

# A comprehensive genome-based diagnostics resource and pipeline for identification of threatening plant pathogens

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<http://cpgr.tigr.org>

## Abstract

Diagnosticians are increasingly using molecular markers developed from genomic data to identify threatening plant pathogens. However, widespread use of this technology has been limited by the paucity of genomic data for certain plant pathogens, a lack of a centralized phytopathogen database and the need for bioinformatics training. We have been funded by the USDA to address these limitations by constructing a comprehensive resource to house publicly available genome sequence and annotation data for plant pathogens including viruses, bacteria, fungi, oomycetes, and nematodes and provide search tools to facilitate the use of genomic data by the community. This database and resource will be coupled to 1) an experimental component in which we develop genomic based diagnostic tools for three proof-of-concept pathogens (*Xanthomonas*, *Pythium*, and *Meloidogyne*) and 2) an educational component involving training of plant pathologists and diagnosticians in genomics, bioinformatics, and molecular diagnostic methods. We will present progress on the Comprehensive Phytopathogen Genomics Resource <http://cpgr.tigr.org>

**CPGR**



The Comprehensive Phytopathogen Genomic Warehouse is a database of finished, draft and in progress genome sequencing projects and EST projects for viral, bacterial, stramenopile, fungal, and nematode plant pathogens. It will be updated on a frequent basis and will be integrated into the main CPGR database.

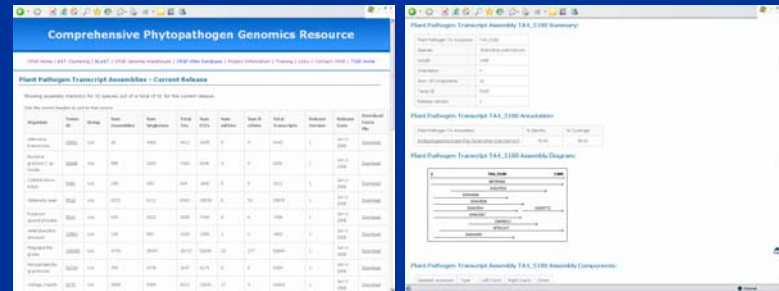
## Current CPGR Genome Warehouse Totals:

Taxon Group	Finished	Draft	In Progress	EST Project
Bacteria	<a href="#">24</a>	<a href="#">12</a>	<a href="#">15</a>	0
Fungi	0	<a href="#">9</a>	<a href="#">6</a>	<a href="#">19</a>
Nematodes	0	0	0	<a href="#">14</a>
Stramenopiles	0	<a href="#">3</a>	<a href="#">2</a>	<a href="#">4</a>
Viruses	<a href="#">624</a>	0	0	0
Viroids	<a href="#">36</a>	0	0	0
<b>Total</b>	684	24	23	37

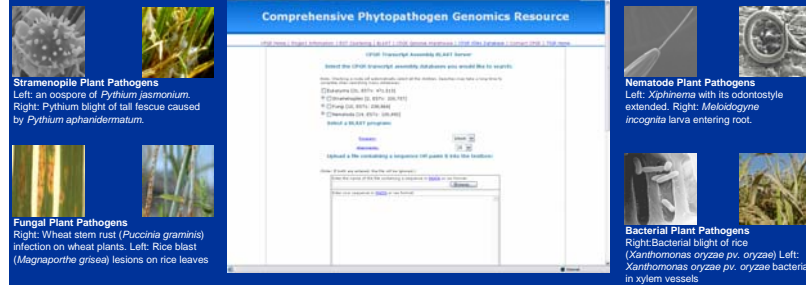
## Proof of Concept

- Develop diagnostic primers to distinguish between *Xanthomonas oryzae* pv. *oryzae* from *X. oryzae* pv. *oryzicola*
- Develop expressed sequence tags (ESTs) from *Pythium ultimum* var. *ultimum* to differentiate *Pythium* at the species level
- Differentiate host races or pathotypes of *Meloidogyne chitwoodii* and closely related species using diagnostic primers

## Transcript Assemblies of ESTs & FLcDNAs



## BLAST Server



## Why use the CPGR?

- It houses all relevant public genomic data available for plant pathogens
- It allows you to mine genomic data and develop specific diagnostic tools
- Stay up-to-date on phytopathogen genomics progress

## CPGR Workshops!

- **March 20-23, 2007**
- **TIGR, Rockville, MD**
- **July 2007**
- **APS Meeting, San Diego, CA**
- **October 23-26, 2007**
- **TIGR, Rockville, MD**



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