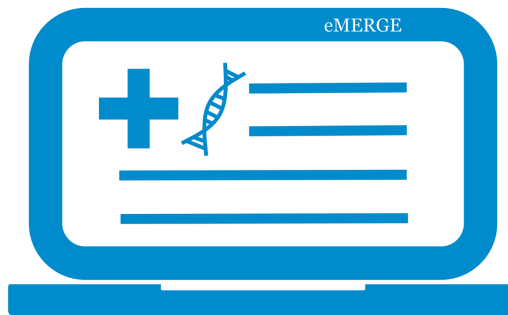


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eMERGE & Beyond Workshop Summary

Sharon E. Plon, MD, PhD, FACMG
National Advisory Council for Human Genome Research
(NACHGR)

February 12th, 2018

eMERGE & Beyond Webpage for Workshop Summary & Video Cast

eMERGE & Beyond: The Future of Electronic Medical Records and Genomics

October 30, 2017



On October 30th, 2017, the National Human Genome Research Institute (NHGRI) is hosting a program review workshop entitled *eMERGE and Beyond: The Future of EHR and Genomics*. The Electronic Medical Records and Genomics (eMERGE) network conducts genomic discovery and clinical implementation research by leveraging data from large biorepositories linked to electronic medical records. The workshop serves to highlight accomplishments of eMERGE as well as identify potential eMERGE future directions. The workshop will identify gaps, discuss challenges and define future opportunities in genomic medicine research.

The workshop will focus on the following four main topics:





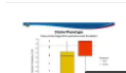
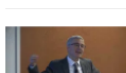

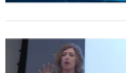



- Evidence generation for genomic medicine
- Identification of novel and disruptive opportunities in genomic medicine
- Electronic phenotyping for genomic research
- Electronic Medical Records (EMR) integration of genomic results and automated decision support.

YouTube Video Playlist

All workshop slides and materials are in PDF format.

[Printable Agenda](#) | [Meeting Roster](#) | [Executive Summary](#) | [Workshop Summary](#)

Agenda	
Opening Remarks	
8:00 - 8:15 a.m.	Welcome, Introduction & Opening Remarks Eric Green, Rongling Li Video
8:15 - 8:30 a.m.	NHGRI Genomic Medicine Portfolio Teri Manolio Video - Slides
8:30 - 9:15 a.m.	eMERGE Program Overview Rex Chisholm Video - Slides

- 
eMERGE & Beyond: Welcome, Introduction & Opening Remarks - Eric Green
 National Human Genome Research Institute
- 
NHGRI Genomic Medicine Portfolio - Teri Manolio
 National Human Genome Research Institute
- 
eMERGE Program Overview - Rex Chisholm
 National Human Genome Research Institute
- 
All of Us Program Synergy with eMERGE - Stephanie Devany
 National Human Genome Research Institute
- 
VA Million Veterans Program Phenomic Science - Michael Gaziano
 National Human Genome Research Institute
- 
Electronic Phenotyping for Genomic Research (eMERGE) - George Hripcsak
 National Human Genome Research Institute
- 
Electronic Phenotyping for Genomic Research - Ken Kawamoto
 National Human Genome Research Institute
- 
Electronic Phenotyping for Genomic Research (Discussion)
 National Human Genome Research Institute
- 
Electronic Phenotyping for Genomic Research - Josh Denny/Marylyn Ritche
 National Human Genome Research Institute
- 
Evidence Generation for Genomic Medicine (eMERGE) - Gail Jarvik
 National Human Genome Research Institute
- 
Evidence Generation for Genomic Medicine (eMERGE) - Marc Williams
 National Human Genome Research Institute

eMERGE & Beyond Workshop Goals

1

Review the current goals and accomplishments of eMERGE

2

Identify concepts and gaps of interest in the field of Genomic Medicine that a potential new phase of eMERGE could address

eMERGE Phases (2007-2019)



- Can EMR and biobank be used for genomic research?

- Genome-wide genotyping
- GWAS

- Can genomic findings be applied in clinical care and how?

- Clinical implementation pilots
- GWAS

- Can sequence data in clinically relevant genes be used to assess penetrance and improve clinical care?

