MedicalXpress

NIH announces $240 million project to map human genomes

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The federal government is funding a monumental project to map 200,000 human genomes in an effort to understand the genetic causes of common diseases such as cardiovascular disease, diabetes, epilepsy and autism.

Four institutions were chosen to take part in the four-year, $240 million project announced Thursday by the National Institutes of Health, the nation's medical research funding agency.

The four institutions will join to form the Centers for Common Disease Genomics. Their combined genetic sequencing and analyzing power will map genomes of the large and diverse populations required to understand how one's genes increase or even protect against the risk of complex diseases such as hypertension, diabetes and mental illness.

The diseases are considered complex because they involve numerous genes and environmental factors; unlike for example, sickle cell anemia, which is caused by just one mutation. They are also unlike cancers, where researchers can sequence one person's tumor cells and healthy cells and look for differences.

"So, what we have to do is sequence people who have the disease and those who don't have the disease and compare their genomes," said Rick Wilson, director of the McDonnell Genome Institute at Washington University School of Medicine, one of the four institutions chosen for the project. "That's fine, but we have to sequence a lot more genomes so

we can figure out what is different because of the disease, or different because these are different people."

The findings could lead to the earliest diagnosis possible, garnered from a needle prick as a newborn. That would allow a person to be vigilant in protective lifestyle choices and detection exams; or use medications to counter the activities of bad genes or boost the protection from good genes.

"If we can identify these genes, we might be able to create new drugs and identify people who are at risk way before they would ever have a heart attack," Wilson said.

The other institutions chosen are the Broad Institute of MIT and Harvard University in Cambridge, Mass.; Baylor College of Medicine in Houston and the New York Genome Center in New York City.

The large-scale effort is mind-boggling, given that just over 10 years ago, it took researchers more than a decade and about $1 billion to first sequence the human genome. The newest machines can sequence 18,000 genomes a year for about $1,000 per genome.

"We are at an extraordinarily exciting time for the field of genomics," said Dr. Eric Green, director of the National Human Genome Research Institute, which is part of the NIH. "What was unfathomable only a decade ago is now within our grasp."

The four research institutions chosen to receive the funding have been at the forefront of the advances and are equipped with the latest sequencing machines, the HiSeq X, released last year and developed specifically for large-scale studies. The machines - at cost of $1 million each - are sold only in groups of 10.

"It is the first time anything has been done on this scale," Wilson said. "There are only a few places in the world that can do this work, and we are excited to be one of those places."

The genome institute in St. Louis established itself as a leader of genomics research early in the game, when it was a key player in the effort to first map the human genome, ultimately contributing 25 percent of the blueprint.

In 2008, the institute was the first to sequence the cancer genome of a leukemia patient, opening the door to the sequencing of hundreds more cancer genomes and discoveries already resulting in improved personalized treatments.

Not only do the partnering institutions have the latest large-scale sequencing technology, they also are able to store and analyze the massive amount of information generated. One human genome alone contains enough data to fill a phone book the size of the Washington Monument.

At the McDonnell Genome Institute, that effort is led by computational biologist Ira Hall, who is constantly developing new methods to make faster and meaningful comparisons. "Having the tools to analyze this data is as important as the sequencing technology itself," Hall said.

In fact, Wilson said, most of the funding will go to such efforts. "Right now we can generate more data than we have the ability to analyze," he said.

The research team at Washington University will spend the first four years of the grant looking for the genetic variants involved in heart disease and diabetes by sequencing up to 40,000 genomes. The research centers already have banks of genetic and biographical material,

collected as part of past studies, so they can get started right away.

Wilson said his team is able to study genomes from diverse ethnic backgrounds, including its thousands of genomes of African-Americans. The institute also is working with 20,000 samples from a unique Finnish population with very similar genes that make it easier to pinpoint differences related to disease.

The team has already discovered a gene responsible for a dangerously high lipid level that puts people at risk for heart disease, and a drug company has a medication in the works, Wilson said. "But we've just scratched the surface."

The money will allow researchers to dig further. "All the work we've been doing so far is looking at a small part of the genome," he said. "We know we need to look at the whole genome."

While promising, the effort to find genetic clues in common diseases has many unknowns, experts acknowledge. Researchers are guessing at the number of genomes that need to be sequenced to make meaningful discoveries, and some don't agree. The complex interplay of multiple genes and environmental factors make finding answers challenging.

"The honest truth is we don't know, " Green said. "This is still exploratory work by nature."

But with the technology now in researchers' hands, it's imperative to try to ease the burden of diseases that affect hundreds of millions across the globe, Wilson said. Coronary heart disease is the leading cause of death worldwide. "We have to start doing something," he said.

One thing is for sure, while St. Louis is no longer an NFL city since it just lost the Rams, the city will continue to lead the way in the field of

genetics.

"We might not have an NFL football team," Wilson said, "but we have a genome center."