

CONSERVATION GENETICS AND RESISTANCE BREEDING AT THE HARRISON EXPERIMENTAL FOREST

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Genetic resistance offers a promising, sustainable option for managing introduced pests and pathogens in forestry. To counter two such introduced pathosystems, chestnut blight and laurel wilt, we are initiating conservation genetics and resistance breeding projects in the host species. Chestnut blight (caused by *Cryphonectria parasitica*) has virtually eliminated American chestnut (*Castanea dentata*) from the landscape since being introduced more than a century ago. We are searching throughout Mississippi for American chestnuts to use in cooperative resistance breeding. Mississippi is a desirable search area, since it represents the most southern portion of the species native range. American chestnuts will be vegetatively propagated, planted in two breeding orchards in Mississippi and genotyped to help validate species identity. To date, 20 putative American chestnuts have been discovered and propagated for orchard planting and genotyping. Laurel wilt (caused by *Raffaelea lauricola*) has killed over 300 million host trees since being discovered in Georgia in 2002. The main host tree has been redbay (*Persea borbonia*) in the southeast, but the disease is now impacting sassafras (*Sassafras albidum*) in areas as far north as Tennessee and Kentucky. Tolerance to the pathogen has been identified in redbay and we will take a similar approach to identify tolerance in sassafras. Specifically, we are propagating putatively tolerant selections of redbay and sassafras and will begin screening them for resistance to identify individuals for our breeding orchard. Currently, eight LW-tolerant redbay selections from the University of Florida are being established in the breeding orchard in Mississippi. A multiagency team is establishing a study to select individual sassafras trees with potential tolerance to laurel wilt. Disease resistance screening will be conducted once selections are propagated. Trees showing levels of resistance will be mated to evaluate the trait's inheritance and to identify candidate trees for breeding and seed orchard development.