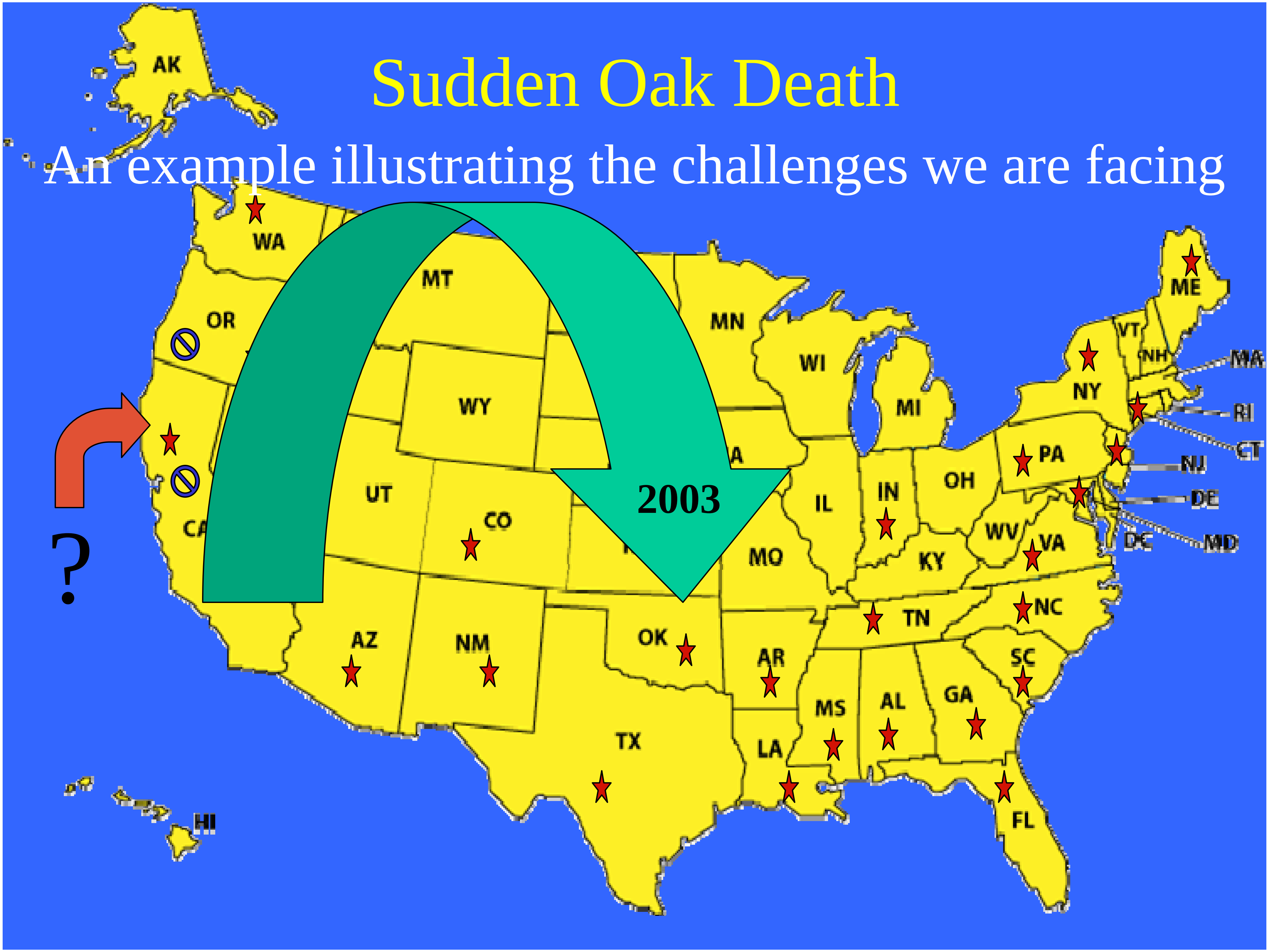
The rapid expansion of global trade and human travel has greatly accelerated the introduction of non-endogenous pathogens and pests.

The global climate change influences pathogen communities both directly and indirectly

Sudden Oak Death

An example illustrating the challenges we are facing



Challenge 1

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.

Challenge 2

"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.

