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CALIFORNIA
Oak death's genes decoded
Unraveling is key step in finding way
to stop spread of pathogen

- [Jane Kay, Chronicle Environment Writer](#)

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Comparing
genome size



Mouse
2.6 billion base pairs 291



Scientists have figured out the complete genetic code of a virulent pathogen that has killed tens of thousands of California native oaks, an important step that scientists said will help them find ways to prevent or stop rampant spread of the disease.

The nonprofit Joint Genome Institute, operated by the University of California for the U.S. Department of Energy, was expected to announce today that it had successfully deciphered the genome of the pathogen that causes sudden oak death.

The scientists also succeeded in decoding the genome of a related pathogen that kills soybean plants.

Sudden oak death has swept through 12 counties in California and southern Oregon, killing native tan oak, coast live oak and black oak. Among the hardest hit regions are Marin, Sonoma and Santa Cruz counties and parts of Napa and Monterey, including Big Sur, where some slopes have been denuded of tan oaks.

With the identification of "molecular markers" of the pathogen, plant scientists will be able to diagnose the disease more easily in oak trees and in about 40 carrier plants.

Currently, plant pathologists have to find cankers on oak trees, then return to the lab to diagnose the material. With the new technique, they could search for the disease in other parts of the tree instead of waiting for the development of the cankers, which are often hard to find. "This will help us diagnose whether plants are infected," said Jeffrey Boore, head of the evolutionary genomics department at the Joint Genome Institute in Walnut Creek.

From the laborious sequencing -- or piecing together the complete arrangement of all the organism's genetic material -- they hope to develop a diagnostic test, Boore said. One detection method would recognize proteins, or strings of amino acids, made from clones of the pathogen's DNA.

Researchers can also look for ways to block the actions of the pathogen's genes, thus halting the fatal infection of the state's signature oak forests and prized yard trees.

One problem that scientists still face is figuring out what genes are necessary to mount an infection. "If we could find some ways to block the action of some of those genes, we

would render them ineffective at infecting other oak trees," Boore said.

The project cost about \$4 million with money from the National Science Foundation, the U.S. Department of Agriculture and the Energy Department. The two pathogens, *Phytophthora ramorum*, which kills oaks, and *Phytophthora sojae*, which kills soybean plants, are among an elite number of pathogens whose genetic codes have been deciphered.

A third pathogen is also of interest to the institute, *Phytophthora infestans*, which caused the Irish potato famine of the late 1840s and continues to cause at least \$3 billion a year in losses. Losses from the soybean pathogen are estimated at \$1 billion a year.

Many interests are competing for the genome decoding expertise of the Joint Genome Institute, which has 60 proposals before it. Selecting the oak and soybean pathogens came about, in part, at the urging of Brett Tyler, a scientist at the Virginia Bioinformatics Institute in Blacksburg, Va., an expert on the soybean disease.

Tyler worked with UC forest pathologist Matteo Garbelotto, one of the early sudden oak death experts along with David Rizzo, a UC Davis plant pathologist. Californians had reported dying trees as long ago as 1994. The two scientists identified the pathogen and diagnosed the disease in June 2000.

Garbelotto helped choose the strain of the oak pathogen that would be deciphered, and with colleague, Kelly Ivors, extracted the DNA on which the institute scientists worked.

Leading the sequencing team were Boore, Tyler and the institute's Dan Rokhsar, head of computational genomics, and Susan Lucas, head of production sequencing. The team sequenced the pathogen eight times to reach the point of reliability before releasing the results.

The oak pathogen has 16,000 genes, compared to 25,000 to 30,000 genes in a human. The pathogen's 60 million chemical DNA units, known as base pairs, compare with 2.9 billion units in humans.

Since March 26, a strict quarantine has been imposed banning any of several ornamental plants that can play host to the pathogen from being shipped out of state. Among them are rhododendrons, viburnums, camellias and azaleas, which suffer from marring lesions caused by the pathogen but apparently don't die.

Regarding the new research, Rizzo said he would welcome aid in diagnosing the disease, particularly if a specific DNA-based test could be used in the field. Blocking infection would be of great value, Rizzo said. "At this point, there's no good fungicide that directly attacks and kills the pathogen."

The spread seemed the worst in the wet mid-1990s through 2000, and has slightly waned with dryer weather. "But it's still out there, and we occasionally find it in new places," Rizzo said.

Knowing the genetic code of the pathogen, Rizzo said, "is helping us learn more about its basic biology. We may not see results immediately, but it's a good first step in finding a control."

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Page B - 3

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