

SOUTHWESTERN NEWS

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SUPER COMPUTER HELPS SPEED GENOME PROJECT

DALLAS — June 24, 1997 — With its blinking lights and sleek case, the machine looks like something from the movie *Star Wars*. It's an appropriate comparison because the speed at which this super computer is generating data and identifying genes is astronomical.

For one researcher at UT Southwestern Medical Center at Dallas, the computer did in a day what previously would have taken about six months.

Dr. Harold "Skip" Garner, professor of biochemistry, formed a collaboration with the computer manufacturer allowing his researchers to use the Hewlett-Packard/Convex Exemplar through May 31, 1999, in UT Southwestern's National Institutes of Health-funded Genome Science and Technology Center (GESTEC).

The machine analyzes more than 1,400 deoxyribonucleic acid (DNA) sequences generated by GESTEC daily as part of the international Human Genome Project. The goal of the worldwide collaboration of scientists participating in the project is to locate, identify and determine the DNA sequence for the 100,000-plus genes in the human body by 2003.

The computer assembles data sequences for submission to the National Database (GenBank) and runs several programs to determine whether the sequences can be identified as genes. The power of this super computer has enabled researchers to explore new approaches to genetic and genomic data analysis, such as artificial intelligence and expert systems for gene prediction.

The Exemplar searches the GenBank to check for previously discovered DNA sequences similar to ones that GESTEC researchers are measuring.

"If an exact match is found, then we have mapped or localized one of our new sequences relative to another one. If one that is close but not identical is found, then perhaps we have found a new gene, the human equivalent of a gene found in another species or a new member of a known gene family," said Garner, holder of the Philip O'Bryan Montgomery Jr., M.D., Distinguished Chair in Developmental Biology.

The Exemplar is actually a series of computers called a parallel processing machine,

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which means it can do a number of tasks at once. The machine at GESTEC is made up of eight processors and has a huge memory — 500 megabytes of RAM and 28 gigabytes of disk space. A typical personal computer has 8 megabytes. Another feature is that the memory is accessible by all eight processors. This is important because all the data the center works with can be stored in the memory, making the gene search even faster.

Because the computer runs a standard UNIX operating system, it is possible to move codes directly to Exemplar from other machines that use the same software. This has made it possible to transfer the many useful codes quickly, easily and without errors.

Parallel-processing computers typically are used in aerospace, plasma physics and weather prediction. Human Genome Sciences (HGS), a private gene-hunting company, is the only other laboratory besides GESTEC using the Exemplar for biology.

"We are able to do a large number of analyses and data reductions that previously were not possible," Garner said. "Now we can analyze not only our data but also data generated by the whole world. Most recently, for example, we have been analyzing a region of DNA on chromosome 3 for Dr. John Minna. This originally was sequenced at Washington University in St. Louis and the Sanger Centre in England, and we wanted to verify the data."

Minna is director of the Nancy B. and Jake L. Hamon Center for Therapeutic Oncology Research and of the W.A. "Tex" and Deborah Moncrief Jr. Center for Cancer Genetics. He also holds the Max L. Thomas Distinguished Chair in Molecular Pulmonary Oncology, the Sarah M. and Charles E. Seay Distinguished Chair in Cancer Research and the Lisa K. Simmons Distinguished Chair in Comprehensive Oncology.

"We interact with Dr. Minna almost daily because he is on a very accelerated, focused hunt for lung-cancer genes," Garner continued. "The best way to go about that is targeted biological experiments that are indicated by this computer analysis.

"If we're going to remain competitive, then we'll need more of these machines on campus, because they are applicable to other areas, such as X-ray crystallography and protein structure. You just have to enter the codes for the particular type of work. At some point, most of the researchers on campus who do those kinds of things will need computing power like this."

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