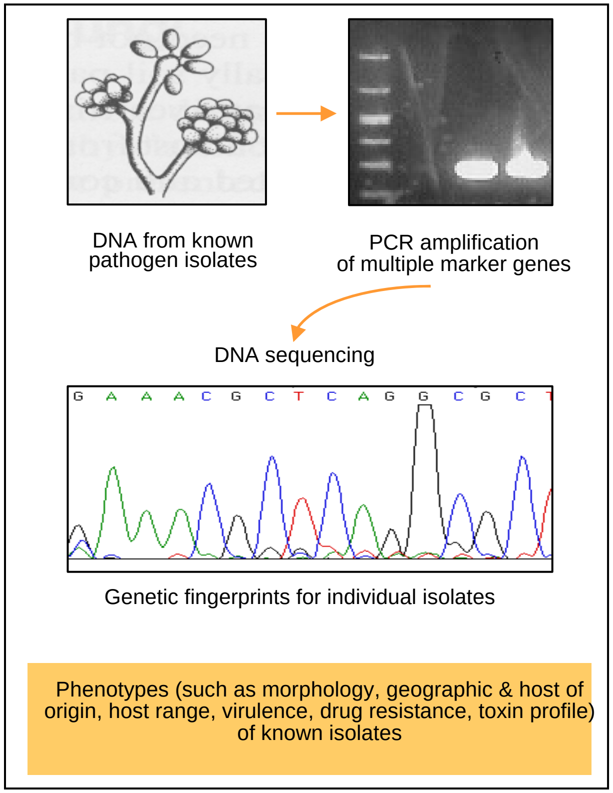
Challenge 3

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



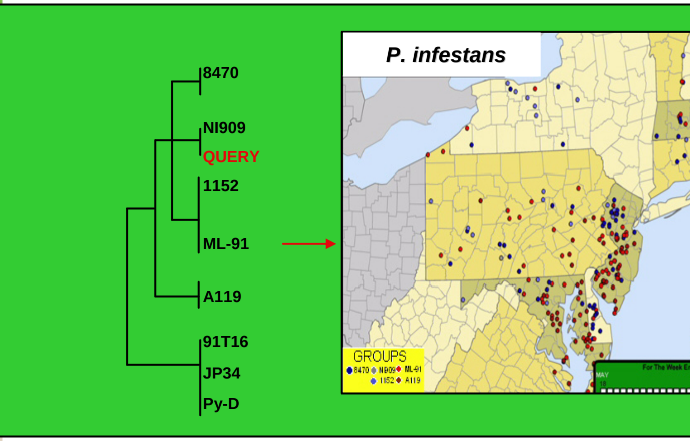
DNA from known pathogen isolates

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

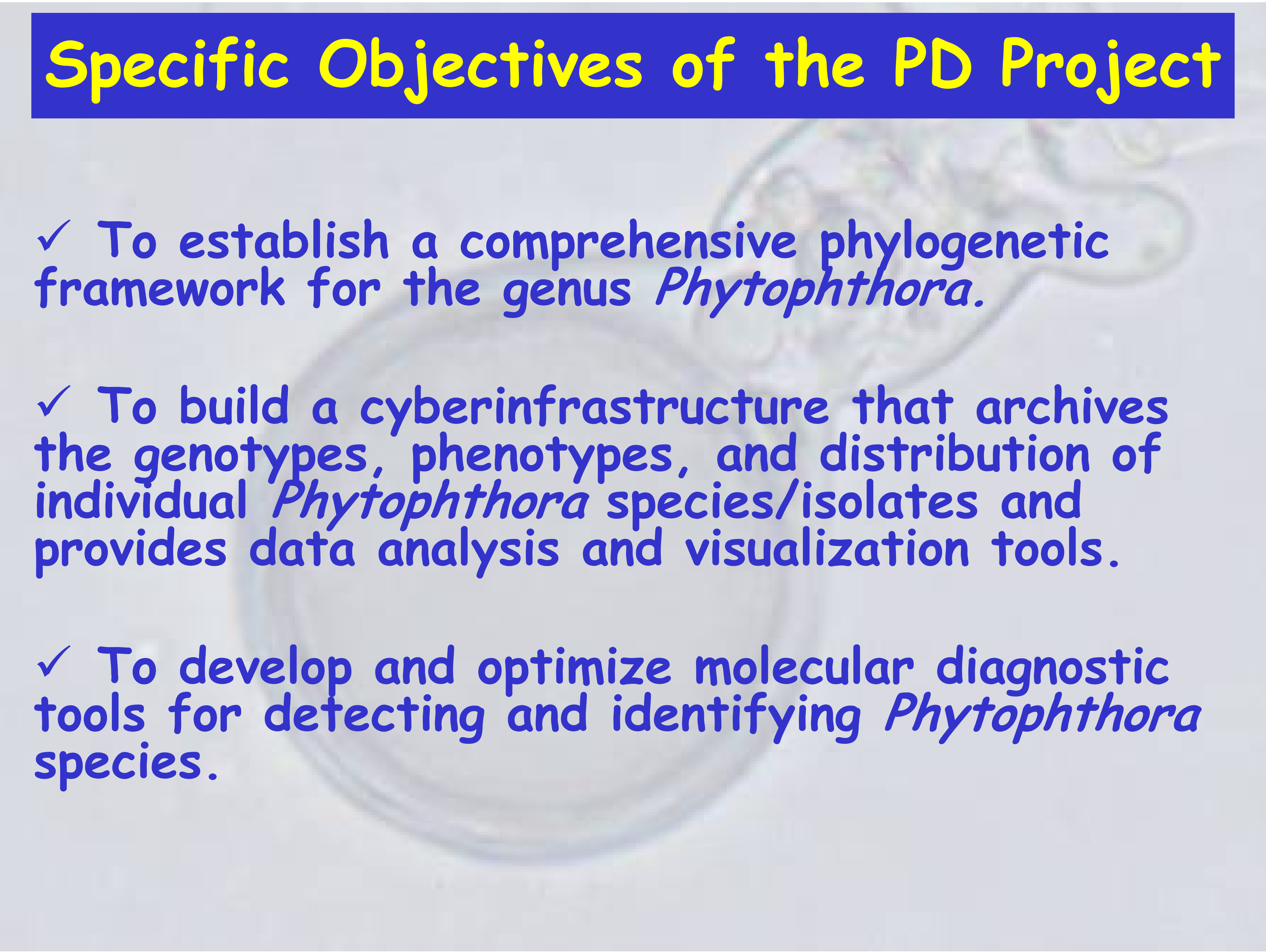
- **Penn State:** Seogchan Kang, David Geiser & Izabela Makalowska
- **UC-Riverside:** Mike Coffey
- **North Carolina State University:** Kelly Ivors
- **USDA-ARS:** Frank Martin & Kerry O'Donnell

USDA-NRI
Plant Biosecurity

THANKS to...

- **Penn State:** J. Blair, S. Park, N. Veeraraghavan, M. Mansfiel & B. Park
- **UC-Riverside:** M. Peiman
- **NC State:** M. Green
- **West Virginia:** Y. Balci
- **PA Dept of Ag:** S. H. Kim & E. Nikolaeva
- **Seoul National University:** Y. Lee, K. Jung & J. Park
- **USDA-ARS SBML:** A. Rossman, D. Farr & E. Cline
- **APS Press:** D. Erwin & O. Ribeiro