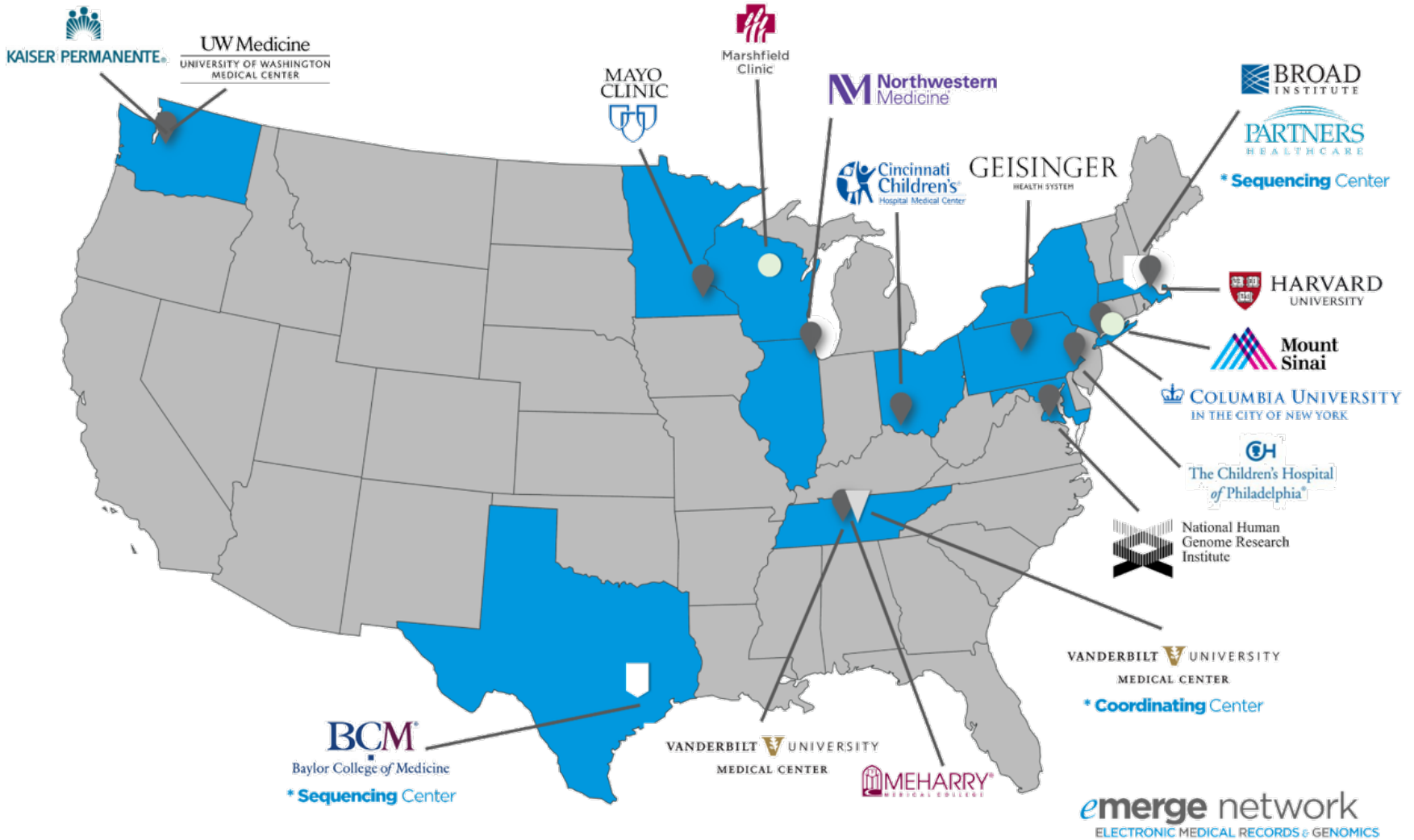
- Electronic phenotyping
- Sequencing
- Clinical implementation
- GWAS

