ASSESSING POTENTIAL *ARMILLARIA* SPP. DISTRIBUTIONS IN WESTERN OREGON, WESTERN WASHINGTON, AND ALASKA: INCLUDING PRELIMINARY CONTEMPORARY AND FUTURE BIOCLIMATIC MODELS FOR *ARMILLARIA SOLIDIPES*

John W. Hanna[1], Mee-Sook Kim[2], Amy C. Ramsey[3], Dan W. Omdal[3], Robin L. Mulvey[4], Betsy A. Goodrich[5], Brennan A. Ferguson[5], Josh J. Bronson[6], Kristen L. Chadwick[7], Jane E. Stewart[8], Helen M. Maffei[9], Geral I. McDonald[1], Eric W.I. Pitman[1], Marcus V. Warwell[1], and *Ned B. Klopfenstein[1]*

INTRODUCTION

Armillaria species are key components of forest ecosystems throughout most regions of western North America. Their ecological roles range from beneficial saprobes to damaging root pathogens, and their impacts vary with environment and host. Under climate change, the impact of pathogenic species within these regions is predicted to increase (Kliejunas et al 2009), which could result in increased tree mortality, growth loss, and hazard trees that threaten public safety. In 2016, a collaborative project was initiated to survey of *Armillaria* spp. distributions in western Oregon, western Washington, and Alaska. Methods and preliminary results of the 2016 and 2017 (ongoing) field surveys/collections are described herein. *Armillaria* isolates derived from collaborative surveys are identified using DNA-based methods (e.g., translation elongation factor-1α gene sequence; *tef1*). DNA-based identification and 19 location-specific climatic variables are used to develop models to predict areas suitable for the occurrence of Armillaria spp. Preliminary predictions of geographic distributions of suitable habitat for *Armillaria* under current and predicted future climates are presented, based on Maximum entropy distribution models (MaxEnt). MaxEnt models are especially useful because of their ability to produce statistically robust models using limited occurrence-only data (see Phillips et al. 2006). This information will contribute to habitat-specific management strategies for reducing impacts and increasing the benefits of these ecologically important fungal species.

OBJECTIVES

The objectives of this project are to (i) survey, collect, isolate, culture, and identify *A. solidipes* and other *Armillaria* species in under-represented areas of western Oregon, western Washington, and Alaska, and (ii) integrate survey data from these under- represented areas with previous surveys of *A. solidipes* (ID, MT, WA, OR, UT, CO, WY, AZ, NM, and other states/ provinces). The combined survey data will be used to evaluate and refine existing bioclimatic models for predicting the contemporary realized climatic niche for *A. solidipes* and projecting its future geographic distribution under climate change in western North America. Any new *Armillaria* species/host combinations within OR, WA, and AK will also be documented.

In: Cleaver, C. & P. Palacios (Comps). Proceedings of the 65th Annual Western International Forest Disease Work Conference; 2017 Oct. 2-6; Parksville, British Columbia. [1]USDA Forest Service, RMRS, Moscow, Idaho. [2]Department of Forestry, Environment and Systems, Kookmin University, Seoul, South Korea. [3]Washington DNR, Olympia, Washington. [4]UDSA Forest Service, FHP Region 10, Juneau, Alaska. [5]UDSA Forest Service, FHP Region 6, Wenatchee, Washington. [6]UDSA Forest Service, FHP Region 6, Central Point, Oregon. [7]UDSA Forest Service, FHP Region 6, Sandy, Oregon. [8]Department of Bioagricultural Sciences and Pest Management, Colorado State University, Ft. Collins, Colorado. [9]USDA Forest Service-Central Oregon Service Center, Bend, Oregon.

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METHODS

Point locations for 378 *Armillaria solidipes* isolates were collected from previous studies of Washington, Oregon, Idaho, Montana, Utah, Wyoming, Arizona, Colorado, New Mexico, British Columbia, and Chihuahua (McDonald et al. 1987, Shaw 1989, Omdal et al. 1995, McDonald et al. 1998, Kim 1999, Kim et al. 2000, Ferguson et al. 2003, Worrall et al. 2004, Hanna 2005, Hanna et al. 2007, Hanna et al. 2008a, Hanna et al. 2008b, Blodgett and Lundquist 2011, McDonald et al. 2011, Klopfenstein et al. 2012, Hanna et al. 2014, Hoffman et al. 2014, Blodgett et al. 2015, and unpublished data). Isolates of *A. solidipes* and other *Armillaria* species from ongoing surveys were identified by DNA sequencing (e.g., *tef1* gene) as described in Kim et al. (2006), Ross-Davis et al. (2012), and/or Elías-Román et al. (2013). Identification of some isolates were validated by somatic incompatibly and/or morphology.

