Yeast’s Value Rises as Scientists Map Its 6,000 Genes

The Human Genome Project announced recently that an international consortium of scientists has finished spelling out the entire genetic code of a species of yeast valuable to scientists and commonly used by bakers and brewers.

This historic achievement, which comes nearly 4 years ahead of schedule and involved ordering 12 million units of DNA, marks the completion of the first full-sequence map of a eukaryotic, or complex, organism.

Because humans also are eukaryotes who share basic cellular properties with this species of yeast, called *Saccharomyces cerevisiae*, the announcement had been anxiously awaited by biomedical researchers. The sequence map paves the way for science to undertake a comprehensive study of the yeast’s genetic blueprint, assembling possibly within a few years the first full description of how a eukaryotic cell works, a longstanding goal of biology and medicine.

“If the human sequence is biology’s moonshot, then having the yeast sequence is like John Glenn orbiting the earth a few times,” said Francis Collins, M.D., Ph.D., director of the National Institutes of Health’s National Center for Human Genome Research, which supported American participation in the initiative.

**Essential to Life**

Although humans and yeast are separated by about 1 billion years on the evolutionary ladder, about one-third of the yeast’s 6,000 genes are related to human genes. That is, the human and yeast genes contain stretches of DNA that are close or identical in sequence, suggesting they are essential to life or else they would have been lost during evolution.

Given these similarities, scientists have spent years fishing around in yeast DNA trying to pull out interesting genes. This hit-or-miss strategy has led to novel insights into human cell biology, triggering major advances in understanding diseases such as neurofibromatosis, ataxia telangiectasia, hereditary nonpolyposis colon cancer, and cystic fibrosis.

But this approach has also been fraught with failure. In over three decades of trawling for genes, scientists say that until recently they had managed to find just 44% of the yeast genome, underscoring the need for a full-sequence map to aid in the gene search.

“In 1992, we made a ‘gentleman’s agreement’ not to compete, but to divide the work among us in order to complete the sequence rapidly with as little duplication as possible,” said Andre Gouffeau, who coordinated the European Union effort from Catholic University of Louvain in Belgium.
"We agreed not to stake out any territory and, on several occasions, DNA fragments to be sequenced were redistributed according to the respective abilities of the sequencing teams."

In 1994 alone, the consortium produced 5 million bases, or subunits, of yeast DNA. This momentum continued into 1996, leading up to the completion of all 16 yeast chromosomes in April.

How Does It Work?

The next step will be to find out how the yeast genome works. In April, the National Cancer Institute and the National Center for Human Genome Research began requesting applications for a new initiative to systematically analyze the function of genes in the yeast genome. Similar efforts are in the works in Europe.

With the yeast data now publicly available to researchers, the complete DNA sequences of other model organisms are on the way. According to Collins, the full-sequence map of the bacteria Escherichia coli should be finished by the end of 1996, with that for the round worm and fruit fly slated for completion well before the year 2000.

Most exciting of all, the Human Genome Project has also begun sequencing human DNA. This spring, the National Center for Human Genome Research (home to the project) launched a 3-year pilot project to evaluate full sequencing of all 3 billion subunits of human DNA. Less than 5% of the human genome has been sequenced by other researchers, but NCHGR is planning to start from scratch and sequence everything. A similar project is under way in England. If all goes well, the complete human blueprint should be finished by the year 2005, if not sooner.

— Bob Kuska

Cancer Researchers Getting Caught Up in the Net

The Internet is a vast and rapidly evolving network that is profoundly influencing everything it touches, including science.

Cancer research is no exception. Researchers are beginning to take advantage of this communications revolution, in activities that range from increasing contact with colleagues to performing prospective quality assurance in clinical trials.

New developments on the net are making it possible for researchers at remote locations to manipulate powerful instruments such as microscopes and nuclear magnetic resonance via the Internet. Others are bringing researchers together in virtual reality meetings, where they can have discussions, share documents, and perform calculations or other scientific manipulations as if they were in the same room. Soon it may be possible to record these events almost as a movie.

The net's most important benefit is instant message-sending that eliminates telephone tag, said Nicholas Restifo, M.D., a senior investigator in the laboratory of Steven A. Rosenberg, M.D., Ph.D., at the National Cancer Institute. "I have collaborations that I wouldn't have otherwise. It's a lot easier to communicate with European colleagues using the 'net' than any other way, because of the time difference. I exchange information with a guy in Spain on an almost daily basis."

Compared with the phone, another big advantage of e-mail is that it leaves a paper trail, and one never has to ask correspondents to spell the names of complex reagents.

Without e-mail, Nicholas J. Vogelzang, M.D., professor of medicine at the University of Chicago, said he would be unable to run the Cancer and Leukemia Group B Prostate Cancer Committee, which he chairs. "I coordinate 12 to 15 sites where various doctors are writing research plans, from ideas to writing the manuscripts we are submitting to the journals. There is virtually no way that I could do this by phone, and the mail is too inefficient."

One Internet institution, the list server, allows researchers to bring their quandaries before large groups of fellows. A list server coordinates a group with a shared interest, sending everyone's e-mail to everyone else on the list.

Dr. Nicholas Restifo

Steve Gore, M.D., assistant professor of oncology at the Johns Hopkins University Cancer Center, subscribes to a list server on a technique called flow cytometry. Recently, he had been trying unsuccessfully to develop methods to measure programmed cell death in CD34-positive bone marrow. A query to the list server got one colleague so fired up that he developed a new technique which he plans to publish and which worked for Gore.