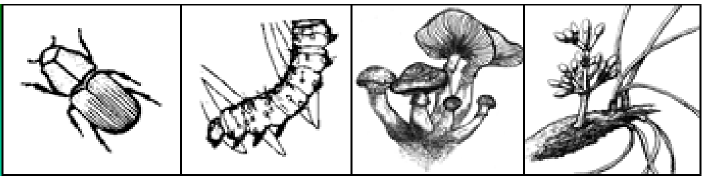
Forest Health Protection



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Assessment of Root Disease Occurrence and Severity Estimated from Climate Models with Forest Inventory and Analysis (FIA) Data

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Summary

Two new climate-based root disease models have been developed for Region 1. One model provides estimates of climatic suitability for root disease and the other provides estimates of potential root disease severity. These models were developed using root disease presence and severity data collected on Forest Inventory and Analysis (FIA) plots and incorporate climatic and biophysical variables to estimate the spatial distributions of suitable climate for root disease and potential severity where root disease may occur. The model outputs are assigned to VMap polygons via ancillary tables. Herein, we compared the numerical outputs from these two models to analogous values derived from the 2011 FIA hybrid summary database for each of the National Forests in Region 1. Maps were also created for each Forest to compare the spatial distributions of root disease occurrence and severity estimated from both the FIA summary database and the climate-based root disease models.

The first of the two models developed by Holden et al. (2020) estimates climatic suitability for root disease over a continuous spatial distribution in Region 1. In general, the model-derived estimates of acres with climate suitable for root disease for the National Forests west of the Continental Divide were consistent with the estimates of area with root disease present based on the overall proportion of FIA plots with root disease, though there were a few exceptions. For the Flathead National Forest, Custer-Gallatin National Forest, and Beaverhead-Deerlodge National Forest, the climatic suitability model underestimated the area with climate suitable for root disease. For others, such as the Idaho Panhandle National Forest, the model indicated that a much higher proportion of the Forest was suitable for root disease than indicated from impacts observed on FIA plots. The climatic suitability model may still have some utility for predicting areas with the potential for root disease to occur but should be used with caution, particularly for the Flathead National Forest and for those Forests east of the Continental Divide. The utility of the climatic suitability model predictions may be improved if combined with information regarding the abundance and distribution of root disease susceptible hosts such that areas with suitable climate and an abundance of highly susceptible hosts can be identified.

Root disease can occur anywhere where virulent pathogen, conducive climate, and susceptible host coexist. While these models do not aim to predict where root disease pathogens occur, they can provide estimates of where generally suitable climate occurs and where susceptible hosts are most abundant. In Region 1, the tree species most susceptible to root disease are Douglas-fir and true firs. The climatic suitability model estimated that over 1.8 million acres (approx. 32%) of Douglas-fir-dominated forest and over 1.3 million acres (roughly 77%) of grand fir-dominated forest occur in areas with suitable climate for root disease.

The second model provides estimates of the potential severity of root disease across Region 1 Forests. Severity of root disease is typically assessed on FIA subplots using the Hagle root disease severity rating system (Hagle 1992), which provides ratings that range from 0-9, with higher values representing more severe root disease impacts. However, the root disease severity ratings for FIA plots that were used as inputs for the model represented the average Hagle rating across FIA subplots. This averaging makes comparisons between FIA plot data and model estimates challenging. Average Hagle severity ratings generated from the model ranged from 0 to 3.26. These low values from the root disease severity model are inherently conservative, with limited potential for predicting severe disease. There are also inconsistencies in the spatial distribution of modeled root disease severity compared to FIA plots. The inherent down-weighting of the severity values combined with spatial inconsistencies in results make it difficult to interpret the model outputs and results in a high potential for misinterpretation and misuse. For these reasons, we are advising that the root disease severity model not be used for any purposes other than use by FHP personnel for internal information gathering and research. Instead, summaries of root disease presence and severity from the FIA summary database should be used for planning and monitoring at the mid- and broad-levels.

The most important factor to consider when using these models is the spatial scale at which they are to be interpreted. The models are not intended for use below the forest level; thus, the broad- to mid-level spatial scales are the only appropriate scales at which to interpret the models. They should not be downscaled to ranger districts, sub-watersheds, or project areas. They are not intended to predict where root disease is currently nor where it will occur; rather, they are meant to provide estimates of where climate is suitable for root disease to potentially occur, and what the potential severity might be if it does occur. There have been no attempts to verify areas differing in probability of root disease suitability with ground surveys, and statistical analyses of error rates associated with the spatial model predictions have not been performed. The models should never be used as a replacement for ground surveys. Resource managers should use their experience and

local knowledge of the presence and severity of root disease to determine whether the model estimates are reasonable for directing ground surveys.