ELSI Research

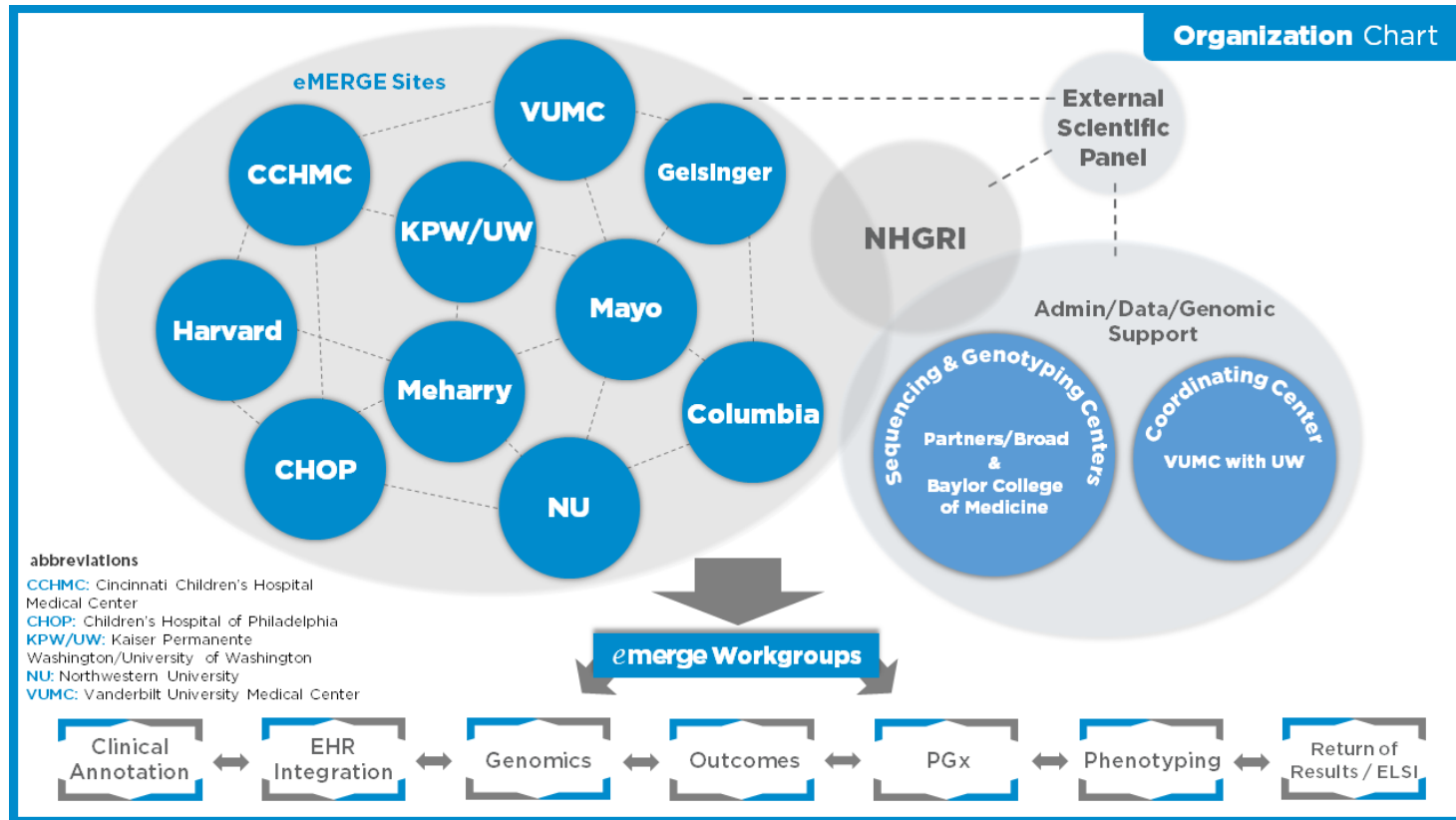
eMERGE Phase III Goals

- 1** Sequence and assess clinically relevant genes in about 25,000 individuals
- 2** Assess the phenotypic implications of these variants
- 3** Integrate genetic variants into EMRs for clinical care
- 4** Create community resources

