

Bioclimatic Models Estimate Areas With Suitable Climate For *Armillaria* Spp. In Wyoming

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INTRODUCTION

Armillaria species range from beneficial saprobes to damaging root pathogens, and their ecological roles and impacts vary with environment and host. *Armillaria solidipes* [pending vote to conserve *A. ostoyae* (Redhead et al. 2011)] is known as an aggressive pathogen of conifers and causes tree mortality and significant growth loss in Wyoming and throughout the world. *Armillaria solidipes* also seems to exist in a non-pathogenic state under certain conditions that vary depending on environment, host, and community (unpublished data). In this case, *A. solidipes* can be difficult to differentiate from other *Armillaria* spp. The ecological role of *A. gallica*, *A. sinapina*, and *A. cepistipes* has been generally characterized as primarily saprophytic to weakly pathogenic. However, *A. gallica* has recently been described as highly pathogenic on hardwoods in some forests (Brazee and Wick 2009). On aspen, *A. gallica* and *A. sinapina* might be more aggressive pathogens than *A. solidipes* (Blodgett 2015, this proceedings, submitted). *Armillaria gallica* and *A. sinapina* are a common components of forest ecosystems and they have recently been found in areas where they were not previously known to occur (Klopfenstein et al. 2009, Kim

et al. 2010, Kim and Klopfenstein 2011, Elías-Román et al. 2013, Nelson et al. 2013, Klopfenstein et al. 2014). Furthermore, all of these typically saprophytic *Armillaria* species are thought to be an important component of forest decline. Under the host/stress/saprogen concept, disease develops when these secondary pathogens, which are already on-site, invade host tissue after environmental stress (Houston 1992). These stressors can include climate, human disturbance, and/or insect/pathogen pests. This type of forest decline is believed to be increasing and generally more severe under climate change as trees become progressively maladapted to their environments (Kliejunas et al. 2009). In this study, we use DNA-based methods to confirm species identification and utilize location-specific climate data for bioclimatic modeling to predict where *Armillaria* spp. are likely to occur and cause disease and forest decline.

OBJECTIVES

The objectives of this study are to 1) determine suitable climate space (potential distribution) for *Armillaria* species in Wyoming and 2) predict which forest areas are at risk to disease and forest decline caused by *Armillaria* spp. in the state.

METHODS

Armillaria isolates were collected from previous studies of the distribution, species, and ecology of *Armillaria* in Wyoming (Blodgett and Lundquist 2011). From these studies, 221 *Armillaria* isolates were recovered from 180 plots. A total of 128 isolates from 102 plots were determined to be *A. solidipes*, 62 isolates

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from 50 plots to be *A. sinapina*, 21 isolates from 17 plots to be *A. gallica*, and 10 isolates from 7 plots to be *A. cepistipes*. All determinations were based on pairing tests against known haploid testers. Representative, subsets of these 221 isolates were then confirmed to species using DNA sequence-based species identification at the USDA Forest Service - Rocky Mountain Research Station, Forestry Science Laboratory in Moscow, Idaho (Kim et al. 2006; Ross-Davis et al. 2012). The 180 plot locations containing *Armillaria* were used in four Maximum Entropy (MaxEnt) species distribution models (Phillips et al. 2006). The models use the plot location of each species within and around Wyoming to map specific potential distributions, based on predicted suitable climate space. Nineteen bioclimatic variables were used in the models (e.g., annual mean temperature, maximum temperature of warmest month, annual precipitation, precipitation of wettest month, precipitation of coldest quarter, etc.). An interpolation grid of ca. 1-km² resolution was used, with data derived from 1950-2000 meteorological records (Hijmans et al. 2005).