Land managers should consider the relative reliability of each of the data sources presented here. The FIA observations are the most reliable source of root disease data and thus should carry the most weight when considering root disease occurrence and severity in the decision-making process. Despite its limitations and potential errors in individual readings, assessment of numbers of acres of root disease that are derived directly from proportions of affected FIA plots, as summarized herein, appear more likely to be useful than the models based on the same data.

Introduction

Collectively, root diseases are a leading contributor to tree mortality in the United States and pose the greatest risk of basal area loss of any biotic agent nationwide (Krist et al. 2014, Lockman & Kearns, eds. 2016). According to National Insect and Disease Forest Risk Assessment (NIDFRA) projections, root diseases could put approximately 1.9 million acres in the Northern Region at risk of losing 25% or more of total basal area between 2013 and 2027 (Krist et al. 2014, Lockman & Kearns, eds. 2016). The root diseases and disease agents that cause the most damage in the Northern Region are Armillaria root disease (*Armillaria spp.*), Heterobasidion root disease (*Heterobasidion occidentale* and *H. irregulare*), laminated root rot (*Coniferiporia sulphurascens* and *C. weirii*), schweinitzii root and butt rot (*Phaeolus schweinitzii*), and tomentosus root disease (*Onnia tomentosa*) (Hagle et al. 2000; Lockman et al. 2016; Lockman & Kearns, eds. 2016). These agents co-occur in many forest types in western Montana and northern Idaho and often co-occur within trees; thus, it is often difficult to determine the contribution of any one pathogen to observed landscape-level root disease damage (Hagle et al. 2000; Lockman et al. 2016). These agents are much more common and damaging in forests west of the Continental Divide. Although some are locally active in forests east of the Continental Divide, much less is known about their extent of occurrence and impact there (Lockman et al. 2016).

The incidence and severity of root disease in the Northern Region has increased in recent decades due to changes in forest composition resulting from fire exclusion and altered forest management practices. One contributing factor was the widespread selective harvesting used to remove western white pine and other high-value trees following establishment of the invasive pathogen causing white pine blister rust, *Cronartium ribicola* (Byler et al. 1990, Hansen & Goheen 2000, Healey et al. 2016, Lockman & Kearns, eds. 2016). Many forests that were previously dominated by pines (*Pinus* spp.) and western larch, which are more tolerant of root disease, are now dominated by a mixture of highly susceptible hosts such as Douglas-fir (*Pseudotsuga menziesii*), grand fir (*Abies grandis*), and subalpine fir (*A. lasiocarpa*).

Three components are required for root disease to occur. A susceptible tree host must be present, along with a virulent root disease pathogen and a suitable environment (e.g. climate, soil composition, spacing of susceptible trees, etc.). Root disease models aim to estimate the potential for root disease occurrence and the potential impacts where it may occur. These estimates are often derived from data on current or predicted host distributions or other environmental conditions (e.g., bioclimatic variables) associated with root disease. However, care should be taken when interpreting results of these models. This is especially a concern where sampling intensities (i.e. survey plots) may be insufficient to represent variability in host or environmental factors controlling presence and absence of disease. Efforts to validate these models have not assessed how model predictions deviate from actual presence and absence of root disease across the study area.

Recent efforts to assess factors associated with root disease in the Northern Region utilized root disease severity data collected in USFS Forest Inventory and Analysis (FIA) plots (Lockman et al. 2016, Holden et al. 2020). The map developed by Lockman et al. (2016) utilized associations between root disease severity ratings from FIA plots and forest dominance type, potential vegetation type (PVT), and Bailey's Ecoregion categories. In effect, this analysis used forest characteristics as that reflect underlying climatic, water availability, soil condition, and countless unknown biotic, abiotic, and temporal interactions associated with root disease presence and severity. Then, combinations of conditions associated with root disease severity were estimated and represented across western Montana and northern Idaho using the Region 1 existing vegetation database (R1 VMap).

Models recently developed by Holden et al. (2020) aimed to improve upon the forest-associations approach of Lockman et al. (2016). Instead of using information about forest vegetation, this approach analyzed underlying biophysical variables for covariance with root disease occurrence and severity in FIA plots. Biophysical variables included temperature, dewpoint temperature, vapor pressure deficit, evapotranspiration, snow water equivalent and climatic water balance deficit, aspect, slope position and cold air drainage potential (Holden et al. 2020). Many of these variables were derived from previous models developed by Holden et al. (2016, 2018) downscaled to a 30 m grid. Root disease was then estimated across the Northern Region based upon modeled, spatially continuous, high-resolution estimates of the climatic and biophysical factors, while also adjusting for inter-plot spatial covariance. Finally, spatial predictions were attributed to R1 VMap polygons, based on median values, to identify where conducive climatic conditions occurred.

