Centers for Mendelian Genomics
RFA-HG-15-002

Applicant Webinar
3:00-4:30 PM EST

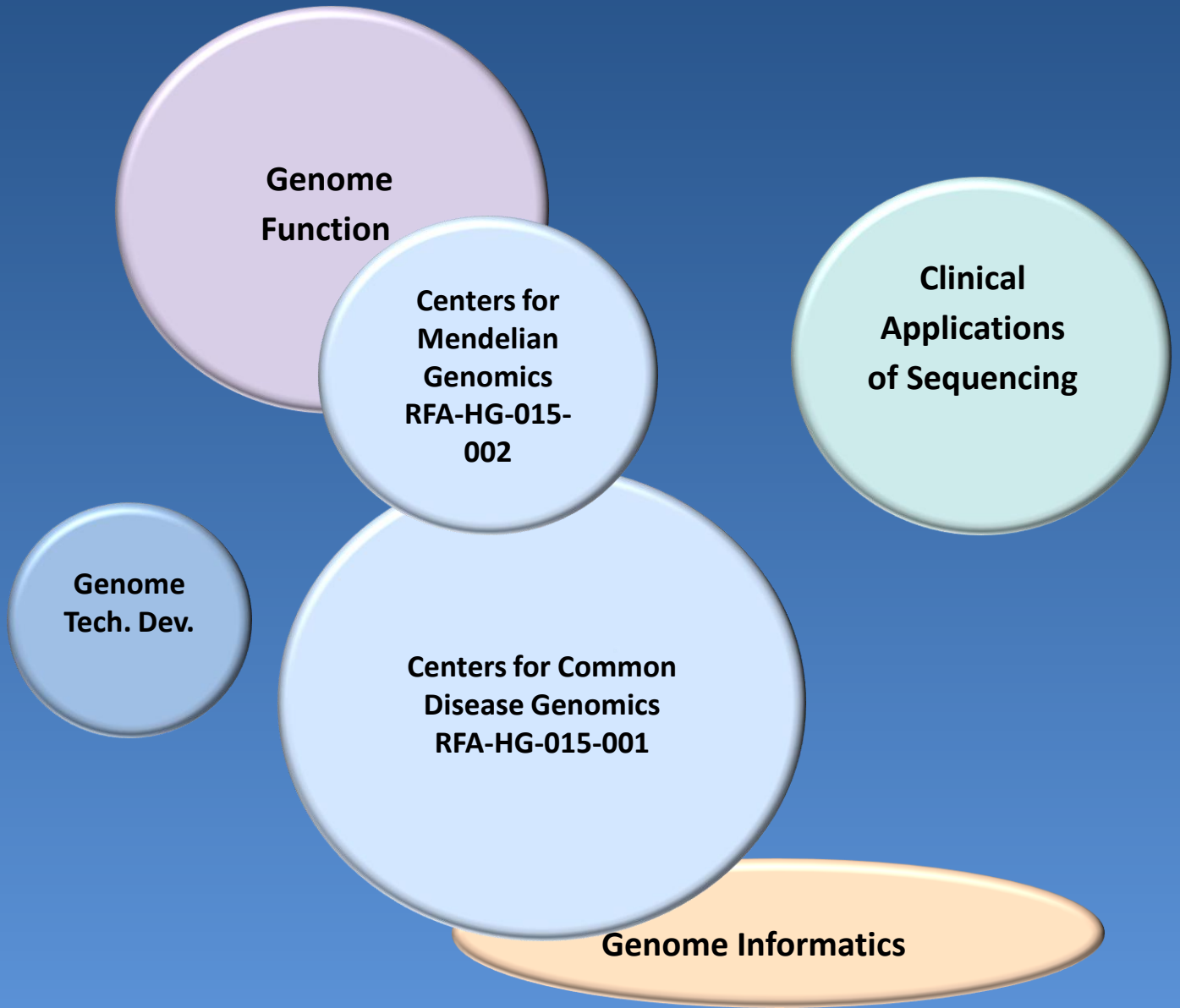
Please email questions to
NHGRISequencingRFAWebinar@mail.nih.gov

National Human Genome
Research Institute

February 18, 2015

Major NHGRI Programs

Structure of Genomes	Biology of Genomes	Biology of Disease	Science of Medicine	Effectiveness of Healthcare



CAVEAT

- *Read the RFA (and any amending Notices) carefully*
- *Read the review and funding criteria*
- *Read the Cooperative Agreement Terms and Conditions*

Centers for Mendelian Genomics

Critical aspects

- Sample availability and solicitation plan
- Plan for genomewide sequencing-based discovery of causal genes for human Mendelian conditions
- Coordination and management plans
- Resource sharing plan

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Program objectives

- Make causal gene discoveries
- Improve methods, costs, and success rates
- Enable others
- Facilitate collaborations and coordination

FAQ's

I. Goals
II. Sample Recruitment, Data Sharing and Informed Consent
III. Format of application
IV. Eligibility and Funding

Selected FAQ's - 1

Question: The RFA heavily emphasizes whole exome sequencing. Can I use a different genomic approach as the main approach for making discoveries of causal genes for human Mendelian conditions?

