

# Future Opportunities for Genome Sequencing and Beyond

## Concept Clearances for the NHGRI Genome Sequencing and Analysis Program Part 2

National Advisory Council on Human Genome Research

February 9, 2015



National Human Genome  
Research Institute

# July 2014 Strategic Planning Workshop

Structure of  
Genomes

Biology of  
Genomes

Biology of  
Disease

Science of  
Medicine

Effectiveness of  
Healthcare

Genome  
Function

(Related  
Tech Dev)

Disease Gene and Variant  
Discovery; Across  
Architectures, Across  
Designs

Clinical  
Applications of  
Sequencing

(Related  
Informatics)

# Workshop Wish-List

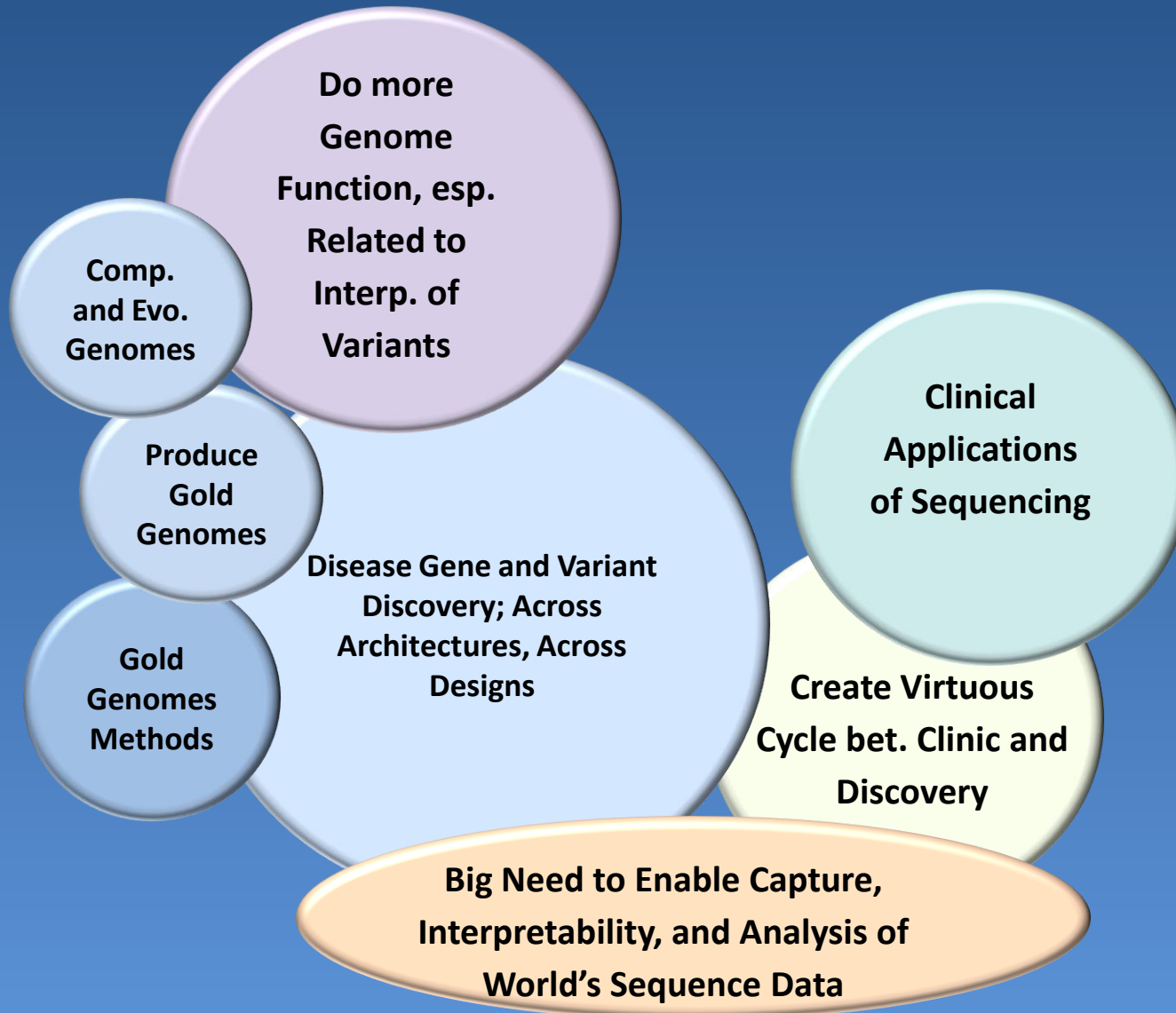
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# Concepts for Clearance

