

Comparative genomics and synteny studies revealing the reservoir of secreted proteins in Phytophthora

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The genus *Phytophthora* belongs to the oomycetes and contains over sixty species that are all notorious plant pathogens. The growth morphology and dispersal strategy of oomycetes resemble that of fungi and the weaponry that oomycetes and fungi use to attack plants appears to be comparable. In the phylogenetic tree, however, oomycetes are positioned on a branch completely separate from fungi. It is very likely that evolutionary history has also shaped the genes and genomes of oomycetes in a unique way. From two *Phytophthora* species, *Phytophthora sojae* and *Phytophthora ramorum*, draft genome sequences are available and we used these sequences to analyze the repertoire of secreted *Phytophthora* proteins. These proteins are of ultimate interest because they might be effector molecules that play important roles in pathogenesis. The presence of signal peptides and transmembrane domains was analyzed on all annotated *Phytophthora* genes resulting in a total of 1570 and 1256 putative secreted protein genes from *P. sojae* and *P. ramorum*, respectively. These were investigated for their sequence diversity, expansion of family members and genome organization. More than 80% of the secreted protein genes form gene families, and many of the families are clustered in the genome. Differences in expansion of gene families in different *Phytophthora* spp. were observed, and these expansion patterns may explain the difference in their pathogenicity. Some genes are located in genomic regions having many re-arrangements and insertions/deletions and these “hotspots” are particularly interesting to explore.