

# Return of Genomic Results Current Applications and Challenges



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On Behalf of the ROR Work Group

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Essentia Health  
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GEISINGER



The Children's Hospital  
of Philadelphia®



# eMERGE ROR

Co-chairs	Workshop Panel members
Gail Jarvik Iftikhar Kullo	Lawrence Meyer, Susan Wolf, Lisa Parker, Iftikhar Kullo, Gail Jarvik

<b>CHOP</b>	John Connolly, Hakon Hakonarson, Brendan Keating
<b>CCHMC/BCH</b>	Armand Antommaria, John Harley, Ingrid Holm, Melanie Myers, Bahram Namjou, Cassandra Perry, Cindy Prows, Sander Vinks, Wendy Wolf
<b>Geisinger</b>	Glenn Gerhard, David Ledbetter, Agnes Sundaresan, Gerard Tromp, Marc Williams
<b>Group Health/UW</b>	Gail Jarvik, David Crosslin, Kelly Ehrlich, Malia Fullerton, Carlos Gallego, Kathy Leppig
<b>MCEIRH/PSU</b>	Murray Brilliant, Terrie Kitchner, Cathy McCarty, Marylyn Ritchie
<b>Mayo</b>	Richard Sharp, Iftikhar Kullo, Jen McCormick,
<b>Mount Sinai</b>	Erwin Bottinger
<b>Northwestern</b>	Steve Persell, Laura Rasmussen-Torvik, Maureen Smith, Cathy Wicklund
<b>Vanderbilt</b>	Kyle Brothers, Ellen Clayton, Julie Field, Tracy McGregor, Dan Roden, Quinn Wells
<b>NIH/NHGRI</b>	Lucia Hindorff, Rongling Li, Rochelle Longbottom, Teri Manolio, Jackie Odgis, Erin Ramos

# **EVOLUTION OF ROR IN EMERGE**

## Return of individual research results from genome-wide association studies: experience of the Electronic Medical Records and Genomics (eMERGE) Network

Stephanie M. Fullerton, DPhil<sup>1</sup>, Wendy A. Wolf, PhD<sup>2</sup>, Kyle B. Brothers, MD<sup>3</sup>, Ellen Wright Clayton, MD, JD<sup>3</sup>, Dana C. Crawford, PhD<sup>3</sup>, Joshua C. Denny, MD<sup>3</sup>, Philip Greenland, MD<sup>4</sup>, Barbara A. Koenig, PhD<sup>5,6</sup>, Kathleen A. Leppig, MD<sup>7</sup>, Noralane M. Lindor, MD<sup>5</sup>, Catherine A. McCarty, PhD, MPH<sup>8,9</sup>, Amy L. McGuire, JD, PhD<sup>10</sup>, Eugenia R. McPeck Hinz, MD<sup>3</sup>, Daniel B. Mirel, PhD<sup>11</sup>, Erin M. Ramos, PhD, MPH<sup>12</sup>, Marylyn D. Ritchie, PhD, MS<sup>13</sup>, Maureen E. Smith, MS, CGC<sup>4</sup>, Carol J. Waudby, MS<sup>8</sup>, Wylie Burke, MD, PhD<sup>1</sup> and Gail P. Jarvik, MD, PhD<sup>1</sup>

- ROR in the context of the EHR
- ROR in the context of age
- Evidence of clinical validity and actionability
- Appropriate methods for ROR
- Diversity of opinion across sites
- Input from lay community, advisory bodies

# Phase II- Genomic medicine pilots

- **Genetic risk scores**
  - Essentia: 7 SNPs assoc with Macular degeneration
  - Mayo: 28 SNPs assoc with heart attack
- **SNPs**
  - Mount Sinai: *ApoL1* for hypertensive renal dz in AA
  - Northwestern: *HFE* and *FV*
- **WGS**
  - Geisinger: Whole genome sequencing in trios
- **PGx**
  - *CYP2D6* results to parents and providers
  - Hypothetical return of *CYP2D6*