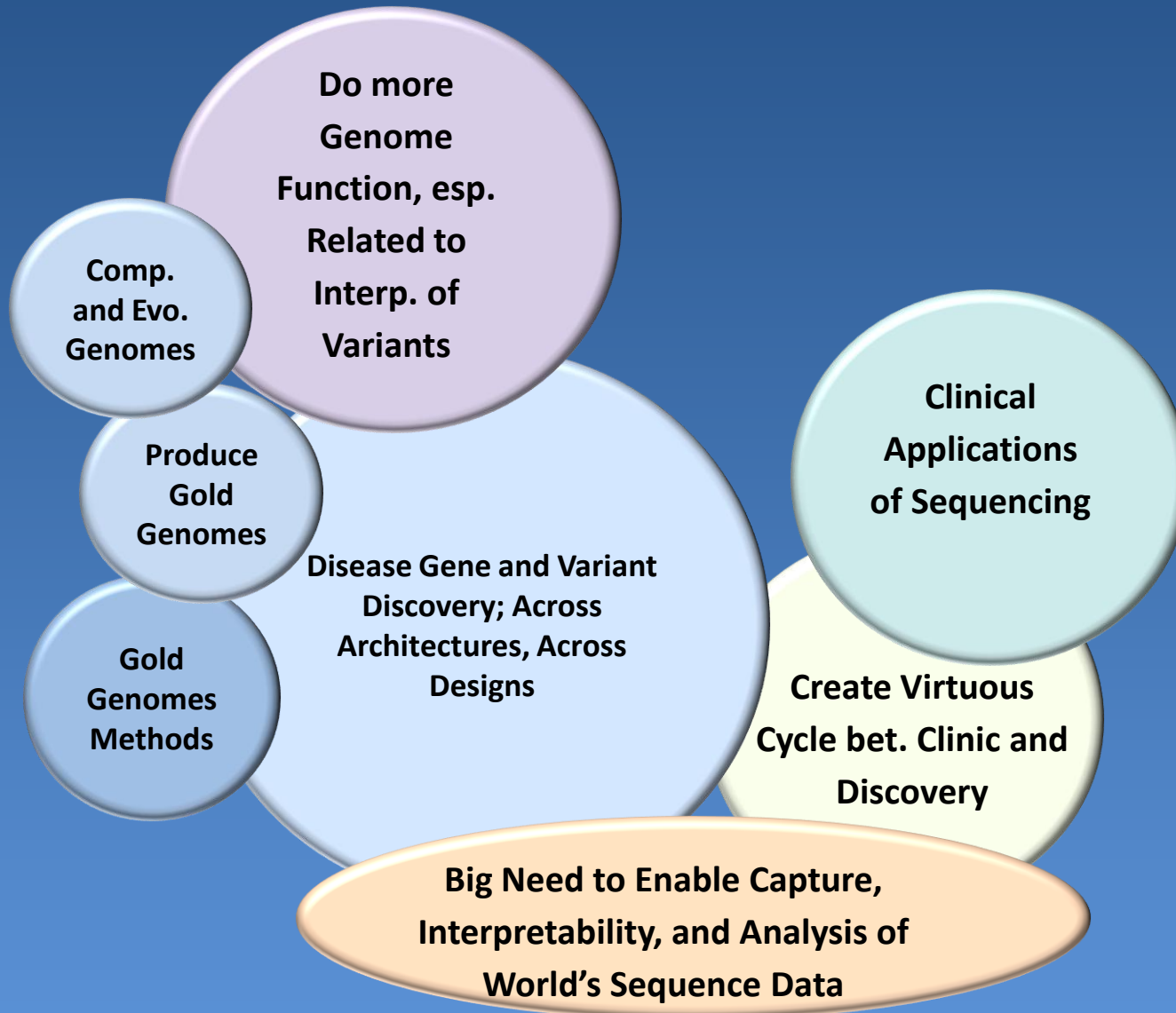
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# Concepts for Clearance

