

ARMILLARIA ALTIMONTANA, A POTENTIAL NATURAL BIOLOGICAL CONTROL AGAINST ARMILLARIA ROOT DISEASE

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Introduction

Root diseases are a primary cause of reduced forest productivity, decreased carbon sequestration, and impaired ecosystem function (e.g., Lockman & Kearns 2016). *Armillaria altimontana* and *A. solidipes* (as *A. ostoyae*) are soil fungi that frequently co-occur (McDonald et al. 2000) and are found in association with western white pine (*Pinus monticola*). *Armillaria solidipes* is well known as a virulent primary pathogen on diverse conifers within inland western regions of the contiguous USA (e.g., Lockman & Kearns 2016). *Armillaria altimontana* is often considered as a weak or secondary pathogen (Brazee et al. 2012). However, little has been documented about the impact of this species on tree health and growth in nature. The objective of this study were to i) identify *Armillaria* isolates associated with each planted western white pine at the species and genet (vegetative clone) level; ii) describe their demography and spatial distribution; and iii) assess the potential influence of each *Armillaria* species on tree growth and survival of western white pine.

Methods

A provenance test of western white pine was planted in 1971 on a 0.8-ha north-facing slope at 970 m.a.s.l at the Priest River Experimental Forest in northern Idaho, USA. The test was designed to examine variation in growth and survival among elevational seed sources in the region (Figures 1 and 2A). In 1987, 2076 living and recently dead trees were measured (e.g., survival, height, and diameter) and inspected/sampled for colonization by *Armillaria* (Figure 2B). Surveys for mycelial fans, wood rot, and resinosis were also conducted in 1987. The root collar and major lateral roots of all remaining trees were inspected for *Armillaria* by excavating 0.3-m deep to a distance of ca. 1-m away from the tree base in three cardinal/ordinal directions. Rhizomorphs, mycelial fans, and rotten wood were used as samples to establish isolates in culture following the methods of McDonald et al. (1987). All isolates were paired against each other to delineate genets using the techniques described in Wu et al. (1996). A final round of diploid-diploid pairings with representatives of each genet were paired against known testers to identify species. Species identification were confirmed using translation elongation factor 1- α (*tef1*) sequences.

Results and Discussion

Armillaria was found in association with 54.9% of the 2076 trees and comprised two species, *A. altimontana* and *A. solidipes*. Based on the spatial distribution of *Armillaria* species and genets and their estimated growth (van der Kamp 1993), *Armillaria* species are estimated to have occupied the site for at least 250 years (Figure 1). *Armillaria solidipes* was uncommon in areas dominated by *A. altimontana* (Figure 1). Trees colonized only by *A. altimontana* exhibited the highest growth and survival and low incidence (1.8 %) of *Armillaria* root disease (Figure 2). *Armillaria solidipes* was frequently (74.7%) associated with *Armillaria* root disease and trees colonized by *A. solidipes* exhibited the lowest growth and survival (Figure 2).

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These findings support the hypothesis that *A. altimontana* is typically non-pathogenic and may function as a beneficial symbiont, epiphyte, or both in western white pine. Furthermore, based on colonization patterns, *A. altimontana* appears to protect western white pine from Armillaria root disease by competitively excluding pathogenic *A. solidipes* in the soil (Warwell et al. 2019). The results support the possibility of new approaches for natural control of Armillaria root disease through management that encourages *A. altimontana*. Further research is needed to determine if, how, and when *A. altimontana* may be beneficial for tree survival and growth. Studies at this site using a metagenomics approach are currently underway to determine soil properties and soil microbes associated with beneficial *A. altimontana* versus virulent *A. solidipes* (Warwell et al. 2019).