The eMERGE Network



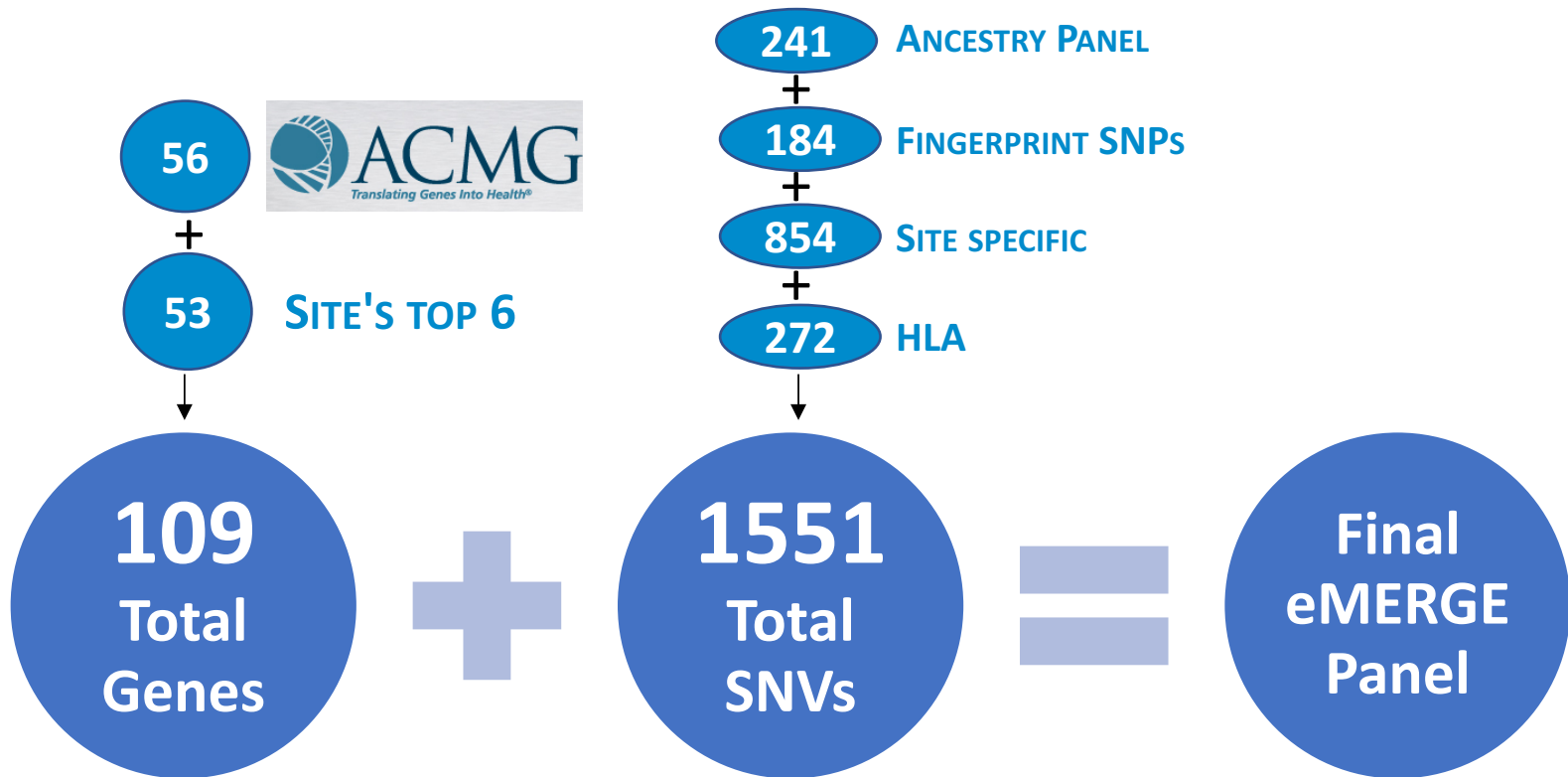
eMERGE Organization Chart



eMERGE SUBGROUPS	
Familial Implications of ROR	HLA
Infobutton	ROR Legal Considerations
Participant Survey	Phenotype Variables

eMERGE SUPPLEMENTS	
Geocoding	Health Care Provider Survey
Phenotyping – OMOP Model	

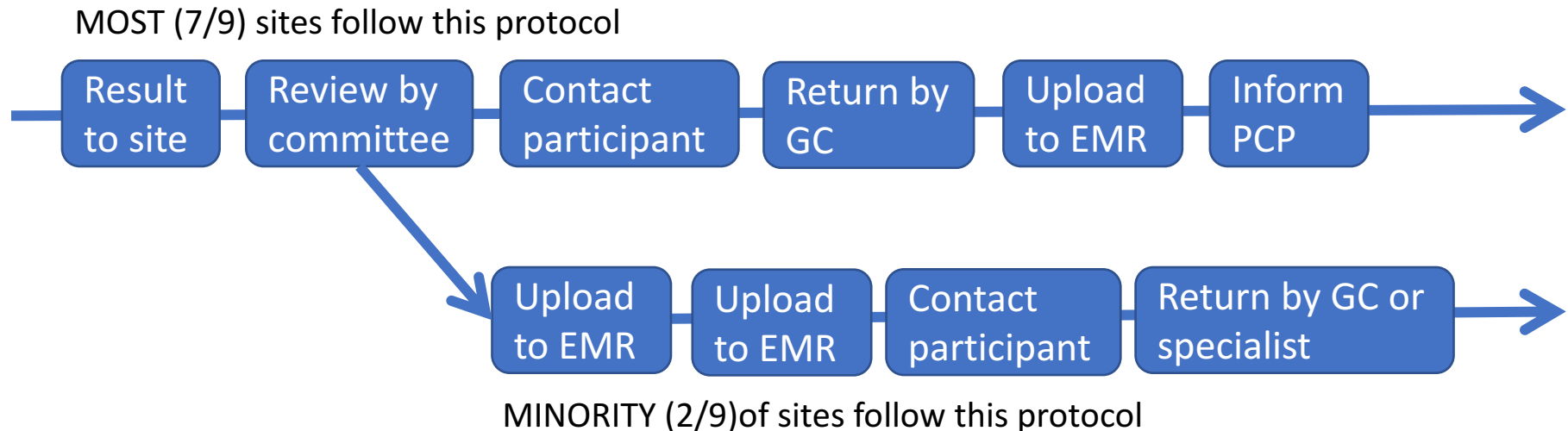
Deliverable: Development of an eMERGEseq Platform



