Survey of *Armillaria* spp. in the Oregon East Cascades: Baseline Data for Predicting Climatic Influences on Armillaria Root Disease

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Abstract

Root disease pathogens, such as *Armillaria solidipes* Peck (recently recognized older name for *A. ostoyae*), will likely have increasing impacts to forest ecosystems as trees undergo stress due to climate change. Before we can predict future impacts of root disease pathogens, we must first develop an ability to predict current distributions of the pathogens (and their hosts). Reliable predictions depend on knowing precise locations of accurately identified pathogens and their host species. Thus, the goal of this study is to obtain baseline information on *Armillaria* spp. distributions in the East Cascades of Oregon. In 2007, a collaborative project was initiated to survey *Armillaria* spp. associated with diverse geographic areas and climate on the eastern slopes of the Oregon Cascades. Data from this project can be incorporated into models that predict current and future distributions of *Armillaria* spp. based on climatic factors. Models to predict distributions of host tree species are currently available. Consequently, predicted host distributions can be compared with predicted distributions of *Armillaria* spp. to assess potential impacts to forest ecosystems under future climate-change scenarios. The methods developed from this project can provide a basis for the modeling of other important pathogens, and help assess the potential for invasive pathogens under climate-change scenarios. Predictions of Armillaria root disease and other diseases under future climates are essential for forest management to strategically reduce future impacts of disease.

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Introduction

Climate change is predicted to increase the impacts of Armillaria root disease in some regions (Sturrock 2007, Kliejunas et al. 2008). Surveys of *Armillaria* spp. distributions provide necessary baseline information for predicting these impacts (Kim et al. 2008). Although pathogenic species, such as *A. solidipes* (recently recognized older name for *A. ostoyae*; Burdsall and Volk 2008), can be detected in the field by trained forest pathologists, it often goes unnoticed in many areas where it can infect trees below ground without anyreadily apparent, above-ground symptoms (Morrison 2000). In addition, *A. solidipes* frequently persists in a non-pathogenic state until host and environmental conditions favor pathogenicity. Thus, the full distribution of accurately identified *A. solidipes* is not well documented. Well-designed surveys are needed to determine distributions of *A. solidipes* and other less pathogenic *Armillaria* spp. Information of the precise location of accurately identified species can be used to model the suitable climate space for the pathogen, which can then be used to predict current and potential future distributions of *Armillaria* spp. Predictions of potential *A. solidipes* distribution can then be compared with predictions for host tree distributions for preliminary assessments of potential climatic influences on Armillaria root disease.

The goal of this study is to obtain baseline information on *Armillaria* spp. distributions in the East Cascades of Oregon. This information will be used to develop predictions of present and future suitable climate space for *Armillaria* spp., which could correspond to species distributions.

Objectives

(1) Document the distributions of *Armillaria* spp. on diverse hosts across a range of climates and geographic areas in the Oregon East Cascades.

(2) Determine suitable climate space for *A. solidipes* and other *Armillaria* spp. in the East Cascades of Oregon.

(3) Project future suitable climate space for *A. solidipes* and other *Armillaria* spp. in the East Cascades of Oregon under various climate models and emission scenarios.

(4) Incorporate information from predictive models into Disease Risk Models/Maps.

Table 1. Summary of preliminary *Armillaria* spp. isolate identifications for 2007 and 2008 collections from the Oregon East Cascades.

NABS I [a]	NABS III-V-VII complex [b]	NABS X [c] or NABS X x III-V-VII hybrid
36 isolates from 23 plots	140 isolates from 44 plots	121 isolates from 45 plots

Note: Two isolates are not yet identified to species groups. All sequences are currently being analyzed to better characterize these isolates.
[a] North American Biological Species I = Armillaria solidipes (recently known as A. ostoyae)
[b] A complex of closely related species (A. calvescens, A. sinapina, A. gallica)
[c] An unnamed biological species

Table 2. Summary of *Armillaria* spp. by plant association group (PAG) [a].

