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Compiled by:

Gregory J. Reynolds
USDA Forest Service
Forest Health Protection
Albuquerque, New Mexico

Nicholas P. Wilhelmi
USDA Forest Service
Forest Health Protection
Flagstaff, Arizona

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Natural Resources Research Library
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MOLECULAR IDENTIFICATION AND CHARACTERIZATION OF ROOT DISEASES IN THE WESTERN USA

Rachael A. Sitz[1,2], John W. Hanna[1], Jane E. Stewart[2], Mee-Sook. Kim[3], Phil G. Cannon[4], Brent W. Oblinger[5], Jim T. Blodgett[6], John C. Guyon[7], Liz G. Hebertson[7], Robin L. Mulvey[8], Doug J. Westlind[3], Josh J. Bronson[9], Amy C. Ramsey[10], Sara M. Ashiglar[11], Melissa J. Fischer[12], Bill Woodruff[13], Greg J. Reynolds[14], and Ned B. Klopfenstein[1]

Introduction

Root diseases cause extensive damage to forests in the western USA (Blodgett et al. 2015). However, despite their abundance and economic impact (Lockman et al. 2016), we know very little about the identity and distribution of some pathogens responsible for these diseases. Our project addresses this knowledge gap by characterizing root pathogens in forests of the western USA (Kim et al. 2006) and has the potential to result in updated distribution maps, bioclimatic models, as well as first reports.

Materials and Methods

Forest Health Specialists in the western USA were asked to collect samples of diverse root diseases. In 2018, a total of 204 root disease samples were collected from AK, CA, CO, NM, OR, SD UT, and WA by 16 professionals (Figure 1). Root disease samples were cultured to isolate the pathogen, and identified to species using DNA-based technology.

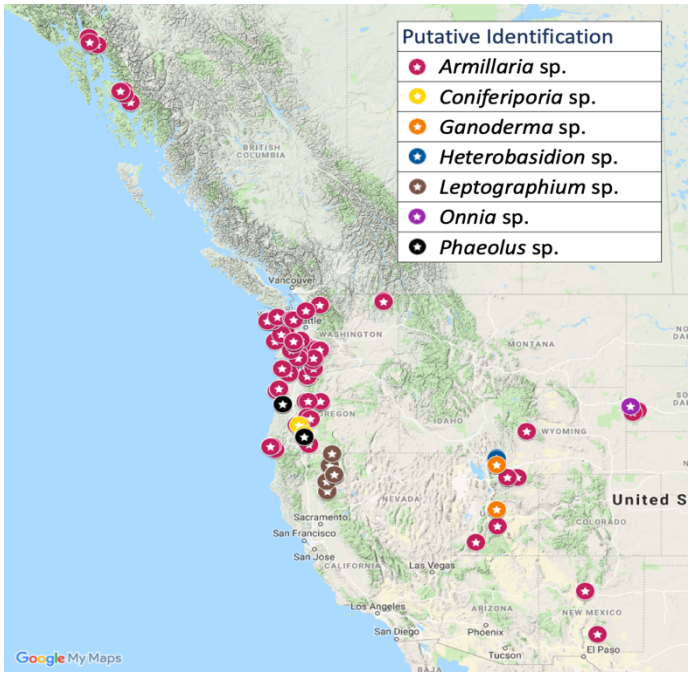

Figure 1: *Map showing the collection locations for the 2018 root disease samples sent to the laboratory for culturing and DNA-based identification.*

Results and Discussion

In total, 228 samples were obtained, yielding 116 successful cultures. Armillaria Root Disease (ARD) comprised the majority of samples (Figure 2), confirming that it is a major root disease in the western USA. DNA sequence-based identification, although in its initial stages, identified several ARD samples as *Armillaria solidipes* (= *A. ostoyae*), and other *Armillaria* spp. were confirmed. Black stain root disease (*Leptographium wagneneri*) was the next most

[1]USFS Rocky Mountain Research Station, Moscow, ID. [2]Colorado State University, Department of Bioagricultural Sciences and Pest Management, Fort Collins, CO. [3]USFS Pacific Northwest Research Station, Corvallis, OR. [4]USFS Forest Health Protection (FHP), Region 5, Vallejo, CA. [5]USFS FHP Region 6, Bend, OR. [6]USFS FHP Region 2, Rapid City, SD. [7]USFS FHP Region 4, Ogden, UT. [8]USFS FHP Region 10, Juneau, AK. [9]USFS FHP Region 6, Central Point, OR. [10]Washington State Department of Natural Resources, Olympia, WA. [11]Washington State Department of Fish and Wildlife, Clarkston, WA. [12]Washington State Department of Natural Resources, Colville, WA. [13]USFS FHP Region 5, Susanville, CA. [14]USFS FHP Region 3, Albuquerque, NM

commonly sampled pathogen, but the methods employed to culture this pathogen were unsuccessful. Much less abundant in our samples are root diseasescaused by *Coniferiporia* (formerly *Phellinus*), *Heterobasidion*, *Phaeolus*, *Onnia*, and unknown pathogens. Overall, the success rate was highly variable for establishing pathogen isolates in culture. The pathogen, type of sample, storage conditions, and time stored before isolation likely influenced the success of pathogen isolations.

