

**Stewart, S.M.;** Dorrance, A.E.; and Robertson, A.E. 2010. Using microsatellite markers to assess diversity of *Phytophthora sojae* in Iowa. *Phytopathology* 100:S123.

*Phytophthora* root rot (PRR) caused by *Phytophthora sojae* can infect soybeans at all growth stages, causing pre- and post-emergence damping-off, root and stem rot. The most effective way to manage PRR is through the use of resistant cultivars however, the pathogen continues to diversify making resistant genes present in cultivars ineffective. Deployment of durable R-gene mediated resistance depends on understanding the factors that contribute to changes in the pathogen population diversity. Twenty four single sequence repeat (SSR) loci were used to analyze the genetic diversity of sixty seven mono-zoosporic isolates of *P. sojae*, collected from diseased plants and soil throughout Iowa. Fifty percent of the loci assessed were polymorphic, and the maximum number of alleles per locus was 2, with an average of 1.5. Isolates were predominantly homozygous. The highest observed heterozygosity for an individual locus was 0.045 with an average 0.005. Selfing was estimated in  $s = 0.985$ , which agrees with previous reports of low levels of outcrossing due to the homothallic nature of the pathogen. The diversity of the population of *P. sojae* in Iowa will be compared to the diversity of *P. sojae* populations from Ohio, Missouri and South Dakota.