Long-Awaited Bacterial Genome Debuts

Last week, Frederick R. Blattner of the University of Wisconsin-Madison made the announcement that the microbiology community had been anxiously anticipating: He and his colleagues have finished sequencing the genome of *Escherichia coli*, the bacterium studied for decades by biologists.

"It's the most important bacterium there is," says Eric C. Lander of the Whitehead Institute for Biomedical Research in Cambridge, Mass. "*E. coli* is the bacterium of choice for studying how bacteria work. It's an invaluable sequence."

Blattner broke the news publicly at a meeting on small genomes in Hilton Head, S.C. He revealed that the bacterium's genome consists of 4,638,858 nucleotide base pairs, the chemical subunits of DNA, and appears to contain 4,300 genes. The exact number of genes remains "fluid" as rigorous analysis of the sequence continues, says Blattner.

The first full sequencing of a bacterial genome was announced in 1995, and completion of several other small genomes followed quickly (SN: 6/10/95, p. 367; 5/4/96, p. 278). At the South Carolina meeting, scientists from the Institute for Genome Research (TIGR) in Rockville, Md., reported that they were putting the final touches on four more sequences: the bacteria that cause syphilis, ulcers, and Lyme disease, as well as an archaea, one of the unusual microorganisms that form the so-called third branch of life (SN: 8/24/96, p. 116).

Yet microbiologists have looked forward to having *E. coli's* genome more than any other. "The main advantage of *E. coli* is that there's an enormous biology literature on this organism. That means when you have a gene and a gene product, you can fit them into the vast understanding of its biology," says Monica Riley of the Marine Biological Laboratory in Woods Hole, Mass., who called news of the genome's completion "exhilarating."

"*E. coli* also provides a reference point for all the other small genomes being sequenced, because for many of those organisms there's very little known about their biology," she adds.

As with the other recently unveiled genomes, *E. coli's* offers a bounty of novel genes. Almost 2,500 of them bear no strong resemblance to any known genes, leaving scientists with few clues to their roles.

"All this is going to take a while to analyze. It's a massive amount of data," says Riley, who maintains an online encyclopedia of *E. coli* genes.

That more than half of the bacterium's genome remains a complete mystery may seem a surprise, considering how extensively investigators have utilized *E. coli*. Yet petri dishes and test tubes aren't normal environments for the bacterium, so many of its genes may never have made their presence known to scientists. "I think a lot of the genes in *E. coli* function in niches other than the laboratory," observes Blattner.

Blattner's group, which started the *E. coli* project in 1991, deposited the last few sequences of the genome into public databases on Jan. 16, narrowly beating a Japanese group led by Hirotada Mori of the Nara Institute of Science and Technology. Mori's team, using previously published data from Blattner's group, actually produced a composite sequence of more than one *E. coli* strain. "It was kind of a race at the finish," admits Blattner.

Researchers have just begun to compare the two genomes to see what genes distinguish the strains. Blattner notes that an important project will be to compare these genomes with those of *E. coli* strains that can cause fatal food poisoning. With reference genome sequences in hand, it should become relatively easy to make such comparisons, he says.

The full *E. coli* sequence may even help researchers clean up their growing wealth of data on the human genome, adds Blattner. Some studies suggest that because of laboratory contamination, 15 percent of the human gene sequences now in databases contain parts of the *E. coli* genome. — *J. Travis*

Pathogens push poinsettias to branch out

Like a lot of other people, Ing-Ming Lee still has a Christmas poinsettia hanging around. But the U.S. Department of Agriculture researcher in Beltsville, Md., is less interested in the plant for interior decoration than for its inner workings.

Inside the plant's tissue lives a pathogen—no one has been sure what kind—that turns the otherwise tall, straight tropical plant into a bushy, branching, seasonal showpiece. In the February NATURE BIOTECHNOLOGY, Lee and his colleagues at USDA and Ball FloraPlant in West Chicago, Ill., report that the branching pathogen is not a virus, as had been suspected, but a phytoplasma, the tiniest kind of bacterial cell known.

Phytoplasma is a relatively new term for the plant-associated equivalents of mycoplasmas, an amorphous group of bacteria that infect animal cells. Several hundred different phytoplasmas are known to target plants, causing such diseases as witches' broom and aster yellows.

Like mycoplasmas, phytoplasmas lack cell walls and cannot be grown in the lab. By screening commercial poinsettias with a set of DNA segments, Lee's team could pick up evidence of the pathogen's genetic sequence and thus identify it as a new type of phytoplasma.

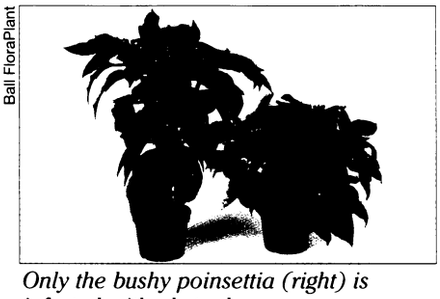
The researchers then performed a series of experiments to demonstrate that the newly detected phytoplasma, not the poinsettia virus, causes the plant's branching. First, they connected poinsettia and periwinkle plants, which do not support the poinsettia virus, with a parasitic plant called dodder. Three to 6 months later, the experimental periwinkles were bushier than control plants.

Then the researchers used dodder as a bridge between the well-branched periwinkles and nonbranching poinsettias. Three to 4 months later, the poinsettias began to turn bushy, and the DNA test showed evidence of the phytoplasma—but not of virus.

"It's extremely well done," says plant microbiologist Robert Goodman of the University of Wisconsin-Madison. Lee's group did not address how the phytoplasma forces the poinsettia to branch out, but Goodman says it fits with a general belief that these agents operate by subverting a plant's growth hormones.

Of the poinsettia phytoplasma, Lee says that "technically, it's a disease. But there's not too much harm for the poinsettia." If anything, the pathogen has improved the plant's survival: 60 million pots of bushy poinsettias are sold each Christmas. Moreover, like the virus responsible for streaked tulips, the phytoplasma is beneficial to growers, generating $325 million annually. — *C. Mlot*

Ball FloraPlant



Only the bushy poinsettia (right) is infected with phytoplasma.