Answer: You may propose to use non-whole exome sequencing genomic approaches to discover causal genes for human Mendelian conditions. Your application should provide justification as to how the proposed approach will lead to successful discovery of causal genes, reasonable and credible advantages in cost and quality, etc. The plan for causal gene discoveries should describe how the chances for discovering novel causal genes will be maximized.

Selected FAQ's - 2

Question: Can I subcontract out sequence production?

Answer: You may propose to subcontract out some or most of sequence production. The capabilities of the sequence data generator should be described in the application. In addition, you will need to demonstrate to reviewers that you understand the project design, detailed technical aspects of how the sequencing platforms perform, and implications of that for data quality, data analysis, and cost. All applicants, whether performing sequencing in-house or contracting out, will also need to demonstrate to reviewers that they will be able to take advantage of evolving sequencing technologies in an optimal timeframe to meet the research objectives with the available funds.

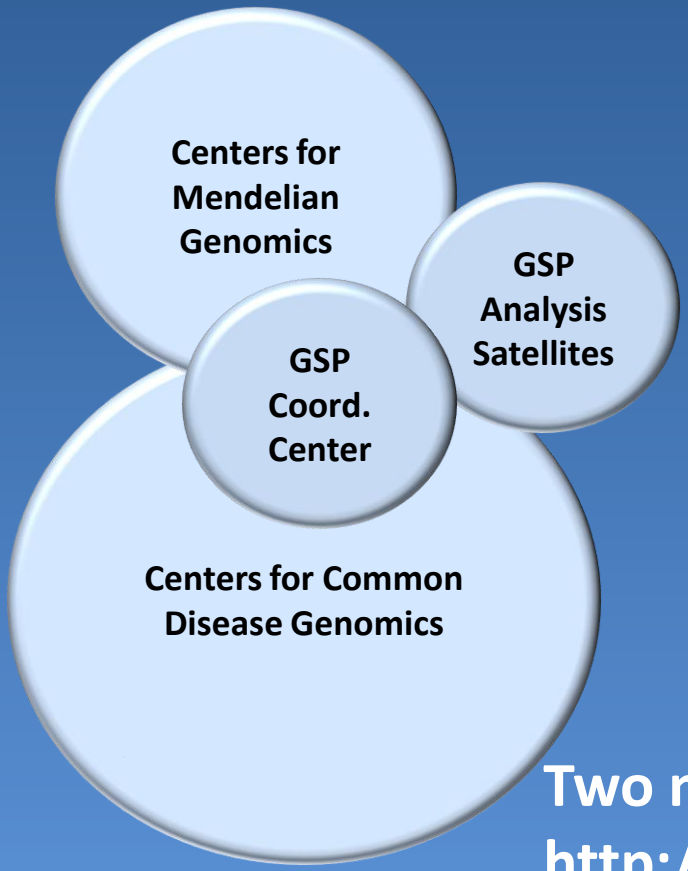
Selected FAQ's - 3

Question: How much time and effort is the PI expected to commit to the proposed CMG?

Answer: The PI is required to devote at least 1.8 person months, based on a 12-month calendar (equivalent to 15% of his/her time and effort) to the proposed CMG. If multi-PI's are proposed, then each PI is expected to commit sufficient time to serve his/her proposed role. Reviewers will be asked to evaluate the *Management Plan* section of the proposal to ensure that adequate effort and organization is proposed.

Core Genome Sequencing Program Additions

Structure of Genomes	Biology of Genomes	Biology of Disease	Science of Medicine	Effectiveness of Healthcare



Two new “Concepts”
http://www.genome.gov/27560312

Contacts

Lu Wang (wanglu@mail.nih.gov): RFA-HG-015-002

Adam Felsenfeld (felsenfa@mail.nih.gov): Overall Genome Sequencing Program, RFA-HG-015-001, new Concepts

Rudy Pozzatti (pozzatr@exchange.nih.gov): Questions about Review

Cheryl Chick (chickc@mail.nih.gov): Administrative questions about budget