

Bioclimatic model-based predictions of potential distributions for four forest root disease pathogens under changing climates in western North America

Duncan R. Kroese¹, Daram Choi^{1, 2}, David C. Shaw², Patrick I. Bennett³, Ned B. Klopfenstein³, and Mee-Sook Kim¹

Introduction:

Root diseases are a major cause of conifer damage in forests of western North America. Two major root diseases in the region, which are caused by native pathogens, are laminated root rot (LRR) disease of Douglas-fir (*Pseudotsuga menziesii*) caused by *Coniferiporia sulphurascens* (Agne et al. 2018; Lockman and Kearns 2016; Thies and Sturrock, 1995), and black stain root disease (BSRD) caused by three fungal pathogens: *Leptographium wageneri* on single-leaf pinyon pine (*Pinus monophylla*) and pinyon pine (*P. edulis*), *L. ponderosum* on ponderosa pine (*P. ponderosa*) and Jeffrey pine (*P. jeffreyi*), and *L. pseudotsugae* on Douglas-fir (Choi et al. 2023).

As the climate changes, suitable climate spaces (potential distribution) for both hosts and pathogens will likely shift (e.g., Kim et al. 2021). Changes in climate that result in increased frequency/intensity of drought and severe heat are also likely to increase forest host stress and damage from root disease (Chmura et al. 2011; Murray and Leslie 2021; Kim et al. 2021). Management options are limited for forest root diseases; however, forest managers can use information about potential distributions of LRR and BSRD pathogens to address these root diseases. This information can be obtained by identifying geographic areas where hosts and pathogens are likely to co-occur based on climatic variables under contemporary and projected future climate scenarios. Establishing and monitoring potential LRR and BSRD risk maps that show potential distributions of pathogens and hosts under contemporary and projected future climates provides critical information to forest managers for minimizing future damage from both root diseases.

Materials and Methods:

Maximum entropy modeling (Maxent version 3.4.4) was performed using presence-only occurrence points (Phillips et al. 2006) for pathogens and hosts. DNA sequence-confirmed, georeferenced location data were used for pathogens: *C. sulphurascens* (N = 50), *L. wageneri* (N=12), *L. ponderosum* (N=10), and *L. pseudotsugae* (N=38). Host location data were obtained from USDA Forest Service, Forest Inventory and Analysis: single-leaf pinyon pine (N=5,219), ponderosa pine and Jeffrey pine (N=29,067), and Douglas-fir (N=45,005). Models were run using 19 bioclimatic variables from WorldClim v2.1 (Fick and Hijmans 2017) at 30-second (ca. 1 km) spatial resolution.

Contemporary (1970-2000) modeling was performed for BSRD (*L. wageneri* – single-leaf pinyon pine; *L. pseudotsugae* – Douglas-fir; *L. ponderosum* – ponderosa pine/Jeffrey pine) and LRR (*C. sulphurascens* – Douglas-fir) (Figs. 1 and 2). Projected future scenarios for *C. sulphurascens* and Douglas-fir (2041-2060 and 2081-2100) modeling was also performed, using Goddard Institute for Space Studies (GISS-E2.1) global climate model (Kelley et al. 2020) under two different shared socioeconomic pathways (SSPs): SSP2-4.5 (a “middle of the road” scenario where trends follow historic patterns in development, energy use, and greenhouse gas emissions) and SSP5-8.5 (a world of rapid, unconstrained growth in economic output, energy use, and greenhouse gas emissions) (Fig. 2).

¹USDA Forest Service – Pacific Northwest Research Station, Corvallis, OR 97331, USA

²Oregon State University, Department of Forest Engineering, Resources & Management, Corvallis, OR 97331, USA

³USDA Forest Service – Rocky Mountain Research Station, Moscow, ID 83843, USA

Conclusions:

For all contemporary models, considerable overlap is evident for the predicted suitable climate spaces of each root disease pathogen and their corresponding hosts (Figs. 1 and 2). However, predicted suitable climate spaces for each host are typically larger than that of their pathogens. Geographic areas with predicted climate suitability for the host but not pathogen represent areas where forest managers should expect fewer root disease outbreaks caused by the respective pathogen.

The future scenarios show a significant reduction in suitable climate spaces for both the LRR pathogen and host (Douglas-fir), with a loss of suitable climate spaces in lower elevation, inland areas. While the areas with suitable climate space were diminished, some predicted suitable climate areas overlap for LRR pathogen and host, and these areas appear suitable for LRR development (Fig. 2).