PAG	Total number of plots sampled	Percent of plots positive for *Armillaria solidipes*	Percent of plots positive for other *Armillaria* spp.	Percent of plots positive for both *A. solidipes* and other *Armillaria* spp.
ABAM Wet	1	100	100	100
ABCO-ABGR Wet	8	38	88	38
ABCO-ABGR Moist	38	21	79	18
ABCO-ABGR Dry	20	5	70	0
ABGR Wet	1	0	0	0
ABGR Moist	2	0	50	0
ABGR Dry	10	30	50	20
TSME Wet	4	0	25	0
TSME Moist	5	0	80	0
TSME Dry	10	40	20	10
TSHE Wet	3	33	67	33
ABMAS Dry	3	33	67	0
PSME Moist	5	0	60	0
PSME Dry	5	0	40	0
PIPO-CADE3 Dry	3	33	0	0
PIPO Dry	40	0	20	0
PIPO Moist	3	0	0	0
PIPO-QUGA Dry	1	0	0	0
PIAL-PICO Dry	1	0	0	0
PICO Dry	3	0	0	0
JUOC Dry	2	0	0	0
Total	168	14	50	9

[a] Twenty-one plots on the Ochoco National Forest were habitat typed based on Johnson and Clausnitzer (1992) and then classified into a PAG equivalent. All other plots were classified into PAGs based on Simpson (2007). ABAM = Abies amabilis, ABCO = Abies concolor, ABGR = Abies grandis, ABMAS = Abies magnifica shastensis, CADE3 = Calocedrus decurrens, JUOC = Juniperus occidentalis, PIAL = Pinus albicaulis, PICO = Pinus contorta, PIPO = Pinus ponderosa, PSME = Pseudotsuga menziesii, QUGA = Quercus garryana, TSHE = Tsuga heterophylla, and TSME = Tsuga mertensiana.

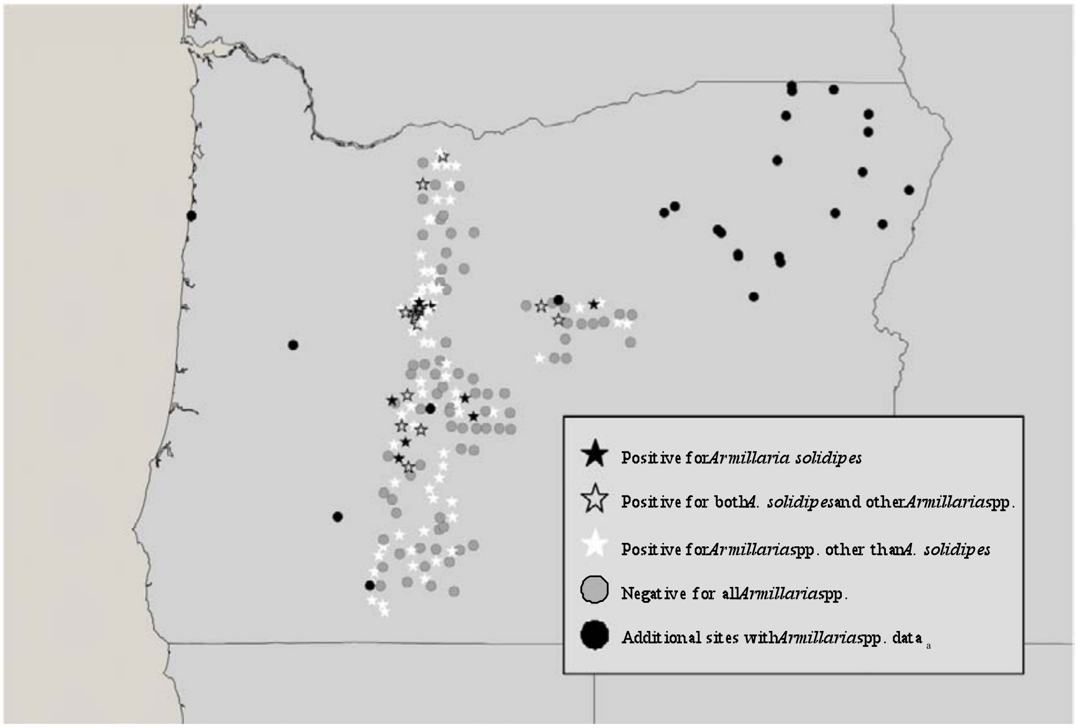

Figure 1. Map of Oregon showing plot locations from 2007 and 2008. Additional sites with Armillaria spp. data suitable for climate modeling (References and/or collector: Ferguson et al. 2003, G.I. McDonald, McDonald et al. 1987, A.L. Smith, and the Intermountain Forest Tree Nutrition Cooperative).

