

UCSD Scientists Win Grant to Develop \$1,000 Genome Sequencing Technology

October 9, 2006

Rex Graham

The current cost to determine the sequence of nucleotide bases in the 6-billion-base-pair human genome is roughly \$10 million, but researchers at UC San Diego and eight other universities and biotech companies hope to use a federal grant to lower the cost to only \$1,000 per human genome sequenced. Determining the genome sequence of individuals is considered crucial to understanding and routinely treating hundreds of inherited diseases, predispositions to other diseases, and cancers.

In order to spur the development of fundamentally new and innovative technologies necessary to reduce the cost of sequencing a genome 10,000-fold, the National Human Genome Research Institute (NHGRI) has awarded \$13 million in new grants to nine universities and corporate groups in the U.S., including UCSD. The institute, which is part of the National Institutes of Health (NIH), is using the grant program as an incentive to expand the routine use of genomics in medical research and health care.

Xiaohua Huang, a professor of bioengineering in UCSD's Jacobs School of Engineering, leads the effort at UCSD to develop a promising technology that shrinks what is currently being done in large genome-sequencing laboratories down to a glass slide the size of a business card. Huang's team will combine micro- and nano-fabrication technologies with innovative chemistry technologies to simultaneously sequence more than 1 billion individual pieces of DNA attached to the surface of single slides.

The latest genome-sequencing grant was announced simultaneously with the announcement of the Archon X PRIZE for Genomics, a \$10 million cash prize to go to the first team that creates the technology to successfully map 100 human genomes in 10 days. The X PRIZE Foundation is a non-profit institute dedicated to fostering radical breakthroughs in space and technology for the benefit of humanity.

"The \$10 million prize may be a nice incentive to researchers, but our group at UCSD is more excited about the challenges of overcoming the daunting technical obstacles that must be overcome to develop a \$1,000 genome technology," said Huang. "Sequencing a genome in a few days for only \$1,000 is an enormously challenging task, but I think we have as good a chance as any group to get there first." Huang's group was awarded \$275,000 for one year with the possibility up to an additional \$3 million over three more years if specified milestones are met in the initial experiments.

Huang will be joined at the Jacobs School by Pavel Pevzner, a professor in the Computer Science and Engineering Department who leads the department's Bioinformatics Laboratory. Sequencing the 23 pairs of human chromosomes extracted from the cells of one individual involves cutting the DNA into tens of millions to hundreds of millions of pieces, and Pevzner is developing the computational techniques needed to computationally reassemble the chromosomes by piecing together the overlapping ends of all the fragments after they have been sequenced.

Bioengineering professor Michael Heller is a third member of the UCSD team. He is an expert on using electric fields to actively manipulate biomolecules and assemblies of nanostructures. His expertise will be utilized to accelerate and enhance the sequencing process.

The UCSD team will use an experimental method for DNA sequencing aimed at developing a method for fabricating high-density arrays of nanoparticles, with one fragment of DNA attached to individual nanoparticles in the arrays. The investigators will attempt to demonstrate that more than 1 billion individual DNA molecules can be sequenced simultaneously.

Media Contact: Rex Graham, (858) 822-3075