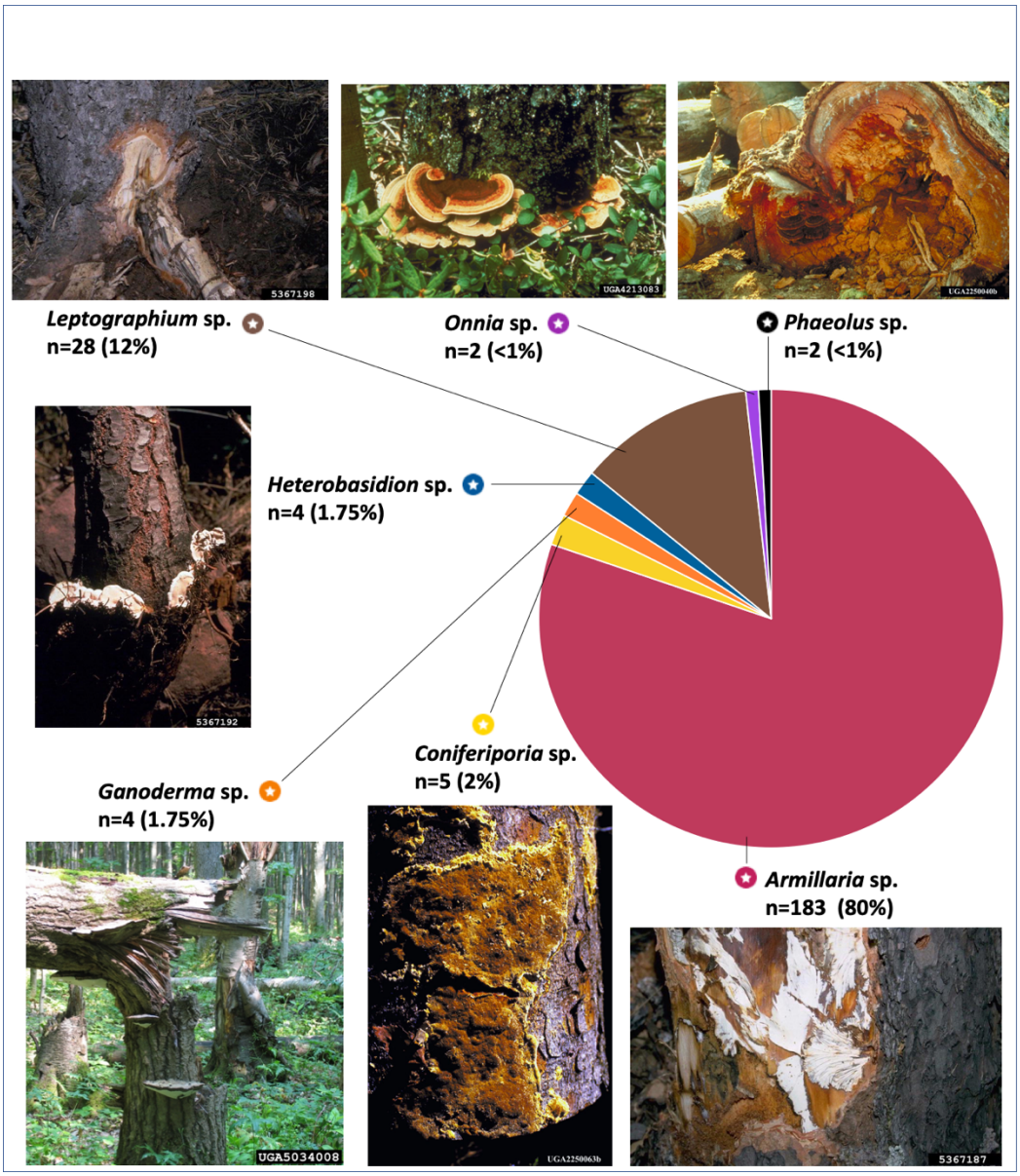

Figure 2: *Pie chart showing the relative proportion of samples obtained that are presumably caused by the fungal genera pictured. Colors indicate different genera and coordinate with the map legend in Figure 1. Photos were obtained from Bugwood Image Database System and include:* Armillaria *spp. William Jacobi Colorado State University 5367187,* Heterobasidion annosum *Mike Schomaker Colorado State Forest Service 5367192,* Phaeolus schweinitzii *USFS Northern and Intermountain region UGA2250040b,* Onnia tomentosa *Minnesota Department of Natural Resources UGA4213083,* Ganoderma *Joseph Obrien USFS UGA5034008,* Coniferiporia weirii *USFS Northern and Intermountain region UGA2250063B, and* Leptographium wageneri*, William Jacobi, Colorado State University 5367198.*

Conclusions

In the upcoming 2019 field season, adjustments such as expediting the time from sample collection to pathogen isolation and using alternate culturing techniques may impact results, especially for difficult-to-isolate pathogens such as *Leptographium*. Moving forward, ARD samples will be used to strengthen previous bioclimatic models of ARD in the western USA. Ultimately, this project will continue to expand upon our knowledge of the fungal species causing root diseases in the western USA and their distributions.

Acknowledgements

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