Molecular Evolution of an Avirulence Homolog (Avh) Gene Subfamily in *Phytophthora ramorum*[1]

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Abstract

Pathogen effectors can serve a virulence function on behalf of the pathogen or trigger a rapid defense response in resistant hosts. Sequencing of the *Phytophthora ramorum* genome and subsequent analysis identified a diverse superfamily of approximately 350 genes that are homologous to the four known avirulence genes in plant pathogenic oomycetes and share with them two protein motifs (RxLR and dEER). These have been termed Avh (avirulence homolog) genes. While as a whole the genes in this superfamily exhibit modest sequence similarity, small groups of closely related genes can be identified. We have investigated the molecular evolution of one such group of seven Avh genes. Microarray data suggests that four of these genes are expressed in isolate Pr-102 whose genome was sequenced. We sequenced the full coding region (approximately 400 bp) and flanking noncoding regions of each gene in the three clonal lineages of *P. ramorum*. The number of polymorphic sites within *P. ramorum* genes ranges from 0 to 35, suggesting different evolutionary pressures among genes. Analysis indicates that these genes contain both codons under purifying selection (e.g. in the signal peptide and RxLR and dEER motifs) and under positive selection. We have also been able to obtain the sequence of homologous Avh genes in the sister taxa *P. hibernalis*, *P. lateralis*, and *P. foliorum* allowing for examination of the evolution of these genes across species.

Key words: *Phytophthora ramorum*, *Phytophthora lateralis*, *Phytophthora hibernalis* effector, RXLR motif.

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