CONCLUSIONS AND FUTURE WORK

Four MaxEnt models provided preliminary predictions of suitable climate space for *Armillaria* species in Wyoming. The predictive capacity will be improved by 1) continuing DNA-based identification of *Armillaria* species from additional field collections, 2) adding more locations confirmed to have *Armillaria*, and 3) adding additional predictive variables (e.g., soil types, solar radiation, etc.). This climate-based prediction window can also be used to examine how various climate-change scenarios may affect potential distribution and disease activity. Methods developed from this project can be used to model other important forest pathogens and examine the potential for invasive species to occupy new areas under climate changes.

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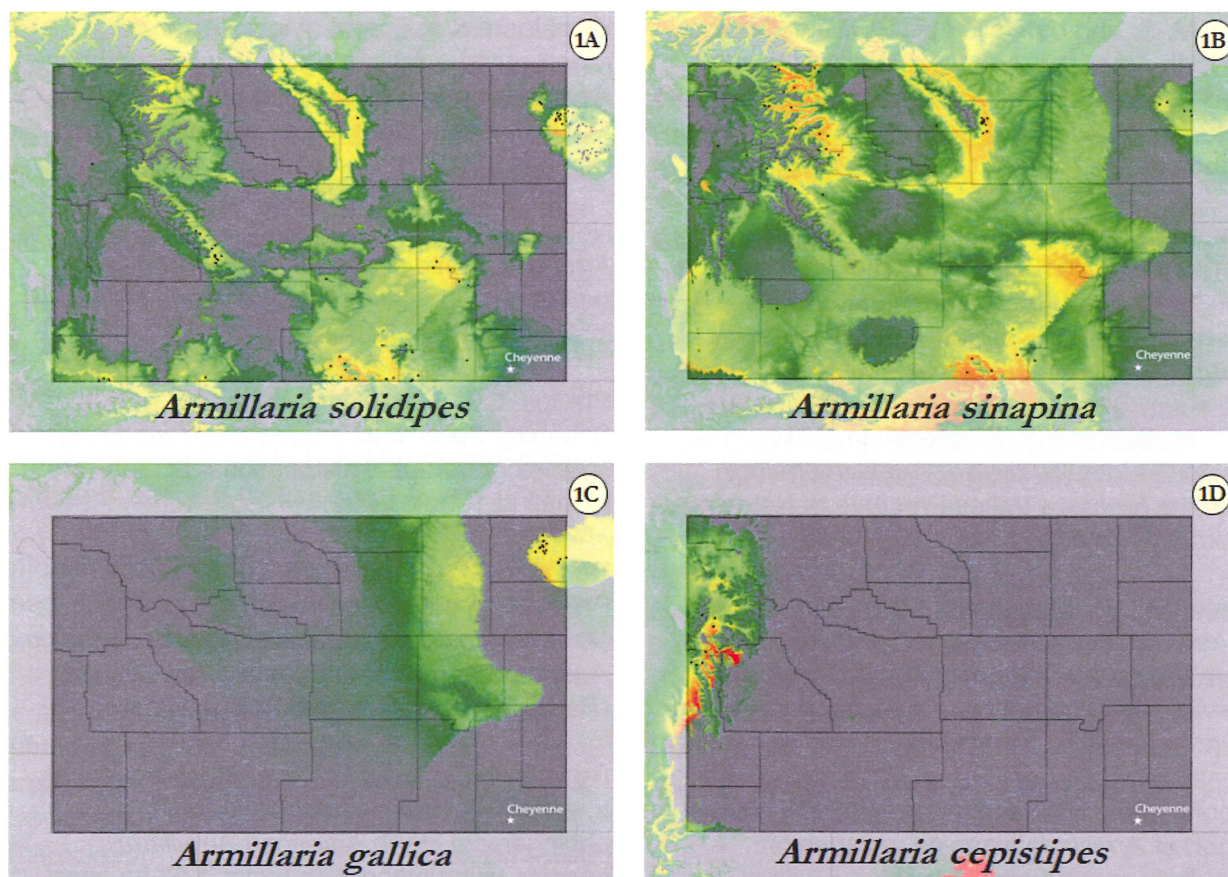