Figure 1. *Armillaria* surveys. Armillaria root disease center (top left); Excavating a root collar to survey for *Armillaria* (top right); Armillaria fruiting bodies or basidioma (bottom left); *Armillaria* rhizomorphs (bottom center); and *Armillaria* mycelial fan (bottom right).

MaxEnt distribution models used 19 bioclimatic variables (e.g., annual mean temperature, maximum temperature of warmest month, annual precipitation, precipitation of wettest month, precipitation of coldest quarter, etc.) in two sets of interpolation grids (ca. 1-km^2 resolution) from worldclim.org (Hijmans 2005). One set containing environmental data for contemporary climate (based on data from 1950-2000) and a set of climate projection grids for the year 2070 (average for 2061-2080) based on data from the Intergovernmental Panel on Climate Change/Coupled Model Intercomparison Project Phase 5 (IPCC/CMIP5). For the 2070

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predictions, we chose to use the representative concentration pathway 8.5 (RCP8.5), which represents a "business-as-usual" continued rise in CO_2 greenhouse gas scenario and the global circulation model (GCM) HadGEM2-ES (Collins et al. 2008, Riahi et al. 2011). Techniques are further described in Klopfenstein et al. (2009).

RESULTS

Surveys are ongoing, with >30 *Armillaria* isolates collected and established in culture to date (Figure 1). Preliminary climate-based, species distribution models using MaxEnt were created [Figures 2A (*A. solidipes* potential distribution under contemporary climate), and 2B (*A. solidipes* predicted potential distribution for project year 2070 climate)] based on the 378 confirmed locations where *A. solidipes* has already been identified.

DISCUSSION

This project is developing methods to monitor and predict potential threats of Armillaria root disease under contemporary and future climate scenarios across the western USA, including Alaska. Predictions of the present and future distribution of *Armillaria* pathogens will guide forest managers for appropriate practices to manage Armillaria root disease, based on contemporary and future climate scenarios. Information from this project will be incorporated into prediction models for the western USA. In addition, this approach can also be adapted for other native and invasive forest pathogens.

