

Martin, F.N. 2010. Mitochondrial genomics of Oomycetes, tools for phylogenetics and development of molecular markers. *Phytopathology* 100:S150.

Due to its comparatively small size, similar number of genes and rate of evolutionary divergence the mitochondrial genome can be a valuable resource for elucidating phylogenetic relationships and development of molecular markers. In an effort to facilitate the use of this region for these purposes the mitochondrial genomes of 15 *Pythium* and 20 *Phytophthora* spp. have been sequenced. Comparative genomics has been useful for identification of genes useful for estimating evolutionary relationships and development of conserved primer sequences for their amplification. A mitochondrial multigene phylogeny for the genus *Phytophthora* was recently completed and efforts are underway to include *Pythium* and other Oomycetes in the analysis using the same regions. Comparison of genomic sequences among *Phytophthora* spp. has identified the types of polymorphisms associated with intraspecific compared to interspecific genome evolution. This has facilitated the identification of regions more prone to evolutionary divergence that are useful for classification of mitochondrial haplotypes. Conserved mitochondrial gene order differences among *Phytophthora* compared to *Pythium* and plants have also been useful for development of a systematic approach for development of multiplexed TaqMan real time PCR diagnostic marker system for identification of *Phytophthora* at a genus as well as species specific level. A similar approach is under investigation for *Pythium* as well.