Materials and methods

A total of 168 0.04-ha.plots (119 FY2007 and 49 FY2008) were established across climatically diverse sites in Oregon's East Cascades (e.g., Warm Springs Indian Reservation, Fremont-Winema NF, Deschutes NF, Mt Hood NF, and Ochoco NF). The majority of plots were selected on the basis of climatic diversity and spatial separation across gridded sections (ca. every 7'30" N and 1° 52'30" W). For each tree and shrub species present, primary root systems and butts of three individuals were thoroughly examined, and samples (i.e., rhizomorphs, mycelial fans, rotten wood) of *Armillaria* spp. were collected along with precise location (i.e., latitude, longitude, elevation, slope, and aspect) and associated environmental data (e.g., vegetation type). *Armillaria* spp. isolates were established in culture, then identified with DNA-based techniques (Kim et al. 2006); (tables 1 and 2; and figures 1, 2a, 2b, and 3).

Preliminary results

We identified a total of 36 isolates of *A. solidipes* (NABS I) and 261 isolates of other *Armillaria* spp. using somatic pairing and DNA sequencing methods (table 1). The occurrence of *Armillaria* spp. associated with Plant Association Groups (PAGs) is shown in table 2. Preliminary evidence indicates that the occurrence of different *Armillaria* spp. varies by PAG type (table 2). These surveys will be used to determine suitable climate space for *Armillaria* spp. Once the suitable climate space is determined, the current and potential future distribution of *Armillaria* spp. can be predicted based on interpolated climatic factors across the landscape.

