

Parkunan, V.; Johnson, C.; and Hong, C. 2010. Diversity of the tobacco black shank pathogen, *Phytophthora nicotianae*, in Virginia. *Phytopathology* 100:S97.

Black shank, caused by *Phytophthora nicotianae*, is a significant problem in tobacco-growing regions throughout the world, including Virginia. A total of 217 isolates of *P. nicotianae* were collected from stem pith samples from flue-cured, burley, and dark fire-cured tobacco sampled from fields in 12 Virginia counties in 2006–09. Isolate race identities were determined using host differential assays. Seventy-six percent of the isolates were race 1, 21% race 0, and 3% race 3. The mating type was determined based on a conventional pairing assay using *P. meadii* and/or *P. nicotianae* testers. In contrast to an earlier North Carolina study, 94 percent of the isolates were of the A² mating type; only 6 percent of the isolates belonged to the A¹ mating type. A single mating type in most of Virginia's tobacco fields may indicate a lower possibility for sexual recombination, possibly creating a biological bottleneck to adaptation by the pathogen population. A detailed genetic diversity study is underway employing simple sequence repeats and random amplified polymorphic DNA markers.