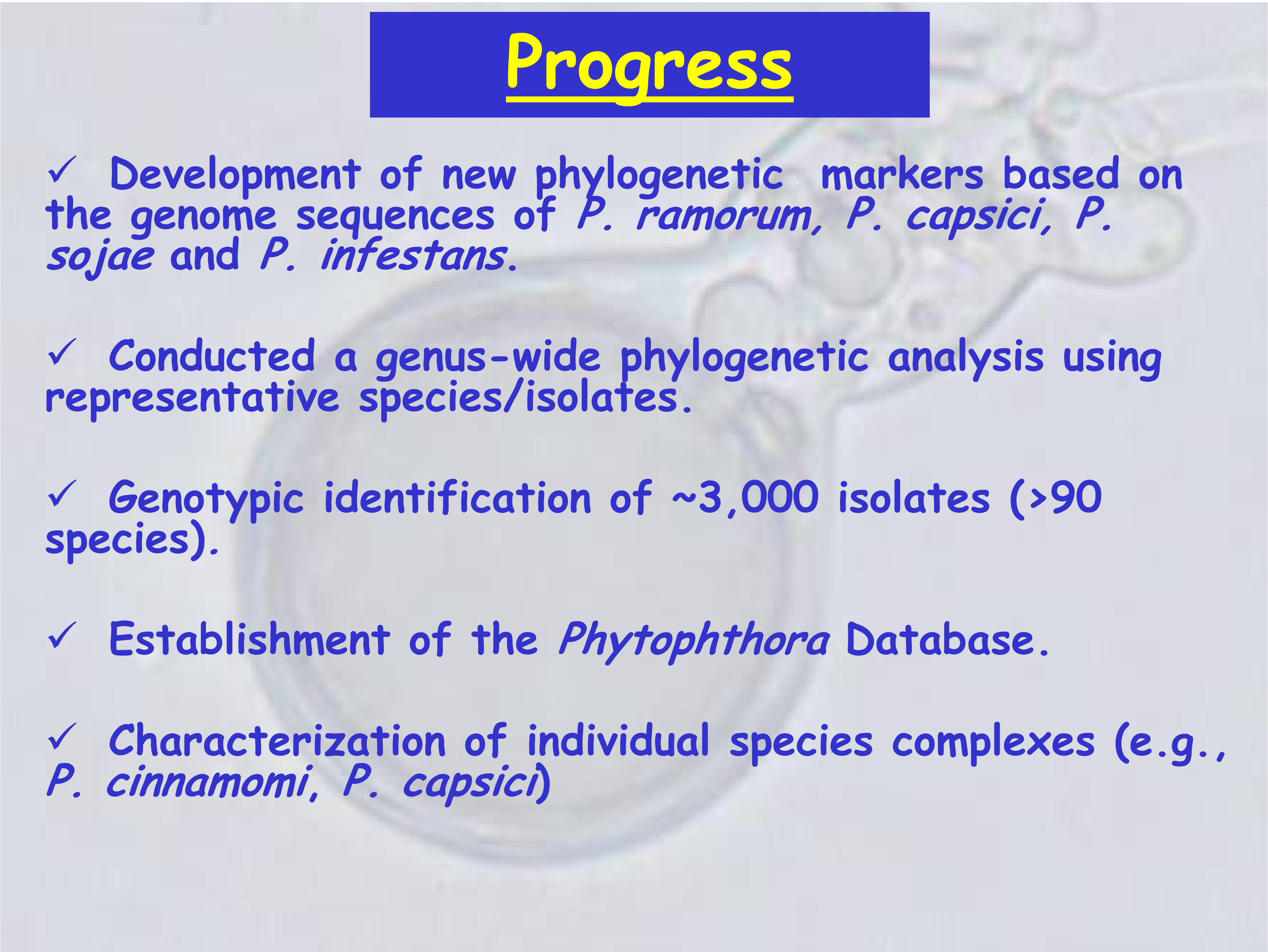
Specific Objectives of the PD Project



✓ 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.



Progress

✓ Development of new phylogenetic markers based on the genome sequences of *P. ramorum, P. capsici, P. sojae* and *P. infestans.*

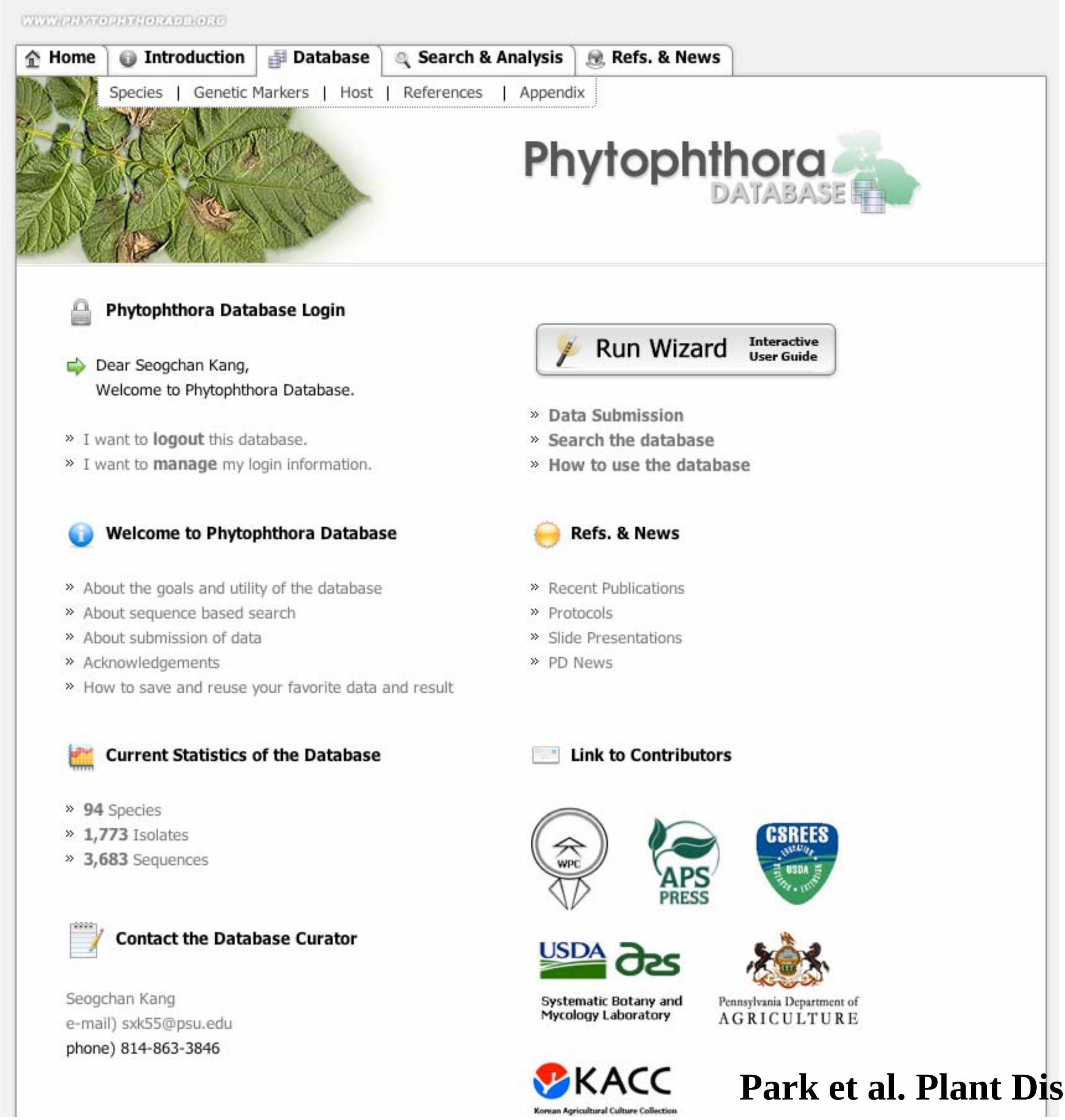
✓ Conducted a genus-wide phylogenetic analysis using representative species/isolates.

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

✓ Establishment of the *Phytophthora* Database.

✓ Characterization of individual species complexes (e.g., *P. cinnamomi, 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.