# An EHR-based genomic medicine pilot study



## What is Your Risk of Heart Attack?

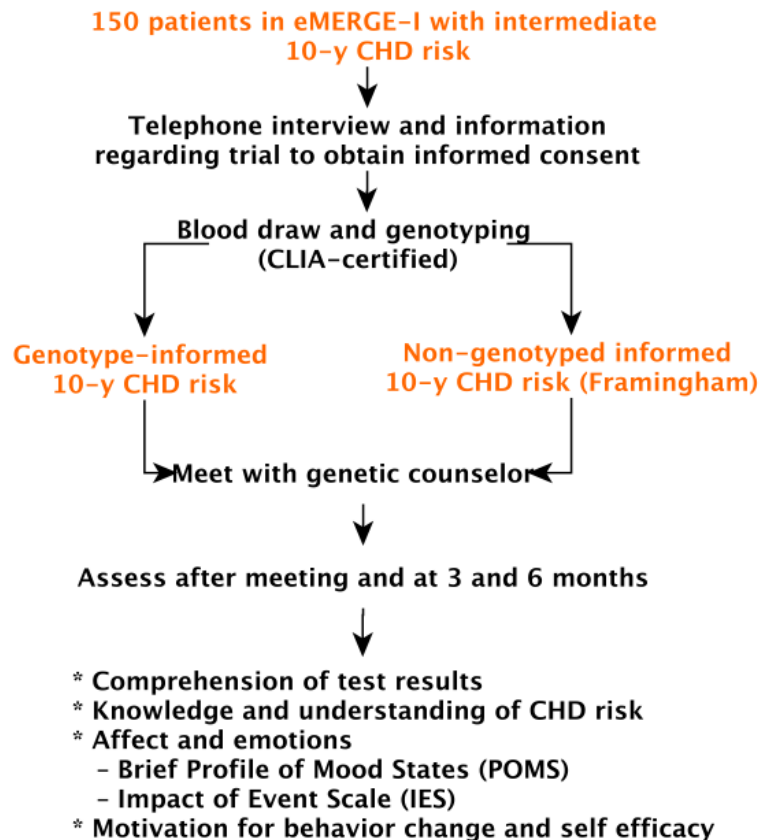
Mayo Clinic is seeking individuals by invitation to participate in the Myocardial Infarction Genes (MI-GENES) Study. The purpose of this study is to understand how genetic information might improve assessment of heart attack risk.

You may be eligible to participate if:

- You are between the ages of 45-70
- You live in Southeast Minnesota
- You do not take statin medications
- You have participated in the Mayo Clinic Biobank or a previous research study at Mayo Clinic

The study includes 4 visits (see back for details). We will ask you to provide blood samples, complete surveys, and meet with a genetic counselor, as well as a clinician. You will be compensated for your time.

For more information, please contact the study team at (507) 293-0177.



# Phase II- Network-wide projects

- eMERGE PGx
- Copy number variation
- *HFE* variants

Site	C282Y/C282Y	C828Y/H63D	H63D/H63D	Sum
Geisinger	12	67	110	189
GHC/Seattle	17	60	72	149
Marshfield	15	52	87	154
Mayo	44	179	206	4
Mt. Sinai	1	12	29	42
Northwestern	19	64	81	164
Vanderbilt	39	152	141	332
<b>Total</b>	<b>147</b>	<b>586</b>	<b>726</b>	<b>1459</b>

# **FUTURE DIRECTIONS**



BIOREPOSITORIES



WIDESPREAD USE  
OF EHRs



GENOME  
SEQUENCING

# ROR: Unique potential of eMERGE

- EHR-based genomic discovery
  - ‘Longitudinal’ phenotypes
  - Pleiotropy (PheWAS)
- EHR based genomic implementation
  - Storage, visualization and integration
  - Decision support
  - Incidental findings
  - Outcomes
- The learning EHR

# ROR - Discovery

- Incidental findings
- Mechanism and timing of ROR
- Consent
- Patient preferences
- CLIA confirmation
- Documentation in EHR
- Family members
- Pediatric setting

Jarvik et al, Manuscript in preparation, joint CSER and eMERGE effort

# ROR - Implementation

## What could be returned

CNV  
? recessive mutations

- Single SNVs
  - PGx
  - Disease risk
- Genetic risk scores  
CHD, AMD, T2D

IFs from resequencing,  
(whole exome, whole genome, targeted)

## Prepare for return

Jurying

CLIA lab testing

Statistical modeling

EHR integration

## Areas of study

ELSI

Storage & Re-interpretation

Clinical Decision Support

Outcomes

# Potential projects

- **WES (n = 1000 each site):** phenotypes, penetrance, pleiotropy, pediatric considerations
- **Targeted sequencing** for the 56 ACMG genes to determine pathogenicity, penetrance, informing kin, etc.
- **Clinically indicated panels:** cardiomyopathies, pediatric syndromes
- **High-density genotyping** - common and rare variants

