Phylogenetics and host distribution of Armillaria in riparian ecosystems of the northern Great Plains

Conference Paper · May 2020

8 authors, including:


Shawn McMurtrey
Oregon State University
2 PUBLICATIONS **0** CITATIONS
SEE PROFILE

Brandon C. Alveshere
University of Connecticut
5 PUBLICATIONS **41** CITATIONS
SEE PROFILE

Patrick Ian Bennett
US Forest Service
8 PUBLICATIONS **12** CITATIONS
SEE PROFILE


Mee-Sook Kim
USDA Forest Service Pacific Northwest Research Station
155 PUBLICATIONS **1,390** CITATIONS
SEE PROFILE

Proceedings of the 66th Western International Forest Disease Work Conference

YMCA of the Rockies, Ram's Horn Lodge
Estes Park, Colorado
June 3-7, 2019

Proceedings of the 66th Western International Forest Disease Work Conference

YMCA of the Rockies, Ram's Horn Lodge
Estes Park, Colorado
June 3-7, 2019

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

Patsy Palacios
Natural Resources Research Library
Quinney College of Natural Resources
Utah State University
Logan, Utah

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.

Citation:
Reynolds, G.J., Wilhelmi, N.P., and Palacios, P (comps.). 2020. Proceedings of the 66th Western International Forest Disease Work Conference, Estes Park, Colorado, 3-7 June 2019.

Special Thanks for Photos go to:
Alex Woods
Greg Reynolds
Kelly Burns
Susanna Keriö

PHYLOGENETICS AND HOST DISTRIBUTION OF *ARMILLARIA* IN RIPARIAN FORESTS OF THE NORTHERN GREAT PLAINS

Shawn B. McMurtrey[1], Brandon C. Alveshere[2], Patrick I. Bennett[1,3], Mee-Sook Kim[4], John W. Hanna[5], Ned B. Klopfenstein[5], James T. Blodgett[6], and Jared M. LeBoldus[1, 7]

Abstract

Root disease pathogens, including *Armillaria* (Fr.) Staude*,* are a leading cause of growth loss and mortality of trees in forest ecosystems of North America (Lockman & Kearns 2016). This panglobal fungus can cause significant reductions in tree growth that can lead to mortality. *Armillaria* spp. have a wide host range, and they also play a vital ecological role in the carbon cycling process via wood decomposition (Raabe 1962, Baumgartner et al. 2011, Heinzelmann et al. 2019). As a native root-disease fungus, *Armillaria* spp. are among the oldest and largest known living organisms on Earth (Ferguson et al. 2003). Armillaria root disease has been found in every region of the United States. Currently, 11 species of *Armillaria*/*Desarmillaria* are known to occur in North America (Kim et al. 2006, Klopfenstein et al. 2017, Elías-Román et al. 2018), each with different ecological roles from pathogenic to saprophytic. Very little work has been done identifying and characterizing the distribution of *Armillaria* spp. in the northern Great Plains region, although *A. gallica* Marxm. & Romagn was previously identified in association with diverse hardwood species in the Niobrara Valley Preserve in Nebraska (Kim & Klopfenstein 2011).

Phylogenetic analyses provide a better understanding of taxonomic relationships among *Armillaria* species, which facilitates mapping spatial distributions and host associations for insights into *Armillaria* ecology. The objectives of this study were to: 1) provide baseline information on *Armillaria* species that are present in the northern Great Plains region; and 2) determine geographic distribution of host trees that are associated with the *Armillaria* species. A broad goal of this study is to provide important missing data that might assist with updating root disease risk maps. Isolates were collected from 78 out of 101 sites surveyed. Host species was recorded, and each tree was inspected for signs/symptoms of root disease (killing of the cambium in a live tree) and butt rot (degrading inner wood in a live tree) (Williams et al. 1986). A total of 57 *Armillaria* isolates were sequenced from 12 different host tree species from sites in North Dakota, South Dakota, and Nebraska. Identification of *Armillaria* isolates was accomplished by comparing nucleotide sequences from the translation elongation factor 1-alpha (*tef1*) gene. All 57 isolates had a >98% general consensus match to *A. gallica*. The locations of *A. gallica* were then mapped (Figure 1). A phylogenetic tree was constructed using maximum-likelihood (ML) algorithms (Figure 2). Statistical support for the branch topology was calculated from 1,000 bootstrap replicate trees. *Armillaria gallica* has a wide host range and geographic distribution, and it is much more widespread in the northern Great Plains region than previously recognized.

