

GENETIC ANALYSES OF THE LAUREL WILT PATHOGEN, *RAFFAELEA LAURICOLA*,  
IN ASIA PROVIDE CLUES TO THE SOURCE OF THE CLONE CAUSING  
THE CURRENT USA EPIDEMIC

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

<sup>1</sup>USDA Forest Service, Southern Research Station, Forest Health Research and Education Center, Lexington, KY; <sup>2</sup>College of Tropical Agriculture and Human Resources, University of Hawaii at Manoa, Hilo, HI; <sup>3</sup>Tropical Research and Education Center, University of Florida, Homestead, FL; <sup>4</sup>Peckerwood Garden Conservation Foundation, Hempstead, TX; <sup>5</sup>School of Forest Resources and Conservation, University of Florida, Gainesville, FL

Laurel wilt is caused by the fungus *Raffaelea lauricola* T.C. Harr., Fraedrich and Aghayeva, a nutritional symbiont of its vector, *Xyleborus glabratus* Eichhoff, the redbay ambrosia beetle. Both are native to Asia but were found in Georgia in the early 2000s and have since spread to much of the southeastern United States killing >300 million trees in the Lauraceae plant family. Our goals were to elucidate the genetic structure of populations of the pathogen, *R. lauricola*, examine its reproductive strategy, and investigate the number of times the pathogen was introduced to the USA. A panel of 12 simple sequence repeat (SSR) markers identified 15 multilocus genotypes (MLGs) among 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 USA a single time. Only three closely related MLGs were detected in the USA, the most prevalent of which (30 of 34 isolates) was also found in Taiwan. MLG diversity was far greater in Asia than the USA with isolates from Myanmar being 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 present results suggest that a Taiwanese origin is possible for the population of *R. lauricola* in the USA, although more work is needed. 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 is being developed. The pathogen population should be monitored so that new genotypes can be identified and incorporated into resistance screening trials.