



Midterm project updates for ongoing *Armillaria* surveys in California: DNA-based identification, bioclimatic modeling, and information for managing *Armillaria* root disease under changing environments

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Introduction

Although *Armillaria* has been previously surveyed in several western states of the USA, little definitive information on *Armillaria* species distribution in California has been provided in the last 20 years (e.g., Baumgartner and Rizzo 2001). Furthermore, it is well established that climate and climate change influence the distribution of *Armillaria* species that cause *Armillaria* root disease, which is a major cause of losses in forest growth and productivity (e.g., Lockman and Kearns 2016; Kim et al. 2021, 2022). This paper details recent progress towards identifying *Armillaria* for subsequent use in bioclimatic modeling to predict the influences of climate and climate change on the distribution of *Armillaria* species in California.

Objectives

The objectives of this project are to (i) culture and/or use DNA sequences to identify *Armillaria* species from collections/surveys across diverse forest areas in California; (ii) use *Armillaria* occurrence data to evaluate and refine bioclimatic models for predicting the present and future suitable climate space (geographic area that is climatically suitable for the species' survival) for representative *Armillaria* species in California; (iii) use bioclimatic models to produce predictive maps for *Armillaria* species to support forest management decisions in relation to *Armillaria* root disease; and (iv) document any new *Armillaria* species/host combinations within California. Resulting bioclimatic models can also be compared with predictive distribution models of important host tree species within the region.

Continued *Armillaria* surveys/collections are needed to supplement under-represented areas for *Armillaria* occurrence across California (Fig.1). To assist in this effort, we are soliciting help from collaborators to conduct surveys within these areas. *Armillaria* samples (e.g., mycelial fans on live trees indicating disease activity, rhizomorphs, and/or fruiting bodies) should be sent to USDA Forest Service RMRS and PNWRS Forest Patholog

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laboratories for identification along with GPS information, associated host/environmental information, and photos.

Methods

Survey, collection, and bioclimatic modeling methods for *Armillaria* follow those as described in Kim et al. (2021, 2023), Hanna et al. (2024), and Hanna et al. (this WIFDWC proceedings volume). Thirty-one locations were used to construct a preliminary example model of potential *A. gallica* distribution based on contemporary bioclimatic data (1970-2000, Fick and Hijmans 2017) using ten replicate runs with the MaxEnt algorithm (Phillips et al. 2006).

Preliminary Results and Discussion

To date, approximately 59 *Armillaria* samples have been identified from California using translation elongation factor 1-alpha (*tef1*) gene sequences (36 *A. gallica*, 10 *A. altimontana*, 5 *A. sinapina*, 6 *A. nabsnona*, and 2 *A. mellea*) (e.g., Ross-Davis et al. 2012; Klopfenstein et al. 2017). Our initial goal for this project is to acquire 30 or more sample locations for each *Armillaria* species to conduct bioclimatic modeling. While species distribution models can be produced using as few as 3-5 locations, sample sizes less than 13-20 are known to potentially decrease model performance (Stockwell and Peterson 2002, Papes and Gaubert 2007, van Proosdij et al. 2016). Our bioclimatic modeling efforts will require expanded *Armillaria* collections within coastal forests from Eureka, CA to the Mexican border. We also hope to obtain *Armillaria* collections within the Trinity, Mendocino, Plumas, Stanislaus, and Sequoia National Forests. Additionally, we currently only have four confirmed samples from southern California where *A. mellea* is presumed to be the most prevalent species. For this reason, we hope to obtain more *A. mellea* samples to allow robust bioclimatic modeling.