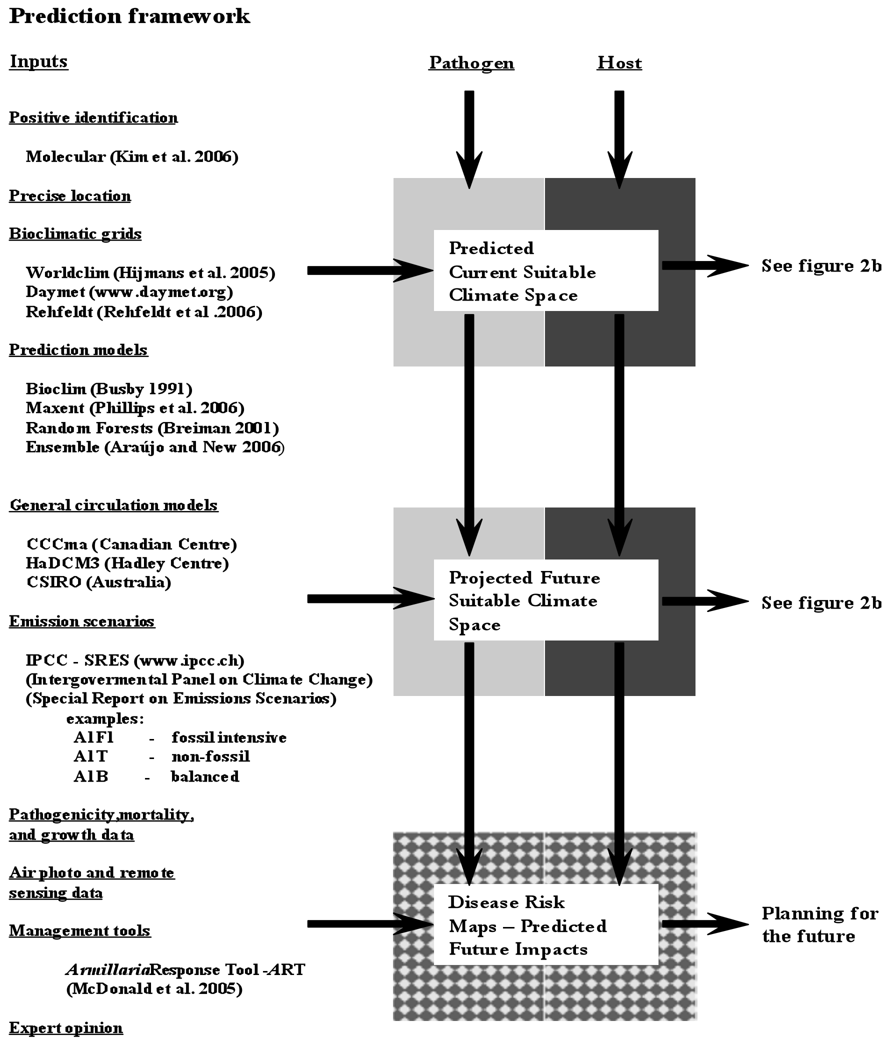

Figure 2a. Prediction framework for determining the impacts of Armillaria root disease in the future.

Future work and refinements

A third field season, to be conducted by the USDA Forest Service Forest Health Protection - Central Oregon Service Center in Bend, OR, is scheduled for 2009 to complete the surveys of Oregon's East Cascades. Continued isolate characterization is also underway at the USDA Forest Service - Rocky Mountain Research Station Forestry Sciences Lab in Moscow, ID. After identification of *Armillaria* spp. isolates is completed, locations confirmed to have *Armillaria* spp. will be used to model suitable climate space (figures 1, 2a, and 2b). This climate window can then be used to predict how various climate change scenarios may affect distribution. Although pathogen distribution may not directly correspond to disease distribution, predictions of pathogen distribution represent an initial step for predicting future disease distribution.

Future tree distribution models show a reduction in suitable climate space for the majority of tree species in the western United States (Rehfeldt et al 2006). In areas where trees become maladapted due to climate change and *A. solidipes* co-exist, it seems reasonable to expect an increase in Armillaria root disease. Weakly pathogenic *Armillaria* spp., also known as saprogens, may also play an increased role in forest disease as trees are stressed by a combination of factors induced by climate change (Boland et al. 2004). The integration of these predictions with other data sources (e.g., pathogenicity, mortality, and growth data) can form a basis for producing or refining National Insect and Disease Risk Maps (figures 2a and 2b). The incorporation of additional data, such as slope, aspect, soil types, and population structure, should improve precision of future predictions. The methods developed from this project can provide a basis for the modeling of other important pathogens. In addition, these predictions can help assess the potential for invasive species to invade new areas under climate-change scenarios. Predictions of Armillaria root disease under future climates are essential for forest management to strategically reduce future impacts of root disease. Similar approaches can be used to mitigate climate-change impacts on other forest diseases.

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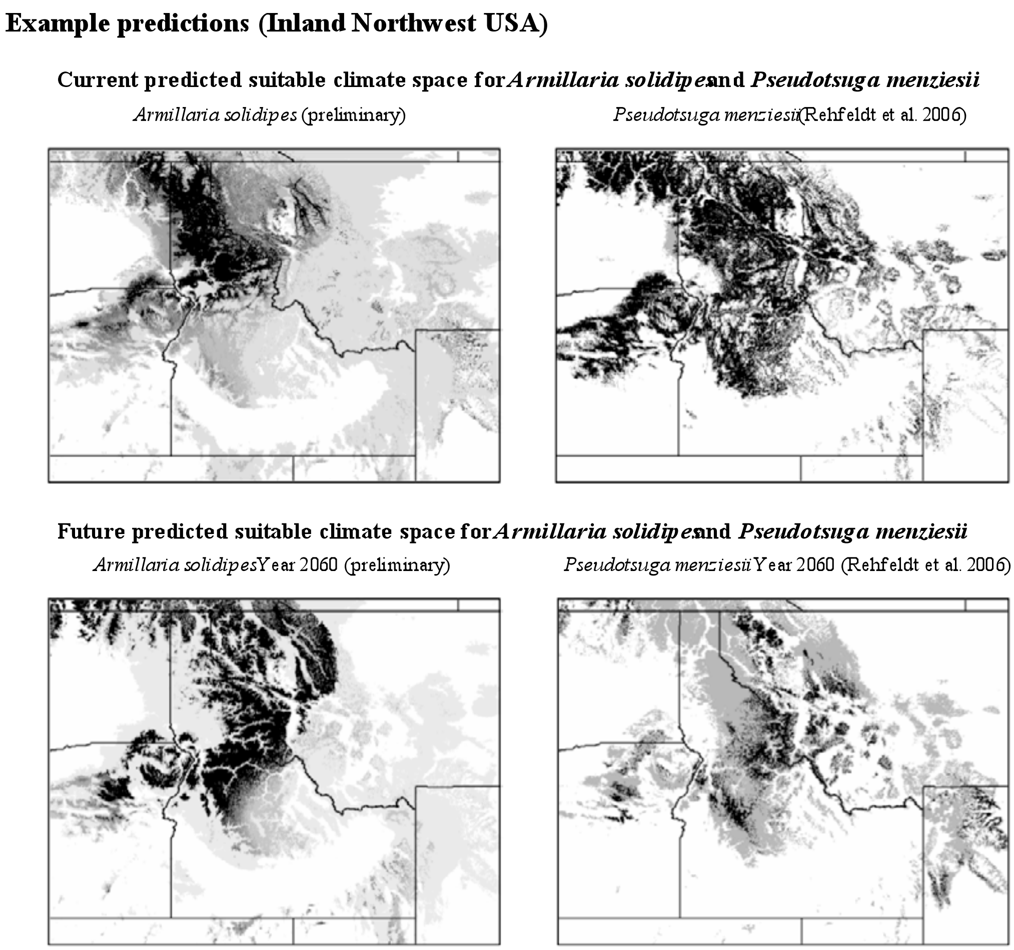