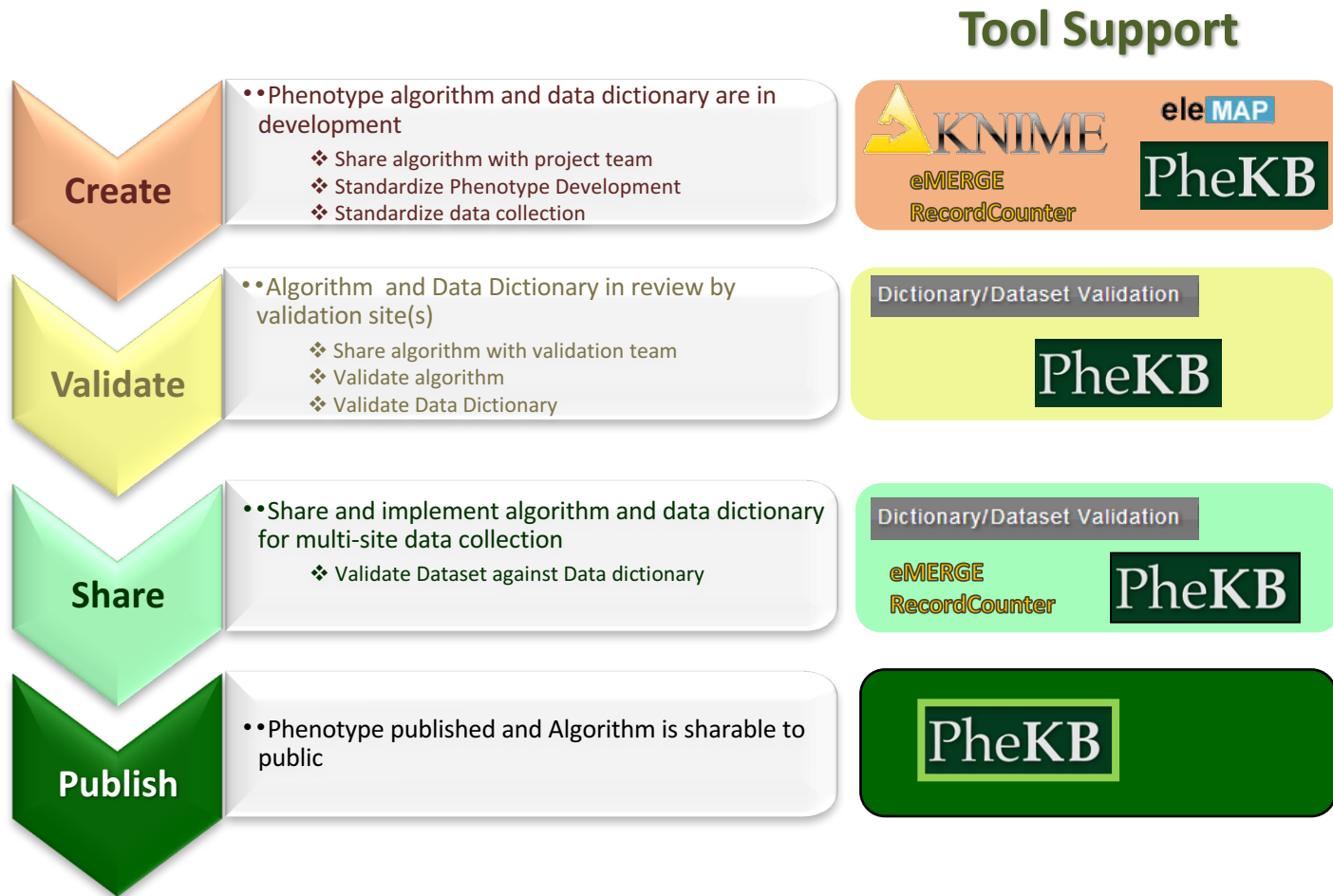
- Clinical reports are generated on the “Consensus Actionable List” and any specific genes or SNVs requested by individual sites

Process of return of results in Phase 3 across the eMERGE sites

All 9 sites return 68 common genes plus institutional genes. However, no two sites have the same process.

