

## BIOCLIMATIC MODELING OF *ARMILLARIA* SPECIES IN SOUTHEASTERN ALASKA, INCLUDING POTENTIALLY INVASIVE *ARMILLARIA* SPECIES UNDER CHANGING CLIMATE

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### Introduction

Armillaria root disease, caused by several *Armillaria* species, is one of most damaging tree diseases throughout the world (Wargo & Shaw 1985). In southeastern Alaska, both *A. sinapina* and *A. nabsnona* have previously been reported, but these species have generally been considered as weak pathogens or saprophytes under natural conditions in this region (Shaw & Loopstra 1988, Adams et al. 2015). More recently, however, *A. sinapina* has been found in pathogenic situations in Alaska (Klopfenstein et al. 2009a, Adams et al. 2015). In Shaw and Loopstra's (1988) study, they also identified two *Armillaria* spp. (*A. sinapina* and *A. nabsnona*) in addition to unknown *Armillaria* sp. from Alaska, which may represent new species. With the discovery of active and potentially increasing *Armillaria* root disease in Alaska and the possibility of new *Armillaria* species in the region, we investigated potential *Armillaria* species distributions using DNA sequence-based identification coupled with bioclimatic modeling (Klopfenstein et al 2009b, Ross-Davis et al. 2012, Elías-Román et al. 2013, and Klopfenstein et al. 2017).

For bioclimatic modeling for southeastern Alaska, we used point locations from the North American Pacific Northwest (southwestern British Columbia, western Washington, western Oregon, northern California) under the future climate scenario of RCP 8.5 for the year 2085. These models show potential invasive threats posed by *Armillaria* from the Pacific Northwest, should these species become established in southeastern Alaska. While non-native *Armillaria* species have yet to be reported as invasive in North America, reports of European/Asian *A. mellea* and *A. gallica* are documented in the literature for South Africa (Coetzee et al. 2001, Coetzee et al. 2003, Mwenje et al. 2006, Wingfield et al. 2010). Inoculum could obviously arrive via natural migration or on woody material infected with rhizomorphs or mycelial fans, which could potentially arrive undetected at ports of entry. Furthermore, introduction of basidiospores, which have been shown to survive on tree bark through an Alaskan winter (Shaw 1981), would not be readily detectable with current technologies.

### Objectives

- (1) Isolate, culture, and identify *Armillaria* species from surveys/sample collections from georeferenced locations in southeastern Alaska
- (2) Predict current suitable climate space distribution of all species identified in the region
- (3) Project these distributions for future time periods under several climate change scenarios
- (4) Predict potentially invasive *Armillaria* species based on modeled contemporary suitable climate for *Armillaria* species of the Pacific Northwest and predicted future climate in southeastern Alaska

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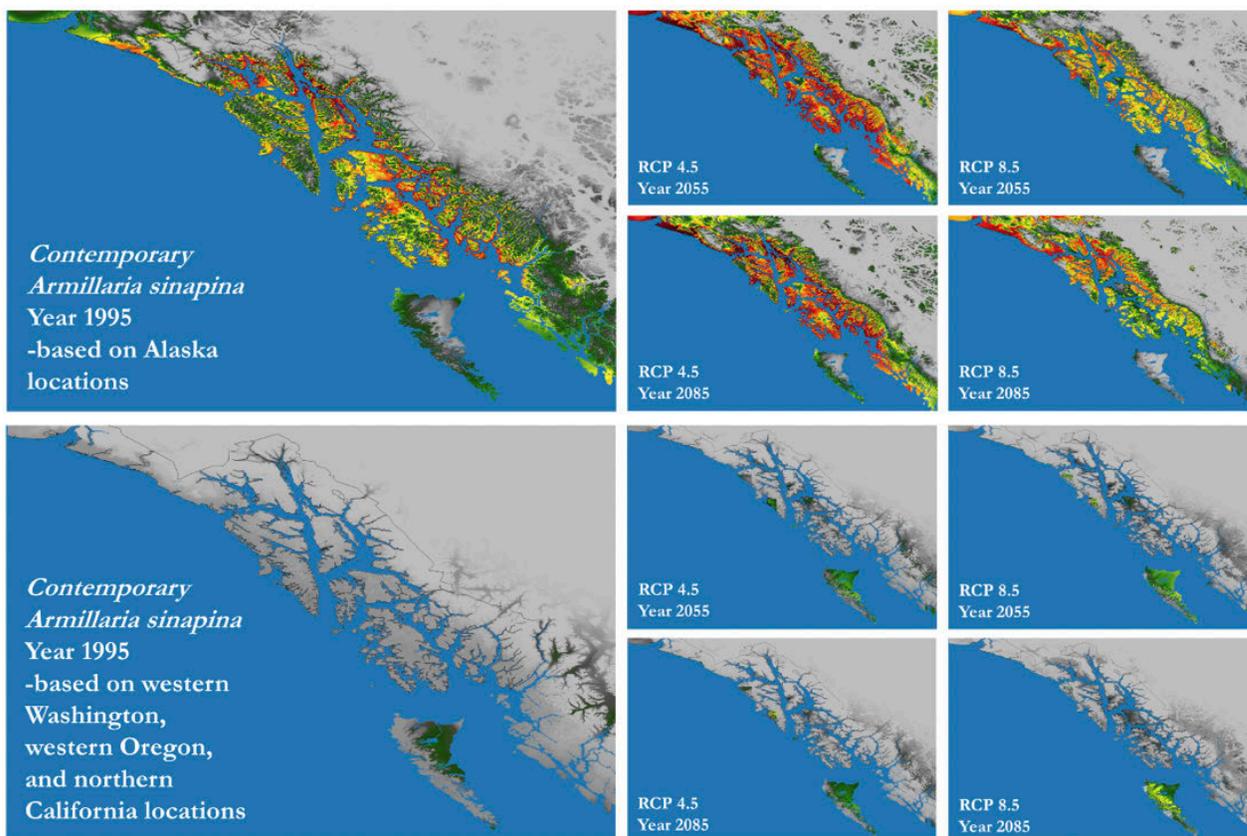
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## Methods

