# Genome sequences for two deadly plant pathogens make major contributions to scientific research

December 15 2010, By Susan Bland

A scientific paper written by an international team of researchers led by scientists at the Virginia Bioinformatics Institute at Virginia Tech and published in the journal *Science* in 2006 has surpassed 200 citations in the ISI Web of Knowledge, an online academic database that documents the impact of scientific publications. The paper presents the draft genome sequences of two deadly plant pathogens, *Phytophthora ramorum* and *Phytophthora sojae*.

*Phytophthora sojae* causes severe damage in soybean crops and results in $1–2 million in annual losses for commercial farmers in the United States. *Phytophthora ramorum*, which causes sudden oak death, has attacked and killed tens of thousands of oak trees in California and Oregon. The sequences of both genomes have served as a resource for the entire scientific community, revealing a recent, large expansion and diversification of many deadly genes involved in infection of the plant hosts of *Phytophthora*.

Virginia Bioinformatics Institute Professor Brett Tyler and his research group who worked on the *Phytophthora* genome sequences analyzed the genetic information using bioinformatic tools and identified an enormous superfamily of pathogen genes involved in the infection of plants. These genes produce virulence proteins that manipulate how plant cells work in such a way as to make the plant hosts more susceptible to infection. The researchers subsequently identified the region of these

virulence proteins containing the amino acid sequence motifs RXLR and dEER that enables them to enter the cells of their hosts by carrying the virulence proteins across the membrane surrounding plant cells without any additional machinery from the pathogen, as well as the fundamental entry mechanism that actually allows dangerous fungal microbes to infect plants and cause disease. These discoveries pave the way for the development of new intervention strategies to protect plant, and even some animal cells, from deadly fungal infections.

The project to sequence the genomes of *Phytophthora ramorum* and *Phytophthora sojae* started in 2002. The sequencing of *Phytophthora ramorum* represented the fastest sequencing of a newly emerged pathogen other than the Severe Acute Respiratory Syndrome virus; *Phytophthora ramorum* was identified in 2000 and its draft sequence was complete by 2004. The work, which was funded by the National Science Foundation, the United States Department of Agriculture's National Research Initiative, and the Department of Energy, was carried out by an international team of scientists led by the Department of Energy's Joint Genome Institute and the Virginia Bioinformatics Institute.

"Both evolutionary biologists and plant pathologists have shown strong interest in our paper," Tyler explained. "But the greatest impact by far has stemmed from the extensive knowledge of oomycete virulence proteins that has originated from the genome sequences."

**More information:** Read the original paper outlining the draft genome sequences of *Phytophthora sojae* and *Phytophthora ramorum*: Tyler BM, Tripathy S, Zhang X, et al. (2006) *Phytophthora* genome sequences uncover evolutionary origins and mechanisms of pathogenesis. *Science* 313:1261–1266. [PMID: 16946064]

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