GOVERNMENT

AFTER REVIEW, DOE'S GTL SHIFTS PLANS, SCRAPS GRANT REQUEST

The Department of Energy's Office of Science has restructured the facilities plan for its Genomics: Genomes to Life program in response to a review by the National Research Council of the National Academies.

Rather than creating four separate facilities devoted specifically to protein production, biomolecular imaging, proteomics, and systems biology, as it had earlier planned, GTL now envisions "one or two vertically integrated centers with a focus on bioenergy research," according to DOE. However, the agency says it could consider building centers for systems biology research into carbon sequestration and bioremediation in future years.

Additionally, DOE canceled its funding opportunity announcement for a planned GTL facility for the production and characterization of proteins and molecular tags, issued in early January. DOE says it plans to issue a new solicitation in the coming months for one or more centers for bioenergy research, and that such research has become an increasing priority for GTL.

The changes follow on the heels of a nonbinding review by NRC that recommended GTL uproot its R&D plan of creating the four technology-specific centers in favor of building four vertically integrated facilities in which the four original disciplines would look for applications for tasks already identified as GTL targets.

"We're recommending a biology-oriented, programmatic approach rather than just building large-scale facilities around innovative technologies," says **Charles Cantor**, chief science officer at Sequenom and one of 12 co-authors of the NRC report. "It's safe to assume that the investment in technologies probably doesn't have to be as large as DOE had previously projected."

According to the NRC report, it would've taken 24 years for DOE's technology-specific facilities to be built and "to reach full capabilities." NRC suggested instead that DOE center the facilities around energy alternatives, legacy waste solutions, and carbon sequestration.

David Kingsbury of the Gordon & Betty Moore Foundation and a report co-author says the reconfiguration would help keep the program dynamic and timely. "There is an opportunity for a broader number of vendors to be engaged early on," he says. "From sequencing to protein production to imagery and mass spectrometry, there is a lot of potential. DOE will be making an investment and making sure they stay state-of-the-art."

— Elizabeth Kiem and Justin Petrone

STRUCTURAL VARIATION

NEW NHGRI DIRECTION FOLLOWS COPY NUMBER VARIATION TREND

Type "copy number variation" into Google and the search engine pulls up close to 43 million hits. The breathless popularity gain seen in this field surprises even pioneers like **Evan Eichler**, who remembers when most scientists thought the concept of quantifying copies of genes and using that information to compare one genome to another was purely "an idiosyncrasy of the genome." He adds, "The people that are now extremely excited about it — they weren't so excited by it 10 years ago" when he was beginning to study it.

Copy number variation, which along with insertions and deletions falls under the broader umbrella of structural variation, has truly come into its own. Recent papers have linked the phenomenon to kidney dis-

The **Multiple Myeloma Research Consortium** kicked off a multi-million-dollar research program called the Multiple Myeloma Genomic Initiative. The program is a collaboration between MMRC, **TGen**, and the **Broad Institute**.

The **UK Biobank** expects to invite 3,000 residents of the south Manchester area to take part in the startup phase of the national DNA database. The project, which aims to collect samples from up to a half million participants between the ages of 45 and 69, is scheduled to launch nationwide later this year.

Genizon raised $10.6 million in debt financing from venture capital firms and other investors, including Illumina. The money will be used to increase its GeneMap and drug target inventory, according to the company.

Renato Paro was named professor for biosystems at **ETH** in Zurich, Switzerland, and will be a founding director of the Center of Biosystems Science and Engineering. The center will have 15 professorships in life sciences, engineering, and informatics and will integrate research activities of ETH Zurich, the **University of Basel**, and the **University of Zurich**.

Stephen Lammert has joined **Stillwater** to lead the development of a new line of mass spectrometers. Lammert has held R&D roles at **Oak Ridge**, and began mass spectrometry work at **PerkinElmer** and **Thermo Finnigan**.

Photos: Mekea Hurwitz

ease, AIDS susceptibility, Alzheimer's, and Parkinson's. With each new connection between phenotype and genome sequence change, it seems, even more people flood into the field. Earlier this year, NHGRI issued its priorities for the production-scale genome centers, and topping the list was an initiative to study structural variation in 48 human genomes.