Structure of  
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Biology of  
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Biology of  
Disease

Science of  
Medicine

Effectiveness of  
Healthcare

Comp.  
and Evo.  
Genomes

Produce  
Gold  
Genomes

Disease Gene and Variant  
Discovery; Across  
Architectures, Across  
Designs

# Concepts for Clearance

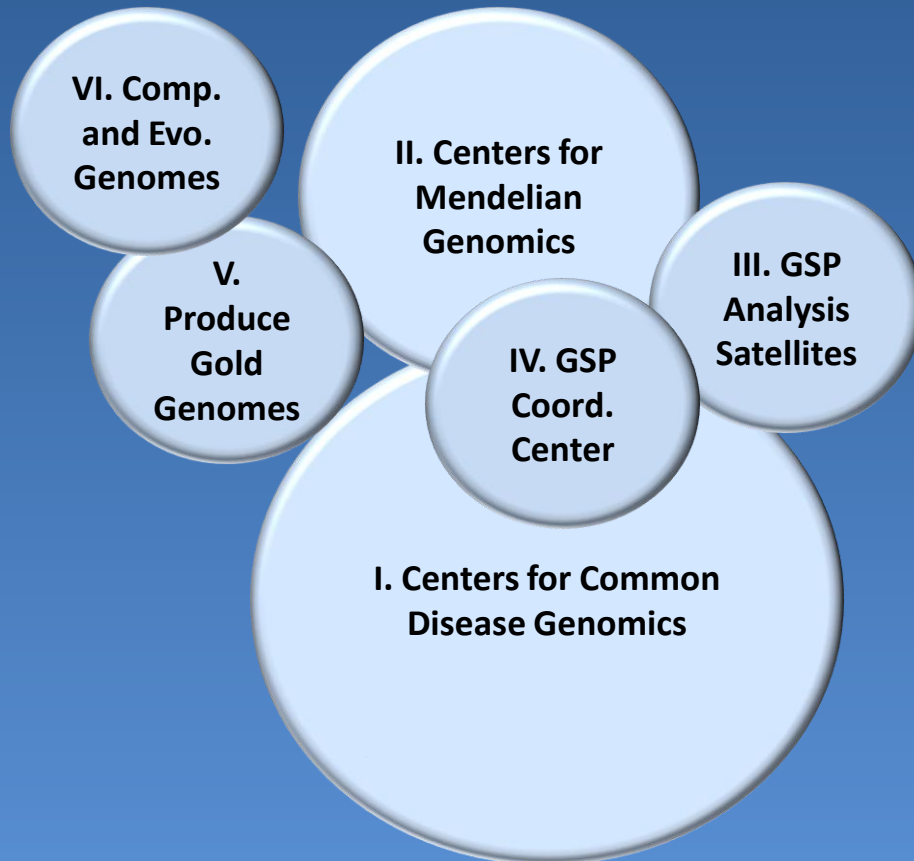
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# Multiple Concepts/RFA's

- I. Centers for Common Disease Genomics (CCDG): RFA-HG-015-001
- II. Centers for Mendelian Genomics (CMG): RFA-HG-015-002
- III. *Genome Sequencing Program Analysis Satellites\**
- IV. *Genome Sequencing Program Coordinating Center\**
- V. *“Gold Genome” Production*
- VI. *Comparative and Evolutionary Genomics*

# The GSP: Analysis and Coordination

Considering both the CCDG and the CMG:

- *A lot of data: Analysis Opportunities → Concept III*
- *A complex structure: Coordination Needs → Concept IV*



# III. GSP Analysis Satellites (GSPAS)

- Will propose and carry out novel, creative analyses of the data produced by the GSP, that will cut across individual projects, grants, and even programs (*not just GSP*)
- Will also help with cross-program analyses that we can define in advance or with the program
- Not routine data processing

# III. GSP Analysis Satellites

- Improved or novel analyses for non-automated aspects of characterizing sequence variants in the data, after variant calling
- Particular interest in questions about association; analyses using existing functional data to help make associations and/or make functional inferences; means to improve study design to increase power; and other higher level analyses
- With overall GSP: when is a common disease study “comprehensive” or complete; characterization and specification of sample sets that could serve as common controls
- Will identify, and in collaboration with the GSP, carry out, other analyses that bridge across multiple grantees

