Disease Notes

Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Armillaria Root Disease Pathogen, *Armillaria gallica*, on *Rhododendron* and *Quercus rubra* in Georgia, U.S.A.

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Armillaria root and butt diseases, which are a global issue, can be influenced by changing environmental conditions. *Armillaria gallica* is a well-known pathogen of diverse trees worldwide (Brazee and Wick 2009). Besides *A. gallica* causing root rot of *Hemerocallis* sp. and *Cornus* sp. in South Carolina (Schnabel et al. 2005), little is reported on the distribution and host range of *A. gallica* in the southeastern United States. In July 2017, three *Armillaria* isolates were obtained from two naturally occurring hosts in Georgia, U.S.A., and cultured on malt extract medium (3% malt extract, 3% dextrose, 1% peptone, and 1.5% agar). One isolate (GA3) was obtained in Unicoi State Park near Helen, Georgia (latitude 34.712275, longitude –83.727765, elevation 498 m) from the basal portion of *Rhododendron* sp. with extensive root/butt decay, but no crown symptoms were evident. GA4 and GA5 (latitude 33.902433, longitude –83.382453, elevation 215 m) were isolated from wind-felled *Quercus rubra* (red oak) with root disease at the State Botanical Gardens in Athens, Georgia. GA4 was associated with a large root ball (~4-m diameter), and GA5 was obtained from a mature tree with infected roots, with characteristic spongy rot of Armillaria root disease. Crown symptoms could not be evaluated because the crowns had been removed before the collections. Several other oaks with Armillaria root disease were noted throughout the State Botanical Gardens. Pairing tests reduced these three isolates (whiteish mycelia with a dark, brownish crust and rhizomorphs) to two genets with GA4 = GA5. Both genets (GA3 and GA4) were identified as *A. gallica* using translation elongation factor 1α (*tef1*) sequences (GenBank nos. MT761697 and MT761698, respectively) that showed ≥97% identity (≥98% coverage) with *A. gallica* sequences (KF156772, KF156775). Also, nine replications of somatic pairing tests showed 33 to 67% compatibility with *A. gallica* (occurs in southeastern United States), compared with 0 to 22% for *A. mexicana*, *A. mellea* (occurs in southeastern United States), *A. solidipes*, and *Desarmillaria tabescens* (occurs in southeastern United States). To our knowledge, this note represents the first report of *A. gallica* on *Rhododendron* and *Q. rubra* in Georgia, U.S.A., which has experienced severe drought in recent decades (e.g., Williams et al. 2017) that could predispose trees to *Armillaria* infection (e.g., Wargo 1996). *Q. rubra* was previously reported as a host of *A. gallica* in Arkansas (Kelley et al. 2009) and Massachusetts (Brazee and Wick 2009), U.S.A. In Missouri, U.S.A., *A. gallica* has been reported as a weak pathogen with potential biological control against *A. mellea* (Bruhn et al. 2000). Other reports from several regions on various hosts suggest pathogenicity of *A. gallica* is associated with changing climate (Kim et al. 2017; Kubiak et al. 2017; Nelson et al. 2013). Wide genetic variation and/or cryptic speciation within *A. gallica* may account for differences in ecological behavior (Klopfenstein et al. 2017), but this is difficult to evaluate because *Armillaria* pathogenicity tests cannot be used on most forest tree seedlings. This study suggests that *A. gallica* is more widespread than previously known, and its adverse impacts on woody plants may intensify over time, depending on the environmental conditions. Further studies are needed to determine environmental influences on *A. gallica*, the full distribution of *A. gallica*, and its effects in forests of the southeastern United States.

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