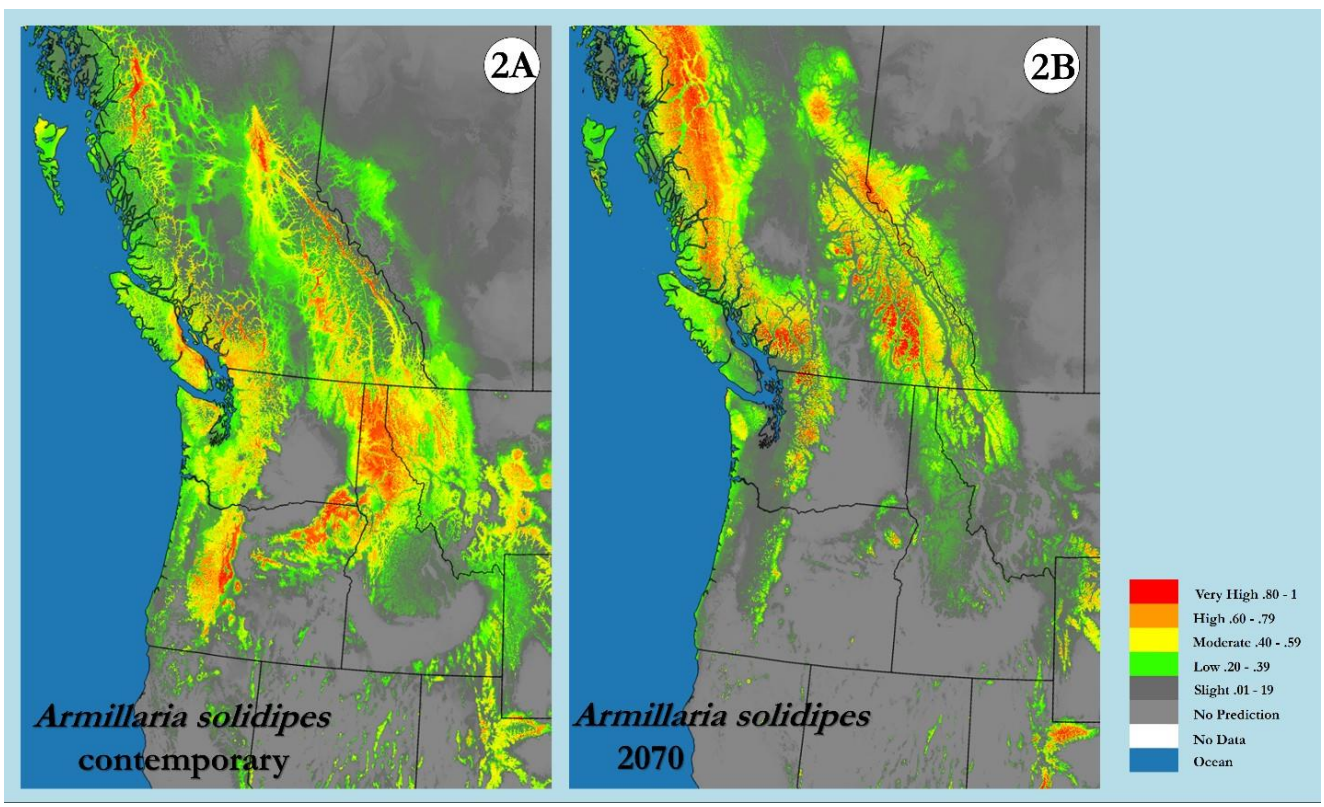

Figure 2. Maximum Entropy bioclimatic model of predicted suitable climate space (potential distribution) for 2A: *Armillaria solidipes* based on contemporary climate; 2B: *Armillaria solidipes* based on the RCP 8.5 "business as usual" climate-change scenario for the year 2070.

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Our preliminary models (Figures 2A and 2B) predict that suitable climate for *A. solidipes* will decrease in Oregon and Washington by the year 2070 RCP8.5 "business as usual" scenario; however, these models are based on the pathogen and should be considered in the context of host trees for a better understanding of climate-change impacts. In addition, the adaptation potential of *Armillaria* spp. remains unknown. Predicted changes in climate may also predispose woody hosts that become maladapted (physiologically stressed by changing climate) to Armillaria root disease. It has been hypothesized that woody hosts that are stressed due to changing climate will have a higher likelihood of susceptibility to pathogens (e.g., Kliejunas et al. 2009, Sturrock et al. 2011, and others). For example, ongoing climate change is projected to increase the elevational distribution of *A. solidipes* which could potentially exacerbate Armillaria root disease in high-elevation areas of the southern Cascadia region, where species such as *Pinus albicaulis* (whitebark pine) are predicted to lose much of their suitable climate space due to climate change (Warwell et al. 2007). It seems plausible that disease caused by *A. solidipes* may increase until maladapted hosts and *A. solidipes* vanish from local landscapes.

To date, *A. solidipes* has not been recorded in California (Baumgartner and Rizzo 2001). Additional surveys/collections are needed from southern Oregon and northern California to determine the southern extent of *A. solidipes* distribution and the distribution of other *Armillaria* spp. along the west coast. Based on the predicted 2070 suitable habitat for *A. solidipes*, collections from these areas appear vital for determining which *Armillaria* species have potential to invade in the Cascadian region under future-climate scenarios. Currently, *A. solidipes* has not been found in Alaska. Bioclimatic model predictions indicate suitable climate space for *A. solidipes* is predicted to greatly increase throughout the southern coast of British Columbia and into southeast Alaska. Hence, caution is warranted for any northward movement of woody materials infected with *Armillaria* because of the increased potential (under future climate change) for *A. solidipes* to survive in northern areas that are currently considered climatically unsuitable for its survival.

The predictive capacity of bioclimatic models for *A. solidipes* and other *Armillaria* sp. can be further improved by 1) Removing bias with bias grids and/or collection of additional isolates from under-represented areas, 2) Adding additional predictive variables (i.e. soil types, solar radiation, topography, predictions of other *Armillaria* species, etc.), and 3) Obtaining population-level data to allow independent predictions based on diverse populations within a species.

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