Lassiter, E.S.; Russ, C.; Nusbaum, C.; Zeng, Q.; Hu, C.; Thorne, J.; and Ristaino, J.B. 2010. Inferring evolutionary relationships of species in the *Phytophthora* Ic clade using nuclear and mitochondrial genes. Phytopathology 100:S68.

Phytophthora infestans the causative agent of potato and tomato late blight is an important pathogen worldwide and caused the Irish potato famine of the 1840's. Two sisters species of *P. infestans* in the Ic clade, *P. andina* and *P. mirabilis* have been described in Ecuador and Mexico, respectively. Coalescent analysis revealed that *P. andina* and *P. infestans* share a common ancestor in Ecuador on wild Solanum species. We have conducted Bayesian analysis of several nuclear genes (beta-tubulin, elongation factor Iα, RAS, and intron 1 of RAS) in isolates from Mexico and Ecuador and document the shared evolutionary history of the three species, which cluster together and are distinct from *P. phaseoli* and *P. ipomoeae*. Multiple heterozygous sites are shared among the three species. This is particularly interesting in the light of suggestion that *P. andina* may be a hybrid of *P. infestans* and *P. mirabilis*. We have also sequenced, annotated and mapped the entire mitochondrial genomes of *P. andina*, *P. mirabilis*, *P. ipomoeae* and *P. phaseoli* and compared then to the mitochondrial genome of *P. infestans*. We will report results of the Bayesian, coalescent and migration analysis using both the nuclear and whole mitochondrial genomes of these species and resolve the evolutionary histories of species of this clade.