The rapid expansion of global trade and human travel has greatly accelerated the introduction of non-endogenous pathogens and pests.

The global climate change influences pathogen communities both directly and indirectly
Sudden Oak Death

An example illustrating the challenges we are facing
Difficulties in accurately determining species/population identity based on morphological traits->
Accurate determination of species/population identity is critical for risk assessment and the implementation of regulatory measures and appropriate disease control strategies.
Issues in Molecular Identification

✓ Molecular identification is not a panacea.
  • Your results may be as good as what you compared with (legacy errors and problems).
  • Different genes may tell different stories.
  • Molecular data without biological contexts have a limited value.

✓ What is species?
  • Biological, morphological, and phylogenetic species concepts.
  • They overlap but not perfectly.
"There are known knowns. These are things we know that we know. There are known unknowns. That is to say, there are things that we know we don't know. But there are also unknown unknowns. There are things we don't know we don't know."

- Donald Rumsfeld -

Limited understanding of pathogen diversity in nature -> There exist many “known knowns, known unknowns & unknown unknowns” threatening agricultural and ecological systems.
Limited efforts and mechanisms to support global cooperation and knowledge sharing-

Mapping and documenting the diversity, distribution, and biology of major pathogens worldwide and sharing this information are essential to improve our ability to track and manage pathogens.
**Phytophthora Database**

Cyberinfrastructure supporting identification and monitoring of *Phytophthora* species

- DNA from known pathogen isolates
- PCR amplification of multiple marker genes
- DNA sequencing
- Genetic fingerprints for individual isolates
- Phenotypes (such as morphology, geographic & host of origin, host range, virulence, drug resistance, toxin profile) of known isolates

www.phytophthoradb.org

**Principal Investigators**

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- **UC-Riverside**: Mike Coffey
- **North Carolina State University**: Kelly Ivors
- **USDA-ARS**: Frank Martin & Kerry O'Donnell
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- West Virginia: Y. Balci
- PA Dept of Ag: S. H. Kim & E. Nikolaeva
- Seoul National University: Y. Lee, K. Jung & J. Park
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- APS Press: D. Erwin & O. Ribeiro
Specific Objectives of the PD Project

✓ To establish a comprehensive phylogenetic framework for the genus *Phytophthora*.

✓ To build a cyberinfrastructure that archives the genotypes, phenotypes, and distribution of individual *Phytophthora* species/isolates and provides data analysis and visualization tools.

✓ To develop and optimize molecular diagnostic tools for detecting and identifying *Phytophthora* species.
Development of new phylogenetic markers based on the genome sequences of *P. ramorum*, *P. capsici*, *P. sojae* and *P. infestans*.

Conducted a genus-wide phylogenetic analysis using representative species/isolates.

Genotypic identification of ~3,000 isolates (>90 species).

Establishment of the *Phytophthora* Database.

Characterization of individual species complexes (e.g., *P. cinnamomoi*, *P. capsici*)
Organization of the *Pytophthora* Database

Phytophthora Database Login

Dear Seogchan Kang,

Welcome to Phytophthora Database.

» I want to logout this database.
» I want to manage my login information.

Welcome to Phytophthora Database

» About the goals and utility of the database
» About sequence based search
» About submission of data
» Acknowledgements
» How to save and reuse your favorite data and result

Current Statistics of the Database

» 94 Species
» 1,773 Isolates
» 3,683 Sequences

Contact the Database Curator

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Refs. & News

» Recent Publications
» Protocols
» Slide Presentations
» PD News

Link to Contributors

KACC

**Phylogenetic Position within the Genus**

This genus-wide phylogenetic tree contains 74 species, including Pythium vexans as the outgroup, and was built using sequences at seven loci (approximately 7000 nucleotides), including 659 Protein Cystatin Domain, 585 Tubulin, 326 Heat Shock Protein 10, Luge Subtilisin-like, TIGR gene fusion, and Translation Elongation Factor 1 alpha (Seren Blair et al., unpublished data).

**Characteristics**

1. **sporulation**
   - Sporangia are oval, ellipsoid to ovoid, brown in color, and compactly clustered, with a sporangial range from 20 to 18 μm (Roubal 1942) in Phytographa. Sporangia are 20 to 30 μm in diameter (Soil 1944). These dimensions are smaller than those of the previous description (15 to 20 μm in diameter, 7 to 9 μm in width), with a sporangial range from 15 to 20 μm in diameter (Eckels 1951).
   - Sporangia are compactly clustered (Figure 4B and 5B in Phytographa), forming a circular cluster at the base of the sporangium (Figure 4C).

2. **Typical host**
   - Neither high nor low sporangia have been reported, except in a paper from Russia by Puchkova (1952), which noted chloroazepine spores in the vascular cambium of its host. Using this information, we can determine the typical host to be Phytographa. This species is also known to have sporangia in the cambium of its host (Figure 5A and 5B).
Functionality of the Pytophthora Database

Marker Sequence Database

Data Submission

Virtual Gel

BLAST Search

Sequence Alignment

Phylogenetic Tree

Data Download & Storage

Cart & Folder
Functionality of the *Pytophthora* Database
Future Direction
Stremenophile/Oomycete Tree of Life?

- Brown Algae
  - Diatoms
    - Hypochohytriomyces
      - Leptomitales*
        - Saprolegniales*
          - Rhipidiales*
            - Lagenidiales*
              - Peronsoporales*
                - Labyrinthulomyces
                  * = Oomycetes
Pythium Database Login

Dear Guest,
Welcome to Pythium Database.

» I want to log out this database.
» I would like to login the DB as guest

Run Wizard
Easy to access work process

» Data Submission
» Search the database
» How to use the database

Welcome to Pythium Database

» About the goals and utility of the database
» Acknowledgements

Current statistics of the database

» 31 Species
» 364 Isolates
» 364 Sequences

Pythium Database News

Link to contributors
Fusarium Database Login

Dear Guest,
Welcome to Fusarium Database.

» I want to logout this database.
» I want to modify my login information.

Welcome to Fusarium Database

» About the goals and utility of the database
» Acknowledgements

Current statistics of the database

» 15 Species
» 915 Isolates
» 2,284 Sequences

Fusarium Database News

Link to contributors