---

[1]Department of Botany and Plant Pathology, Oregon State University, Corvallis, Oregon, USA. [2]College of Agriculture, Department of Natural Resources and the Environment, University of Connecticut, Storrs, Connecticut, USA. [3]USDA Forest Service, Forest Health Protection, Northern and Intermountain Regions, Missoula, Montana, USA. [4]USDA Forest Service Pacific Northwest Research Station, Corvallis, Oregon, USA. [5]USDA Forest Service Rocky Mountain Research Station, Moscow, Idaho, USA. [6]USDA Forest Service, Forest Health Protection, Rocky Mountain Region, Rapid City, South Dakota, USA. [7]Department of Forest Engineering, Resources, and Management, Oregon State University, Corvallis, Oregon, USA

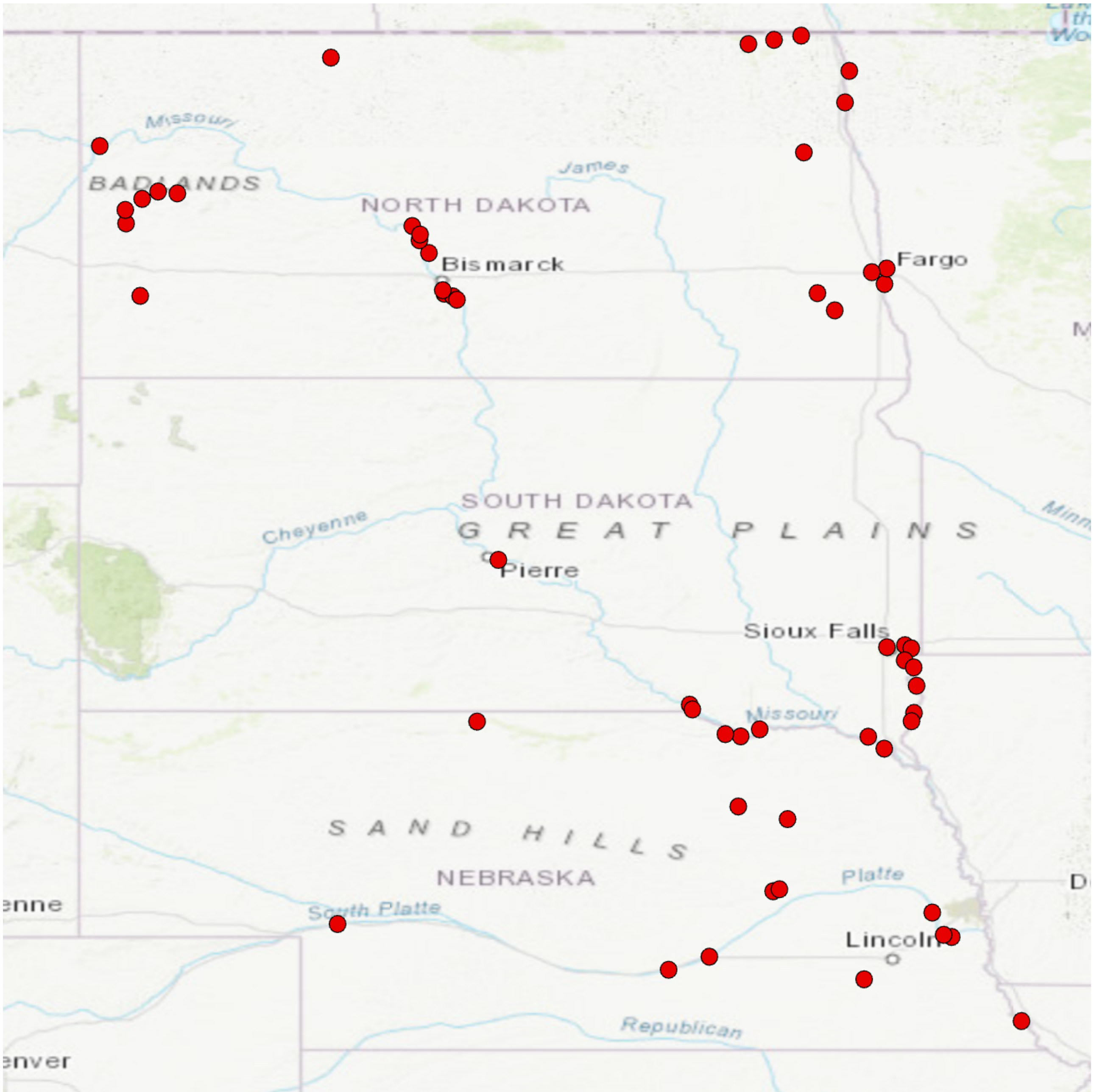

Figure 1: *This map depicts the 57 locations where* Armillaria gallica *was found. Each isolate that was sequenced had pairwise identity matches with* A. gallica *at a > 98% match using translation elongation factor 1-alpha gene comparison.*