These two approaches--using vegetative (Lockman et al. 2016) or climatic (Holden et al. 2020) associations with root disease--each yielded spatial maps. Validation based on an independent set of field plots was not feasible due to the vast land area assessed by the model. For the Holden et al. (2020) model, cross-validation results suggested that using three climatic variables (mean annual dewpoint temperature, evapotranspiration, and climatic water deficit) could explain root disease occurrence reasonably well. A model that added the fourth most significant climatic variable (solar radiation, among dewpoint temperature, climatic water deficit, and evapotranspiration) had much lower predictive accuracy for explaining root disease severity (Holden et al. 2020). The methodology did not present geographic trends of Type 1 and Type 2 errors associated with the assignments of potential for root disease presence and severity.

The objectives of this report were to: 1) compare area estimates of root disease presence and severity from the Holden et al. (2020) models to those derived from FIA summary database to assess the utility of the Holden et al. (2020) models for broad- and mid-level usage and 2) provide guidance to resource managers on the appropriate use of the model data and associated spatial layers.

Methods

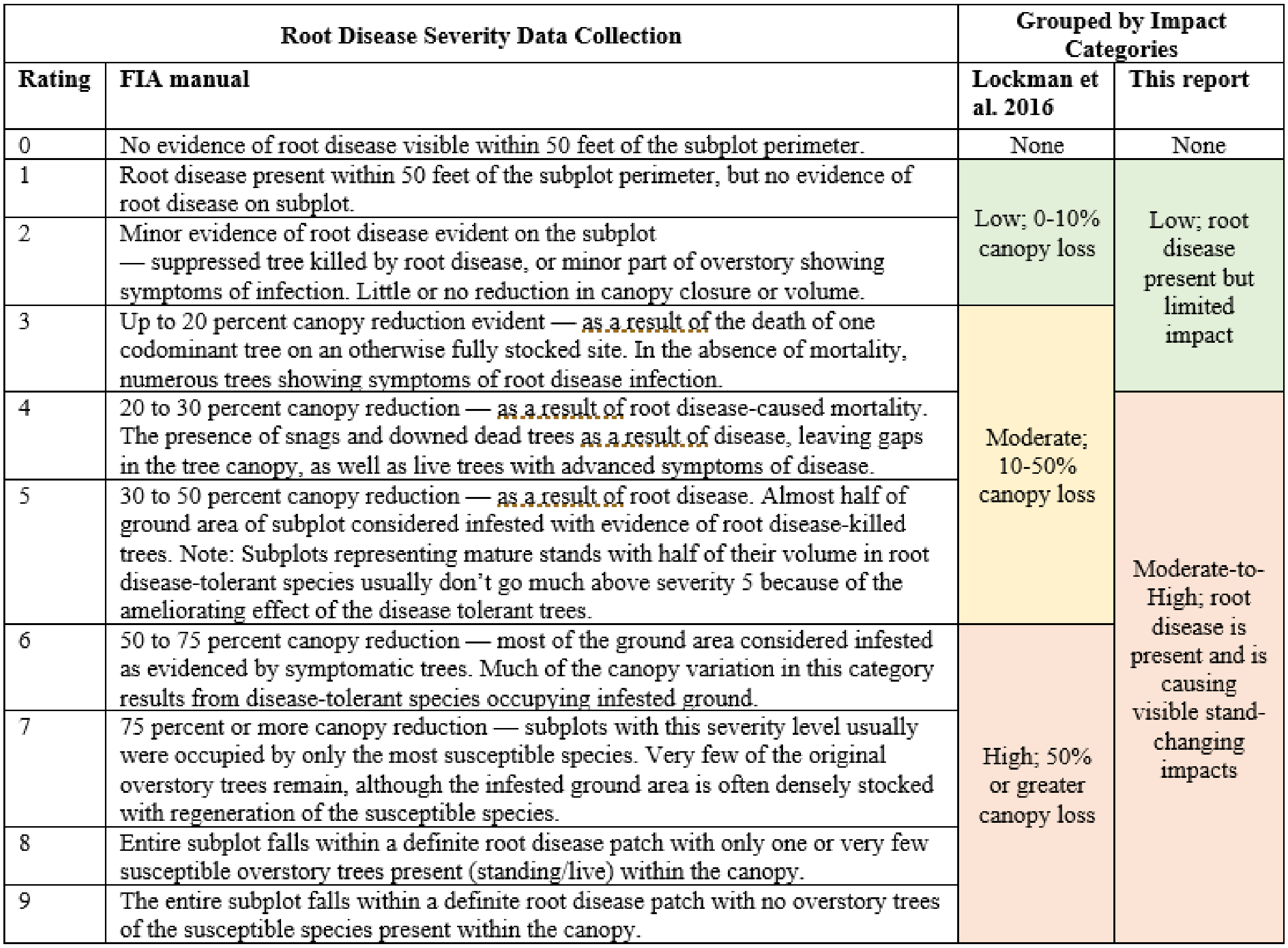
Data Collection

The FIA plots used for the development of the climate-based root disease model and for the summaries presented here represent 3,695 forested plots from the 2011 hybrid version of the Region 1 summary database (Bush 2014, Bush et al. 2018, Bush and Reyes 2020). These data were collected from 1993 to 2011 in a gridded network across Region 1. The FIA plots sampled from 1993-1998 variously consisted of 7 subplots (in earlier years) or 5 subplots (in later years) (Bush and Reyes 2020). As of 1996, each FIA plot has consisted of four circular subplots, each with a 24 ft. radius equivalent to 1/24th of one acre (Bush and Reyes 2020). Ten percent of these plots are surveyed annually, such that inventories are completed every 10 years (Bush and Reyes, 2020).

Root disease severity was estimated on FIA subplots using the Hagle root disease severity rating system (Hagle 1992). FIA field crews received training in this method by Forest Health Protection (FHP) personnel to calibrate visual estimates and maintain consistency among evaluations of root disease severity. Crews estimated canopy loss due to suspected root disease mortality and/or ground area occupied by symptomatic or dead trees and assigned each subplot a rating of 0–9, with higher values representing greater root disease impacts. A rating of 0 indicates that no root disease impacts were observed in the subplot, nor within 50 ft of the subplot. A rating of 1 indicates that no root disease impacts were observed in the subplot but were observed within 50 ft of the subplot. Ratings 2–9 indicate that evidence of root disease was observed on the subplot, with higher values indicating greater canopy loss and/or larger area impacted by root disease (Hagle 1992, Lockman et al. 2016) (Table 1).

