



First Report of *Armillaria* root disease of *Celtis laevigata* caused by *A. gallica* in South Carolina, USA

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Abstract

Celtis laevigata (sugarberry, southern hackberry) is an important, shade-tolerant, deciduous hardwood tree species that occurs naturally in flood plains, along streams and rivers, and in urban landscapes of the southeastern USA (Kennedy 1990). In recent years, dieback and mortality of *C. laevigata* have been commonly observed in some areas of South Carolina (SC) and Georgia (GA) (Poole et al. 2021). In April/May of 2018, the crown conditions and root systems were examined for three *C. laevigata* trees in North Augusta, SC. The crown of each tree was visually assessed using the method of Poole et al. (2021). Root samples were obtained by excavating two main roots ca. 2 meters away from the stem of each tree. Tree SB474 (N33 29.472, W81 59.082, elev. 55.8 m) exhibited > 66% crown loss and decaying roots with white mycelial fans and dark rhizomorphs characteristic of *Armillaria*. Tree SB913 (N33 29.830, W81 59.349, elev. 58.8 m) exhibited ca. 34-66% crown loss, while tree SB914 (N33 29.837, W81 59.338, elev. 57 m) appeared healthy with no apparent crown loss. Roots of trees SB913 and SB914 appeared healthy, although rhizomorphs were attached to the root surfaces. Roots and/or attached rhizomorphs were surface disinfested and plated on a basidiomycete-selective medium (Hendrix and Kuhlman 1962). Three *Armillaria* isolates, one from each corresponding tree, were paired with each other, and two genets were identified (SB474 and SB913 = SB914). The two genets (SB474 and SB913) were used in somatic pairing tests against three known tester isolates for each of the following species: *A. solidipes*, *A.*

mellea, *A. gallica*, *A. mexicana*, and *Desarmillaria caespitosa* (= *A. tabescens*). Pairing of isolates SB474 and SB913 showed the highest compatibility with *A. gallica* (isolates ST22, ST23, and M70) with 100% and 89%, respectively. These isolates were definitively confirmed as *A. gallica* by translation elongation factor 1 α gene sequences (*tef1*; Klopfenstein et al. 2017) (GenBank accession nos. OM993577 and OM993578 for SB474 and SB913, respectively). GenBank nucleotide BLAST showed *tef1* similarity for both SB474 and SB913 isolates was highest for *A. gallica* ($\geq 98.7\%$; GenBank accession nos. MT761696, MT761697, and KF156772). This is the first report of *A. gallica* associated with Armillaria root disease of *C. laevigata*. Rhizomorphs on the surface of apparently healthy tree roots and root colonization in severely declining trees are a common sign of *A. gallica* (Baumgartner and Rizzo 2001). Pathogen colonization of root surfaces may provide an opportunity for infection of highly damaged trees, resulting in root disease (Gregory 1985). Primary agents of *C. laevigata* dieback and mortality in SC and GA remain undefined, but continued study is needed to confirm the role of *A. gallica* in *C. laevigata* dieback and mortality. Although pathogenicity tests are impractical for Armillaria, these *A. gallica* occurrences in SC further adds to our knowledge of this pathogen's distribution in the southeastern USA, where it has also been confirmed in Tennessee in hardwood forests (Bruhn et al. 1997), SC on *Hemerocallis* sp. (Schnabel et al. 2005), and GA on a *Rhododendron* sp. and *Quercus rubra* (Hanna et al. 2020). The distribution and host range of *A. gallica* is likely more widespread in the southeastern USA than existing records indicate. Documenting Armillaria distribution, including *A. gallica*, is essential for predicting climate-change impacts on Armillaria root diseases (Kim et al. 2022).

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