

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

J.W. Hanna¹, M.V. Warwell¹, R.A. Sitz¹, J.C. Guyon², E.G. Hebertson², A.L. Saavedra³, J.T. Blodgett⁴, M.-S. Kim⁵, J.E. Stewart⁶, S.M. Ashiglar^{1,7}, G.I. McDonald¹, and N.B. Klopfenstein¹

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 under-represented 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.

¹USDA Forest Service, RMRS, Moscow, ID, USA. ²USDA Forest Service, FHP Region 4, Ogden, UT, USA. ³USDA Forest Service, FHP Region 4, Boise, ID, USA. ⁴USDA Forest Service, FHP Region 2, Rapid City, SD, USA. ⁵USDA Forest Service, PNW, Corvallis, OR, USA. ⁶Dept. of Bioagricultural Science and Pest Management, Colorado State University, Fort Collins, CO, USA. ⁷Washington State Department of Fish and Wildlife, Clarkston, WA, USA

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).

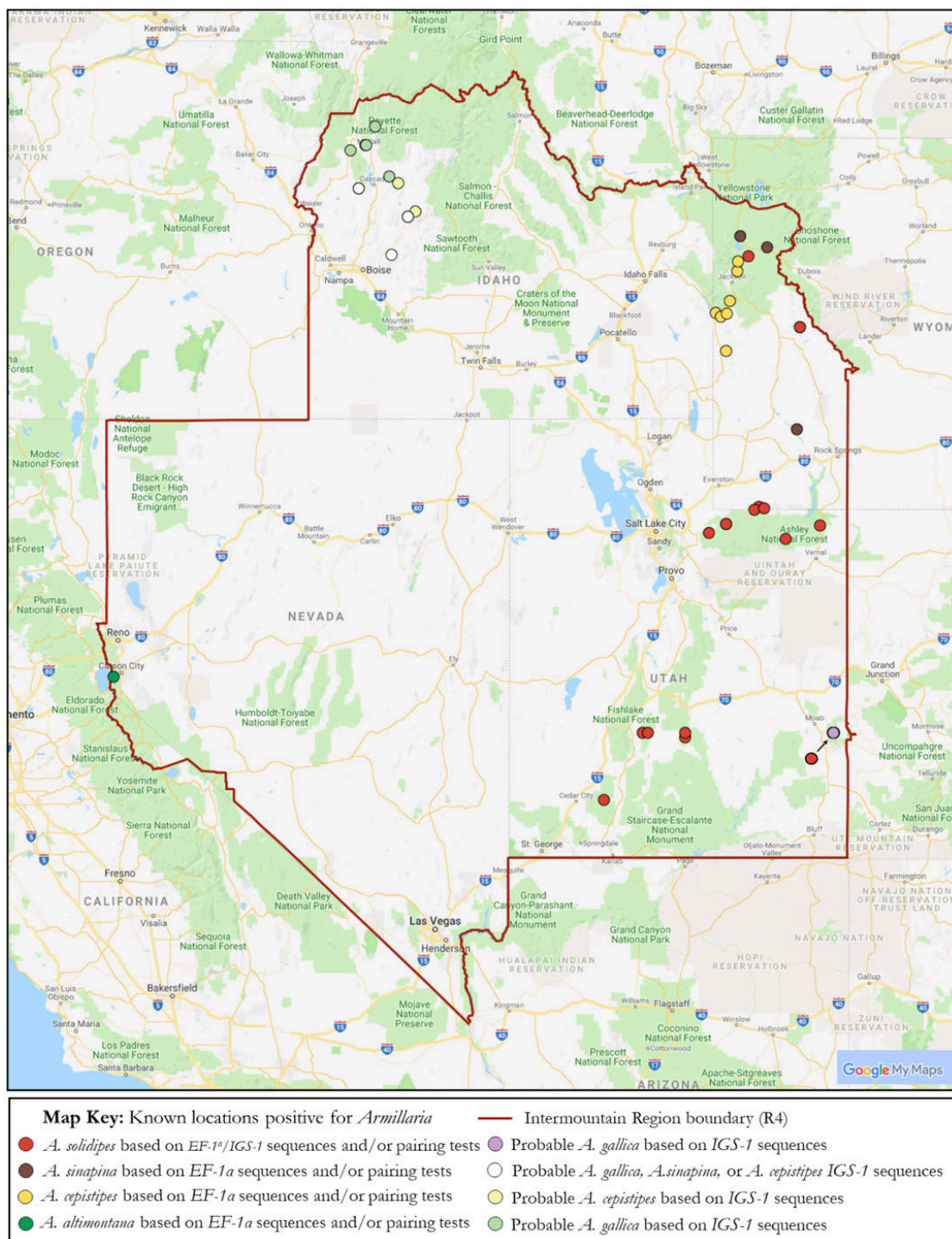


Figure 1: USDA Forest Service Intermountain Region (R4) - Study area.



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.