The fine-scale severity ratings recognized by this system have often been grouped by their level of impact. Lockman et al. (2016) used four impact levels as follows: None (rating 0), Low (ratings 1–2; 0–10% canopy loss), Moderate (ratings 3–5; 10–50% canopy loss) and High (ratings 6–9; 50% or greater canopy loss). However, FHP pathologists working with FIA data analysts have also considered that a more useful classification system for land managers is one that uses a single group for severity ratings that indicate significant current or imminent impacts from root disease on the stand. The system used for this report is as follows: rating 0= none, indicating that the plots are on forested land, but no root disease is present; ratings 1-3= L (low) indicating that root disease is present but with limited impact thus far and for the next decade (Lockman et al. 2016); ratings 4-9= MH (moderate-to-high) indicating that root disease is present and is causing visible stand-changing impacts (Table 1).

Table 1. Hagle (1992) root disease severity rating system. Impact categories combining multiple severity ratings differed slightly between Lockman et al. (2016) and this report.



Root Disease Severity Data Collection		**Grouped by Impact Categories**	
Rating	**FIA manual**	**Lockman et al. 2016**	**This report**
0	No evidence of root disease visible within 50 feet of the subplot perimeter.	None	None
1	Root disease present within 50 feet of the subplot perimeter, but no evidence of root disease on subplot.	Low; 0-10% canopy loss	Low; root disease present but limited impact
2	Minor evidence of root disease evident on the subplot — suppressed tree killed by root disease, or minor part of overstory showing symptoms of infection. Little or no reduction in canopy closure or volume.		
3	Up to 20 percent canopy reduction evident — as a result of the death of one codominant tree on an otherwise fully stocked site. In the absence of mortality, numerous trees showing symptoms of root disease infection.	Moderate; 10-50% canopy loss	
4	20 to 30 percent canopy reduction — as a result of root disease-caused mortality. The presence of snags and downed dead trees as a result of disease, leaving gaps in the tree canopy, as well as live trees with advanced symptoms of disease.		Moderate-to-High; root disease is present and is causing visible stand-changing impacts
5	30 to 50 percent canopy reduction — as a result of root disease. Almost half of ground area of subplot considered infested with evidence of root disease-killed trees. Note: Subplots representing mature stands with half of their volume in root disease-tolerant species usually don't go much above severity 5 because of the ameliorating effect of the disease tolerant trees.		
6	50 to 75 percent canopy reduction — most of the ground area considered infested as evidenced by symptomatic trees. Much of the canopy variation in this category results from disease-tolerant species occupying infested ground.	High; 50% or greater canopy loss	
7	75 percent or more canopy reduction — subplots with this severity level usually were occupied by only the most susceptible species. Very few of the original overstory trees remain, although the infested ground area is often densely stocked with regeneration of the susceptible species.		
8	Entire subplot falls within a definite root disease patch with only one or very few susceptible overstory trees present (standing/live) within the canopy.		
9	The entire subplot falls within a definite root disease patch with no overstory trees of the susceptible species present within the canopy.		

