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

1 α (*tef1*) sequences (GenBank nos. MT761697 and MT761698, respectively) that showed $\geq 97\%$ identity ($\geq 98\%$ 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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