

A POPULATION GENETICS STUDY OF THREE FLORIDA PERSEA SPECIES EFFECTED BY THE LAUREL WILT EPIDEMIC

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Laurel wilt disease was introduced into the southeastern US in 2002 and since then has spread as far west as Texas. The causative fungus, *Raffaelea lauricola*, is a symbiont of the redbay ambrosia beetle, *Xyleborus glabratus*. The fungus has a host range that includes a variety of lauraceae family members including avocado, sassafras and redbays. Ecologically important Florida *Persea* species effected by the disease include redbay (*Persea borbonia*), swampbay (*Persea palustris*) and silkbay (*Persea humilis*). Particularly devastating losses have occurred in populations of redbay and swampbay, an important component of tree islands in the Florida Everglades. At Florida sand scrub preservation sites, all three *Persea* species occur relatively near one another. Silkbay grows exclusively on sandhill, xeric sites, swampbay grows in wetlands and swamps and redbay grows on high spots along the edges of streams, swamps or hammocks. Differences between redbay and swampbay habitats can be subtle, making identification tricky at times and underscoring the need to choose replanting sites carefully. Twenty samples per species were collected from five Florida sandhill preservation sites. Genetic diversity of species and population differentiation between species and locations was determined using SSR (simple sequence repeat) markers, at twelve loci. The fact that *Persea* are outcrossing and generally diverse species was confirmed by this study. Genetic differentiation between species was highest between silkbay and swampbay and lowest between silkbay and redbay. Given the restricted range of silkbay and its genetic similarity to redbay, silkbay could be an ecotype of redbay. In general, a better understanding of the genetics within and between these closely related species will inform replanting of areas effected by laurel wilt disease.