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

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

Refs. & News

» Recent Publications
» Protocols
» Slide Presentations
» PD News

Current Statistics of the Database

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

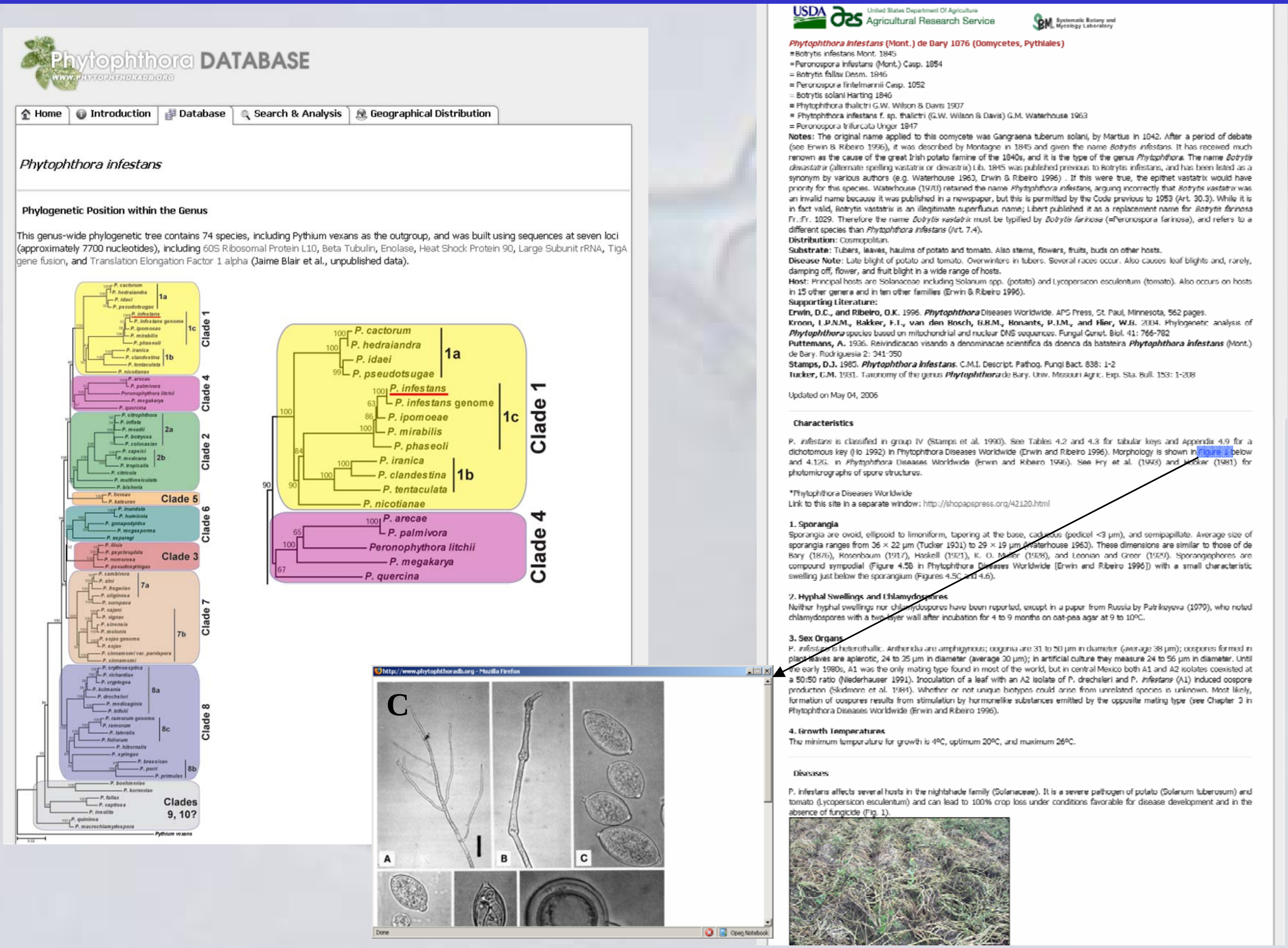
Link to Contributors

Contact the Database Curator

Seogchan Kang
e-mail) sxk55@psu.edu
phone) 814-863-3846

Park et al. Plant Disease (2008) 92: 966-972

Species Information Page



Phytophthora infestans

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 7700 nucleotides), including 60S Ribosomal Protein L10, Beta Tubulin, Enolase, Heat Shock Protein 90, Large Subunit rRNA, TigA gene fusion, and Translation Elongation Factor 1 alpha (Jaime Blair et al., unpublished data).

***Phytophthora infestans* (Mont.) de Bary 1076 (Oomycetes, Pythiales)**

=Botrytis infestans Mont. 1845
=Peronospora infestans (Mont.) Casp. 1854
= Botrytis fallax Desm. 1846
= Peronospora fintelmannii Casp. 1052
= Botrytis solani Harting 1846
= Phytophthora thalictri G.W. Wilson & Davis 1907
= Phytophthora infestans f. sp. thalictri (G.W. Wilson & Davis) G.M. Waterhouse 1963
= Peronospora trifurcata Unger 1847

Notes: The original name applied to this oomycete was Gangraena tuberum solani, by Martius in 1042. After a period of debate (see Erwin & Ribeiro 1996), it was described by Montagne in 1845 and given the name *Botrytis infestans*. It has received much renown as the cause of the great Irish potato famine of the 1840s, and it is the type of the genus *Phytophthora*. The name *Botrytis devastatrix* (alternate spelling vastatrix or devastrix) Lib. 1845 was published previous to Botrytis infestans, and has been listed as a synonym by various authors (e.g. Waterhouse 1963, Erwin & Ribeiro 1996) . If this were true, the epithet vastatrix would have priority for this species. Waterhouse (1970) retained the name *Phytophthora infestans*, arguing incorrectly that *Botrytis vastatrix* was an invalid name because it was published in a newspaper, but this is permitted by the Code previous to 1953 (Art. 30.3). While it is in fact valid, Botrytis vastatrix is an illegitimate superfluous name; Libert published it as a replacement name for *Botrytis farinosa* Fr.:Fr. 1829. Therefore the name *Botrytis vastatrix* must be typified by *Botrytis farinosa* (=Peronospora farinosa), and refers to a different species than *Phytophthora infestans* (Art. 7.4).
Distribution: Cosmopolitan.
Substrate: Tubers, leaves, haulms of potato and tomato. Also stems, flowers, fruits, buds on other hosts.
Disease Note: Late blight of potato and tomato. Overwinters in tubers. Several races occur. Also causes leaf blights and, rarely, damping off, flower, and fruit blight in a wide range of hosts.
Host: Principal hosts are Solanaceae including Solanum spp. (potato) and Lycopersicon esculentum (tomato). Also occurs on hosts in 15 other genera and in ten other families (Erwin & Ribeiro 1996).
Supporting Literature:
Erwin, D.C., and Ribeiro, O.K. 1996. ***Phytophthora*** Diseases Worldwide. APS Press, St. Paul, Minnesota, 562 pages.
Kroon, L.P.N.M., Bakker, F.T., van den Bosch, G.B.M., Bonants, P.J.M., and Flier, W.G. 2004. Phylogenetic analysis of ***Phytophthora*** species based on mitochondrial and nuclear DNS sequences. Fungal Genet. Biol. 41: 766-782
Puttemans, A. 1936. Reivindicacao visando a denominacae scientifica da doenca da batateira ***Phytophthora infestans*** (Mont.) de Bary. Rodriguesia 2: 341-350
Stamps, D.J. 1985. ***Phytophthora infestans***. C.M.I. Descript. Pathog. Fungi Bact. 838: 1-2
Tucker, C.M. 1931. Taxonomy of the genus ***Phytophthora*** de Bary. Univ. Missouri Agric. Exp. Sta. Bull. 153: 1-208

