

## GENETIC DIVERSITY IN THE LAUREL WILT PATHOGEN, *RAFFAELEA LAURICOLA*, AND THE CONSEQUENCES FOR RESISTANCE BREEDING

Tyler J. Dreaden<sup>1</sup>, Marc A. Hughes<sup>2</sup>, Randy C. Ploetz<sup>3</sup>, Adam Black<sup>4</sup>, and Jason A. Smith<sup>5</sup>

Laurel wilt is caused by *Raffaelea lauricola*, a fungal nutritional symbiont of its vector, *Xyleborus glabratus*, the redbay ambrosia beetle. Both the fungus and beetle are native to Asia but were found in Georgia in the early 2000s. The disease has spread to much of the Southeastern United States killing >300 million host trees in the Lauraceae family. The objectives of this research were to elucidate the genetic structure of populations of *R. lauricola*, examine its reproductive strategy, and determine the number of USA introductions. A panel of 12 simple sequence repeat (SSR) markers identified 15 multilocus genotypes (MLGs) in a collection of 59 isolates from the USA (34 isolates), Myanmar (18), Taiwan (6) and Japan (1). Limited diversity in the USA isolates and the presence of one MAT idiomorph (mating type locus) indicated that *R. lauricola* was probably introduced into the country once. MLG diversity was far greater in Asia than the USA. Only three closely related MLGs were detected in the USA, the most prevalent of which (30 of 34 isolates) was also found in Taiwan. Although more work is needed, the present results suggest that a Taiwanese origin is possible for the population of *R. lauricola* in the USA. Isolates of *R. lauricola* from Myanmar were distinct from those from Japan, Taiwan and the USA. Although both MAT idiomorphs were present in Myanmar and Taiwan, only the population from Taiwan had the genetic structure of a sexually reproducing population. The results highlight the need to prevent the introduction of additional genotypes and the second mating type into the USA because this could allow the pathogen to rapidly overcome the resistance that has been developed. The pathogen population needs to be monitored so that new genotypes can be identified and incorporated into resistance screening trials if they are found.

<sup>1</sup> Forest Health Research and Education Center, Southern Research Station, USDA Forest Service, Lexington, KY 40546, (tdreaden@usda.gov).

<sup>2</sup> College of Tropical Agriculture and Human Resources, University of Hawaii at Manoa, HI 96720.

<sup>3</sup> Tropical Research & Education Center, University of Florida, Homestead, FL 33031.

<sup>4</sup> Peckerwood Garden Conservation Foundation, Hempstead, TX 77445.

<sup>5</sup> School of Forest Resources and Conservation, University of Florida, Gainesville, FL 32611.

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