# III. GSP Analysis Satellites

Relationship to other HG activities:

- NHGRI funds other sequence analysis activities both investigator-initiated and HG-initiated
- We will encourage proposals that will take best advantage of the GSP, and discourage those that would duplicate other ongoing or routine analysis efforts
- The GSPAS will be an integral part of the GSP

# III. GSP Analysis Satellites

## Mechanism:

- Cooperative agreements to facilitate coordination with the GSP as a whole, while simultaneously encouraging creative proposals
- Investigators and key personnel from CMG or CCDG grants will not be eligible to be funded, in order to encourage dissemination
- We will write the FOA to increase the chances that each GSPAS will have a different area of focus

## Funds:

- \$3M per year for four years; 3-4 awards. Start as soon possible in time to other GSP elements



# IV: GSP Coordinating Center (GSPCC)

## Two Realities:

- The current GSP is already a large, complex program; the new one will be more complex: More elements; more data; multiple large projects (and the collaborators that they bring)
- There are some cross-program “deliverables”. We need scientific help spurring, leading, and tracking those

# IV: GSP Coordinating Center: Two Roles

1. Leadership/coordination roles for cross-program objectives we can identify now:

- Specification for common controls
- When is a project “comprehensive”?
- Joint allele frequency analysis for CMG

*And others that may arise over time*

*Will bring leadership and a sense of mission to the items above; will need to work with other program components for bulk of analysis and to ensure consensus. Requires scientific expertise.*

# IV: GSP Coordinating Center

## 2. Administrative/logistic/outreach:

- Tracking progress (project status, costs, etc.)
- Logistical coordination within program and among collaborators (calls, meetings, hosting of documents, etc.)
- Policy coordination/dissemination (e.g., data access within the program)
- The program overall will need at least a minimum level of outreach: e.g.: what projects are underway, progress, collaborators, highlights, how the community can get the data
- Possible role in facilitating process for choosing new CCDG projects

*In both leadership and administrative roles, the CC will work collaboratively with the rest of the program and with NHGRI. The CC will be co-equal with the other components.*



# IV. GSP Coordinating Center

## Relationship to other HG activities:

- None

## Mechanism:

- Cooperative Agreement (e.g., U24) is required to ensure coordination with NHGRI staff and the GSP
- CCDG and CMG investigators will not be eligible for funding

## Funds:

- \$1M/year for four years; one award. FOA to be released as soon as possible to allow funding to begin at about the same time as the rest of the GSP

# The Core GSP

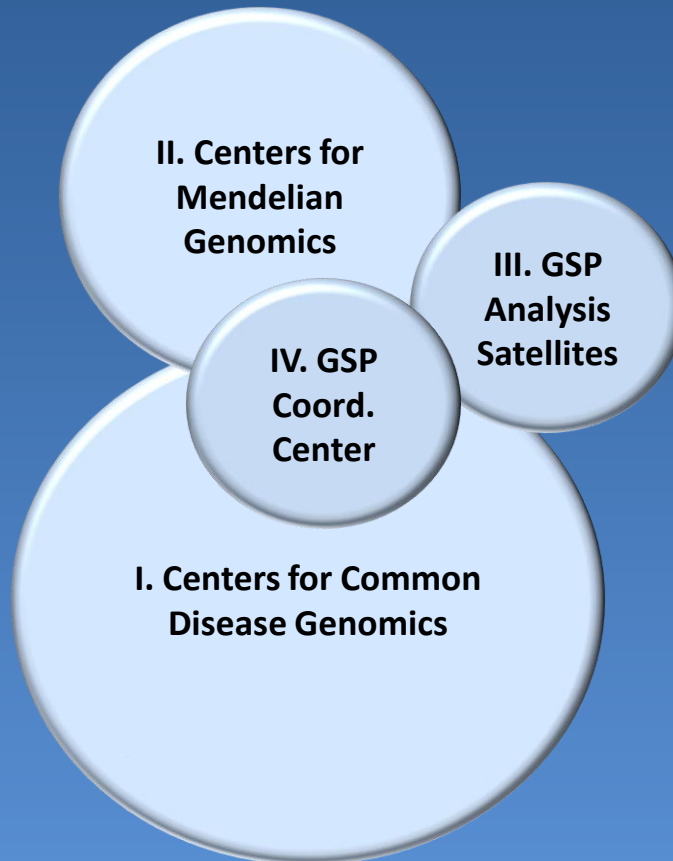
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# V: Gold Genomes