Updated on May 04, 2006

Characteristics

P. *infestans* is classified in group IV (Stamps et al. 1990). See Tables 4.2 and 4.3 for tabular keys and Appendix 4.9 for a dichotomous key (Ho 1992) in Phytophthora Diseases Worldwide (Erwin and Ribeiro 1996). Morphology is shown in Figure 1 below and 4.12G. in *Phytophthora* Diseases Worldwide (Erwin and Ribeiro 1996). See Fry et al. (1993) and Hooker (1981) for photomicrographs of spore structures.

*Phytophthora Diseases Worldwide
Link to this site in a separate window: http://shopapspress.org/42120.html

1. Sporangia
Sporangia are ovoid, ellipsoid to limoniform, tapering at the base, caducous (pedicel <3 µm), and semipapillate. Average size of sporangia ranges from 36 × 22 µm (Tucker 1931) to 29 × 19 µm (Waterhouse 1963). These dimensions are similar to those of de Bary (1876), Rosenbaum (1917), Haskell (1921), K. O. Müller (1928), and Leonian and Greer (1929). Sporangiophores are compound sympodial (Figure 4.5B in Phytophthora Diseases Worldwide [Erwin and Ribeiro 1996]) with a small characteristic swelling just below the sporangium (Figures 4.5C and 4.6).

2. Hyphal Swellings and Chlamydospores
Neither hyphal swellings nor chlamydospores have been reported, except in a paper from Russia by Patrikeyeva (1979), who noted chlamydospores with a two-layer wall after incubation for 4 to 9 months on oat-pea agar at 9 to 10ºC.

3. Sex Organs
P. *infestans* is heterothallic. Antheridia are amphigynous; oogonia are 31 to 50 µm in diameter (average 38 µm); oospores formed in plant leaves are aplerotic, 24 to 35 µm in diameter (average 30 µm); in artificial culture they measure 24 to 56 µm in diameter. Until the early 1980s, A1 was the only mating type found in most of the world, but in central Mexico both A1 and A2 isolates coexisted at a 50:50 ratio (Niederhauser 1991). Inoculation of a leaf with an A2 isolate of P. drechsleri and P. *infestans* (A1) induced oospore production (Skidmore et al. 1984). Whether or not unique biotypes could arise from unrelated species is unknown. Most likely, formation of oospores results from stimulation by hormonelike substances emitted by the opposite mating type (see Chapter 3 in Phytophthora Diseases Worldwide (Erwin and Ribeiro 1996).

4. Growth Temperatures
The minimum temperature for growth is 4ºC, optimum 20ºC, and maximum 26ºC.

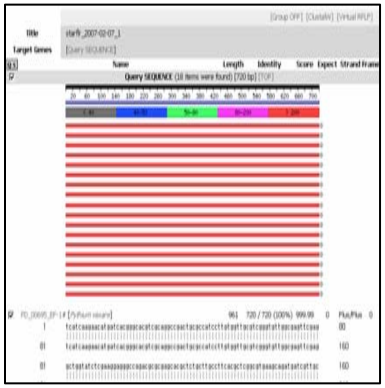
Diseases

P. infestans affects several hosts in the nightshade family (Solanaceae). It is a severe pathogen of potato (Solanum tuberosum) and tomato (Lycopersicon esculentum) and can lead to 100% crop loss under conditions favorable for disease development and in the absence of fungicide (Fig. 1).

Functionality of the *Pytophthora* Database

Marker Sequence Database

BLAST Search

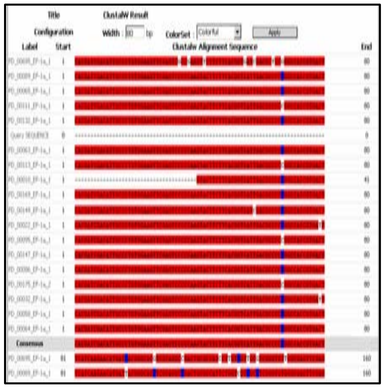


Title: start_2007-02-07_1

Target Genes: [Query SEQUENCE]

Query SEQUENCE (18 items were found) [720 bp] [TOP]

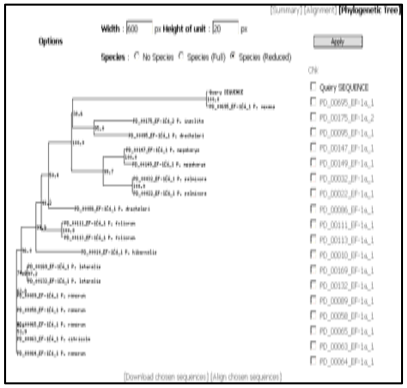
Sequence Alignment



Title: ClustalW Result

Configuration: Width: 60 bp ColorSet: Colorful

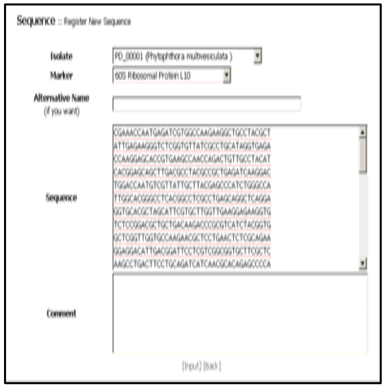
Phylogenetic Tree



Options: Width: 600 px Height of unit: 20 px

Species: ○ No Species ○ Species (Full) ● Species (Reduced)