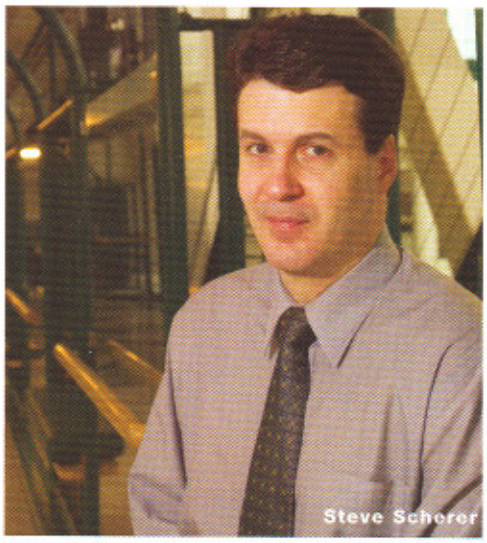
Steve Scherer, director of the Centre for Applied Genomics at the Hospital for Sick Children, was one of the organizers of the first copy number variation meeting held last September in his home base of Toronto. "It was quite timely because there had not been a meeting really on this at all because it's such new science," he says. About 60 participants came, and the meeting was such a hit that it will actually merge with the annual SNP conference; the first co-meeting will be held in Hong Kong this September.

For most people, copy number variation research has a fairly brief history. The first papers describing this on a genome-wide scale came out in 2004 — one from **Mike Wigler**'s lab at Cold Spring Harbor and another from Scherer and **Charles Lee** at Harvard. That was the first time, Scherer says, that the technology was available to study this in a large-scale, rigorous manner. "We knew about it for a long time, we just didn't have the technology to prove it," he says. "We started to look genome-wide in 2002 when array CGH became more available to us."

Most copy number variation research relies on BAC- or oligo-based arrays, but those don't show broader structural variation events like insertions and deletions, says Eichler. Sequencing technology, on the other hand, gives more comprehensive information but for many researchers is prohibitively expensive.

Scherer says a genome-wide scan can be done with current array technology for $1,000, but he adds, "If we could bring it down 10-fold, it brings it into the realm of the average laboratory experiment" — which will likely be necessary to get this technology into the hands of clinical scientists.

Scherer has also been an organizer of a consortium that aims to analyze samples


Steve Scherer

from the HapMap project for their copy number variation content. "We've been working on that for a year and a half now," he says. "We'll be preparing our data for publication this year sometime." Going forward, Scherer hopes the consortium will look at more samples from a broader global population and do more disease-association studies too.

Both Eichler and Scherer point to the need for improved database work in the field. Scherer says there should be a common repository that allows scientists to compare all of the data in this area, while Eichler says developing a quality control system — preferably one in which data is vetted and distributed by people other than those who generated it — will be key. They look forward to improvements in the variation detection technology as well. "The technology is there," Scherer says, "but it's there in a rudimentary form."

Looking ahead, Scherer says, "the ultimate success story would be if in the next [few] years every single genetic disease study incorporated a component of copy number variation or structural variation in their experiment design."

Eichler's view of the field in a couple of years is a little less rosy. "There's a lot of excitement and there should be a lot of excitement, but right now we might be a little over the top," he cautions. "Two years from now there'll be a little bit of after-the-party blues." — *Meredith Salisbury*

Deltadot, a London-based firm that develops tools for protein and nucleic-acid analysis, raised £6 million in a round of venture capital financing.

Shaun Lonergan, vice president of business development at **454 Life Sciences**, has left the company. 454 has named **Katherine Webster** vice president of sales.

Jenny Graves, head of the comparative genomics research group at the Research School of Biological Sciences at the **Australian National University** and director of the ARC Centre for Kangaroo Genomics at ANU and the **University of Melbourne**, was selected Asia-Pacific laureate of the L'oréal-Unesco 2006 awards for Women in Science.

Qiagen has created a high-throughput RNAi user forum open to all scientists. The forum, which will meet semiannually, will be coordinated by **Spyro Mousses** at **TGen**, **John Hogenesch** from **Scripps**, **NCI**'s **Natasha Caplen**, **Carl Novina** at **Harvard**, and **Lucas Pelkmans** from the **Swiss Federal Institute of Technology**.

Guy della Cioppa, who served as vice president of business development at **Predictive Diagnostics** until last June and was most recently head of business development at **Advanced Ideas in Medicine**, died March 3 when his vehicle veered off a road near Davis, Calif., and hit a tree. He was 56.