Figure 2b. Preliminary *Armillaria solidipes* predictions for the Inland Northwest, USA, using the Maxent prediction model (based on data from McDonald et al. 1987 and climate surfaces developed by Rehfeldt et al. 2006). The *A. solidipes* predictions are shown on a gradient from black (high suitability) to light grey (low suitability). The *Pseudotsuga menziesii* models use the Random Forest prediction model, black indicates suitable habitat for *Pseudotsuga menziesii* (>75% Random Forest decision tree votes) and grey indicates less suitable habitat (50-75% Random Forest decision tree votes) (Rehfeldt et al. 2006).

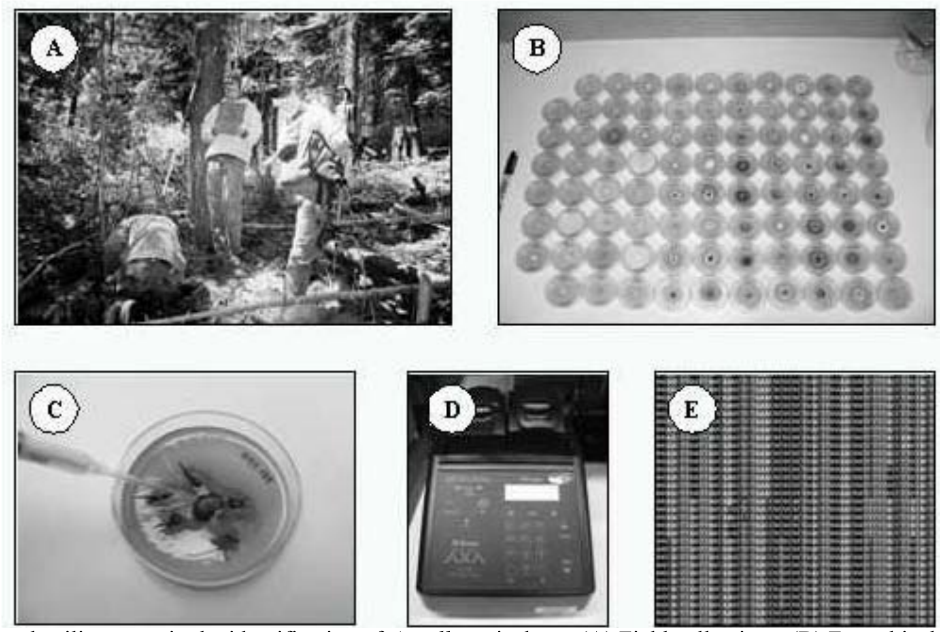

Figure 3. Photos detailing steps in the identification of *Armillaria* isolates. (A) Field collections, (B) Fungal isolation, (C) DNA scrapings, (D) PCR thermocycler, and (E) Data analysis.

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