FIA Summary Data

The summaries of root disease acres from FIA root disease data presented here were derived from the Region 1 summary database using the Region 1 Vegetation Classification, Mapping, Inventory, and Analysis Group's Estimator Form (Bush et al. 2018). This program uses a plot expansion factor that estimates forested acres represented by each FIA plot (Pugh et al. 2018). For each of the root disease estimates, a 95% confidence interval was constructed from 40,000 bootstrap samples (Leach 2005). Other FIA data used for these analyses included the characterization of tree species most abundant in the canopy as "dominance 40% plurality" (DomMid40). This descriptor shows a site's single most abundant species if its abundance is 40% or greater, or if no single species has at least 40% dominance, the mixed species composition is coded HMIX for hardwood mixes, IMIX for shade-intolerant conifer mixes, and TMIX for shade-tolerant conifer mixes (Barber et al. 2011).

The coordinates of FIA plots and subplots in the maps herein do not reflect their exact locations. All such coordinates have been altered slightly to protect the confidentiality and integrity of FIA plots, in accordance with the Food Security Act of 1985 (reference 7 USC 2276 § 1770) (Burrill et al. 2018). Model development was conducted using accurate coordinates by those with privileged access to the unaltered data.

Holden et al. (2020) Root Disease Model Outputs

Holden et al. (2020) described a climate-based presence/absence model, hereinafter referred to as the "climatic suitability" model, and a root disease severity model. The climatic suitability model estimates the match between a location's climate and climate that was determined most associated with root disease occurrence at FIA subplots across the region. In this model, the root disease severity for each subplot was converted into a categorical response variable whereby subplots with a Hagle rating of 0 were coded as root-disease "absent", while those with any non-zero Hagle rating were coded as root-disease "present" (Holden et al. 2020). The only predictors considered for this model were the climatic and biophysical variables described above (i.e. host abundance was not included as a potential predictor) (Holden et al. 2020). The outputs of this model were scaled as a continuous variable from 0-1. For this report, the continuous variable output was converted to a binary variable to facilitate comparisons with presence/absence data from the FIA summary database. Values less than 0.5 were considered to represent a low probability of suitable climate for root disease occurrence and those greater than or equal to 0.5 to represent a high probability of suitable climate. Maps for each forest showing climate suitability values in four categories (0-0.25, 0.25-0.5, 0.5-0.75, and 0.75-1) were also produced (Appendix A). However, correspondence of these ranges in climate suitability values with presence or absence of root disease and of specific root diseases is unavailable.

The root disease severity model uses the correspondence between Hagle severity ratings on FIA plots and environmental variables to output values similar in concept to Hagle root disease severity ratings, but as a continuous response variable that can be imputed across the modeled landscape. The Hagle severity ratings for the four subplots per FIA plot were averaged to give a single value for each FIA plot. For the purposes of scoring whether different FIA plots in an area were affected by root disease for this report, values less than one were assigned to root disease severity class 0 (no root disease). Values greater than or equal to one were assigned to the root disease severity class L (low). None of the values from the root disease severity model outputs were greater than or equal to four, which would represent root disease severity class MH (moderate-to-high). These categorical values from the model were then considered to correspond to the Hagle (1992) root disease severity values and were combined into severity classes (Table 1).

The model outputs including probability of suitable climate (RD_SUITABILITY), root disease severity (RD_SEVERITY), and host abundance (RD_SUSCEPTIBLE_SPP) for each National Forest in Region 1 are available in VMAP as ancillary tables appended to forest VMap layers. Herein, model data was displayed on VMap polygons by Forest (Appendix B). The use of VMap also allowed depiction of the spatial distribution of root-disease susceptible tree species (Appendix C). Douglas-fir and true firs were displayed as the most susceptible hosts to most root diseases in Region 1. The abundance of these root disease susceptible hosts was derived from the VMap attribute DomMid40 and was represented in three categories- Absent (0%), Limited (< 40% BA), and Abundant (≥ 40% BA). R1 VMap coverage is comprehensive and thus is not restricted to federal lands within National Forest boundaries. However, for the purposes of the data comparisons presented here, the R1 VMap layers were clipped to the National Forest boundaries for all forests in Region 1.

