

Introducing the *Phytophthora* Database: An Integrated Resource for Detecting, Monitoring, and Managing *Phytophthora* diseases¹

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Abstract

Its virulence and ability to spread rapidly throughout the world by various means establishes *Phytophthora* as one of the most important groups of plant pathogens. Discoveries of inter-specific hybridization among *Phytophthora* species in nature, which could yield novel pathogens, further underscore the threat posed by members of this genus. The ability to accurately and rapidly identify the causal agent of a disease is crucial for developing effective regulatory and disease management strategies, and facilitates the monitoring of changes in pathogen communities as they respond to agricultural practices and environmental changes. The *Phytophthora* database (PD) (<http://www.phytophthoradb.org>) project was initiated in 2005 to enhance our capability of rapid detection and diagnosis of *Phytophthora* spp. by archiving genotypic and phenotypic diversity of *Phytophthora* in a highly integrative cyber infrastructure that can easily be accessed and searched.

To establish a more comprehensive phylogenetic framework for the genus *Phytophthora*, informative molecular markers from multiple nuclear loci were identified using the available genome sequences for *P. ramorum* and *P. sojae*, in conjunction with the large number of expressed sequence tags (ESTs) available for *P. infestans*. We sequenced up to nine loci of selected isolates that represent most of the known species within *Phytophthora* (228 isolates from 80 species), (Blair and others, unpublished), including (i) two loci in the nuclear ribosomal RNA (rRNA) encoding genes: the internal transcribed spacer (ITS) regions and the 5' portion of the large subunit rRNA, (ii) nuclear genes encoding 60S ribosomal protein L10, beta-tubulin, enolase, heat shock protein 90, TigA fusion protein, and translation elongation factor 1 alpha, and (iii) a mitochondrially-encoded *coxII* gene and spacer region between *coxI* and *coxII*. The resulting phylogeny supports the division of *Phytophthora* into approximately eight major groups, and also resolves the overall relationships among these groups with moderate support. In addition to those regions, four additional mitochondrially encoded genes are being sequenced from the same isolates to construct a mitochondrially based phylogenetic framework.

To support the identification of unknown *Phytophthora* isolates via comparison of their sequences with corresponding sequences derived from archived isolates, we generated and deposited sequence data from more than 1,100 isolates representing the known diversity of

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the genus. Since ITS sequences have been commonly used for identifying oomycete species and isolates, the ITS region was sequenced from all isolates archived in the database. Although sequences for multiple loci are present for a group of isolates representing individual species, the database is currently dominated by ITS sequences. Because the PD provides applied and molecular information on *Phytophthora* species along with a suite of data analysis tools, we feel the PD has more utility than GenBank. In addition, the data stored at the PD is provided by specialists actively working with *Phytophthora*, hence proper identification of reference cultures should be less prone to error. This project is on-going; sequence and species data are continually being deposited to increase utility and breadth of this database. Scientists interested in *Phytophthora* are encouraged to use and contribute to the database.

The phylogenetic framework established at this database supports the development and validation of molecular diagnostic approaches designed primarily for species identification. The use of genotyping will greatly assist the study of newly isolated oomycetes by researchers who have limited experience in taxonomy, or by regulatory agency scientists who must quickly assess the threat of a new population and track its change and movement. The significance of this project to agricultural and forest biosecurity is the establishment of a baseline for monitoring the emergence of new and foreign *Phytophthora*. In addition, this database should serve as a model data collection system that could be easily adapted to develop databases for other important pathogen groups.

Key words: *Phytophthora* disease, invasive pathogen, genomics, population genetics, systematics, taxonomy.