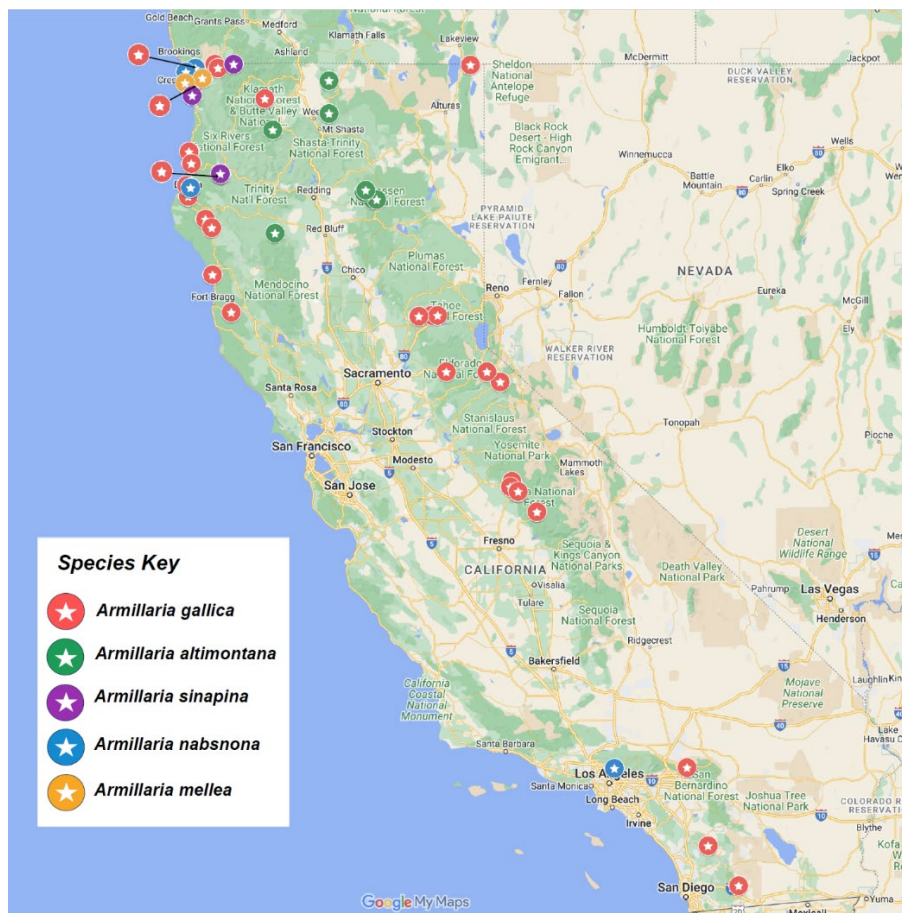


Figure 1. *Armillaria* collections in California identified using translation elongation factor 1-alpha gene sequencing.

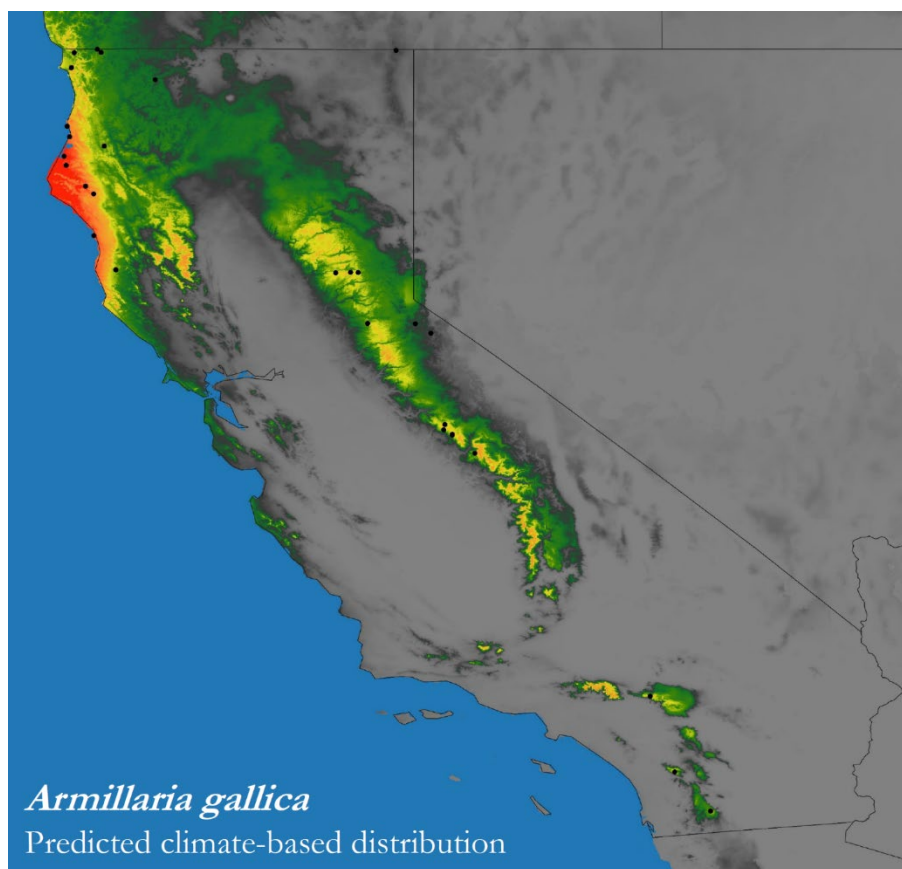


Figure 2. Preliminary bioclimatic model using MaxEnt to predict potential distribution of *Armillaria gallica* in California. Darkest gray represents the predicted empirical MaxEnt climate suitability, with dark green, light green, yellow, orange, and red indicating increased probabilities of climatic suitability, respectively.

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