



DEVELOPING A PREDICTION MODEL FOR *ARMILLARIA SOLIDIPES* IN ARIZONA

N.B. Klopfenstein¹, J.W. Hanna¹, M.L. Fairweather², J.D. Shaw³,
R. Mathiasen⁴, C. Hoffman⁴, E. Nelson⁴, M. -S. Kim⁵, and
A.L. Ross-Davis^{1,6}

ABSTRACT

In 2010, a collaborative project was started to determine the distribution of *Armillaria solidipes* (= *A. ostoyae*) in Arizona. The methods and preliminary accomplishments of the 2010 and 2011 (ongoing) field surveys/collections are summarized. During the next phase of this project, surveys will be completed and remaining *Armillaria* isolates will be identified using DNA-based methods. In addition, a preliminary prediction map based on 25 locations positive for *A. solidipes* is presented. Sites positive for *A. solidipes* are associated with climate data to predict the potential current distribution (and disease activity) of *A. solidipes* within the region. Data from this region can be added to global *A. solidipes* datasets that will help develop bioclimatic models for predicting the future distribution and disease activity of *Armillaria solidipes* under various climate-change scenarios.

INTRODUCTION

Severity of *Armillaria* root disease appears to increase with increased forest management (McDonald et al. 1987). This causes a dilemma for forest managers because it can be difficult to determine if a site is at risk for *Armillaria* root disease unless symptoms are prominent. The pathogenic species *A. solidipes* [pending vote to conserve *A. ostoyae* (Redhead et al. 2011)] is often difficult to identify from other saprophytic *Armillaria* spp., and *A. solidipes* seems to exist in a non-

pathogenic state in some areas (unpublished data). Recently, DNA-based methods became available to identify North American *Armillaria* species (Kim et al. 2006, Ross-Davis et al. 2011). In this study, we are using DNA-based identification and location-specific climate data for bioclimatic modeling to predict where *A. solidipes* is likely to occur and cause disease under different forest management regimes.

OBJECTIVES

- (1) Determine suitable climate space for *Armillaria solidipes* in Arizona.
- (2) Predict which Arizona forest areas are at risk to disease caused by *Armillaria solidipes*.
- (3) Develop habitat-specific management strategies to reduce impacts of *Armillaria* root disease.
- (4) Incorporate information into a bioclimatic model to predict the potential future (e.g., 2030, 2060, and 2090) distribution (and disease activity) of *Armillaria solidipes*.

METHODS

Currently, 115 0.04-ha plots in Arizona have been surveyed for *Armillaria* spp. (Figures 1 and 2). Actual plot locations were selected on the basis of plot availability within a given section, accessibility by road, and maximizing the variation in elevation, slope, and vegetation types encountered on the landscape. Three live or dead trees and shrubs of each species present were inspected for the presence of *Armillaria* spp. "Large", "Medium", and "Small" trees (relative to tree sizes found on plot) of each species were selected for inspection and sampling. Tree inspection and sampling was

In: Zeglen, S. Comp. 2012. Proceedings of the 59th Annual Western International Forest Disease Work Conference; 2011 October 10-14; Leavenworth, WA.

¹USDA Forest Service, RMRS, Moscow, ID. ²USDA Forest Service, FHP, Region 3, Flagstaff, AZ. ³USDA Forest Service, RMRS, FIA, Ogden, UT. ⁴Northern Arizona University, Flagstaff, AZ. ⁵Kookmin University, Seoul, Korea. ⁶Western Forestry Conservation Association, Portland, OR.

conducted by excavating at least one main root and the nearest portion of root collar to a radial distance of approximately 0.5 m from the bole. Shrubs were sampled by extracting the root system. If present, rhizomorphs were collected from trees and shrubs. If resinosis or other symptoms of disease were

apparent, the root collar was cut to inspect and collect bark-fan samples, if present. *Armillaria* samples were kept cool and mailed to the Forestry Sciences Laboratory in Moscow, where isolates were established in culture in preparation for DNA-based species identification.