Maxent modeling has demonstrated potential as a valuable tool for guiding forest disease management (Kim et al. 2021). However, Maxent modeling is not without limitations, such as overfitting of models with relatively few occurrence points (Phillips et al. 2006), as could be reflected in the limited availability of presence data for the LRR and BSRD pathogens. And, while a large amount of information on climatic conditions are encompassed in the bioclimate variables used, other environmental conditions, such as water drainage, soil characteristics, slope, elevation, etc., may also influence the distribution of root disease pathogens, hosts, and resulting diseases.

For better informed management decisions, more DNA sequence-verified occurrence points of the LRR and BSRD pathogens would increase the predictive power of these bioclimatic models, and predictive modeling of other host species of *C. sulphurascens*, such as mountain hemlock (*Tsuga mertensiana*), grand fir (*Abies grandis*), and white fir (*A. concolor* and *A. concolor* x *grandis*), would also benefit from more verified occurrence points for each host species.

Though disease management options are limited, predicted overlapping distributions of the hosts and pathogens represent areas for targeting present and future forest management actions, such as reducing site disturbances, planting or favoring of less susceptible tree species, or other silvicultural treatments to reduce pathogen spread.

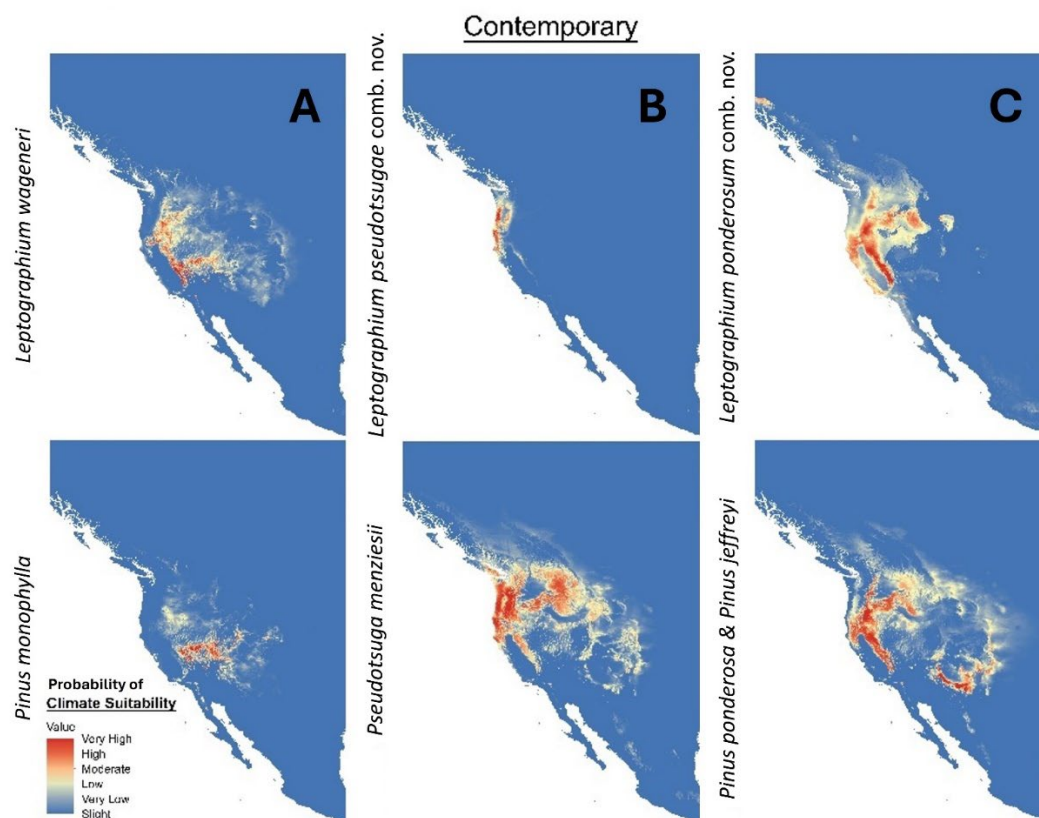


Fig. 1: Maxent bioclimatic predictive models under a contemporary scenario (1970-2000) for black-stain root disease: *Leptographium wageneri* and single-leaf pinyon pine (*Pinus monophylla*) (A), *L. pseudotsugae* and Douglas-fir (*Pseudotsuga menziesii*) (B); and *L. ponderosum* and ponderosa pine/Jeffrey pine (*P. ponderosa*/*P. jeffreyi*) (C).



