EARTH SCIENCE

# Precise Positioning for All Is Coming

The White House threw a coming-out party last week for the Global Positioning System (GPS), predicting that the technology will blossom into an $8 billion market by 2000. But businesses hoping to capitalize on GPS weren't the only revelers. Besides giving assurances that signals from the network of 24 U.S. satellites will continue to be broadcast to all the world at no cost, the White House also vowed to end the practice of degrading the signals available to civilians. The degradation was meant to preserve the most accurate position information for the U.S. military, GPS's owner, but it has long been a costly irritant to researchers.

Earth scientists have come to depend on GPS for everything from locating geologic outcrops to measuring the drift of the continents (*Science*, 17 April 1992, p. 318), and they have been quick to exploit schemes for compensating for the fuzzy signal. Their own experience, they say, implies that the policy is unlikely to be keeping accurate GPS information out of the wrong hands. "I think that President Clinton recognized that the ability to know where you are very precisely is going to be accessible to everyone, whether or not the United States decides to make its GPS accessible," says Randolph Ware of the University NAVSTAR Consortium in Boulder, Colorado, a group of U.S. and foreign universities cooperating on scientific uses of GPS. "It's a part of being in the space age, just as in the age of sail if you turned on a lighthouse anyone could use it."

**In from the cold.** Military restrictions on GPS will be lifted, eventually.

The U.S. military doesn't see it that way. Even under the new policy, the satellite signal that civilian GPS receivers pick up will continue to be degraded for the next 4 to 10 years. Until the military develops electronic jamming techniques that would deny an enemy the use of GPS in wartime, civilian positioning will be accurate to only 100 meters rather than the 15 meters' accuracy available to the military.

Still, "anybody who wants better than 100-meter precision is doing it right now," says Thomas Herring of the Massachusetts Institute of Technology, who measures continental drift. "The only way the military can deny accurate positioning to civilians is to turn the satellites off." By using sites with known positions as benchmarks to correct for the intentional fuzzing of the satellite signal, for example, so-called differential GPS achieves accuracies of 1 to 10 meters, which is even better than that of the military GPS signal.

The big drawback, Herring says, is the added cost: Degrading the signal "is ineffective and is costing us money." For now, that's the price tag on the military's best gift since it gave the world the Internet.

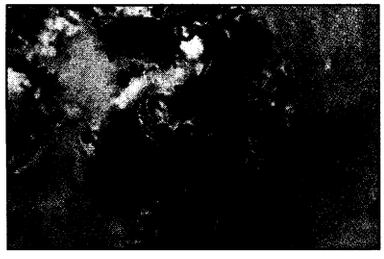
–Richard A. Kerr

GENOME SEQUENCING

# Europeans Move On From Yeast to TB

For European geneticists, this month marks the official completion of one major genome sequencing project and the start of two others. A consortium of groups across the continent has just finished sequencing the genome of the brewer's yeast *Saccharomyces cerevisiae* (*Science*, 29 March, p. 1798). Now, Britain's Wellcome Trust, the country's biggest private funder of biomedical research, is sponsoring efforts to sequence the genomes of two of the world's biggest killers: the organisms responsible for tuberculosis and malaria.

Wellcome announced last week that it will spend more than $2 million on a project to sequence *Mycobacterium tuberculosis*. The organism is believed to infect one third of the world's population, and it kills some 3 million people each year. Researchers are keen to develop new approaches to treating the disease but are hampered by the difficulty of working with the slow-growing organism. "Little is known about the proteins and metabolism of the bacterium, and researchers looking for new routes for therapy are working in a completely blind manner," says Stewart Cole, a tuberculosis researcher at the Institut Pasteur in Paris, who heads one of the groups in the project. "The spur for the sequencing work is its potential to identify all the proteins in the organism and develop rational targets."



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**Deciphering a killer.** Genome of *Mycobacterium tuberculosis* (shown here in sputum) is one third the size of the yeast genome but is harder to sequence.

*M. tuberculosis*'s genome, at an estimated 4.5 million base pairs, is small compared to yeast's 14 million, but it presents sequencers with quite a challenge. It has an imbalance in the bases that make up DNA, with guanine and cytosine accounting for about two thirds of the bacterium's genome. And that makes sequencing difficult because long strands of DNA can fold into a hairpin shape during the sequencing process, says Bart Barrell, head of the team at the Sanger Centre in Hinxton, near Cambridge, U.K., which will carry out the main sequencing work. "It makes life more difficult, but we think this problem can now be overcome," thanks to the experience gained through other sequencing projects, he says. Wellcome, which funds the Sanger Centre, will provide $2 million to Barrell's team and $100,000 to Cole's group at the Institut Pasteur. The two groups will collaborate on the project, which is expected to be completed within a year.

*M. tuberculosis* presents a daunting enough challenge, but Wellcome's other target, the malaria parasite *Plasmodium falciparum*, is an even tougher customer. It poses a similar kind of problem: Almost 80% of the total genome is made up of the other two bases, adenine and thymidine. When genes are being cloned from the parasite, the strands of DNA tend to recombine and the genetic information tends to get scrambled, says John Stephenson, program manager at the Wellcome Trust. Moreover, the whole genome is estimated to contain around 27 million base pairs—twice the size of the yeast genome.

For these reasons, Wellcome is taking a cautious approach. The grant will also fund Barrell for a pilot project to sequence *P. falciparum*'s chromosome 3, which consists of about 1.2 million base pairs. Barrell's team hopes to know within a year whether it can overcome the problems using a "shotgun" approach of cloning short fragments. If so, Barrell believes a full-scale sequencing project would be a good successor to the yeast project. "The genomes are similar in structure, with 14 chromosomes in malaria compared to 16 in yeast, and span a similar size range," says Barrell. "But we don't know how difficult it is going to be," he says. "That's why it's a pilot project."

–Nigel Williams