

PHYLOGENETICS AND HOST DISTRIBUTION OF *ARMILLARIA* IN RIPARIAN FORESTS OF THE NORTHERN GREAT PLAINS

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Abstract

Root disease pathogens, including *Armillaria* (Fr.) Staude, are a leading cause of growth loss and mortality of trees in forest ecosystems of North America (Lockman & Kearns 2016). This panglobal fungus can cause significant reductions in tree growth that can lead to mortality. *Armillaria* spp. have a wide host range, and they also play a vital ecological role in the carbon cycling process via wood decomposition (Raabe 1962, Baumgartner et al. 2011, Heinzelmann et al. 2019). As a native root-disease fungus, *Armillaria* spp. are among the oldest and largest known living organisms on Earth (Ferguson et al. 2003). *Armillaria* root disease has been found in every region of the United States. Currently, 11 species of *Armillaria/Desarmillaria* are known to occur in North America (Kim et al. 2006, Klopfenstein et al. 2017, Elías-Román et al. 2018), each with different ecological roles from pathogenic to saprophytic. Very little work has been done identifying and characterizing the distribution of *Armillaria* spp. in the northern Great Plains region, although *A. gallica* Marxm. & Romagn was previously identified in association with diverse hardwood species in the Niobrara Valley Preserve in Nebraska (Kim & Klopfenstein 2011).

Phylogenetic analyses provide a better understanding of taxonomic relationships among *Armillaria* species, which facilitates mapping spatial distributions and host associations for insights into *Armillaria* ecology. The objectives of this study were to: 1) provide baseline information on *Armillaria* species that are present in the northern Great Plains region; and 2) determine geographic distribution of host trees that are associated with the *Armillaria* species. A broad goal of this study is to provide important missing data that might assist with updating root disease risk maps. Isolates were collected from 78 out of 101 sites surveyed. Host species was recorded, and each tree was inspected for signs/symptoms of root disease (killing of the cambium in a live tree) and butt rot (degrading inner wood in a live tree) (Williams et al. 1986). A total of 57 *Armillaria* isolates were sequenced from 12 different host tree species from sites in North Dakota, South Dakota, and Nebraska. Identification of *Armillaria* isolates was accomplished by comparing nucleotide sequences from the translation elongation factor 1-alpha (*tef1*) gene. All 57 isolates had a >98% general consensus match to *A. gallica*. The locations of *A. gallica* were then mapped (Figure 1). A phylogenetic tree was constructed using maximum-likelihood (ML) algorithms (Figure 2). Statistical support for the branch topology was calculated from 1,000 bootstrap replicate trees. *Armillaria gallica* has a wide host range and geographic distribution, and it is much more widespread in the northern Great Plains region than previously recognized.

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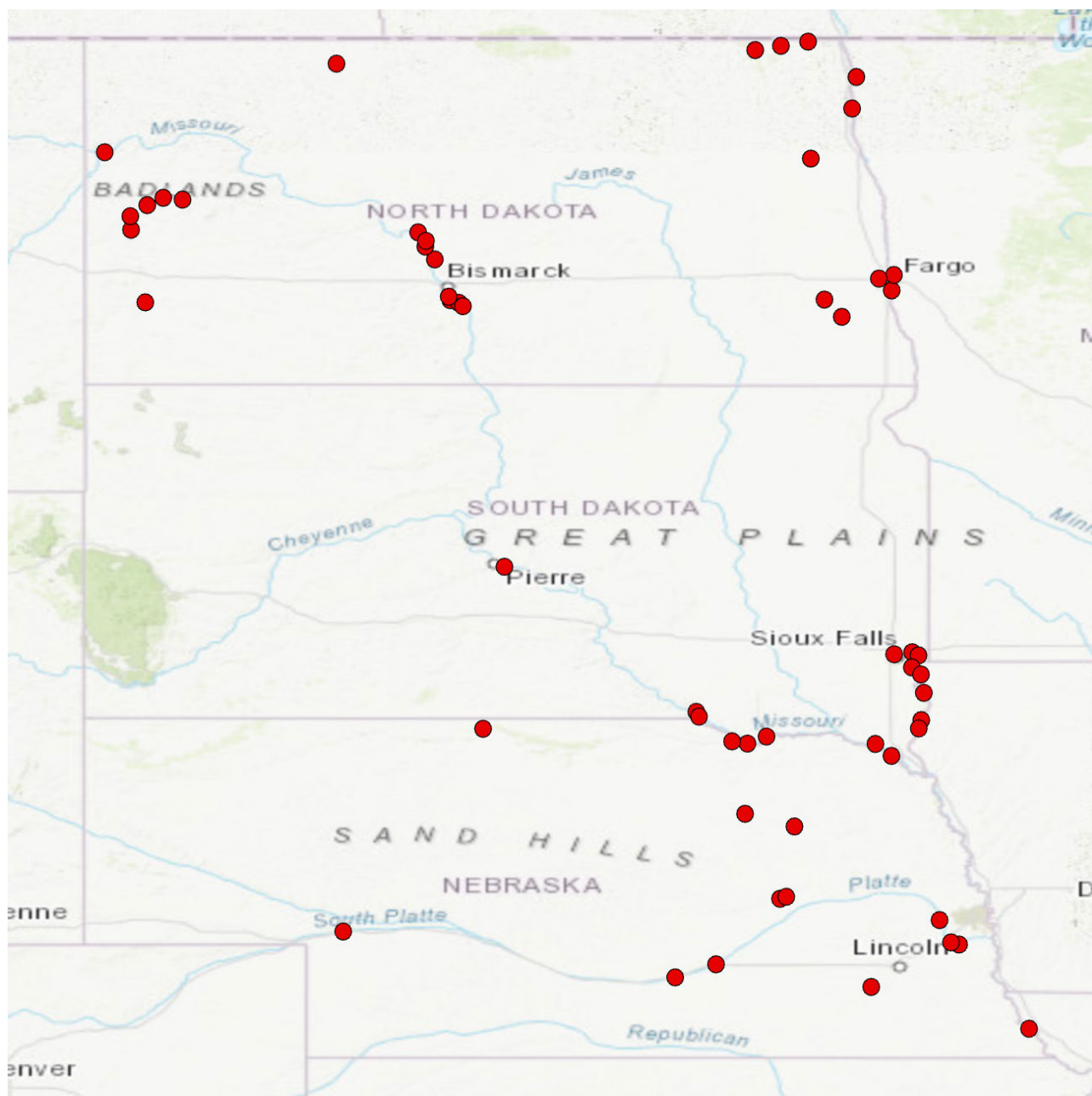


