POPULATION GENETICS OF THE LAUREL WILT PATHOGEN, *RAFFAELEA LAURICOLA*

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Laurel wilt is an emerging disease of members of the Lauraceae plant family in the southeastern United States. The disease is characterized by systemic wilt and rapid mortality. It is caused by *Raffaelea lauricola*, a fungus in the Ophiostomatales that is vectored by the redbay ambrosia beetle (*Xyleborus glabratus*) that was likely introduced to the southeastern United States from Asia around 2002. It was hypothesized the disease resulted from a single introduction event and the fungus has clonally replicated in the US. To test this hypothesis and guide resistance screening efforts, a population genetics study of *R. lauricola* using isolates from Burma, Japan, Taiwan, and the southeastern United States, using 11 microsatellite loci was conducted. A single multilocus genotype and a single mating type was found in the US and multiple multilocus genotypes and two mating types were found in the Asian isolates. Our findings support the single US introduction hypothesis, aid in the development of resistance screening methods and highlight the need to prevent the introduction of additional *R. lauricola* genotypes.

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