## Purpose:

Produce high quality\* finished genomes at “current costs” in the next three years

- Human (25-50) and Select Non-Human Primate (10-12)
- Develop more specific definition of “high-quality finished”
- Use state-of-the-art methods to maximize quality/quantity

# V: Gold Genomes

## Why?

### Human:

The reference is good but can be made better:

- gaps
- incomplete representation of SV
- move from a mosaic to a faithful haplotype representation
- can better represent world populations

### Non-human primates:

Primate genomes are key to understanding fundamental questions about human genome evolution, but existing assemblies mostly fall short of being reference quality

# V: Gold Genomes

## What is “high quality”?

- Well beyond what is achievable by current “short-read only” methods
- Can state in absolute terms, e.g., haplotype-resolved; contiguity, number of gaps, specific lists of known “difficult” regions, etc.
- Can state in terms of gain in biomedical utility
- Practical issues need to be considered (a moving state of the art; cost)
- FOA language will need to consider all, and also encourage creative proposals

# V: Gold Genomes

## Relationship to other activities:

- The NHGRI Genome Reference Consortium award already funds 5-7 very high quality human genomes; will need to coordinate effort with GRC (production AND integration into references)
- No overlap for primate genomes
- May need some community input re. selection of samples

## Mechanism:

Cooperative Agreement for a resource

## Funds:

\$2M/year for three years; one or two awards





# VI: Comparative and Evolutionary Genomics

## Purpose:

Encourage *investigator-initiated* applications for comparative and evolutionary genomics projects, of wide scope and of high interest to the NIH research community, that address fundamental questions about genome biology, evolution, and function

# VI: Comparative and Evolutionary Genomics

## Some examples:

- Characterizing basic comparative features of genome structure leading to inferences about mechanisms of origin or function—e.g., whole genome duplication, repeats, orthology, paralogy, loss and gain, horizontal transfer, mobile elements; also differences in evolutionary rates, selection, lineage-specific changes, etc.
- Resolving conserved regulatory sequences in human and other sequenced genomes and inferences about function
- Discovering genomic innovation (e.g., origins of proteins, biochemical pathways, core metazoan developmental program, etc.)
- Defining the genomic basis of phenotypic innovations ranging from major taxonomic innovations – e.g., multicellularity or the adaptive immune system -- to those occurring on a shorter time scale, for example, differences between closely related species or within species

# VI: Comparative and Evolutionary Genomics

- Animal, fungal, protist, but not others
- Multi-species or perhaps multiple individuals within a population
- De-prioritize those with a narrow focus more appropriate to another funder
- Prioritize those with some relevance to human biomedical science

# VI: Comparative and Evolutionary Genomics

## Relationship to other HG activities:

- No direct overlaps; NHGRI has no other announced mechanism to consider proposals for organismal genome sequencing
- Opportunity for synergy with Functional Genomics program

## Mechanism:

- PAR for investigator-initiated R01 applications: this allows for a written FOA, a single review date; applications reviewed together. Second release in a year depending on response.

## Funds:

- We estimate the activity will require ~\$2M/year but will not set aside funds in advance; one or two awards; three years



# NHGRI GSP

I. Centers for Common Disease Genomics:	\$60M/year; 4 years
II. Centers for Mendelian Genomics:	\$10 M/year; 4 years (+\$2M/year from NHLBI)
<i>I. GSP Analysis Satellites</i>	<i>\$3M/year; 4 years</i>
<i>II. GSP Coordinating Center</i>	<i>\$1M/year; 4 years</i>
<i>I. Gold Genome Production:</i>	<i>\$2M/year; 3 years</i>
<i>II. Comparative and Evolutionary Genomics:</i>	<i>\$2M/year; 3 years</i>
<b>Year 1 Total:</b>	<b>\$78M (+\$2M)</b>

# Thanks To Many

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