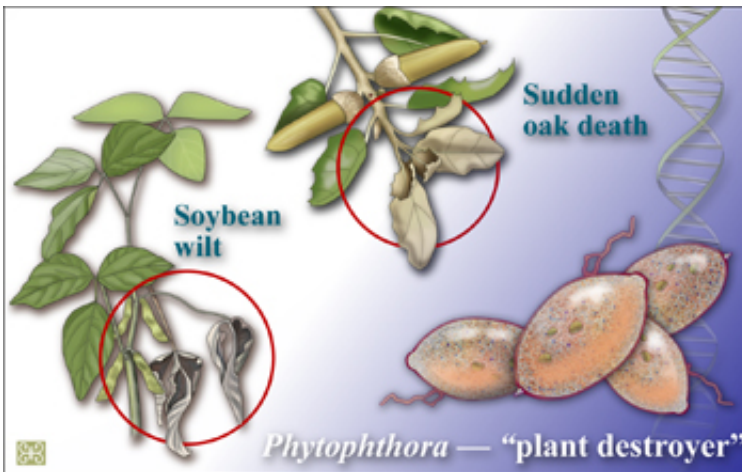


Genome Info from 'Plant Destroyers' Could Save Trees, Beans and Chocolate

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Scientists have sequenced the genomes from two species of *Phytophthora*, a group of plant pathogens that attacks a broad range of plants including soybeans and oak trees. Credit: Zina Deretsky, National Science Foundation

An international team of scientists has published the first two genome sequences from a destructive group of plant pathogens called *Phytophthora*--a name that literally means "plant destroyer." The more than 80 species of fungus-like *Phytophthora* (pronounced "fy-TOFF-thor-uh") attack a broad range of plants and together cost the agriculture, forestry and nursery industries hundreds of billions of dollars each year.

Even though *Phytophthora* are similar to fungi, most fungicides are ineffective at controlling them. The information gained from studying

the genomic sequences of *P. ramorum* and *P. sojae* will help scientists devise strategies to combat not only these two species, but also other disease-causing Phytophthora.

The study appears in the Sept. 1 issue of the journal *Science*.

Phytophthora sojae, an endemic pathogen of soybeans, is responsible for \$1 billion to \$2 billion in losses worldwide each year. *Phytophthora ramorum* is associated with sudden oak death, a disease that has devastated the nursery industry and oak ecosystems in California, Oregon and Washington. More than 1 million native oak and tanoak trees have been lost to the disease.

In addition to soybean and oak, *Phytophthora* species cause disease in avocado, coconut, papaya, pineapple, potato, strawberry and watermelon, to name a few. The pathogen also destroys an estimated 450,000 tons of cocoa beans with a resulting \$400 million loss in chocolate production each year.

The researchers found the pathogens have nearly twice as many genes as other fungal pathogens, and that more than 40 percent of the genes in each of the two species are undergoing rapid change. Many of the rapidly evolving genes encode toxins and other proteins that may debilitate plants.

"We speculate that the rapidly changing genes are being driven to evolve by pressure from the defense systems of the pathogens' host plants," said Virginia Bioinformatics Institute's Brett Tyler, the project's principal investigator.

"The *Phytophthoras*, in addition to their great economic importance, are fascinating organisms with very distinct and interesting biology," said Maryanna Henkart, NSF's division director for molecular and cellular

biosciences, which helped fund the work. "These new genome sequences will contribute to our basic understanding of normal plant-microbe relationships as well as their roles in disease," she said.

Source: NSF

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