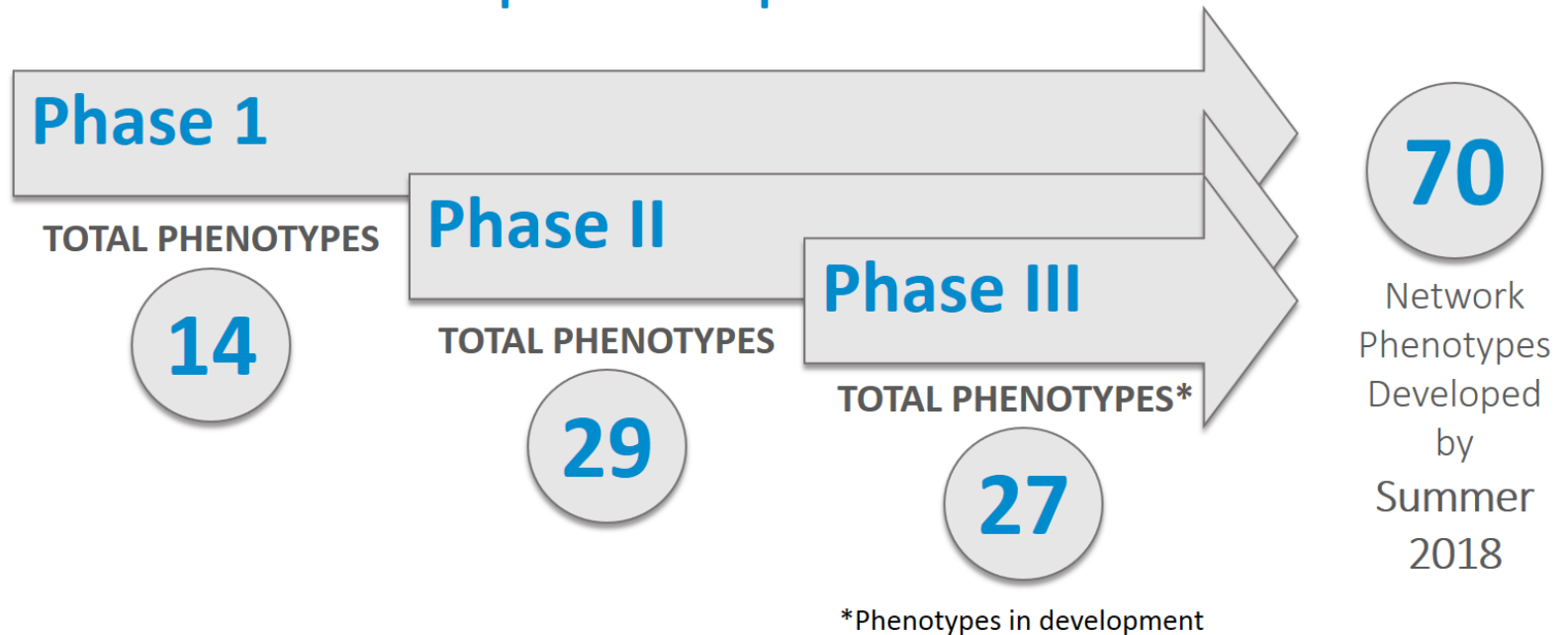


EMR Phenotypes Development Workflow



Development of EMR Phenotypes in eMERGE

PHENOTYPES: Development & Implementation



eMERGE & Beyond Workshop 10/30/2017

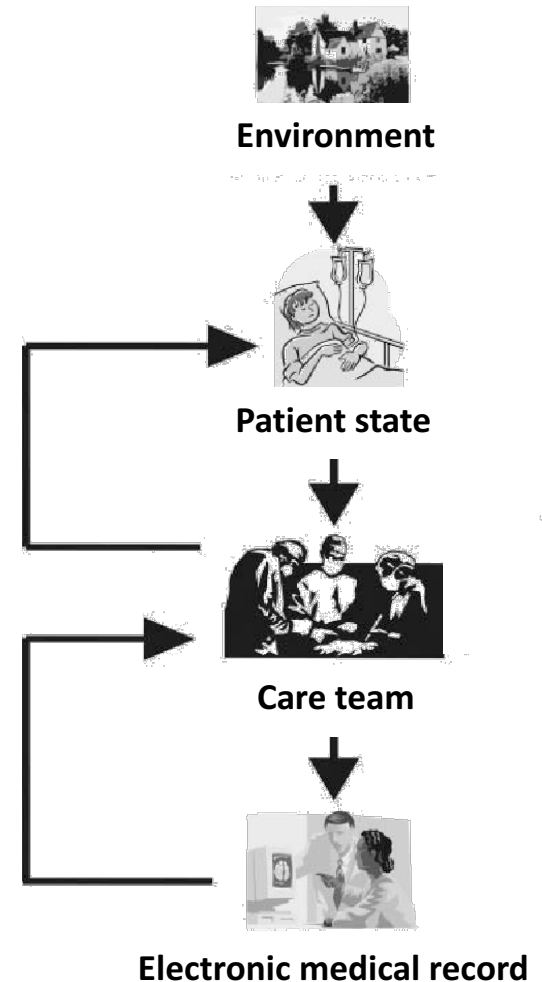
Major topics discussed and recommendations developed

1. Electronic Phenotyping for Genomic Research
2. Evidence Generation for Genomic Medicine
3. EMR Integration of Genomic Results and Automated Decision Support
4. Novel and Disruptive Opportunities in Genomic Medicine