Figure 1. Occurrence locations of *Armillaria* spp. (depicted with small black dots). **1A.** *A. solidipes* (106 locations); **1B.** *A. sinapina* (51 locations); **1C.** *A. gallica* (17 locations); and **1D.** *A. cepistipes* (7 locations) from Wyoming surveys of Blodgett and Lundquist (2011), which are part of an ongoing USDA Forest Service Special Technology Development Project. Preliminary Maximum Entropy bioclimatic models of suitable climate space (potential distribution) for species in Wyoming based on occurrence points in Wyoming surveys of Blodgett and Lundquist (2011). Dark green represents predicted suitable climate space for *Armillaria*, with light green, yellow, orange, and red indicating increased suitability, respectively.

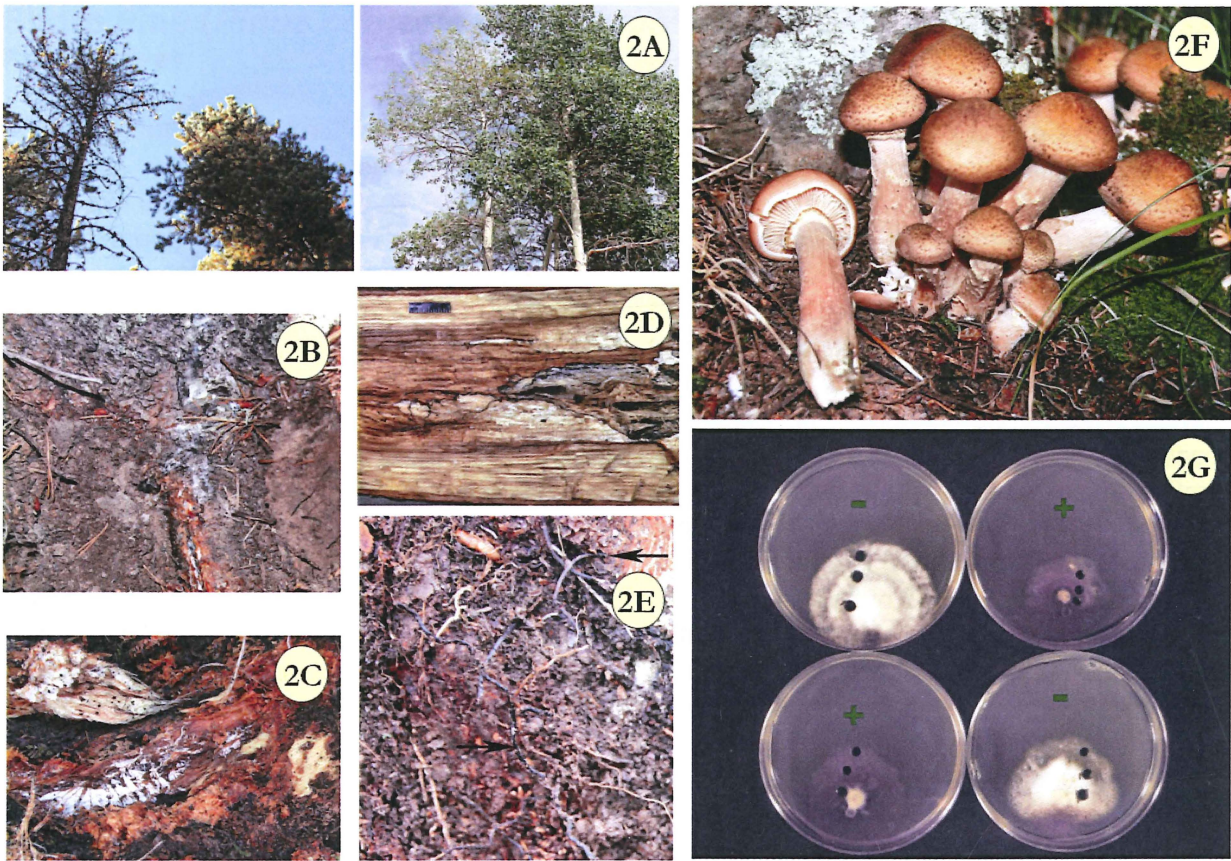
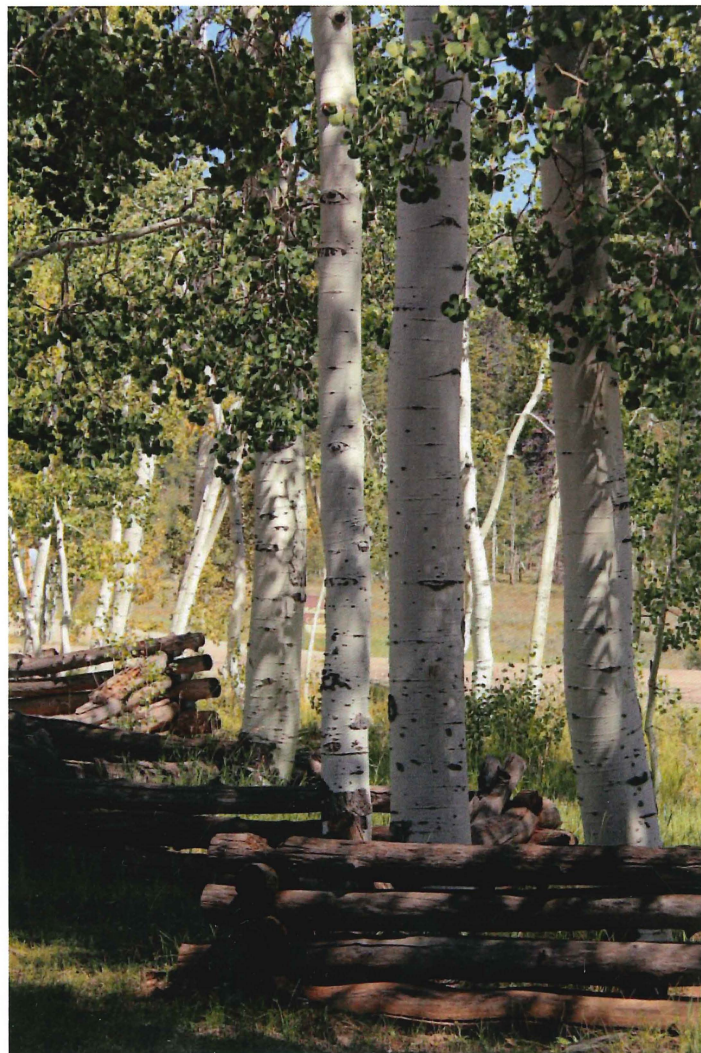


Figure 2. Armillaria collection photos: **2A.** Chlorotic foliage with extensive dieback is a typical symptom of lodgepole pine (*Pinus contorta*; left) and aspen (*Populus tremuloides*, right) with Armillaria root disease. **2B.** Lodgepole pine with Armillaria root disease showing resinosis at the root collar. **2C.** A diagnostic sign of Armillaria root disease is the characteristic mycelial fan, seen here on aspen. **2D.** Armillaria white rot with zone lines. **2E.** Rhizomorphs (gray to black, see arrows) in soil growing into a root and root collar are diagnostic signs of Armillaria root disease. **2F.** Fruiting bodies of an *Armillaria* sp. at the base of a paper birch (*Betula papyrifera*). **2G.** Species identification of unknown diploid isolates using haploid tester isolates in mating tests. Photos 2A, 2B, 2D, 2E, 2F, and 2G: James T. Blodgett, USDA Forest Service. Photo 2C: Daniel H. Brown, USDA Forest Service, Bugwood.org.

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