Major roots and butts of trees and shrubs were examined, and samples (i.e., rhizomorphs, mycelial fans, rotten wood) of *Armillaria* species were collected along with precise location information and associated environmental data. Cultured *Armillaria* isolates from southeastern Alaska were then identified based on current DNA sequencing methods (e.g., translation elongation factor 1-alpha: *tef1* gene) as described (Ross-Davis et al. 2012, Elías-Román et al. 2013, and Klopfenstein et al. 2017). Forty-nine collections were made from 2016 to 2018. From positively identified isolates, a dataset of coordinates was created for use in bioclimatic modeling. Duplicate species isolates collected within 0.25 km were eliminated from analyses. After these isolates were eliminated from the analyses, 12 locations for *A. sinapina* were obtained for bioclimatic modeling (Figure 1). A single isolate of *A. nabsnona* was identified from Prince of Wales Island, but this was insufficient for bioclimatic modeling (Figure 2. *A. nabsnona* map). *Armillaria* locations from the Pacific Northwest were used to model potentially invasive *Armillaria* species for this region. For details about the Pacific Northwest isolate numbers and locations used in modeling, please refer to another WIFDWC proceeding paper by Hanna et al. (Maximum entropy-based bioclimatic models predict areas of current and future suitable habitat for *Armillaria* species in western Oregon and western Washington) in this volume.

Models for each *Armillaria* species were created using Maximum Entropy (Maxent) software (Phillips et al. 2006). Input data for Maxent calculations in suitability models consisted of “samples with data” (SWD) files for each species that linked climate variable values for each of 26 bioclimatic variables with geographic coordinates (presence point localities). Additional input into Maxent included sets of interpolation grids (ca. 1-km<sup>2</sup> resolution) for current and projected climate data for North America (CMIP5 scenarios) provided by the AdaptWest Project (Wang et al. 2016). These consisted of a set based on contemporary climate normals for the year 1995 (an average from 1981-2010) and two future sets for year 2055 (average from 2041-2070) and year 2085 (average from 2017-2100). For the future data, we chose a single atmosphere-ocean general circulation model (AOGCM), Hadley Global Environment Model 2 - Earth System (HadGEM2-ES), rather than an ensemble of dissimilar models (Bellouin et al. 2007, Collins et al. 2011, Martin et al. 2011). HadGEM2-ES is one of the eight available datasets from the AdaptWest Project; it fits in the middle of climate model genealogy for CMIP5 (performs similarly to an ensemble) and has been shown to be a top performer for the Pacific Northwest USA (Knutti et al. 2013, Rupp et al. 2013, Wang et al. 2016). The gridded climate layers were unprojected from Lambert Conformal Conic to an acceptable format for Maxent in degrees of latitude and longitude and then clipped to 141° W, 40° N, 120° W, 60° N so that random background points selected by Maxent would be located within the study area of *Armillaria* locations, which is different than the approach used by Hanna et al. (2019). In all, grids for 26 biologically relevant variables, including seasonal and annual means, extremes, growing and chilling degree days, snow fall, potential evapotranspiration, and several drought indices were considered.

