

An open-access T-BAS phylogeny for emerging *Phytophthora* species

Allison Coomber^{1,2} Amanda C. Saville¹ Ignazio Carbone^{1,4} Jean Beagle Ristaino^{1,3}

¹Department of Entomology and Plant Pathology, NC State University, Raleigh, North Carolina, United States of America; ²Functional Genomics Program, NC State University, Raleigh, North Carolina, United States of America; ³Emerging Plant Disease and Global Food Security Cluster, NC State University, Raleigh, North Carolina, United States of America; ⁴Center for Integrated Fungal Research, NC State University, Raleigh, North Carolina, United States of America

Phytophthora species cause severe diseases on food, forest, and ornamental crops. Since the genus was described in 1876, it has expanded to comprise over 190 formally described species. There is a need for an open access phylogenetic tool that centralizes diverse streams of sequence data and metadata to facilitate research and identification of *Phytophthora* species. We used the Tree-Based Alignment Selector Toolkit (T-BAS) to develop a phylogeny of 192 formally described species and 33 informal taxa in the genus *Phytophthora* using sequences of eight nuclear genes. The phylogenetic tree was inferred using the RAxML maximum likelihood program. A search engine was also developed to identify microsatellite genotypes of *P. infestans* based on genetic distance to known lineages. The T-BAS tool provides a visualization framework allowing users to place unknown isolates on a curated phylogeny of all *Phytophthora* species. Critically, the tree can be updated in real-time as new species are described. The tool contains metadata including clade, host species, substrate, sexual characteristics, distribution, and reference literature, which can be visualized on the tree and downloaded for other uses. This phylogenetic resource will allow data sharing among research groups and the database will enable the global *Phytophthora* community to upload sequences and determine the phylogenetic placement of an isolate within the larger phylogeny and to download sequence data and metadata. The database will be curated by a community of *Phytophthora* researchers and housed on the T-BAS web portal in the Center for Integrated Fungal Research at NC State. The TBAS web tool can be leveraged to create similar metadata enhanced phylogenies for other Oomycete, bacterial or fungal pathogens.