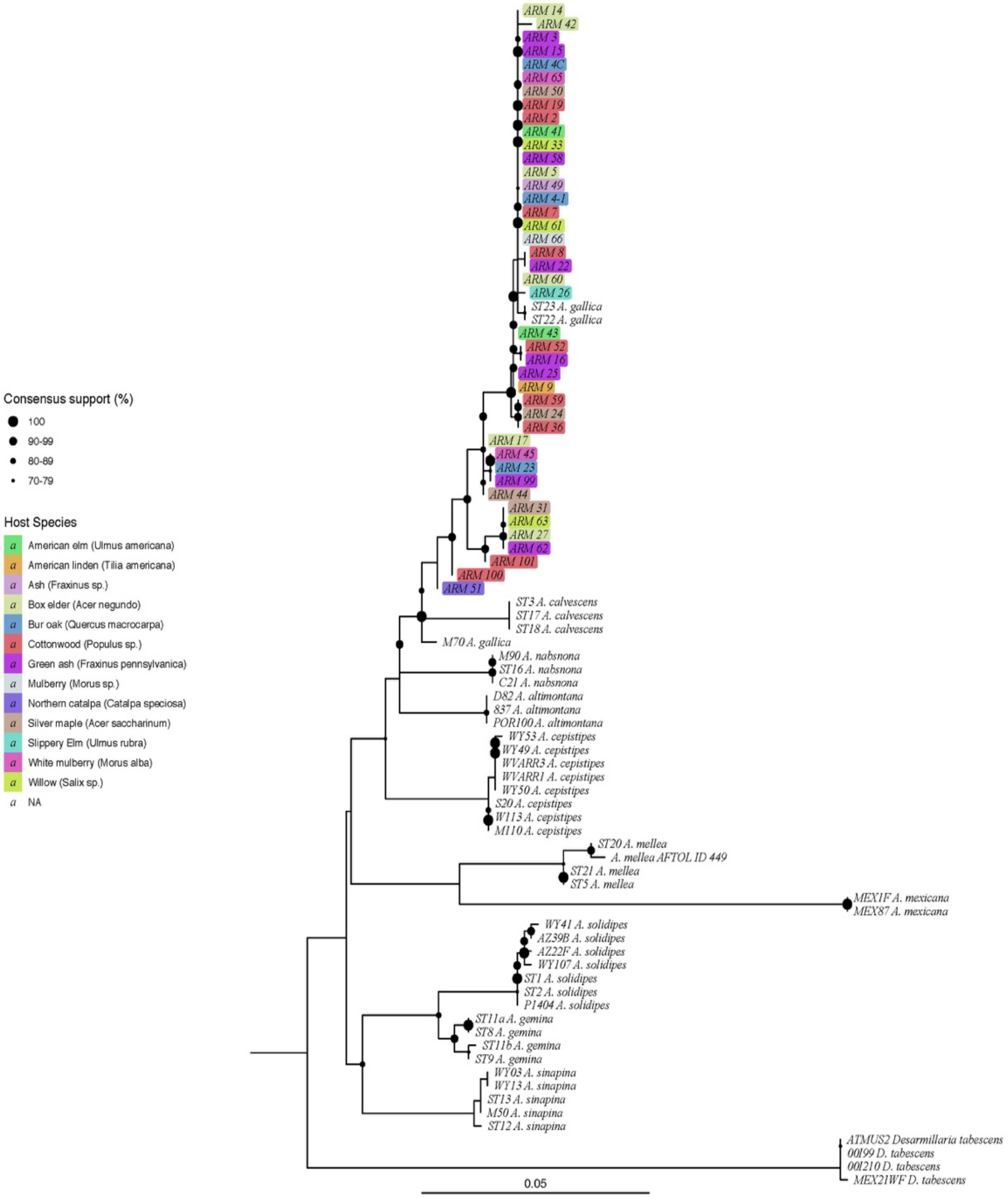

Figure 2: *Phylogenetic trees were constructed using maximum-likelihood (ML) algorithms, and statistical support for the branch topology was calculated from 1,000 bootstrap replicate trees. Colors represent host species shown in the legend. The sizes of the circles at nodes represent bootstrap support. Only values > 70% are shown. This phylogenetic tree shows 42 of the 57 isolates that were sequenced.*

Literature Cited

Baumgartner, K., Coetzee, M.P.A., Hoffmeister, D. (2011). Secrets of the subterranean pathosystem of *Armillaria*. *Molecular Plant Pathology, 12(6), 515–534. https://doi.org/10.1111/j.1364-3703.2010.00693.x*

Elías-Román, R.D., Medel-Ortiz, R., Alvarado-Rosales, D., Hanna, J.W., Ross-Davis, A.L., et al. (2018). *Armillaria mexicana*, a newly described species from Mexico. *Mycologia, 110(2), 347-360. Armillaria mexicana, a newly described species from Mexico*

Ferguson, B.A., Dreisbach, T.A., Parks, C.G., Filip, G.M., Schmitt, C.L. (2003). Coarse-scale population structure of pathogenic *Armillaria* species in a mixed-conifer forest in the Blue Mountains of northeast Oregon. *Canadian Journal of Forest Research, 33(4), 612-623. https://doi.org/10.1139/x03-065*