Results

Comparisons of Root Disease Occurrence on FIA Plots with the Estimated Climatic Suitability for Root Disease from the Climatic Suitability Model

The 2011 hybrid FIA summary database contains root disease occurrence and severity data for 14,682 subplots representing approximately 22,517,661 forested acres in Region 1 (Table 2). Root disease was present on 5,155 FIA subplots from across the region; this represents an estimated 7.9 million acres and is equivalent to approximately 35% of the total forested acres on National Forest lands in Region 1 (Table 2, Fig. 1). The climatic suitability model estimated suitable climate for root disease greater than or equal to 0.5 occurred on nearly 6.2 million acres, approximately 30% of the total forested VMap acres on National Forest lands in Region 1 (Table 3, Fig. 1). Note that slight differences in total forested land-area estimates for the Region between the FIA summary database and VMap outputs occurred and may reflect differences in the estimation of forest coverage based on forested PVT (FIA database) and acres for which the LIFEFORM attribute was listed as “TREE” (VMap) as well as some differences in land ownership in the two data sets.

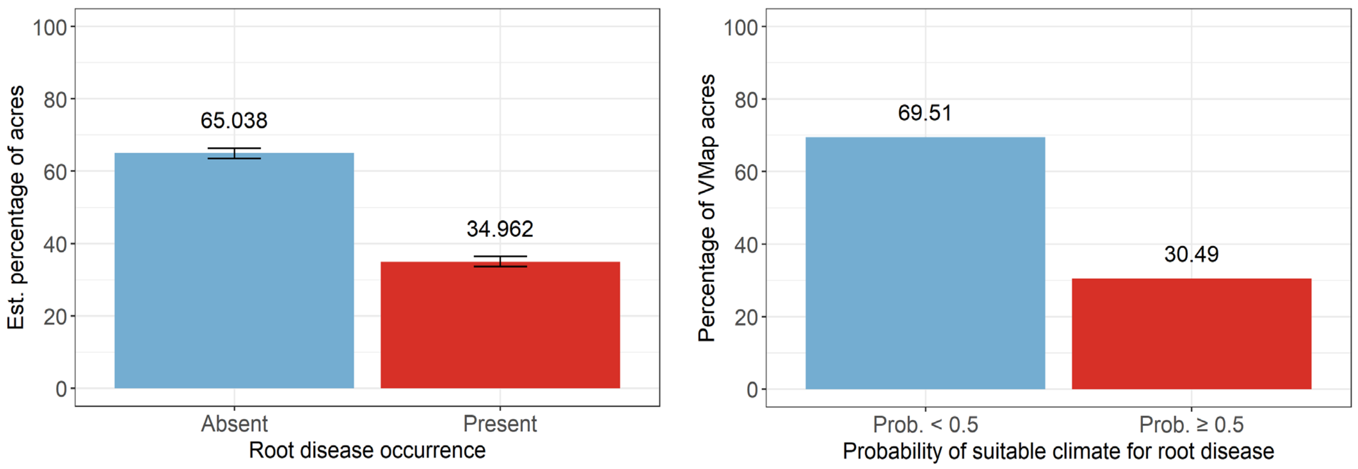


Figure 1. Left: Root disease incidence in Region 1 from the 2011 hybrid FIA summary database, expressed as a percentage of total acres. Error bars represent 95% confidence intervals for the estimate calculated from 40,000 bootstraps. All FIA subplots occurred on forested potential vegetation type (PVT) and were on National Forests in Region 1. Right: Probability of suitable climate for root disease from the Holden et al. (2020) climatic suitability model. Numbers of acres reflect the percentage of total acres for all VMap polygons (or portions of polygons) within National Forest boundaries for which LIFEFORM = 4000 (TREE).

Table 2. Region-wide summary of root disease occurrence with land-area estimates based on FIA plot sampling.

Root Disease Occurrence	FIA Subplots	Acres	Acres [95% C.I.]	Percentage of Acres	Percentage of Acres [95% C.I.]
Absent	9,527	14,611,480	[14,304,794 – 14,953,078]	65.0	[63.5 – 66.4]
Present	5,155	7,906,180	[7,569,086 – 8,216,019]	35.0	[33.6 – 36.5]
Total	14,682	22,517,660		100	

[a]Numbers of FIA subplots reflect only those occurring on forested potential vegetation type (PVT) with root disease data available, [b]confidence intervals calculated from 40,000 bootstraps.

Table 3. Region-wide summary of the probability of suitable climate for root disease from the Holden et al. (2020) climatic suitability model with land-area estimates from Region 1 VMap.

Probability of suitable climate for root disease	VMap tree acres[a]	Percentage of VMap tree acres
Prob. < 0.5	14,119,112	69.5
Prob. ≥ 0.5	6,194,516	30.5
Total	20,313,628	100.0

[a]Acreage values reflect the sum of acres for all VMap polygons (or portions of polygons) within National Forest boundaries for which LIFEFORM = 4000 (TREE).

