

**Mammella, M.A.;** Schena, L.; Coffey, M.D.; Cacciola, S.O.; Martin, F.N. 2010. Intraspecific analysis of *Phytophthora nicotianae* from diverse hosts and geographic locations using mitochondrial and nuclear markers. *Phytopathology* 100:S76.

*Phytophthora nicotianae* is an economically important pathogen with a worldwide distribution that causes disease in hundreds of plant species. In Italy it is a particular problem on citrus, where it primarily causes root rot. In an effort to better understand the population structure of isolates recovered from citrus in Italy and how these relate to those recovered from different hosts and geographic regions we have been examining the mitochondrial haplotype for a collection of over 90 isolates. Four regions of the mitochondrial genome (totaling 3 kb) have been sequenced for this purpose with a total of 49 haplotypes identified thus far. Interestingly 17 isolates from citrus recovered from Italy, California and Philippines represent 9 haplotypes that cluster closely together (these are differentiated by a total of 9 SNPs and 5 deletions occurring in two homopolymeric thymine regions). Single citrus isolates from Tunisia, Trinidad and Italy have distinctly different haplotypes. Some isolates from other host species exhibited a similar type of grouping, with many isolates recovered from tobacco and ornamentals clustering in their individual host associated clades. Investigations classifying nuclear genotypes for the same group of isolates are currently under way and their correlation with mitochondrial haplotypes will be discussed.