Fig. 2: Maxent bioclimatic predictive models under five climate scenarios [Left to right: Contemporary (1971-2000), 2041-2060 SSP2-4.5, 2081-2100 SSP2-4.5, 2041-2060 SSP5-8.5, and 2081-2100 SSP5-8.5] for laminated root rot disease: host Douglas-fir (*Pseudotsuga menziesii*) (A) and pathogen (*Coniferiporia sulphurascens*) (B).

Acknowledgments:

Funding: USDA Forest Service (FS) - Western Wildland Environmental Threat Assessment Center and USDA FS, Forest Health Protection – Special Technology and Development Program (STDP R5-2020-03). Findings and conclusions are those of the authors and should not be construed to represent any official USDA determination or policy.

Literature Cited:

- Agne, M.C., Beedlow, P.A., Shaw, D.C., Woodruff, D.R., Lee, E.H., Cline, S.P., Comeleo, R.L. 2018. Interactions of predominant insects and diseases with climate change in Douglas-fir forests of western Oregon and Washington, U.S.A. *Forest Ecology and Management* 409: 317-322.
- Chmura, D.J., Anderson, P.D., Howe, G.T., Harrington, C.A., Halofsky, J.E., Peterson, D.L., Shaw, D.C., St Clair, B.J. 2011. Forest responses to climate change in the northwestern United States: ecophysiological foundations for adaptive management. *Forest Ecology and Management* 261: 1121-1142.
- Choi, D., Harrington, T.C., Shaw, D.C., Stewart, J.E., Klopfenstein, N.B. Kroese, D.R., Kim, M.-S. 2023. Phylogenetic analyses allow species-level recognition of *Leptographium wagneri* varieties that cause black stain root disease of conifers in western North America. *Frontiers in Plant Science* 14: 1286157.
- Fick, S.E., Hijmans, R.J. 2017. WorldClim 2: new 1-km spatial resolution climate surfaces for global land areas. *International Journal of Climatology* 37: 4302-4315.
- Kelley, M., Schmidt, G. A., Nazarenko, L., Bauer, S. E., Ruedy, R., Russell, G. L., Ackerman, A. S., Aleinov, I., Bauer, M., Bleck, R., Canuto, V., Cesana, G., Cheng, Y., Clune, T. L., Cook, B. I., Cruz, C. A., Del Genio, A. D., Elsaesser, G. S., Faluvegi, G., Kiang, N. Y., Kim, D., Lacis, A. A., Leboissetier, A., LeGrande, A. N., Lo, K. K., Marshall, J., Matthews, E. E., McDermid, S., Mezuman, K., Miller, R. L., Murray, L. T., Oinas, V., Orbe, C., Pérez García-Pando, C., Perlwitz, J. P., Puma, M. J., Rind, D., Romanou, A., Shindell, D. T., Sun, S., Tausnev, N., Tsigaridis, K., Tselioudis, G., Weng, E., Wu, J., Yao, M.-S. 2020. GISS-E2.1: Configurations and Climatology. *Journal of Advances in Modeling Earth Systems* 12: e2019MS002025.
- Kim, M.-S., Hanna, J.W., Stewart, J.E., Warwell, M.V., McDonald, G.I., Klopfenstein, N.B. 2021. Predicting present and future suitable climate spaces (potential distributions) for an *Armillaria* root disease pathogen (*Armillaria solidipes*) and its host, Douglas-fir (*Pseudotsuga menziesii*), under changing climates. *Frontiers in Forests and Global Change* 4: 740994.
- Lockman, I.B., Kearns, H.S., 2016. Black stain and related root diseases - *Leptographium* Species. Forest root diseases across the United States. Gen. Tech. Rep. RMRS-GTR-342. Ogden, UT: U.S. Department of Agriculture, Forest Service, Rocky Mountain Research Station. 55 p.
- Murray, M.P., Leslie, A. 2021. Climate, radial growth, and mortality associated with conifer regeneration infected by root disease (*Armillaria ostoyae*). *The Forest Chronicle* 97: 43–51.
- Phillips, S.J., Anderson, R.P., Schapire, R.E. 2006. Maximum entropy modeling of species geographic distributions. *Ecological Modelling* 190: 231-259.
- Thies, W.G., Sturrock, R.N. 1995. Laminated root rot in western North America. Gen. Tech. Rep. PNW-GTR-349. Portland, OR: U.S. Department of Agriculture, Forest Service, Pacific Northwest Research Station. 32 p. In cooperation with: Natural Resources Canada, Canadian Forest Service, Pacific Forestry Centre.