

## Abstract- Summer Research Symposium

### Genetic structure of modern U.S. genotypes of *Phytophthora infestans*

The oomycete, *Phytophthora infestans* (Mont.) de Bary, is the plant pathogen responsible for late blight, which causes billions of dollars in crop damage each year. The fungus-like organism was first described in the 1840s when it decimated Ireland's potato crop during the famine. Modern isolates of this pathogen have been collected, isolated, and stored in labs around the U.S. so that the genetic diversity of the pathogen can be analyzed. The purpose of this study was to examine the genetic structure of modern strains of *P. infestans* that are prevalent in the US based on four nuclear genes: Intron Ras, Ras, AVR2 (as well as its haplotype AVR2-like), and AVR3. The two avirulence genes allow the pathogen to infect resistant plants containing R2 and R3 genes. DNA was extracted from 61 samples and amplified using PCR. The PCR product was sequenced and analyzed with SNAP Workbench. Phylogenetic trees were made to examine the evolutionary relationships among the genotypes. This information along with phenotypic data (fungicide sensitivity) will be used to help track outbreaks of the disease and recommend management options to growers via the USAblight.org web portal.