Data Submission



Sequence :: Register New Sequence

Isolate: PD_00001 (Phytophthora multivesiculata)

Marker: 60S Ribosomal Protein L10

Alternative Name (if you want):

Sequence:

```
CGAAACCAATGAGATCGTGGCCAAGAAGGCTGCCTACGCT
ATTGAGAAGGGTCTCGGTGTTATCGCCTGCATAGGTGAGA
CCAAGGAGCACCGTGAAGCCAACCAGACTGTTGCCTACAT
CACGGAGCAGCTTGACGCCTACGCCGCTGAGATCAAGGAC
TGGACCAATGTCGTTATTGCTTACGAGCCCATCTGGGCCA
TTGGCACGGGCCTCACGGCCTCGCCTGAGCAGGCTCAGGA
GGTGCACGCTAGCATTCGTGCTTGGTTGAAGGAGAAGGTG
TCTCCGGACGCTGCTGACAAGACCCGCGTCATCTACGGTG
GCTCGGTTGGTGCCAAGAACGCTCCTGAACTCTCGCAGAA
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AAGCCTGACTTCCTGCAGATCATCAACGCACAGAGCCCCA
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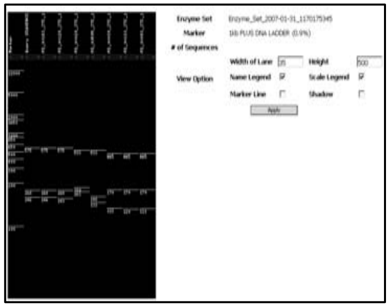
Comment:

Virtual Gel



Enzyme Set: Enzyme_Set_2007-01-31_1170175345

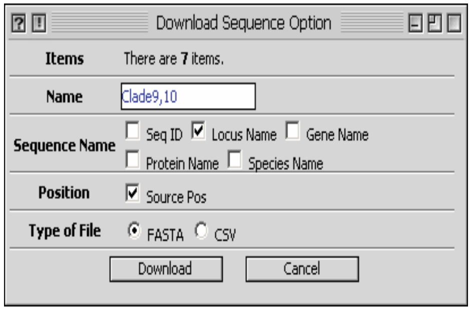
Marker: 1kb PLUS DNA LADDER (0.9%)

\# of Sequences

