Disease Note

Diseases Caused by Fungi and Fungus-Like Organisms

First Report of the Armillaria Root Disease Pathogen, *Armillaria solidipes*, on Black Oak (*Quercus velutina*) in North Carolina, U.S.A.

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Armillaria root disease is among the largest causes of mortality and lost productivity of widely ranging horticultural, urban, and forest trees and shrubs in diverse boreal, temperate, and tropical regions around the world (Kim et al. 2022). Damage from Armillaria root disease will likely increase in response to changing climate and extreme weather because environmental stress can predispose host trees to Armillaria root disease (Kim et al. 2021; Murray and Leslie 2021). On 14 August 2021, a mature black oak (*Quercus velutina*) ca. 29 m in height and 64 cm in diameter at breast height experienced a complete structural failure originating at the root plate, falling onto a major highway within the Pisgah National Forest near Brevard, North Carolina (35°16′50.876″N, 82°42′51.785″W, elevation 680 m) during sunny, calm conditions. No aboveground indications of predisposing disturbance, injury, or insect or disease activity were observed. Advanced wood decay, however, was present in several structural roots of the exposed root plate; abundant rhizomorphs attached to the surfaces of most roots were noted. One large primary root (ca. 23 cm in diameter) exhibited clear signs of Armillaria root disease at the point of failure as evidenced by an extensive decay column, abundant black rhizomorphs on the root surface, and white mycelial fans (a sign of pathogenicity) within the root itself. Rhizomorph samples were established in culture, two *Armillaria* isolates (PNF#001R-1 and PNF#001R-2) were examined, and pairing tests showed that both isolates belonged to the same genet (PNF#001R-1 = PNF#001R-2). Based on translation elongation factor 1α (*tef1*) sequences, both isolates (one genet) were identified as *A. solidipes* (GenBank accession no. OP823701), showing 98% similarity with *A. solidipes tef1* sequences (e.g., MH879015) in GenBank. Also, nine replications of somatic incompatibility tests of the isolate with five North American *Armillaria* spp. (*A. solidipes*, *A. mellea*, *A. gallica*, *A. mexicana*, and *Desarmillaria caespitosa* [=*Armillaria tabescens*]) showed 67% compatibility with *A. solidipes*, compared with 0 to 22% for *A. mellea*, *D. caespitosa*, *A. gallica*, and *A. mexicana*. All test species but *A. mexicana* are reported to occur in the eastern and/or southern United States, while *A. mexicana* occurs in a similar environment in Mexico (Elías-Román et al. 2018). To our knowledge, this is the first confirmed report of *A. solidipes* in North Carolina, where it was causing disease on black oak, and this is the most southerly confirmed case of *A. solidipes* in eastern North America. Although *Armillaria* inoculation tests are impractical, black oak was previously reported as a host of *A. solidipes* in Massachusetts, U.S.A. (Brazee and Wick 2009). *A. solidipes* is considered to be the most important Armillaria root disease pathogen of conifer forests in the western United States (Lockman and Kearns 2016), but it has been suggested that *A. solidipes* can thrive in northern hardwood forests that reside near conifer forests (Brazee and Wick 2009). Climate change is predicted to increase damage caused by *A. solidipes* on conifers in the western United States (Kim et al. 2021); however, it is undetermined if the occurrence of *A. solidipes*-caused disease in North Carolina is related to climate change or how climate change could influence this disease across the region. More surveys are needed to assess the impact of Armillaria root disease on health of mixed forests in the eastern United States.

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