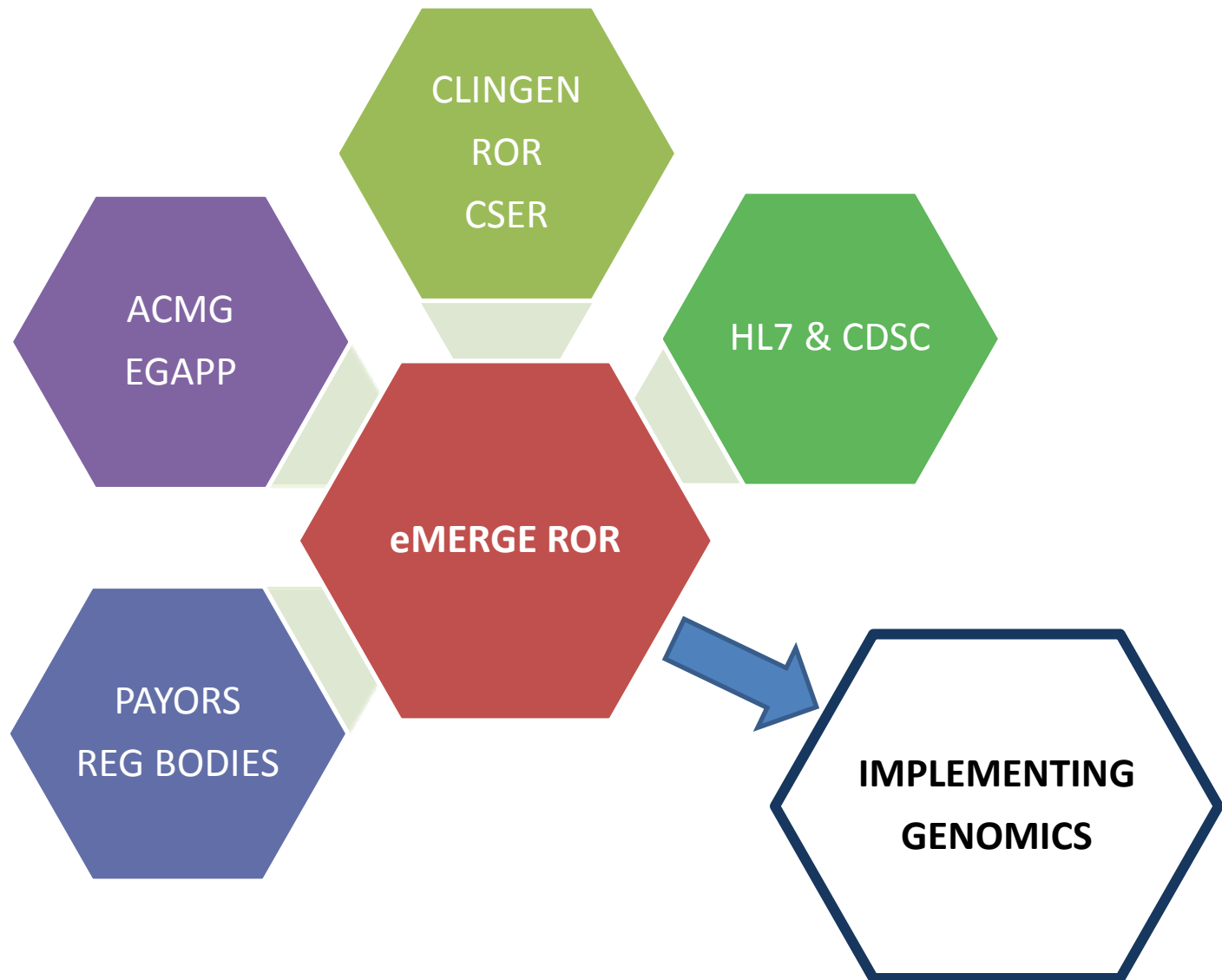
# Consent

- Participant **privacy** and potential vulnerability to adverse social consequences
- Consent to include genomic **data in the EHR**
- **Recontact** to ascertain preferences and re-consent
- **Electronic ascertainment of preferences** over time

# Stakeholders

- **Participants**, parents/guardians in pediatric projects, legally authorized representatives for adult incompetents, deceased
- **Family members**
- **Care providers**
- **Laboratorians**
- **Investigators**
- **Biorepository scientists**

# eMERGE ROR interactions





# Summary

- eMERGE is uniquely positioned to address these knowledge gaps and challenges
  - Linkage to EHR with deep and diverse phenotypes
  - Diversity of clinical settings and EHRs
  - Diversity of genomic information
  - Best practices for implementation
  - n=50,000 including pediatric patients