Width of Lane: 25 Height: 500

View Option: Name Legend ☑ Scale Legend ☑ Marker Line ☐ Shadow ☐

Data Download & Storage



Download Sequence Option

Items: There are 7 items.

Name: Clade9,10

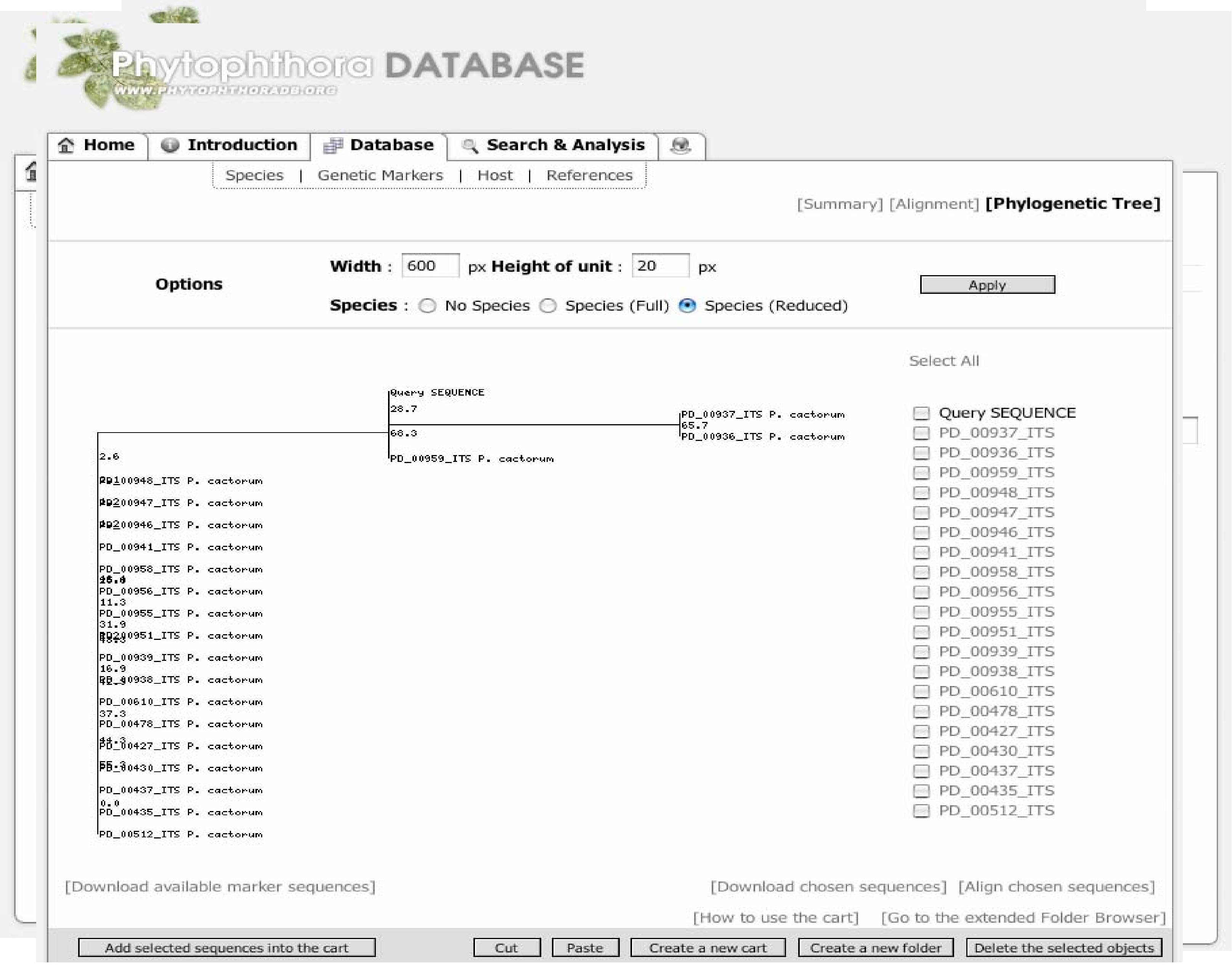
Sequence Name: ☐ Seq ID ☑ Locus Name ☐ Gene Name ☐ Protein Name ☐ Species Name

Position: ☑ Source Pos

Type of File: ● FASTA ○ CSV

Cart & Folder

Functionality of the *Pytophthora* Database



Options

Width : 600 px **Height of unit :** 20 px

Species : ○ No Species ○ Species (Full) ● Species (Reduced)

☐ Query SEQUENCE
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☐ PD_00936_ITS
☐ PD_00959_ITS
☐ PD_00948_ITS
☐ PD_00947_ITS
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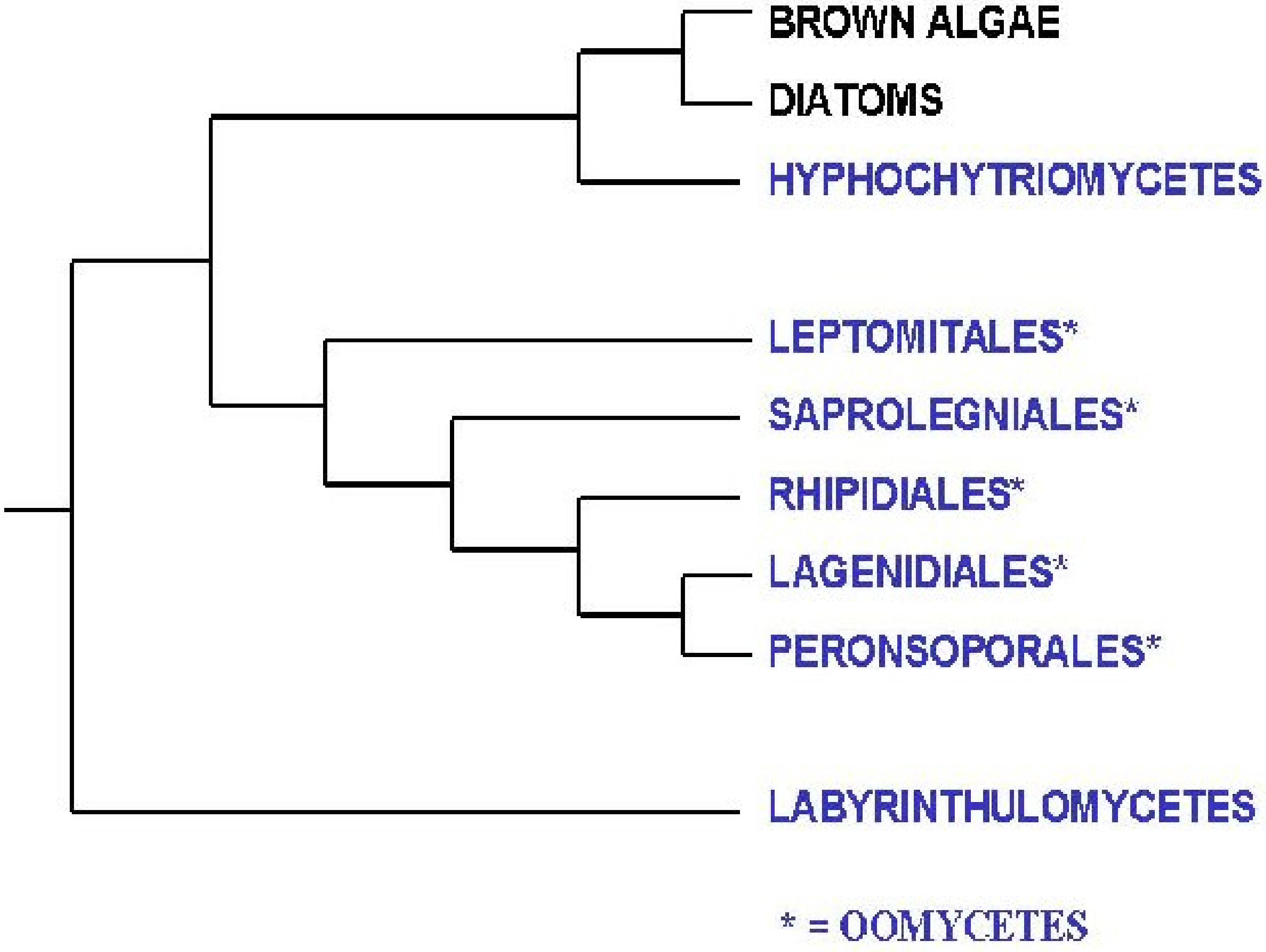
☐ PD_00610_ITS
☐ PD_00478_ITS
☐ PD_00427_ITS
☐ PD_00430_ITS
☐ PD_00437_ITS
☐ PD_00435_ITS
☐ PD_00512_ITS

Future Direction