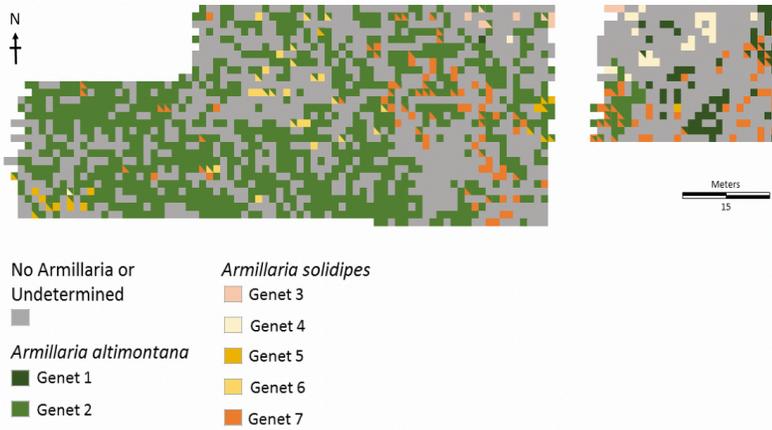


Figure 1: “Armillaria species and genet distribution within the Ida Creek plantation (0.8 ha) at the Priest River Experimental Forest, Idaho, USA. Each square pixel represents 1.2 m x 1.2 m (a single tree location) and colored pixels indicate trees associated with Armillaria altimontana, A. solidipes, or both. Cells split diagonally show the two unique genets that were identified on that single tree. Grey pixels indicate trees where neither *A. altimontana* nor *A. solidipes* were found or trees that were either missing or died early from unknown causes” (Warwell et al. 2019).

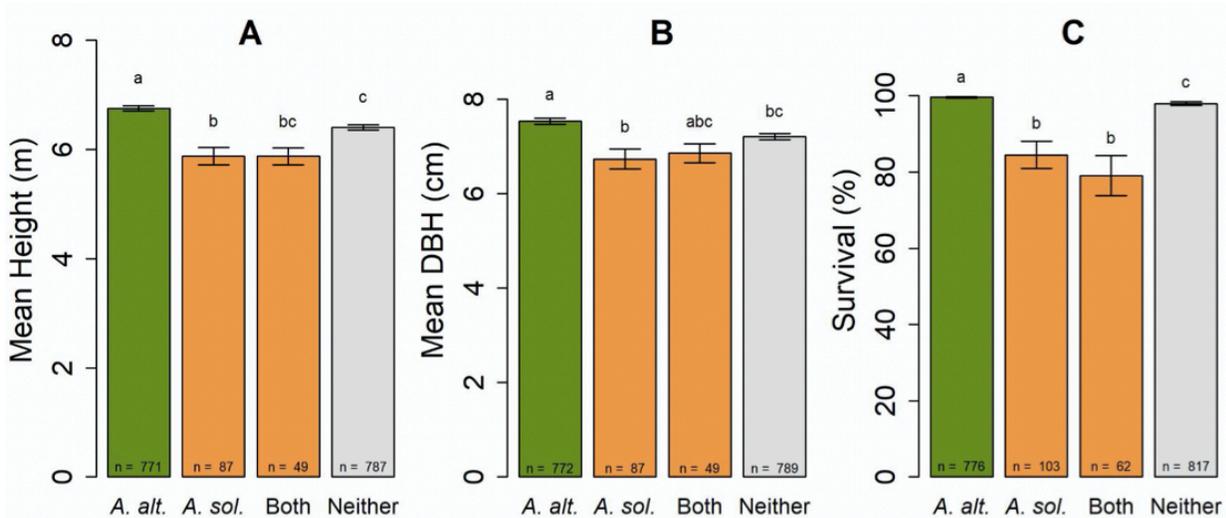


Figure 2: “(A) mean height, (B) mean diameter at breast height (DBH), and (C) percent survival among western white pine (*Pinus monticola*) growing in association with *Armillaria altimontana* (*A. alt.*), *A. solidipes* (*A. sol.*), both *A. altimontana* and *A. solidipes* (Both), or neither *Armillaria* species (Neither) at 16 years post-planting at Priest River Experimental Forest, northern Idaho, USA. Height and DBH measures were not available for every live tree in the data set. Bars show standard error. Means sharing a lower-case letter within each bar graph (i.e., A, B, and C) are not significantly different ($p < 0.05$) by Tukey-adjusted means separation” (Warwell et al. 2019).

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