

## Using Genetic Information to Inform Redbay Restoration in Laurel Wilt Epidemic Areas

**Smith, KE**<sup>1,2</sup>; **Hughes, MA**<sup>2</sup>; **Echt, CS**<sup>1</sup>; **Josserand, SA**<sup>1</sup>; **Nelson, CD**<sup>1,3</sup>; **Davis, JM**<sup>2</sup> and **Smith, JA**<sup>2</sup>

<sup>1</sup>School of Forest Resources and Conservation, University of Florida, 136 Newins-Ziegler Hall, Gainesville, Florida, USA

<sup>2</sup>Southern Institute of Forest Genetics, USDA Forest Service, Southern Research Station, 23332 Success Road, Saucier, Mississippi, USA

<sup>3</sup>Forest Health Research and Education Center, University of Kentucky, 105 T.P. Cooper Hall, Lexington, KY 40546, USA

Laurel wilt disease is incited by the exotic fungus *Raffaelea lauricola* and transmitted by the Asian redbay ambrosia beetle (*Xyleborus glabratus*). The disease has spread from Savannah, Georgia in 2002 across the coastal southeast as far south as the Everglades and in 2014 was discovered as far west as Texas. Mortality is severe with locations in Florida reporting more than 90% loss of redbays, 3-4 inches in diameter and greater. Surviving redbays from coastal maritime forest ecosystems have been collected and propagated for the study of disease resistance and ultimately restoration planting. Disease severity of artificially inoculated parental trees and their open pollinated offspring will supply evidence for whether resistance is inherited simply as a dominant versus recessive trait, or as a complex, quantitative trait. In order to confirm parentage and potentially discover loci segregating with disease resistance simple sequence repeat (SSR) genotyping is underway in this population. Primer sequences were obtained from the Hardwood Genomics Project public resource (<http://www.hardwoodgenomics.org/content/redbay-gssrs>). Initially 96 tetranucleotide repeat primer pairs were tested in 7 survivor trees from 5 locations. Of the 92 loci with successful PCR outcomes, 25 were monomorphic and 33 produced between 2 and 7 scorable alleles. These data will be used to assess genetic diversity of surviving trees, as well as, to identify and guide deployment of resistant (or tolerant) materials in areas where redbay has been decimated by laurel wilt disease.