Additional settings for each Maxent model included 10 replicates with the bootstrapping method (sampling with replacement) and a 25% test percentage. “Random seed” was also selected. Maxent uses background locations or pseudo-absences to train the models. Background points for each model were created from 10,000 randomly selected geographical locations within the geographic range of the collected isolates. Maxent’s cumulative output (an index of probability from 0 to 100) was chosen for easier conceptualization compared to Maxent’s raw exponential model. Two separate contemporary (year 1995) models (and four corresponding future projections for each – year 2055 and 2085 x RCP 4.5 and RCP 8.5) based on the 12 *A. sinapina* locations from southeastern Alaska and based on *A. sinapina* locations from the Pacific Northwest are shown in Figure 1. To investigate potential invasiveness of *Armillaria* species into southeastern Alaska, the same future-climate models were run for the five other species locations of the Pacific Northwest, but only year 2085 – RCP 8.5 (Figure 2).

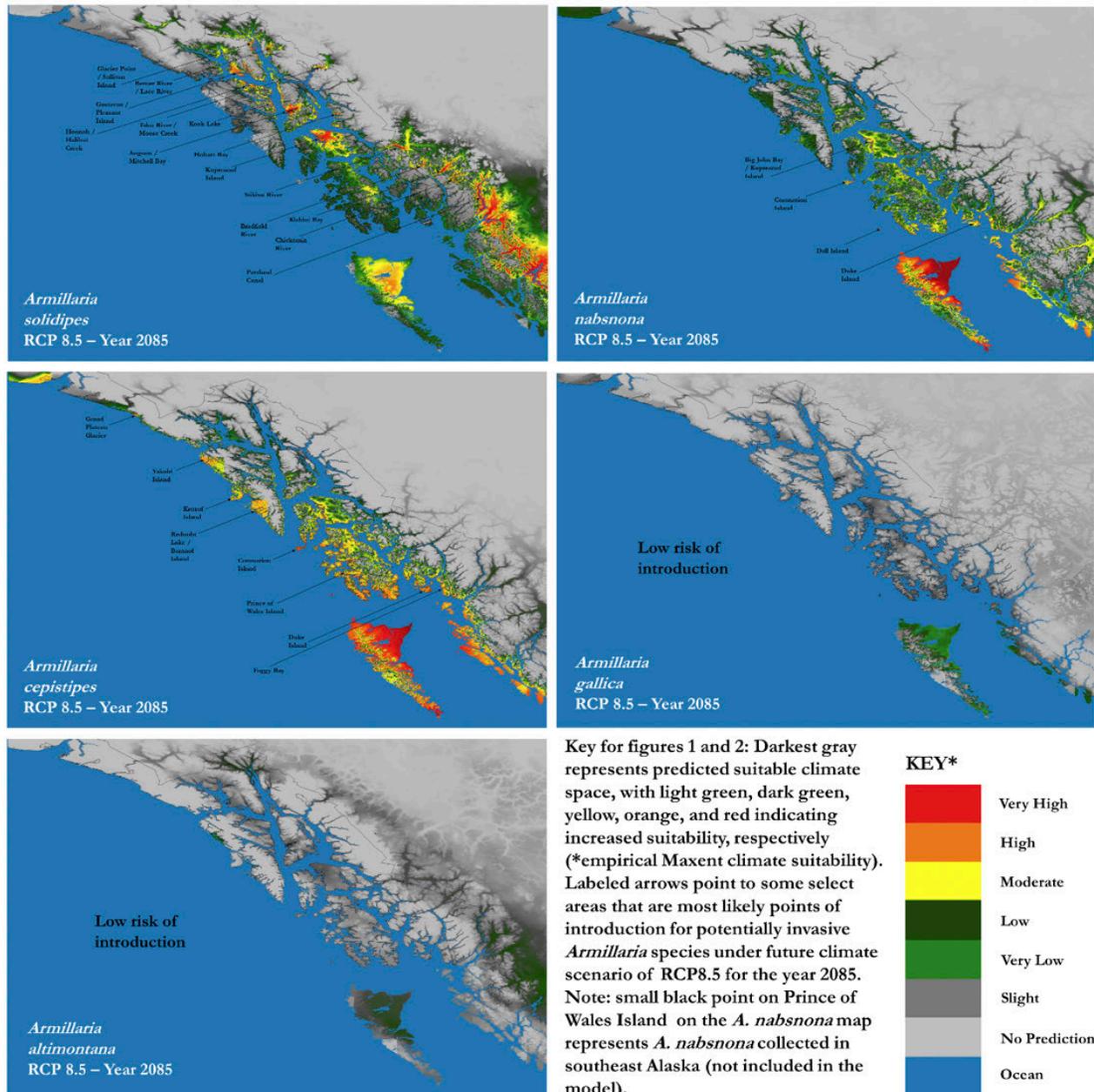


**Figure 1:** Modeled suitable climate for *Armillaria sinapina* based on southeastern Alaska locations (top) versus based on northern California, western Oregon, and western Washington locations (bottom). Does this show populations adapted to different climate niches or does *A. sinapina* have a great ability to adapt to dissimilar climates? (Note: see Figure 2 for KEY).

## Results and Discussion

Our surveys from 2016 – 2018 in southeastern Alaska yielded 49 sample collections. Using DNA sequences of the *tef1* gene, 32 isolates were confirmed as *A. sinapina* and one isolate as *A. nabsnona*. This result confirms previous surveys that showed these *Armillaria* species are present in southeastern Alaska (e.g., Klopfenstein et al. 2009a, Shaw & Loopstra 1988).

Results were limited by the low number of occurrence locations for three of the six Pacific Northwest *Armillaria* species (13 occurrence locations for *A. altimontana*, *A. cepistipes*, and *A. nabsnona*) and only 12 occurrence locations for *A. sinapina* from southeastern Alaska. However, Maxent has been shown to be one of the best performing models based on limited presence data (Wisz et al. 2008). Pearson et al. (2007) had successful results with as few as five occurrence records while Proosdij et al. (2016) indicated 13 occurrence records as a minimum to model “widespread” species. AUC [Area Under the ROC (Receiver Operating