Stremenophile/Oomycete Tree of Life?



BROWN ALGAE

DIATOMS

HYPHOCHYTRIOMYCETES

LEPTOMITALES*

SAPROLEGNIALES*

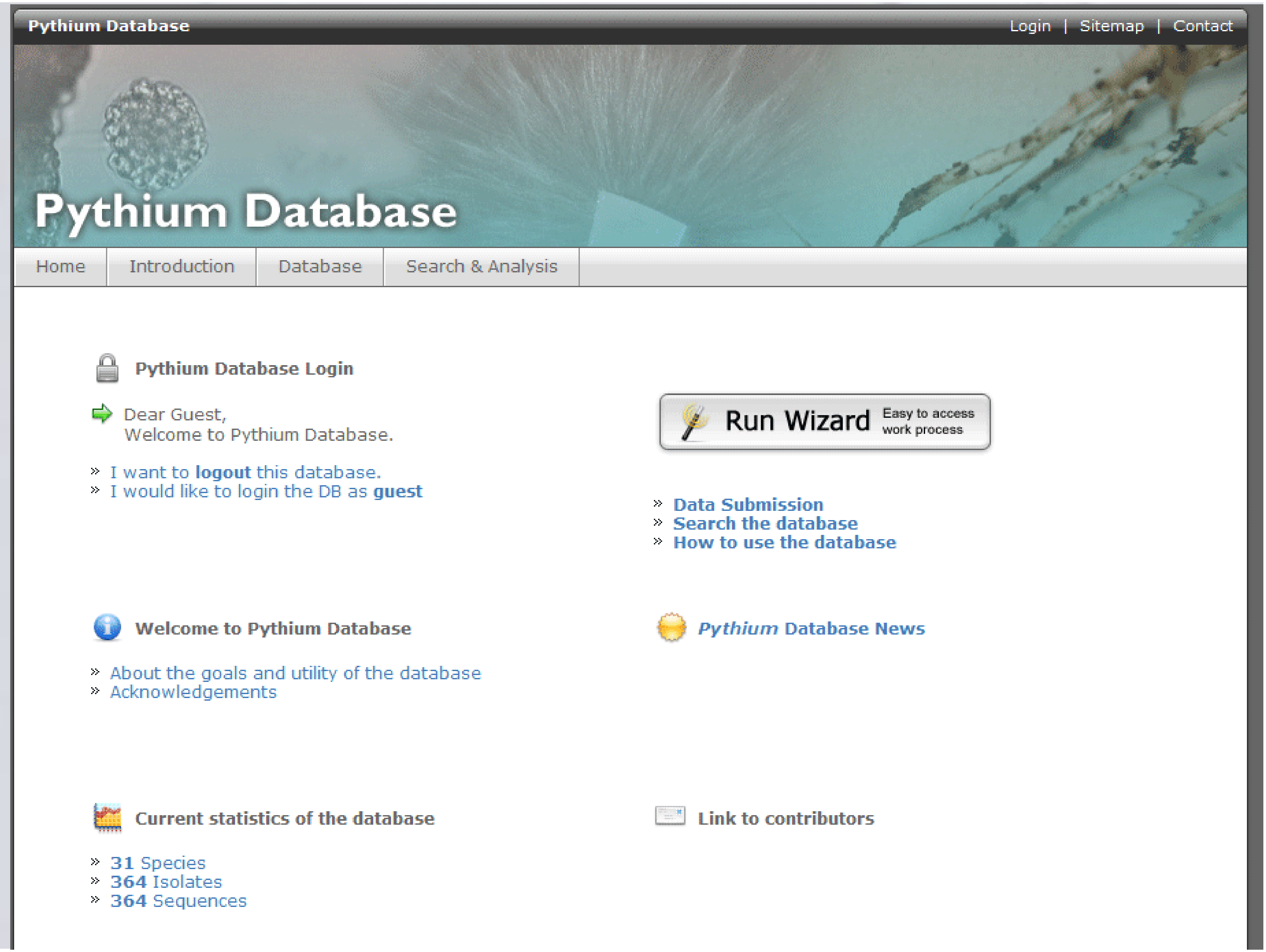
RHIPIDIALES*

LAGENIDIALES*

PERONSOPORALES*

LABYRINTHULOMYCETES

* = OOMYCETES



Pythium Database Login

Dear Guest,
Welcome to Pythium Database.

- I want to **logout** this database.
- I would like to login the DB as **guest**

- **Data Submission**
- **Search the database**
- **How to use the database**

Welcome to Pythium Database

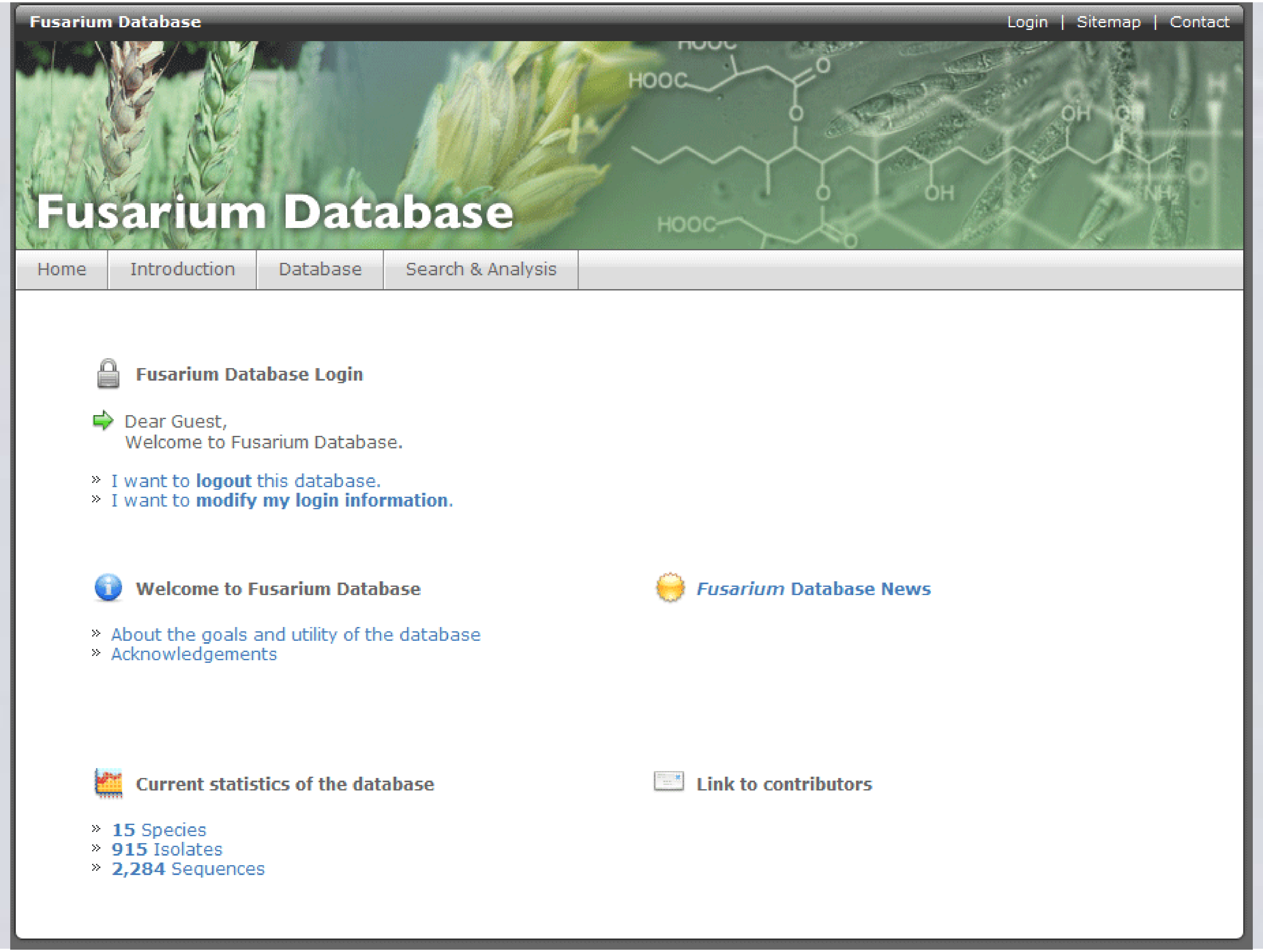
- About the goals and utility of the database
- Acknowledgements

***Pythium* Database News**

Current statistics of the database

- **31** Species
- **364** Isolates
- **364** Sequences

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

***Fusarium* Database News**

Current statistics of the database

- **15** Species
- **915** Isolates
- **2,284** Sequences

Link to contributors