Figure 1: This map depicts the 57 locations where *Armillaria gallica* was found. Each isolate that was sequenced had pairwise identity matches with *A. gallica* at a > 98% match using translation elongation factor 1-alpha gene comparison.

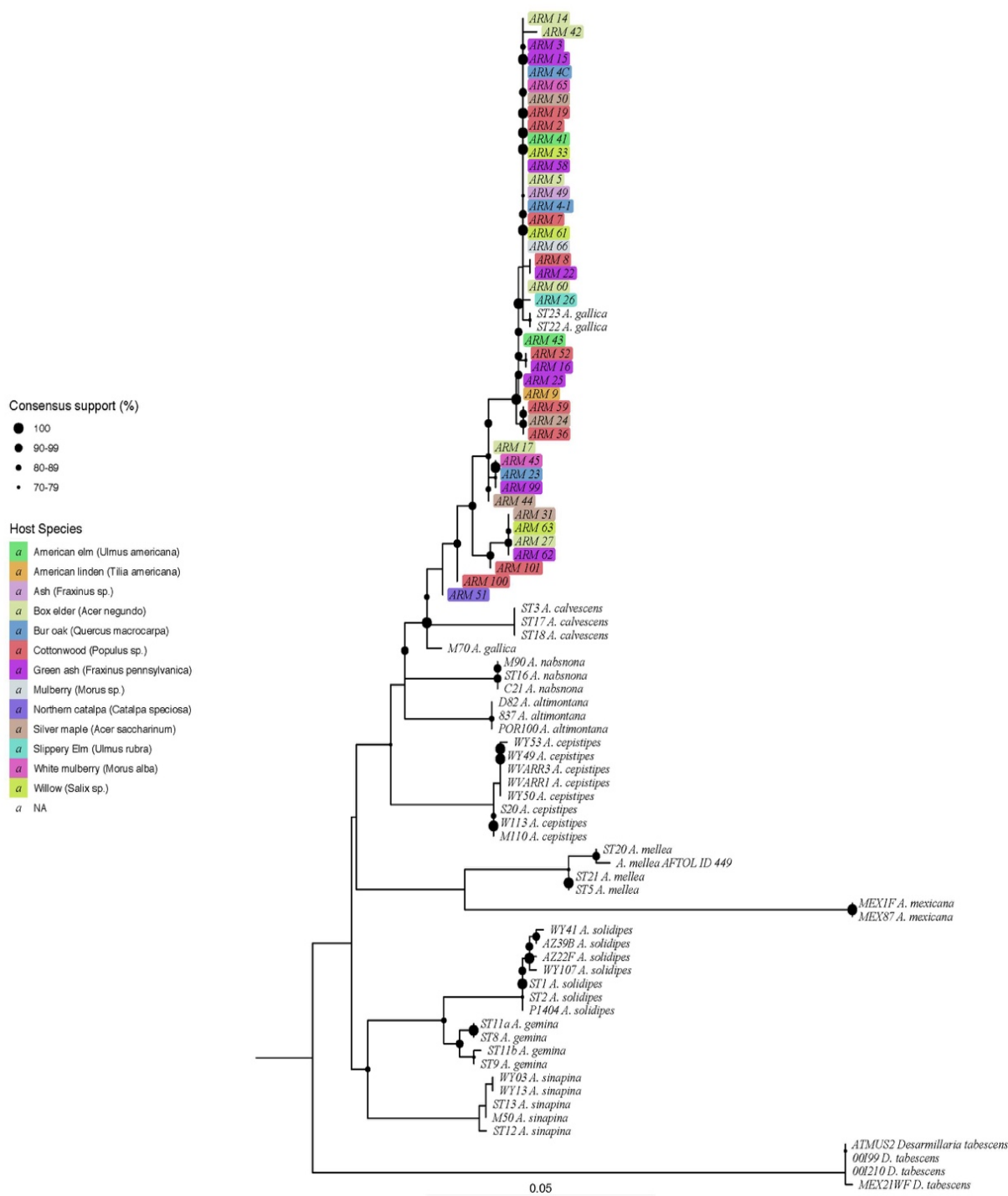


Figure 2: Phylogenetic trees were constructed using maximum-likelihood (ML) algorithms, and statistical support for the branch topology was calculated from 1,000 bootstrap replicate trees. Colors represent host species shown in the legend. The sizes of the circles at nodes represent bootstrap support. Only values > 70% are shown. This phylogenetic tree shows 42 of the 57 isolates that were sequenced.

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