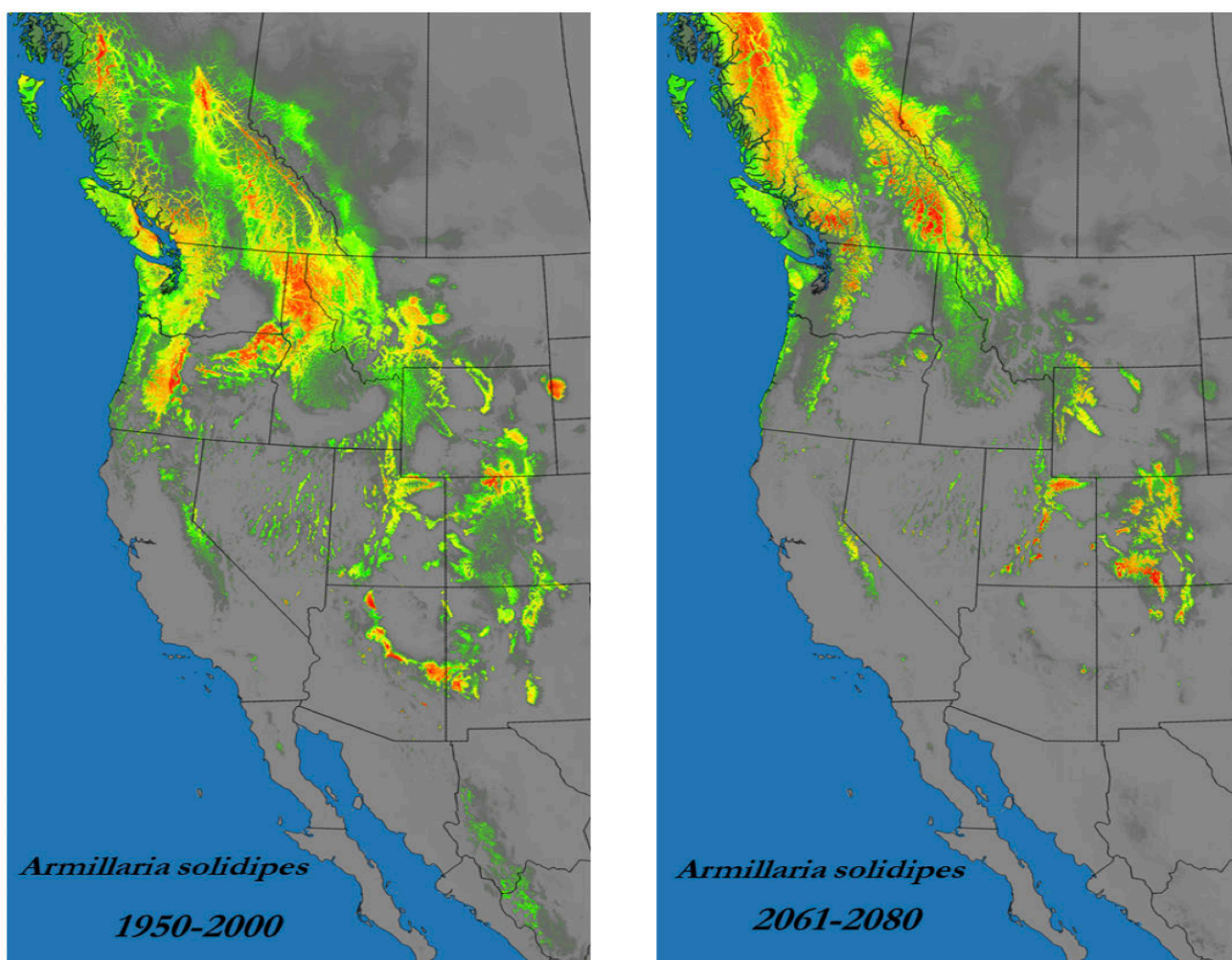


Figure 4: Preliminary example (based on limited data) Maximum Entropy bioclimatic model of realized climate niche for predicted contemporary *Armillaria solidipes* (left image) and predicted for the years 2061-2080 *Armillaria solidipes* (right image). Darkest gray represents predicted suitable climate space, with light green, yellow, orange, and red indicating increased suitability, respectively.

Acknowledgements

This project is supported by USDA – Forest Service, State and Private Forestry, Forest Health Protection – Special Technology Development Program and Rocky Mountain Research Station – Forest Woodland Ecosystems Program.