Root disease occurrence by National Forest

Area estimates were summarized at the National Forest level for all forests in Region 1 to compare FIA database estimates and climatic suitability model outputs. The range in numbers of acres of forested land with root disease for different National Forests based on FIA data was from 257,917 acres (approx. 9%) on the Beaverhead-Deerlodge National Forest (BDNF) to 1,813,281 acres (45%) on the Nez Perce-Clearwater National Forest (NPCNF) (Table 4; Fig. 2). The Idaho Panhandle National Forests (IPNF) had the greatest percentage of area (62%) estimated as having root disease present, followed by the Kootenai National Forest (KNF) with 51% (Table 4, Fig. 2). In contrast, the total area with climate estimated to be suitable for root disease (i.e., climate suitability value ≥ 0.5) from the climatic suitability model ranged from zero for the BDNF to 2.3 million acres (90%) on the IPNF (Table 5; Fig. 3). The climatic suitability model suggested low probability of suitable climate on the Helena-Lewis and Clark (HLCNF) and Custer-Gallatin National Forests (CGNF). The model indicated very few acres on these forests with probabilities of 0.5 or greater (Table 5; Fig.

3). The model's estimation of area with suitable climate for root disease on the NPCNF (1.5 million acres, 45%) very closely approximated the observed root disease occurrence from the FIA database (1.8 million acres, 45%) (Tables 4, 5), though the distribution of FIA plots with infection often differed from the areas considered by the model to have suitable climate (Appendix B). The climatic suitability model underestimated the area with suitable climate for root disease for some National Forests with less than 40% of forested FIA plots infected. For the FNF, there was even greater underestimation of the area with climate suitable for root disease. The FIA database estimates indicated that root disease was present on over 1.1 million acres, approximately 50% of the forested land on the FNF (Table 4; Fig. 2), while the climatic suitability model estimated suitable climate for root disease (Prob. ≥ 0.5) on just over 337,000 acres (approx. 17%) (Table 5; Fig. 3).

Table 4. Root disease occurrence on FIA subplots on National Forests in Region 1.

Forest	Root disease occurrence	FIA Subplots	Acres	Acres [95% C.I.][a]	Percentage of Acres	Percentage of Acres [95% C.I.][a]
Beaverhead-Deerlodge	Absent	1,693	2,630,439	[2,563,503 – 2,697,118]	91.1	[88.8 – 93.4]
	Present	166	257,917	[191,614 – 324,218]	8.9	[6.6 – 11.2]
Bitterroot	Absent	746	1,136,871	[1,064,882 – 1,215,090]	75.7	[70.6 – 80.5]
	Present	244	371,845	[293,958 – 444,528]	24.3	[19.5 – 29.5]
Custer-Gallatin	Absent	1,331	2,088,167	[2,017,572 – 2,174,203]	85.2	[81.9 – 88.3]
	Present	239	374,960	[288,580 – 444,816]	14.8	[11.7 – 18.1]
Flathead	Absent	812	1,203,407	[1,067,083 – 1,285,105]	50.3	[45.5 – 54.8]
	Present	770	1,141,162	[1,058,995 – 1,278,282]	49.7	[45.2 – 54.5]
Helena-Lewis and Clark	Absent	1,377	2,109,240	[2,016,844 – 2,209,746]	78.2	[74.5 – 81.6]
	Present	390	597,388	[496,829 – 690,353]	21.8	[18.4 – 25.5]
Idaho Panhandle	Absent	602	928,015	[825,307 – 1,041,682]	38.4	[33.9 – 42.7]
	Present	979	1,509,180	[1,395,051 – 1,612,838]	61.7	[57.2 – 66.2]
Kootenai	Absent	767	1,095,710	[960,572 – 1,169,627]	49	[44.1 – 53.7]
	Present	758	1,082,853	[1,007,651 – 1,218,732]	51	[46.3 – 55.9]
Lolo	Absent	860	1,336,563	[1,241,531 – 1,439,719]	63	[58.4 – 67.7]
	Present	509	791,059	[686,860 – 885,941]	37	[32.3 – 41.6]
Nez Perce-Clearwater	Absent	1,339	2,207,258	[2,072,950 – 2,362,348]	55.2	[51.6 – 58.8]
	Present	1,100	1,813,281	[1,656,945 – 1,949,962]	44.8	[41.2 – 48.5]

[a]confidence intervals calculated from 40,000 bootstraps.

Table 5. Probability of suitable climate for root disease by National Forest based on outputs from the Holden et al. (2020) climatic suitability model.

