Huge virulence gene superfamily responsible for devastating plant diseases

April 2 2008

A research team from the Virginia Bioinformatics Institute at Virginia Tech has identified an enormous superfamily of pathogen genes involved in the infection of plants. The Avh superfamily comprises genes found in the plant pathogens Phytophthora ramorum and Phytophthora sojae. The pathogen genes produce effector proteins that manipulate how plant cells work in such a way as to make the plant hosts more susceptible to infection.

The results suggest that a single gene from a common ancestor of the both pathogen species has spawned hundreds of very different, fast-evolving genes that encode for these highly damaging effector proteins.

P. sojae causes severe devastation in soybean crops and results in $1–2 million in annual losses for commercial farmers in the United States. P. ramorum, which causes sudden oak death, has attacked and killed tens of thousands of oak trees in California and Oregon. Both pathogens belong to the oomycete group of organisms that also includes the potato late blight pathogen responsible for the Irish potato famine. The scientists probed the recently published genome sequences of both organisms using bioinformatic tools that can look for specific amino acid sequences or motifs.

Advanced searches of the genome sequences (BLAST and Hidden Markov Model) revealed that the P. sojae and P. ramorum genomes encode large numbers of effector proteins (374 from P. ramorum and 396 from P. sojae) that likely facilitate the infection of their host plants.

Given that there are more than 80 species of Phytophthora pathogens, these findings imply that there are more than 30 000 members of this superfamily within the genus Phytophthora.

Proteins arising from the Avh superfamily have very different amino acid sequences but share two common motifs at one end of the protein (N-terminus). The readily identified RXLR and dEER motifs (single letter code for amino acids) are required for entry of the proteins into plant host cells. Similar motifs are also found in the effector proteins produced by the malarial parasite Plasmodium as it invades red blood cells.

The team also detected some conserved amino acid motifs (W, Y and L) at the other end (C terminus) of some of the proteins that have been selected over years of evolution. These C-terminal motifs are usually arranged as a module that can be repeated up to eight times. The functions of these C-terminal motifs are being investigated further.

The Avh gene superfamily is one of the most rapidly evolving parts of the genome. Duplications of genes are common and presumably responsible for the rapid expansion of the family. The diversity and duplication of genes noted in the sequences are consistent with maximizing the number of effector genes in the pathogens while making it increasingly difficult for the host defense systems to recognize invading molecules, ideal features for effector proteins aimed at wreaking havoc on susceptible plant hosts.

Professor Brett Tyler of the Virginia Bioinformatics Institute, the leader of the project, remarked: “The extraordinary speed with which the Avh genes are evolving suggests that these genes are key to the pathogens’ ability to outwit the defense systems of the plants.”

Source: Virginia Tech

Citation: Huge virulence gene superfamily responsible for devastating plant diseases (2008, April 2) retrieved 27 April 2024 from https://phys.org/news/2008-04-huge-virulence-gene-superfamily-responsible.html