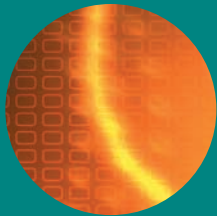




**Peoples Genetics:**  
**Unleashing the Power of Large Populations**

# Unleashing the Power of Large Populations

Now, for the first time, genomics researchers can analyze tens of thousands of DNA samples — reliably, quickly, and economically. The result is breakthrough statistical power and scientific insight, at a level never before possible.



## Peoples Genetics' Technology Benefits

### Discovery, not scoring

- Peoples Genetics does not require *a priori* knowledge of SNPs.
- We simultaneously discover *and* quantify mutations.

### Comprehensiveness

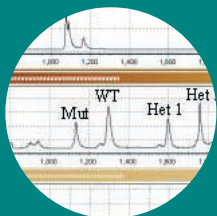
- We discover the identity and frequency of virtually all the alleles (down to a detection threshold of  $5 \times 10^{-5}$ ) for any region scanned.

### Statistical power

- Our combination of large sample sizes and a highly sensitive process ensures greater statistical power and less sample variance than alternative approaches.
- Our process enables comparisons of multiple (not just single) alleles, increasing statistical resolution.

### Savings and speed

- The Peoples Genetics process for scanning large populations is faster, and far more economical than alternatives — by roughly two orders of magnitude.



Peoples Genetics conducts gene/disease causation experiments of unprecedented scale. We employ a process that allows us to pool and analyze samples containing DNA from up to 100,000 individuals, discovering the identity and frequency of nearly every mutation present in any gene studied. We deliver such data at less cost and in less time than any genomics organization in the world.

For over a decade, science has searched for the genetic causes of common diseases, in hope of designing more effective, customized therapies and diagnostic tools. Researchers now recognize that much larger population studies are needed to test the leading hypotheses of genetic causation. Peoples Genetics makes these large-scale tests feasible for the first time.

## The Value of Our Approach

Until now, large-population genetic variation studies simply have not been feasible. The costs of alternative techniques, such as gene sequencing, grow linearly with the size of the sample populations. A single large experiment could cost millions of dollars and take months to complete.

Because Peoples Genetics' technology pools DNA samples, our experiments are virtually insensitive to the size of the population. Therefore, our process, from sample handling to scanning, is far less time-consuming and less expensive than other technologies — in fact, cheaper by roughly two orders of magnitude. This makes it practical, for the first time, to conduct genetic variation studies with tens of thousands of samples.

Large-population studies are essential to making further advances against common diseases, such as cancer and diabetes. Scientists exploring these areas have grown frustrated at the limited success of conventional studies, which typically involve only a few hundred patients and the results of which often cannot be replicated. Increasingly, it is thought that the genetic components of common maladies do not lie in single alleles or even single genes — hypotheses that require large populations to test. For example:

- Genetic risk for common diseases may be distributed over multiple alleles in risk-associated genes (multiallelic causation).
- Any of multiple genes may carry multiple alleles resulting in a disease with a single diagnosis (multigenic causation).
- Mutations in more than one gene, together, may be required to create risk for a disease in a single individual (polygenic causation).
- Environmental factors also may be necessary to influence an individual's risk, even when an independent, essential mutation is present (incomplete penetrance).

To test these hypotheses, researchers ultimately must detect all the alleles of any gene studied and measure fine differences between their frequencies in cases and controls. Only studies involving many thousands of DNA samples can provide the necessary comprehensiveness and statistical power.

## Our Technology Platform and Sample Library

Peoples Genetics' technology allows us to analyze DNA samples from a population of up to 100,000 persons and detect all mutations present at a frequency of 1 part per 20,000.

The power of Peoples Genetics' approach begins with the pooling of DNA. Rather than sequencing each DNA sample from a population, we pool the samples and isolate sequences of interest. Our process then creates conditions that separate

mutant and non-mutant DNA molecules, identifying specific gene variations present in the pool.

This process utilizes our patented form of capillary electrophoresis, Constant Denaturant Capillary Electrophoresis (CDCE), which we conduct at high-throughput levels. We also employ high-fidelity PCR and other sample preparation procedures.

In addition, Peoples Genetics draws upon its own DNA library, representing a wide range of cohorts. These include disease-affected populations — for diabetes, cancers, hyperlipidemia, and other maladies — as well as a young-adult reference population of 100,000.

Peoples Genetics' technology was developed by its founding scientists, William Thilly, Sc.D., and Barry Karger, Ph.D., in a collaboration between the Massachusetts Institute of Technology and Northeastern University.



## A Complement to Current Research

The Peoples Genetics approach complements other genomics technologies by picking up where they leave off. While current techniques work to identify areas of the genome that contain disease-causing alleles, we identify the causal alleles themselves. For gene expression studies, SNP association studies, and other discovery efforts, we act as a “finishing shop,” pinpointing mutations of interest within any set of nominated genes and, critically, eliminating false positives.

Biopharmaceutical companies, research institutions, and other organizations can add value to their own studies by contracting with Peoples Genetics. Drawing on our high-throughput infrastructure and extensive sample library, we provide a turnkey solution for clients who require in-depth genetic analysis.

In addition, we can customize our analysis to the level of sensitivity a client requires. Our Deep Intelligence Scan allows the discovery of all alleles at a frequency as low as 1 part per 20,000 and permits researchers to make a clear determination of gene/disease causation. Our Reconnaissance Scan, which targets alleles at or above a 1% frequency, is ideal for researchers who require a cost-effective interrogation of larger areas of the genome. In both scans, we apply our analysis to pools of up to 100,000 samples, delivering unparalleled statistical power.

---

#### **About Peoples Genetics**

Peoples Genetics, Inc., is a privately held genomics company that is discovering the genetic causes of common diseases through experiments of unprecedented scale. The company provides services for biopharmaceutical companies and research institutions, while also pursuing its own genetic discoveries for future development of proprietary molecular diagnostics. Peoples Genetics holds exclusive licenses from the Massachusetts Institute of Technology and Northeastern University, and was founded in November 2000 by Joseph P. Kennedy II, William Thilly, Sc.D., and Barry Karger, Ph.D. The company is headquartered in Woburn, Massachusetts.

For more information about Peoples Genetics and its services, please contact us by phone at (781) 933-6068 or by e-mail at **[info@peoplesgenetics.com](mailto:info@peoplesgenetics.com)**.

© 2002 by Peoples Genetics, Inc.

9/2002



Peoples Genetics, Inc.  
6-C Gill Street  
Woburn, MA 01801  
781.933.6068  
[www.peoplesgenetics.com](http://www.peoplesgenetics.com)