Concept Clearance Centers for Mendelian Genomics Program Renewal

National Advisory Council for Human Genome Research September 8, 2014



Centers for Mendelian Genomics Program Renewal Purpose

- "Solve" Mendelian disorders at scale at funded centers
- Enable and coordinate with others

"Solve" all or most Mendelian disorders

Centers for Mendelian Genomics (CMGs) Funded by NHGRI and NHLBI Nov 2011 – Current

- 1. Demonstrated the power of sequencing at scale for solving Mendelian disorders
- 2. Discovered the genomic basis of ("solved") over 165 Mendelian disorders; over 100 publications
- 3. Revealed the extent of pleiotropy and genetic heterogeneity underlying Mendelian disorders
- 4. Developed and disseminated resources and innovative methods

Remaining Mendelian Disorders to Solve

Mendelian disorders

~7,300

 Mendelian disorders with known molecular basis ~3,600

 Mendelian disorders with unknown molecular basis ~3,700

 Additional Mendelian disorders described every year

Much work remains to be done in order to solve all Mendelian disorders

CMG Program Renewal Scope and Objectives - 1

- Solving 300 or more Mendelian disorders to learn what it will take to solve all Mendelian disorders
- 2. Enabling others and coordination
 - Developing methods and tools
 - Disseminating resources
 - Outreach and coordination

- 1. Solving 300 or more Mendelian disorders
 - Expecting improvement of efficiency and costs, but fewer "low-hanging fruit" disorders
 - Studying disorders exhibiting a wide range of phenotypes
 - Understanding the genetic characteristics of Mendelian disorders
 - Learning what it will take to solve all Mendelian disorders
 - New features
 - Implementing whole genome sequencing
 - Performing small-scale function assays
 - Solving additional disorders with potentially available funds

2. Enabling and coordinating with others

- Refining/developing methods and tools
 - Approaches genotype driven, phenotype driven, or combination with non-sequencing genomic methods (through collaborations), etc.
 - Tools for collection and evaluation of phenotype information
 - Efficiency and cost improvement for sequence data production
 - Data analyses of difficult genomic regions, such as repeat expansions, CNVs, fusions, etc.

- 2. Enabling and coordinating with others
 - Dissemination
 - Methods and tools
 - Data
 - o dbGaP
 - "Causal" allele information at the CMG Browser and other sites
 - Allele counts

- 2. Enabling and coordinating with others
 - Outreach and coordination
 - Reaching out to individual researchers; training
 - International Rare Diseases
 Research Consortium (IRDiRC)
 activities
 - Coordination (sharing lists of disorders, matching samples or candidate disease genes, etc.)

The goal of solving most/all MCs requires unprecedented cooperation & coordination among clinicians & scientists worldwide – Rod McInnes



CMG Program Renewal Relationship to Other NIH Programs

- Proposed Common Disease Variant Discovery Centers (CDVD Centers)
- Proposed Genome Sequencing Program Coordinating Center
- NHGRI Clinical Sequencing Exploratory Research (CSER)
- NIH Undiagnosed Diseases Network (UDN)

CMG Program Renewal Proposed Mechanism and Funds

Mechanism

- Cooperative agreement mechanism
- Advice and guidance from an external scientific panel (ESP)
- Steering committee and working groups

Funds

- \$40 M NHGRI funds for Nov 2015 Nov 2019, \$10 M annually
- Seek co-funding from other NIH Institutes

RFA

- Up to three CMGs
- RFA open to all applicants

CMG Program Renewal Summary of Concept

- Solve 300 or more Mendelian disorders using genome-wide sequencing
- Enable others with methods and resources, and coordinate projects worldwide
- Cooperative agreement mechanism
- \$40 M total NHGRI funds