15 April 2004

One-Stop Shopping for cDNA

TOKYO--Genetics researchers received a new tool today. A database of annotated, full-length human complementary DNAs (cDNAs), compiled by an international team led by Japanese researchers, has been opened for public access. The database is expected to be a boon for research related to drug development, gene hunting, molecular evolution, and comparative genomics.

Crunch time. Human genome scientists met in Japan in 2002 for a marathon annotation session that laid the groundwork for a new cDNA database.

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cDNA is basic tool of biotechnology. It's a lab-made copy of an organism's DNA--crucially, just the protein-coding parts--that researchers concoct using an enzyme called reverse transcriptase. Normally, DNA is transcribed into RNA, then edited and made into proteins. Reverse transcriptase goes the other way around, building a gene from its messenger RNA. That enables researchers to create copies of active genes without having to hunt through the unedited genome.

The new database pools and builds on information from six major cDNA projects, including the Mammalian Gene Collection of the U.S. National Institutes of Health, the German Human cDNA project, work at the Chinese National Human Genome Center in Shanghai, and three projects in Japan. Takashi Gojobori, deputy director of the Japan Biological Information Research Center in Tokyo, says that scientists involved in the various projects were looking for ways to make their work more accessible to all researchers and to augment the value of individual collections. "One project can't cover everything, but put them all together and they are very complementary," he says.

The database includes data on more than 20,000 unique cDNA sequences, including everything known about function, structure, tissue expression patterns, disease relationships, and orthologs in common experimental animals. Researchers who want a copy of a particular cDNA clone can contact the appropriate institute. A second annotating marathon held last November produced data on 15,000 additional clones, which will be uploaded as soon as they are processed. The database is also prepared to accept submissions. Analysis of the annotated data has already led to the identification of several thousand previously unidentified candidate genes.

Gojobori imagines the database as the ultimate repository of information on cDNAs and sees it as one of Japan's major contributions to the field. Japan was late getting started on its contribution to human genome sequencing efforts, contributing only about 6% of the total. In contrast, the three Japanese projects contributed about 60% of the cDNA data going into the H-Invitational

Database. "I think Japanese researchers wanted to make a unique contribution to genomic efforts," he says.

--DENNIS NORMILE

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