HRS Genetic Data Products

A Resource for Genetic Research in the Behavioral and Health Sciences

Study Design

With financial support from the National Institute of Health (NIH) Director's Opportunity for Research awards using American Reinvestment and Recovery Act funds (RC2 AG036495-01, RC4 AG039029-01), the HRS has genotyped almost 20,000 respondents who provided DNA samples and signed consent forms in 2006-2012. The result is a publicly-available resource of linkable genotype, phenotype, and environmental conditioning variables that can be used widely in the scientific community.

"The addition of genetic data provides a major new dimension for the study and is expected to result in much deeper insights into how we age," said Richard Hodes, director of the National Institute on Aging. "With detailed information on genetic background, combined with the wealth of data on important aspects of the lives of older people, researchers will be better able to describe the spectrum of behavioral and environmental risk factors for disease and disability, as well as those that may protect our health."

Equally important, the HRS is built for comparability with other studies, creating potential for replication and pooling that is crucial for future advances in genetic discovery. This resource creates new horizons for research in behavioral and health sciences.

Genotype Data (2006-2010)

In 2006, saliva was collected using a mouthwash collection method. In 2008 and beyond, saliva was collected using the Oragene DNA collection kit (OGR-250). Saliva completion rates were 83% in 2006, 84% in 2008, and 80% in 2010 among new cohort enrollees. Data for samples for 2012 are forthcoming.

The genotyping was performed by the NIH Center for Inherited Disease Research (CIDR, X01HG005770-01, http://www.cidr.jhmi.edu/) using the Illumina HumanOmni2.5-4v1 and HumanOmni2.5-8v1 arrays, with coverage of approximately 2.5 million single nucleotide polymorphisms (SNPs).

Current dbGaP data products also include imputation of approximately 21 million DNA variants from the 1000 Genomes Project. (http://www.1000genomes.org.) Imputation will increase the number of available markers and will make possible comparisons across platforms that do not assay the same genome-wide SNP panel.

The genotype data and a limited set of phenotype measures have been deposited in the NIH GWAS repository (dbGaP), and provides a convenient method of distribution to researchers who meet NIH requirements for access. Researchers who wish to link to other HRS measures not in dbGaP can apply for access from HRS.

Candidate Genes and SNP Files

The purpose of the HRS Candidate Gene and SNP files is to provide data users access to carefully selected subsets of the HRS genotype data available on dbGaP. These are smaller and more manageable files designed for data users who are interested in a specific gene or SNP. Users must have dbGaP approval before requesting and gaining access to these files from HRS.

Currently, there are two sets of files available:

1) Cognition and Behavior and 2) Longevity. The specific SNPs and genes included in each package and file description documents with details on each data package are available on the HRS website.

Telomere Data 2008

The 2008 Telomere Data release (Final, Version 1.0) includes average telomere length data from 5,808 HRS respondents who consented and provided a saliva sample during the 2008 interview wave. Assays were performed by Telome Health (Telomere Diagnostics, http://www.telomehealth.com/). Average telomere length was assayed using quantitative PCR (qPCR) by comparing telomere sequence copy number in each patient's sample (T) to a single-copy gene copy number (S). The resulting T/S ratio is proportional to mean telomere length. Funding was provided by the National Institute on Aging provided funding (NIH U01 AG09740 and RC4 AG039029).

Exome Data 2006-2010

Exonic variants have been measured using the Illumina Human Exome BeadChip v1 on the approximately 15,500 samples collected from 2006 through 2010. These exome data are available from HRS.

Data Access

Several genetic data products derived from these samples are available. Some data are distributed through the NIH GWAS repository (dbGaP) and others are HRS data products. Detailed information can be found on each product's page on the website. Researchers wishing to use the HRS genetic data must first apply to dbGaP for access to the genotyped data. The process to request access to any dbGaP study is done via the dbGaP authorized access system. Some products will also require a Sensitive Data Use Agreement.

Documentation

Data documentation is available to the public at hrsonline.isr.umich.edu. Click on Genetics Data under Quick Links or the link to Genetics Data under Data Products.

Contact Information

HRS Help Desk: HRSQuestions@umich.edu

HRS Website: hrsonline.isr.umich.edu

Terms

dbGaP is the database of Genotypes and Phenotypes which is a data bank developed by the National Institutes of Health to archive and distribute the results of studies that look at the interaction of genotype and phenotype.

Genotype is the inherited instructions an organism carries within its genetic code.

Phenotype is any observable characteristic or trait of an organism: such as its size and shape, development, biochemical or physiological properties, or behavior. Phenotypes result from the expression of an organism's genes as well as the influence of environmental factors and possible interactions between the two.

GWAS stands for genome-wide association studies. It is a method of studying the complete genomes across many samples of individuals to look for genetic variations associated with particular traits or diseases.

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