Key Recommendations: Electronic Phenotyping for Genomic Research

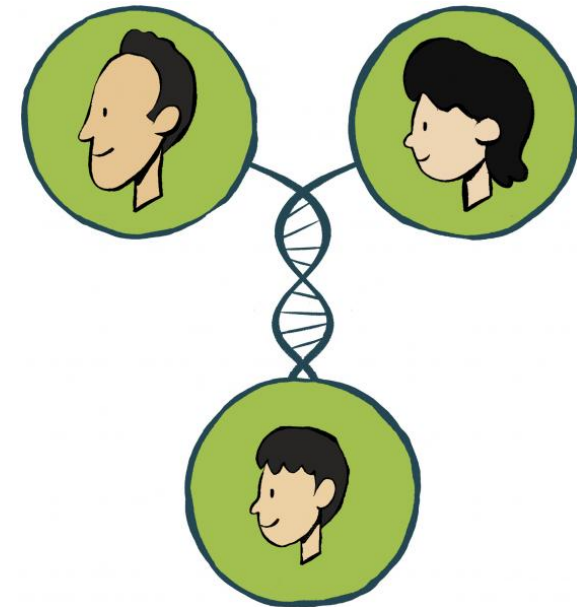
- Focus on developing **better phenotyping methods** and technologies, such as:
 - Continuum of disease severity rather than absent/present binary disease
 - Longitudinal phenotyping to gain information on the time course of conditions
- Experiment with alternative or more automated phenotyping strategies to **improve speed and efficiency**
 - Alternate approaches to manual phenotype validation
- Find more efficient ways to **pool, normalize and analyze data across consortium sites**





Key Recommendations: Evidence Generation for Genomic Medicine

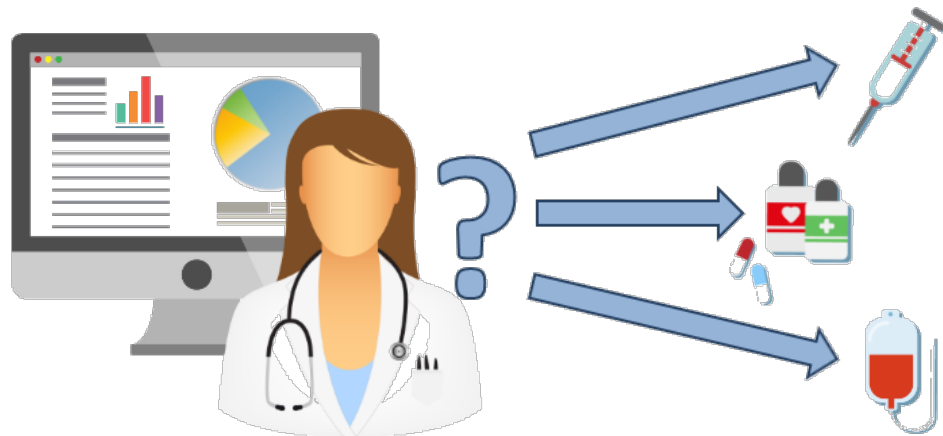
- Develop and **document best practices** from the studies already completed in eMERGE
- Seek appropriate **balance between standardization and experimentation** with study designs
- Improve capture of **standardized family history data** across all site
- **Consider different study designs** including more automated ROR to clinicians
- Study the value and **impact of reporting negative results**
- **Create data standards** for new types of genomic medicine “data objects”
- Ensure study designs provide for **longer-term outcomes assessment** of testing, ROR and downstream testing





Key Recommendations: EMR Integration of Genomic Results and Automated Decision Support

- **Further automate clinical pipelines for variant classification**
- **Develop tools and standardized displays** to synthesize and present information at the point of care with a focus on decision support
- **Narrow the scope of eMERGE** to develop CDS in high-priority areas
- **Develop user-centered designs** through eCDS
- Build foundations that **promote shareable eCDS across centers**
- **Develop closed-loop CDS** with automated outcome assessment tools



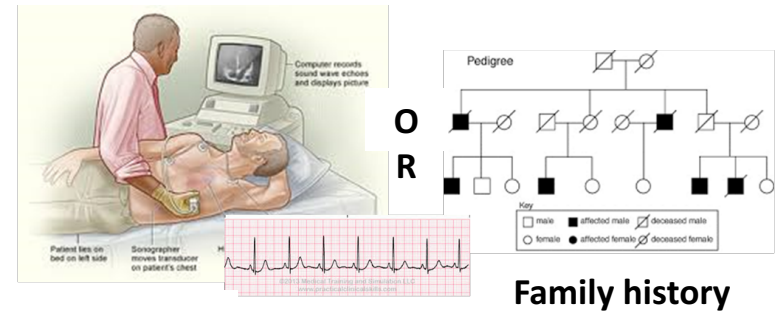
Key Recommendations: EMR Integration of Genomic Results and Automated Decision Support (cont)