Literature Cited

- Aslam, A.J., Magel, E.A. (2018). Influence of drought and season on compartmentalization of black locust (*Robinia pseudoacacia* L.) inoculated with *Armillaria mellea*. *European Journal of Plant Pathology*, 152, 21-31. <https://doi.org/10.1007/s10658-018-1444-5>
- Blodgett, J.T., Lundquist, J.E. (2011). Distribution, species, and ecology of *Armillaria* in Wyoming. In: Fairweather, M.L., Palacios, P. (comps). *Proceedings of the 58th Western International Forest Work Conference*. 4-8 October 2010, Valemount, BC, Canada. (cited in figure 1 legend). p. 58

- Blodgett, J.T., Hanna, J.W., Pitman, E.W.I., Ashiglar, S.M., Lundquist, J.E., et al (2015). Bioclimatic models estimate areas of suitable habitat for *Armillaria* spp. in Wyoming. In: Murray, M., Palacios, P. (coms). *Proceedings of the 62nd Western International Forest Disease Work Conference (WIFDWC)*. 8-12 September 2014, Cedar City, UT. p. 29-33
- Dempster, R.W. (2017). Impact of climate on juvenile mortality and *Armillaria* root disease in lodgepole pine. *The Forestry Chronicle*, 93(2), 148-160. <https://doi.org/10.5558/tfc2017-021>
- Hanna, J.W., Klopfenstein, N.B., Kim, M.-S., McDonald, G.I., Moore, J.A. (2007). Phylogeographic patterns of *Armillaria ostoyae* in the western United States. *Forest Pathology*, 37(3), 192-216. <https://doi.org/10.1111/j.1439-0329.2007.00497.x>
- Hanna, J.W., Warwell, M.V., Maffei, H., Fairweather, M.L., Blodgett, J.T., et al. (2016). Bioclimatic modeling predicts potential distribution of *Armillaria solidipes* and *Pseudotsuga menziesii* (Douglas-fir) under contemporary and changing climates in the interior western U.S.A. In: Ramsey, A., Palacios, P. (comps). *Proceedings of the 63rd Annual Western International Forest Disease Work Conference*. 21-25 September 2015, Newport, OR. p. 117-123.
- Kim, M.-S., Klopfenstein, N.B., Hanna, J.W., McDonald, G.I. (2006). Characterization of North American *Armillaria* species: genetic relationships determined by ribosomal DNA sequences and AFLP markers. *Forest Pathology*, 36(3), 145–164. <https://doi.org/10.1111/j.1439-0329.2006.00441.x>
- Kliejunas, J.T., Geils, B., Glaeser, J.M., Goheen, E.M., Hennon, P., et al (2009). *Climate and Forest Diseases of Western North America: A Literature Review*. PSW-GTR-225. Albany, CA.: USDA, Forest Service, Pacific Southwest Research Station. 56 p.
- Klopfenstein, N.B., Kim, M.-S., Hanna, J.W., Richardson, B.A., Lundquist, J.W. (2009). *Approaches to Predicting Potential Impacts of Climate Change on Forest Disease: An Example with Armillaria Root Disease*. Research Paper RMRS-RP-76. Fort Collins, CO.: USDA, Forest Service, Rocky Mountain Research Station. 10 p.
- Klopfenstein, N.B., Stewart, J.E., Ota, Y., Hanna, J.W., Richardson, B.A., et al. (2017). Insights into the phylogeny of Northern Hemisphere *Armillaria*: Neighbor-net and Bayesian analyses of translation elongation factor 1- α gene sequences. *Mycologia*, 109(1), 75-91. <https://doi.org/10.1080/00275514.2017.1286572>
- Kubiak, K., Żółciak, A., Damszel, M., Lech, P., Sierota, Z. (2017). *Armillaria* pathogenesis under climate changes. *Forests*, 8(4), 100. <https://doi.org/10.3390/f8040100>
- Lockman, I.B., Kearns, H.S.J., eds. (2016). *Forest Root Diseases Across the United States*. Gen. Tech. Rep. RMRS-GTR-342. Ogden, UT.: USDA, Forest Service, RMRS, Ogden, UT, USA. 55 p.
- McDonald, G.I. (1999). Preliminary report on the ecology of *Armillaria* in Utah and the Inland West. In: Trummer, L.,(comp). *Proceedings of the 46th Western International Forest Disease Work Conference*. 28 September – 2 October 1998, University of Nevada-Reno, Reno, NV. p. 85-92
- Phillips, S.J., Anderson, R.P., Schapire, R.E. (2006). Maximum entropy modeling of species geographic distributions. *Ecological Modelling*, 190(304), 231-259. <https://doi.org/10.1016/j.ecolmodel.2005.03.026>
- Rehfeldt, G.E., Crookston, N.L., Warwell, M.V., Evans, J.S. (2006). Empirical analyses of plant-climate relationships for the western United States. *International Journal of Plant Sciences*, 167(6), 1123-1150. <https://doi.org/10.1086/507711>
- Ross-Davis, A.L., Hanna, J.W., Kim, M.-S., Klopfenstein, N.B. (2012). Advances toward DNA-based identification and phylogeny of North American *Armillaria* species using elongation factor-1 alpha gene. *Mycoscience*, 53, 161-165. <https://doi.org/10.1007/s10267-011-0148-x>
- Sturrock, R.N., Frankel, S.J., Brown, A.V., Hennon, P.E., Kliejunas, J.T., et al. (2011). Climate change and forest diseases. *Plant Pathology*, 60(1), 133-139. <https://doi.org/10.1111/j.1365-3059.2010.02406.x>