Heinzelmann, R., Dutech, C., Tsykun, T., Labbé, F., Soularue, J.-P., et al. (2019). Latest advances and future perspectives in *Armillaria* research. *Canadian Journal of Plant Pathology, 41(1), 1-23. https://doi.org/10.1080/07060661.2018.1558284*

Kim, M.-S., Klopfenstein, N.B. (2011). Molecular identification of *Armillaria gallica* from the Niobrara Valley Preserve in Nebraska. *Journal of Phytopathology, 159(1), 69-71. https://doi.org/10.1111/j.1439-0434.2010.01718.x*

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(3), 145–164. https://doi.org/10.1111/j.1439-0329.2006.00441.x*

Klopfenstein, N.B., Stewart, J.E., Ota, Y., Hanna, J.W., Richardson, B.A., et al. (2017). Insights into the phylogeny of Northern Hemisphere *Armillaria*: Neighbor-net and Bayesian analyses of translation elongation factor 1-α gene sequences. *Mycologia, 109(1), 75-91. https://doi.org/10.1080/00275514.2017.1286572*

Lockman, I.B., Kearns, H.S.J., eds. (2016). *Forest Root Diseases Across the United States.* Gen. Tech. Rep. RMRS-GTR-342. Ogden, UT: USDA, Forest Service, Rocky Mountain Research Station. 55 p.

Raabe, R.D. (1962a). Host list of the root rot fungus, *Armillaria mellea*. *Hilgardia, 33, 25-88. https://dx.doi.org? 10.3733/hilg.v33n02p025*

Williams, R.E., Shaw, C.G, III, Wargo, P.M., Sites, W.H. (1986). *Armillaria Root Disease*. Forest Insect & Disease Leaflet 78. Washington D.C.: USDA, Forest Service. 8 p.