- Explore **patient-specific factors** that might increase or decrease the importance of genomic information in the CDS
- **Develop roadmap** for naïve adopters of genomic data implementation in EMR
- **Develop standard extraction of EMR** for research across sites within and outside eMERGE



Key Recommendations: Novel and Disruptive Opportunities in Genomic Medicine

- Develop **real time variant interpretation** using publicly available data (eg ClinGen) matched to patient's phenotype
- Assess **crowdsourcing** of variant interpretation
- Develop methods to efficiently **re-interpret genomic results over time**
- **Apply deep learning techniques** to the characterization of uncertain variants, drug targets, etc.

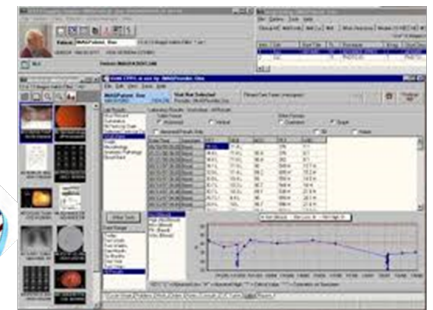
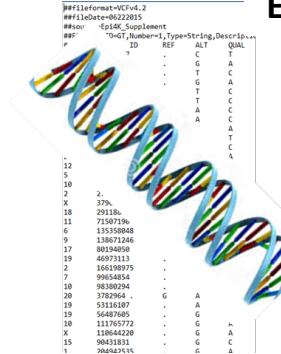


Symptoms



Family history

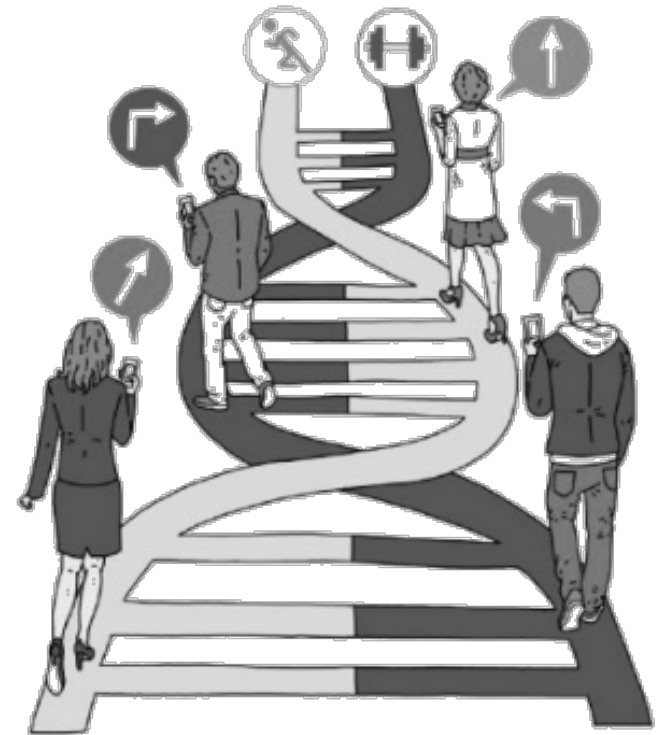
EMR with Genomic data (VCF file)





Key Recommendations: Novel and Disruptive Opportunities in Genomic Medicine (cont.)

- **Link EMR-derived phenotypes** with other classes of -omics data
- Develop **innovative ways to present sequence** information (apps) to physicians
- **Enhance clinical methods** for assessing pathogenicity and penetrance
- Encourage **patient-centered data governance**
- Evaluate the legal and ethical implications of **directly contacting relatives of patients** potentially harboring deleterious variants





Overall Summary of Recommendations

- Decide on the **appropriate balance between innovation and standardization** across sites to increase power of data analysis
- **Expedite variant classification** by automation, machine learning and crowdsourcing.
- Test **innovative ways to present genomic results** to physicians, patients and perform longitudinal follow-up of patients. Try to shift sequencing and ROR early in the funding cycle.
- Increase **efficiency of developing EMR-derived phenotypes**
- **Increase engagement of diverse patient populations** on ELSI issues related to genomic testing and use of electronic health records
- **Facilitate usefulness of eMERGE tools and analyses across multiple research consortia and diverse healthcare systems**

Acknowledgements

Planning Committee

- Rex Chisholm
- Dan Masys
- Howard Mcleod
- Sharon Plon

Workshop Attendees

- eMERGE attendees
- External attendees

eMERGE NHGRI Program Staff

- Jyoti Gupta
- Sheethal Jose
- Rongling Li
- Teri Manolio
- Robb Rowley
- Ken Wiley

<https://www.genome.gov/27569445/>

