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DISEASE NOTES

First Report of Laurel Wilt Disease Caused by *Raffaelea lauricola* on Sassafras in North Carolina

A. E. Mayfield III,† USDA Forest Service, Southern Research Station, Asheville, NC 28804; **C. Villari** and **J. L. Hamilton**, D. B. Warnell School of Forestry & Natural Resources, University of Georgia, Athens, 30602; **J. Slye** and **W. Langston**, North Carolina Forest Service, Goldsboro, 27530; **K. Oten**, North Carolina Forest Service, Clayton, 27520; and **S. W. Fraedrich**, USDA Forest Service, Forestry Sciences Laboratory, Athens, GA 30602.

Laurel wilt is a vascular disease of plants in the family Lauraceae caused by *Raffaelea lauricola* T.C. Harrin., Aghayeva & Fraedrich, a fungal symbiont of the redbay ambrosia beetle, *Xyleborus glabratus* Eichh. The beetle and pathogen are native to Asia and have spread rapidly in the southeastern United States since 2002 (Fraedrich et al. 2015). In natural forests, laurel wilt has killed millions of redbay, *Persea borbonia* (L.) Spreng., and swampbay, *Persea palustris* (Raf.) Sarg., trees (Hughes et al. 2017) and is killing sassafras, *Sassafras albidum* (Nutt.), in areas where *Persea* spp. hosts are present or absent (Fraedrich et al. 2015). As of early 2018, laurel wilt had been confirmed on redbay in 10 North Carolina counties, but it had not yet been confirmed on sassafras. In April 2018, a roadside forest edge containing at least 20 dead sassafras trees (5 to 13 cm diameter at 137 cm height) was investigated in Duplin County, near Greenevers, NC (34.841153, –77.955354). Laurel wilt had been confirmed in Duplin County on redbay by 2015, and dead redbays were present in the adjacent forest. Bark was removed from four symptomatic sassafras trees, which exhibited black streaks of discoloration in the outer sapwood, evidence of small-diameter beetle holes (approximately 1 mm) near the base of the stem, and absence of flowers or expanding leaves. We did not confirm the presence of *X. glabratus* and did not determine whether infection of individual trees occurred via beetle

vectors or root transmission. Samples of discolored sapwood were collected from two trees, and wood chips from the samples were plated on malt extract agar amended with cycloheximide (200 ppm) and streptomycin (100 ppm). A fungus was consistently isolated from the chips and identified as *R. lauricola* based on its unique mucoid growth, conidiophores, and size and shape of its budding conidia (Harrington et al. 2008). The identity of two representative isolates was further confirmed by sequencing the β-tubulin region with the primers bt2a and bt2b and comparing the obtained sequences with those available in GenBank. Consensus sequences (GenBank accessions nos. MH636807 and MH636808, respectively) showed 100% homology to *R. lauricola* voucher Hulcr4530 (GenBank accession no. KX267116.1). The isolates were also tested with a polymerase chain reaction primer set specific to *R. lauricola* (i.e., chk-f and chk-r) (Dreaden et al. 2014), which resulted in positive amplification. This is the first documentation of laurel wilt on sassafras in North Carolina and, at the time of this writing, represents the northernmost record and the eighth U.S. state report of the disease on this host. Unlike redbay, which is primarily restricted to the southeastern U.S. Coastal Plain region, sassafras occurs in a variety of forest types throughout much of the eastern half of the United States. Resource managers are concerned that the beetle and disease will continue to spread northward through sassafras, which is more common in the northern portions of its range. Recent models suggest that *X. glabratus* can survive the low temperature extremes that occur over much of the sassafras range (Formby et al. 2017). Laurel wilt represents a threat to sassafras, and forest health personnel should be alert to the possibilities of the disease occurring in more northerly states.

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