

Disease Notes

First Report of **Laurel Wilt** Disease Caused by *Raffaelea lauricola* on Camphor in Florida and Georgia

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Laurel wilt is a recently described (1) vascular disease of redbay (*Persea borbonia* (L.) Spreng) and other plants in the family Lauraceae. The **wilt** is caused by *Raffaelea lauricola*, a fungus vectored by the nonnative redbay ambrosia beetle (*Xyleborus glabratus* Eichhoff) (1,2). Since 2003, **laurel wilt** has caused widespread mortality of redbay in Georgia, South Carolina, and Florida (1) and has recently been found on **avocado** in Florida (4). Since June of 2007, **wilted** shoots and branch dieback have been observed in several camphor trees (*Cinnamomum camphora* (L.) Sieb.) in residential areas of McIntosh and Glynn counties in Georgia and Baker County in Florida. Symptomatic camphor trees ranged from 4.5 to 12 m high and occurred in areas where redbay mortality due to **laurel wilt** has been frequently observed during the last 2 to 3 years. In some camphor trees, only the smaller branches (<2 cm in diameter) were **wilting** or dead, whereas in other trees (e.g., Baker County, Florida), the larger branches and substantial portions of the crown were also symptomatic. Rapid **wilt** that affects entire trees that is usually observed in redbay, has not been observed in camphor. Some camphor trees in residential areas of Jekyll Island, Georgia (Glynn County), where extensive **wilt** of redbay has occurred, have exhibited only localized **wilt** of some shoots or branches and other camphors remain asymptomatic. Removal of bark from **wilted** branch sections revealed black-to-brownish staining in the sapwood, characteristic of **laurel wilt**. Although no evidence of ambrosia beetles was observed on these samples, more extensive surveys are needed to determine the role of this vector in **laurel wilt** of camphor. Wood chips from symptomatic areas of branches were surface sterilized and plated on cycloheximide-streptomycin malt agar as previously described (1,4) and *R. lauricola* was routinely isolated. Small subunit (18S) sequences from rDNA were amplified by PCR and sequenced using primers NS1 and NS4 (3). BLASTn searches revealed homology to *R. lauricola* C2203 (GenBank Accession No. EU123076, 100% similarity, *e*-value of 0.0, and a total score of 1,886). The small subunit rDNA sequence for this isolate has been deposited into GenBank (<http://www.ncbi.nlm.nih.gov/Genbank/index.html>) and has been assigned Accession No. EU 853303. The presence of **laurel wilt** in camphor provides an opportunity to understand the pathogen distribution and possible resistance mechanisms in this host, which could have implications for efforts to remediate the impacts of the disease in redbay and other species in the Lauraceae in the southeastern United States.

References: (1) S. W. Fraedrich et al. *Plant Dis.* 92:215, 2008. (2) T. C. Harrington et al. *Mycotaxon* 104:399, 2008. (3) M. A. Innis et al. *PCR Protocols, A Guide to Methods and Applications*. Academic Press. San Diego, CA, 1990. (4) A. E. Mayfield, III et al. *Plant Dis.* 92:976, 2008.

Cited by

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