

**2008 APS CENTENNIAL MEETING
MINNEAPOLIS CONVENTION CENTER, MINNEAPOLIS, MN
JULY 26-30, 2008**

<http://www.apsnet.org/meetings/abstracts.asp>

Levesque, C.A.; de Cock, A.W.A.M.; Robideau, G.; Desaulniers, N.; and Bala, K. 2008. The Oomycota. *Phytopathology* 98:S184.

Oomycetes are no longer part of the Eumycota, or true fungi. Although oomycetes are different from true fungi in many ways, the two groups still have many common ecological features. Molecular taxonomy and phylogenies have confirmed for the most part the traditional classification of oomycetes. The two main orders of Saprolegniales and Peronosporales are still well separated by phylogenies. Most important plant pathogen genera such as *Pythium* and *Phytophthora* are still monophyletic and their species morphological taxonomy is generally supported by molecular analyses. There are a few exceptions though. There are some species that are being split (e.g. *Py. irregulare*), genera that are within a genus clade (e.g. *Pythiogeton*), and clades that might require a new genus status (e.g. *Pythium vexans* clade). Most phylogenetic studies of oomycetes have been done with the ribosomal DNA cistron and mitochondrial cytochrome oxidase genes but multigene phylogenies were performed in *Phytophthora*. These were made possible by the large amount of genome sequence information available for different species of this genus. The genome of *Pythium ultimum* was recently sequenced, opening new possibilities of multigene studies in Peronosporales. There are also efforts to sequence the genome of *Saprolegnia parasitica* which would greatly facilitate broader phylogenetic studies in oomycetes.