TOWARD DNA-BASED AND BIOCLIMATIC MODELING TOOLS TO IDENTIFY ARMILLARIA PATHOGENS, PREDICT HOST/PATHOGEN DISTRIBUTIONS, AND MANAGE ARMILLARIA ROOT DISEASE IN THE INTERMOUNTAIN REGION (USA) UNDER CHANGING ENVIRONMENTS

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Introduction

Armillaria root disease is one of the leading causes of growth loss and mortality in coniferous forests of the western USA (Lockman & Kearns 2016). Recent surveys suggest Armillaria root disease is increasing on trees in Utah (John Guyon, per. comm.). To maintain forest resilience and productivity, we must determine (1) which Armillaria species are involved in current root diseases and associated mortality in forests across the region, (2) where these Armillaria species occur/will occur across the current and future landscapes, and (3) where changing climates could exacerbate this disease. Previous studies suggest that Armillaria root disease is more severe in trees that are maladapted to climate-induced stress (e.g., Klopfenstein et al. 2009, Kliejunas et al. 2009, Sturrock et al. 2011, Dempster 2017, Kubiak et al. 2017, Aslam & Magel 2018). Thus, it is likely climate change will further exacerbate damage from Armillaria root disease.

Although Armillaria root disease is known to occur in the Intermountain Region (USDA Forest Service Region 4) of the USA, only A. solidipes (previously A. ostoyae) was identified within the region (McDonald 1999). Based on recent data and data from neighboring regions, other Armillaria species also occur in Region 4, including A. sinapina, A. cepistipes, A. gallica, and A. altimontana (Blodgett & Lundquist 2011, Blodgett et al. 2015, RMRS collections, Figure 1). Additional information for these species is needed to predict current and future distributions and associated threats to tree health (Figures 2 and 3). With newly acquired data, we can use DNA-based methods to identify Armillaria species, and bioclimatic models to predict pathogen and host distributions across the region (Klopfenstein et al. 2009, Figure 4).

Data from this project will be incorporated into existing bioclimatic models from other regions in western North America (USDA Forest Service Regions 2, 3, 6, and 10) to build west-wide bioclimatic models for Armillaria. This will improve the model accuracy and expand the geographic extent. These tools predict geographic areas where climate change is predicted to exacerbate Armillaria root disease and can predict areas where tree species that are tolerant to Armillaria root disease will be climatically adapted.

Objectives

The objectives of this project are to: (i) identify Armillaria species from collections/surveys of underrepresented areas in the Intermountain Region; and (ii) use the occurrence data to evaluate and refine bioclimatic models for predicting the present and future suitable climate space (potential distribution or the geographic area that is climatically suitable for a species’ survival). New Armillaria species/host combinations within the region will be documented.

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To supplement under-represented areas, additional *Armillaria* surveys/collections are needed in the Intermountain Region (Figure 1). We have asked collaborators to survey for *Armillaria* within these areas and send us *Armillaria* samples (e.g., mycelial fans on live trees indicating disease activity or rhizomorphs) along with GPS information and host/environmental information (Figure 3).

**Figure 1:** USDA Forest Service Intermountain Region (R4) - Study area.
Figure 2: Armillaria surveys. Armillaria root disease center (upper left); Excavating a root collar to survey for Armillaria (upper right); Armillaria fruiting bodies or basidioma (lower left); Armillaria rhizomorphs (lower center); and Armillaria mycelial fan (lower right).

Methods

Conduct DNA sequence-based diagnostics to identify Armillaria species collected from across the Intermountain Region: Primary root systems and butts of trees and shrubs will be examined, and samples (e.g., rhizomorphs, mycelial fans, rotten wood) of Armillaria spp. collected along with precise location and associated environmental data (Figures 2 and 3). Cultured Armillaria isolates from each site will be identified based on DNA sequencing (Kim et al. 2006, Hanna et al. 2007, Ross-Davis et al. 2012, Klopfenstein et al. 2017). Sampling locations will initially be selected based on information of Armillaria root disease from FHP personnel, and other areas with vegetation that could support Armillaria spp.
Figure 3: Armillaria sample collection. GPS location (left), labeled collection bag for mycelial fans and/or infected wood (center); and labeled tubes for rhizomorphs (right).

Armillaria survey data will be integrated into a bioclimatic model to predict suitable climate space (potential distribution) across the Intermountain Region. A bioclimatic model, such as MaxEnt (Phillips et al. 2006), will be used to determine which climatic factors contribute to the occurrence of Armillaria spp. across the landscape. Future distributions of suitable climate space for Armillaria will be predicted based on various General Circulation Models and greenhouse gas-emission scenarios (Klopfenstein et al. 2009, Hanna et al. 2016), and compared with present realized niche and its predicted distribution under future climate scenarios for many host tree species, which have already been predicted (Rehfeldt et al. 2006). In addition, predictions will be updated with improved climate surfaces, as available. In general, potential distribution of Armillaria root disease will be predicted for areas where the pathogen is climatically adapted, with increased risk associated with areas where the host is climatically maladapted.

Bioclimatic data will be made available for incorporation into web-based, decision tools: Management recommendations will be provided to reduce Armillaria root disease for projected future climates (e.g., 2050, 2080). These decision-support tools will provide guidance for field units for project planning, NEPA documents, forest plan revisions, and show at risk habitat in regard to endangered species.

Expected Outcomes and Benefits

Products from this project will guide forest management by producing decision-support tools that predict potential distribution of Armillaria root disease under present and future climate scenarios. Management recommendations will offer strategies to reduce Armillaria root disease for projected future climates (e.g., 2050s, 2080s, etc.) based on climatic adaptation of tree species in relation to Armillaria. This information can also be incorporated into National Disease Risk maps, which will help develop appropriate disease management protocols. In addition, this project can be readily adapted to other important forest diseases (endemic and invasive). We plan to share our products among the community of forest health professionals and share accompanying information via publications, presentations, on-site workshops, and online.
Figure 4: Preliminary example (based on limited data) Maximum Entropy bioclimatic model of realized climate niche for predicted contemporary Armillaria solidipes (left image) and predicted for the years 2061-2080 Armillaria solidipes (right image). Darkest gray represents predicted suitable climate space, with light green, yellow, orange, and red indicating increased suitability, respectively.

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Literature Cited