Figure 1: Field crew establishing a plot (left); Tree showing possible symptoms of *Armillaria* root disease (center); *Armillaria* spp. basidiocarps at the base of a tree (right).

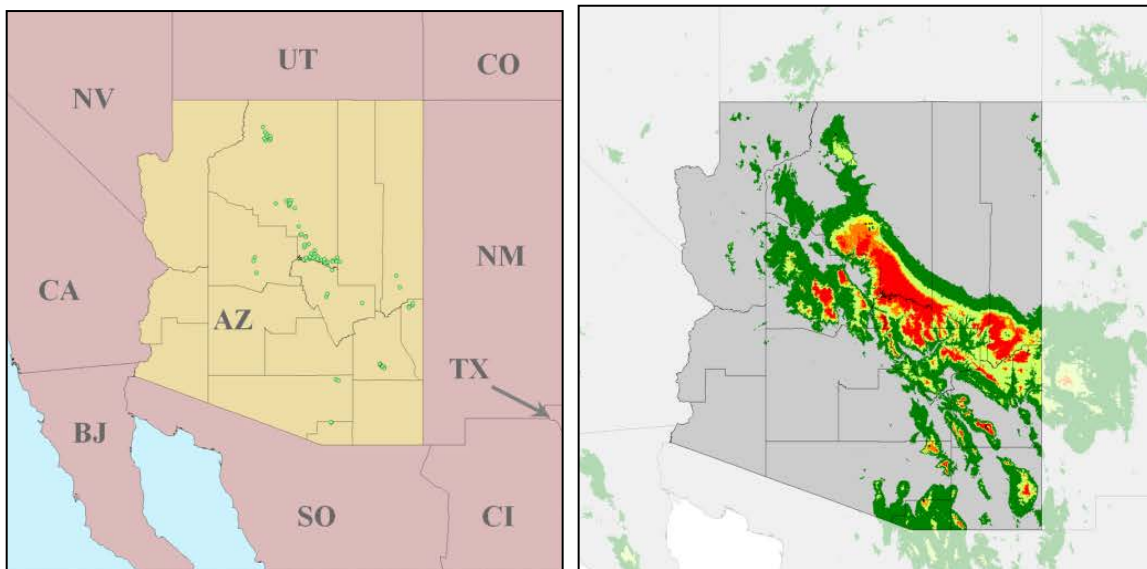


Figure 2: Map of Arizona showing collection sites during the 2010 and 2011 field seasons (left); Preliminary example of predicted suitable climate space for *Armillaria solidipes* in Arizona based on 25 locations positive for *A. solidipes* collected in 2010. Dark green represents predicted suitable climate space for *A. solidipes* with light green, yellow, orange, and red indicating increased likelihood of suitable climate space, respectively (right).

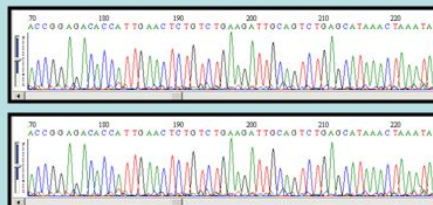
PROJECT OVERVIEW

Phase One - Data Collection



Digging for rhizomorphs (left) Mycelial bark fan colonizing the root collar of a tree (middle) Slope, aspect, location, elevation, plant association, and site description are some of the data recorded at each plot (right).

Phase Two - Identification



After pure fungal cultures of *Armillaria* sp. are obtained scrapings of mycelium are taken from the isolates (left) and added to PCR reagents. The samples then undergo PCR reactions in a thermocycler (middle). Successfully amplified DNA fragments are then sequenced and unique genetic code (right) can be analyzed to identify *Armillaria* spp. (Kim et al. 2006).

Phase Three - Analysis and Products

<http://forest.moscowisl.wsu.edu/fuels/art>

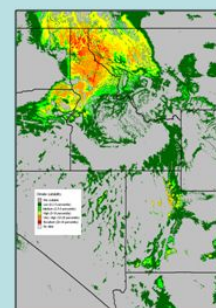


Probability of *Armillaria* presence: HIGH in this subseries.