Characteristics) Curve] values 0.5 to 0.6 represent a failed model while 0.6 to 0.7 is poor, 0.7 to 0.8 is fair, 0.8 to 0.9 is good and 0.9 to 1 is excellent (Swets 1988). The AUC performance measure of the model from the 12 southeastern Alaska *A. sinapina* locations had a value of 0.988 (excellent). The Pacific Northwest model AUC values were *A. altimontana* = 0.970 (excellent), *A. cepistipes* = 0.973 (excellent), *A. gallica* = 0.986 (excellent), *A. nabsnona* = 0.969 (excellent), *A. sinapina* = 0.977 (excellent), and *A. solidipes* = 0.981 (excellent).



**Figure 2:** Potential *Armillaria* species invasiveness based on a relatively high climate-change scenario (RCP8.5 for the years 2085). Bioclimatic model predictions are based on current *Armillaria* occurrences in southern British Columbia, western Oregon, and western Washington.

Based on our model results, *A. sinapina* in southeastern Alaska appears to exist under significantly different climatic conditions than *A. sinapina* in the Pacific Northwest (Figure 1). *Armillaria sinapina* from the Pacific Northwest does not appear to have much suitable climate space in the southeastern Alaska region even when we look at the high climate-change scenario (RCP 8.5 for the year 2085). At this point, we can only speculate as to whether these results indicate that *A. sinapina* comprises different populations that are adapted to different climates or a high adaptability for climate within *A. sinapina*. Also, of note is climatic conditions in southeastern Alaska are predicted to greatly expand suitable climate space for *A. sinapina* by the year 2055 under the RCP 4.5 scenario, and this trend continues into 2085. Under the RCP 8.5 scenario, suitable climate space for *A. sinapina* is reduced in the south but increased in the north.

Based on the modeling of *Armillaria* species locations from the Pacific Northwest, the models show *A. nabsnona*, *A. cepistipes*, and *A. solidipes* all appear to have locations with suitable climate for survival in southeastern Alaska by the year 2085. And, perhaps unfortunately, we predict that future suitable climate space for *A. altimontana*, a potential biocontrol against *A. solidipes* (Warwell et al. 2019), will not exist within this region under the projected future climate scenario. Adding to this scenario, host trees may also be more susceptible to pathogenic *Armillaria* spp. due to maladaptive stress in a new environment under changing climate.

### Acknowledgements

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