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

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Fig. 1. *Armillaria* mushrooms on a pine.

INTRODUCTION

Armillaria root disease is caused by a complex of species that infect many conifer and hardwood tree hosts (Fig. 1 and 2). Variability in host range, aggressiveness, and site preferences may be due to the occurrence or co-occurrence of different *Armillaria* species.

This disease is associated with various forest tree declines worldwide and can play a role in tree mortality often attributed solely to insects. *Armillaria* is a major forest pest in the states neighboring Wyoming, yet little is known about its occurrence or distribution within this state. Recent Forest Health Monitoring detection surveys documented widespread tree decline and mortality in Wyoming, which motivated this study. This is the first statewide evaluation monitoring study of Armillaria root disease in Wyoming.

Knowing distributions of the different species, understanding differences in host ranges and aggressiveness, and determining optimal growth conditions can help determine disease management measures.

OBJECTIVES

❶ Examine the geographic distribution of different *Armillaria* species in Wyoming.

❷ Characterize relationships among hosts, site conditions, and *Armillaria* species.

MATERIALS & METHODS

Sample locations included federal, state, and tribal forested lands throughout Wyoming. Selections were made, site-unseen, based on ownership, vegetation type, and accessibility (Fig 3). All major forest cover types were included.

Plots are 15 m square. Plot variables recorded include: slope; aspect; forest cover type; organic matter thickness; frequency of rhizomorphs in the soil; number of stumps, snags, and logs per plot; and tree species and diameter at breast height (DBH) for all live trees per plot. Soil samples are being analyzed for organic matter content, pH, and texture.

Host tree variables recorded include: species, DBH, host condition (living or dead), crown position, percentage live crown, and associated stress/mortality agents.

Armillaria species are being determined in the laboratory from samples collected from the hosts (Fig 4).

Fig. 2. Mycelial fan of *Armillaria* on a root.

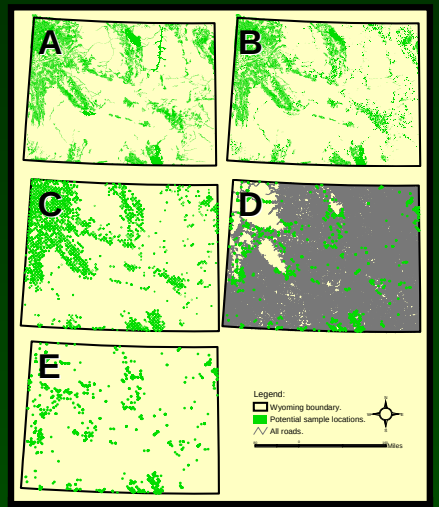

Fig 3. Selection of proposed sample locations. (A) Forest cover in Wyoming; (B) forest cover on federal, state, and tribal lands; (C) a grid was used to systematically select locations; (D) accessibility was considered; (E) final proposed sample locations.

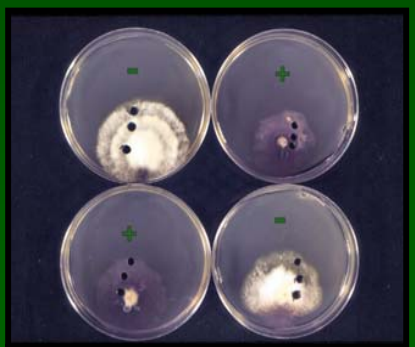

Fig. 4. Species identification of unknown diploid isolates using haploid tester isolates in mating tests. The upper inoculum is an identified haploid tester strain and the lower inoculum is the isolate to be identified in each plate.

RESULTS

We completed 300 plots in 12 different forest cover types (Fig. 5). *Armillaria* was found at 89 locations. One hundred and thirty three isolates were collected, and these are being identified to species. Four *Armillaria* species have been identified so far, with *A. sinapina* being the most common, followed by *A. ostoyae*, *A. gallica*, and *A. cepistipes*.

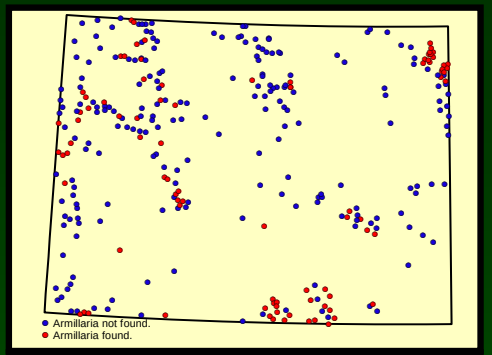

Fig. 5. Sample plots completed. Blue dots show where *Armillaria* was not found, and red dots show where *Armillaria* was found.

FUTURE RESULTS / PRODUCTS

❶ New data about an important forest health issue.

❷ Information regarding *Armillaria* species in Wyoming and their associated hosts and forest cover types.

❸ Descriptions of associated soil and stand ecology of different *Armillaria* species.

❹ Coarse-scale distribution and hazard maps.

❺ Spatial distribution of *Armillaria* compared with Forest Health Monitoring detection survey data, precipitation, and climate data.

❻ Baseline information for future monitoring and surveys of this important disease.

COOPERATORS

Les Koch, Wyoming State Forestry Division; Jim Hoffman and John Guyon, USDA-Forest Service, Forest Health Protection (R4); Roy Renkin, USDI-NPS Yellowstone Center for Resources, Yellowstone National Park; Eric Rhodenbaugh, Bureau of Indian Affairs, Wind River Agency.