Distribution, Species, and Ecology of *Armillaria* in Wyoming

Western International Forest Disease Work Conference
Valemount, British Columbia. October 2010.

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Introduction

Armillaria root disease is caused by a complex of *Armillaria* species associated with many conifer and hardwood hosts worldwide. *Armillaria* species differ in mating types, morphology, culture growth form, molecular sequence, chemical composition, aggressiveness, host range, and ecology. This root disease can play a role in tree mortality often attributed solely to insects or a different disease. In this study, a field survey was conducted to determine the geographic distribution of *Armillaria* spp. in various forest types throughout Wyoming, and to characterize their relationships in hosts and aggressiveness, soils, site conditions, and climate.

Methods

Previous to field visits, plot locations were systematically selected using a geographic information system. One plot was located in each cell of a three-by-three-mile grid across the state in accessible forested areas of public ownership (federal, state, and tribal lands). Stand selection was stratified by forest cover type. Variables recorded included: altitude; slope; aspect; forest cover type; organic matter thickness; frequency of rhizomorphs in the soil; number of stumps, snags, and logs; tree species and diameter at breast height for all live trees; and observations of other diseases, insects, and damage. Soil samples were analyzed for organic matter content, pH, and texture. For recent dead host trees, root disease was confirmed if the root collar or a major root had resin and mycelial fans. For live hosts, root disease was confirmed if mycelial fans were observed in the root collar or a major root. Variables recorded for infected host trees include: species, DBH, host condition (living or dead), crown position, percentage live crown, and associated stress/mortality agents. *Armillaria* spp. were isolated from affected trees and identified in the laboratory by crossing them with haploid tester isolates of known *Armillaria* spp.

Results and Conclusions

Three hundred plots were assessed in 12 different forest cover types. *Armillaria* was found at 89 (= 30%) locations. A total of 133 isolates were collected. Four *Armillaria* species were identified. *A. solidipes* (= *A. ostoyae*) was the most common (40 plots; 63 isolates) followed by *A. sinapina* (32 plots; 43 isolates). *A. gallica* (11 plots; 15 isolates) and *A. cepistipes* (8 plots; 11 isolates) were rarely collected.

Results suggest that *A. solidipes* is the most common *Armillaria* species in Wyoming. This species was frequently associated with conifer hosts and cover types, which are far more common than hardwoods in Wyoming, and was found mainly in the south and northeast parts of the state. *A. sinapina* was associated with conifer and hardwood hosts and cover types, and was widely distributed, but not in the central area of the state. *A. gallica* was found mostly in oak and other hardwood hosts and cover types, and only in northeast Wyoming. *A. cepistipes* was found mostly in hardwoods, but also in conifers in hardwood cover types, and only in west-central Wyoming.

For all species combined, root disease was identified from 66% of the collections. *Armillaria* species differed in hosts, forest cover types, soils, and other site conditions. Differences in aggressiveness among *Armillaria* species were not evident with the combined data, but clear differences become apparent at the host level. Results here suggest that *A. solidipes* is the most aggressive species in conifers. This is in contrast to the often encountered statement that *A. solidipes* is the most aggressive species. Other *Armillaria* species were more aggressive in aspen and other hardwood species. *A. gallica* was the most aggressive species in oak.

Armillaria root disease is considered to be a major driver of stand structure and composition in many forest ecosystems. Determining the species of *Armillaria* in a stand by host can contribute significantly to understanding its disease dynamics.