RESTORATION AFTER THE LAUREL WILT DISEASE EPIDEMIC

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The causative fungus of laurel wilt disease, *Raffaelea lauricola*, is a symbiont of the redbay ambrosia beetle, *Xyleborus glabratus*. The beetle was likely introduced to the United States through the port of Savannah in 2002. Since then the disease has spread across the southeast causing massive losses to redbay (*Persea borbonia*) and swamp bay (*Persea palustris*) populations. Restoration efforts will involve replanting of resistant genotypes and preservation of germplasm at botanical gardens and on public lands. Beginning in 2007, redbay survivor trees were collected from epidemic areas and propagated with rooted cuttings. This material was then screened for resistance using fungal inoculation. In this work, 22 genotypes with 3 to 21 replicates were tested. Least squared means rankings for 12 of the genotypes were compared to previous inoculation experimental rankings. This showed that most genotypes are highly susceptible to fungal inoculation, while only one genotype showed high tolerance in multiple experiments. In addition, many other *Lauraceae* species, including silkbay, sassafras, and avocado have been affected by laurel wilt disease. In further work, the population genetic structure of three ecologically important *Persea* species redbay, swamp bay, and silk bay (*Persea humilis*), from five different Florida sandhill habitat locations were studied. Twenty trees were sampled per species at each location and data for 16 microsatellite loci were determined for each sample. Results show genetic differences between species and the strongest location differences among redbay. Taken together these data can be used to aid restoration efforts of both the *Persea* species in Florida and redbay across the southeast.

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