Armillaria outline: High risk on arid species

The following conifer species may occur in the Cool/WH subseries for North_ID

Species	Subseries	Average Expected Cover (%)	Potential disease impact
ABSP	C	43.5	High if disturbed
PIPE	1/S	35.0	High
PRIN	1/S	6.1	High
PRIO	1/S	1.8	Low
LAOC	1/S	1.1	Low
ABLA	C	1	High out low occurrence
PRIO	1/S	0.9	High if planted trees <20 yrs old
THSL	1/S	0.6	Low in this subseries



Data from this project can be incorporated into tools for land managers such as the *Armillaria* Response Tool (ART – shown to the left and center) (McDonald et al. 2005) or be used to model climate profiles (Rehfeldt et al. 2006) for *Armillaria ostoyae* and predict the affects of climate change on *Armillaria ostoyae* (example map -right).

FUTURE WORK

We will continue to conduct DNA-based identification of *Armillaria* species at the RMRS Forestry Sciences Lab in Moscow, ID. After all *Armillaria* isolates are identified, locations confirmed to have *A. solidipes* will be used to predict suitable climate spaces for this pathogen (Figure 2). This

climate window can also be used to examine how various climate-change scenarios may affect *A. solidipes* in Arizona. The methods developed from this project can also be used to model other important forest pathogens and examine the potential for invasive species to occupy new areas under a changing climate.

ACKNOWLEDGEMENTS

This project was partially funded by the Forest Health Protection, Special Technology Development Program (R6-2010-02: Developing and applying methods to predict present and future climatic influences on *Armillaria* root disease), USDA Forest Service, RMRS, Interior West Region Forest Inventory and Analysis, Joint Venture Agreement (07-JV-11221662-285), and Mission Research Program, School of Forestry, Northern Arizona University, Flagstaff, AZ.

REFERENCES

- 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*. 36:145-164.
- McDonald, G.I., Martin, N.E., Harvey, A.E. 1987. *Armillaria* in the northern Rockies: Pathology and host susceptibility on pristine and disturbed sites. USDA Forest Service, Research Note INT-371. Intermountain Research Station, Ogden, UT. 5 p.
- McDonald, G.I., Tanimoto, P.D., Rice, T.M., Hall, D.E., and others. 2005. Fuels planning: science synthesis and integration; environmental consequences fact sheet 13: Root Disease Analyzer-*Armillaria* Response Tool (ART). USDA Forest Service, RMRS-RN-23-13WWW. Rocky Mountain Research Station, Fort Collins, CO. 2 p.
- Redhead, S.A., Bérubé, J., Cleary, M.R., Holdenrieder, O., and others. (2033) Proposal to conserve *Armillariella ostoyae* (*Armillaria ostoyae*) against *Agaricus obscurus*, *Agaricus occultans*, and *Armillaria solidipes* (Basidiomycota). *Taxon*. 60(6):1770-1771.
- 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 Science*. 167:1123-1150.
- Ross-Davis, A.L., Hanna, J.W., Kim, M.-S., Klopfenstein, N.B. 2011. Advances toward DNA-based identification and phylogeny of North American *Armillaria* species using elongation factor-1 alpha gene. *Mycoscience*. Published online first 8/13/11, DOI 10.1007/s10267-011-0148-x.



***Proceedings of the 59th Annual
Western International Forest Disease
Work Conference***

**October 10-14, 2011
Leavenworth, Washington**



Proceedings of the 59th Annual Western International Forest Disease Work Conference

*October 10th-14th, 2011
Enzian Inn
Leavenworth, Washington*

Compiled by:
Stefan Zeglen
BC Ministry of Forests, Lands and Natural Resource Operations, Nanaimo, BC

and

Patsy Palacios
S.J. and Jessie E. Quinney Natural Resources Research Library
College of Natural Resources
Utah State University, Logan, UT

©2012, WIFDWC

Papers are formatted and have minor editing for language, and style, but otherwise are printed as they were submitted. The authors are responsible for content.