Forest	Probability of suitable climate for root disease	VMap tree acres[a]	Percentage of VMap tree acres
Beaverhead-Deerlodge	Prob. < 0.5	2,303,837	100.0
	Prob. ≥ 0.5	0	0.0
Bitterroot	Prob. < 0.5	1,158,096	97.9
	Prob. ≥ 0.5	24,417	2.1
Custer-Gallatin	Prob. < 0.5	1,862,322	100.0
	Prob. ≥ 0.5	1,630	0.0
Flathead	Prob. < 0.5	1,667,949	83.2
	Prob. ≥ 0.5	337,153	16.8
Helena-Lewis and Clark	Prob. < 0.5	2,376,438	99.7
	Prob. ≥ 0.5	7,564	0.3
Idaho Panhandle	Prob. < 0.5	269,148	10.3
	Prob. ≥ 0.5	2,338,227	89.7
Kootenai	Prob. < 0.5	895,318	37.8
	Prob. ≥ 0.5	1,470,982	62.2
Lolo	Prob. < 0.5	1,766,022	78.0

Forest	Probability of suitable climate for root disease	VMap tree acres[a]	Percentage of VMap tree acres
	Prob. ≥ 0.5	497,209	22.0
Nez Perce-Clearwater	Prob. < 0.5	1,819,981	54.5
	Prob. ≥ 0.5	1,517,335	45.5

[a] Acreage values reflect the sum of acres for all VMap polygons (or portions of polygons) within National Forest boundaries for which LIFEFORM = 4000 (TREE).

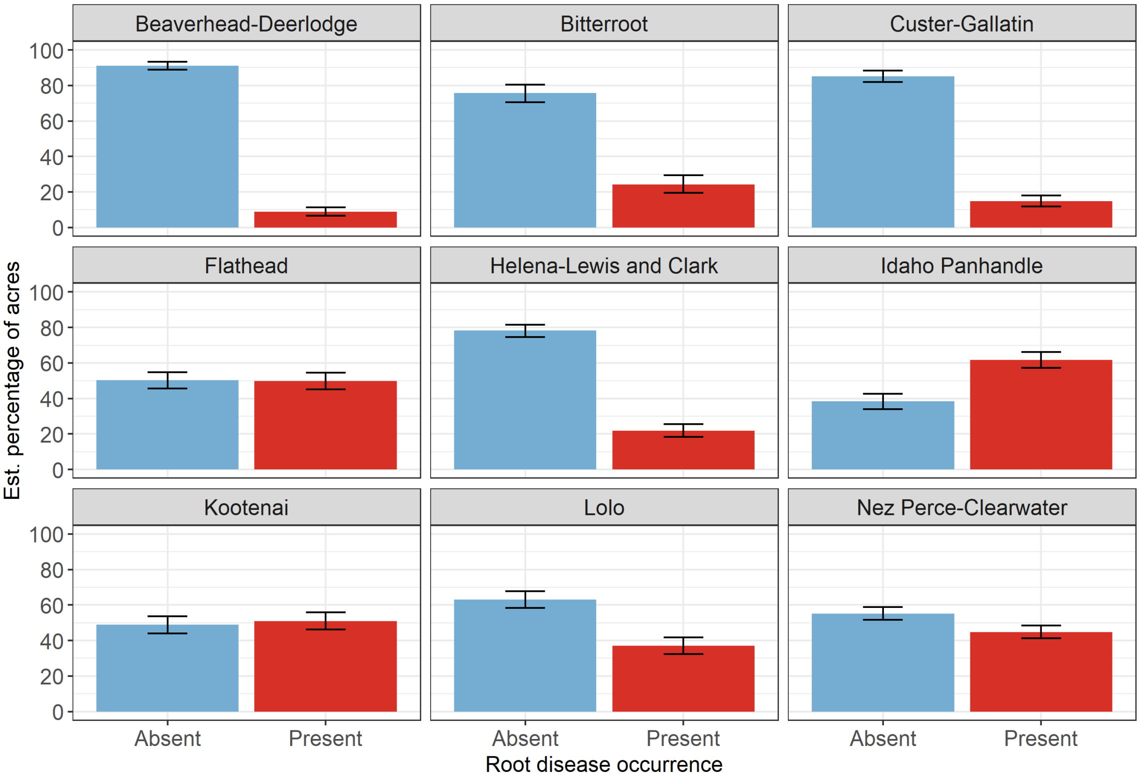


Figure 2. Root disease occurrence on FIA subplots on National Forests in Region 1. Absent = average FIA plot severity rating < 1; Present = average severity rating 1-9. Estimated percentage of acres from FIA summary database with error bars representing 95% confidence intervals for the estimates calculated from 40,000 bootstraps.

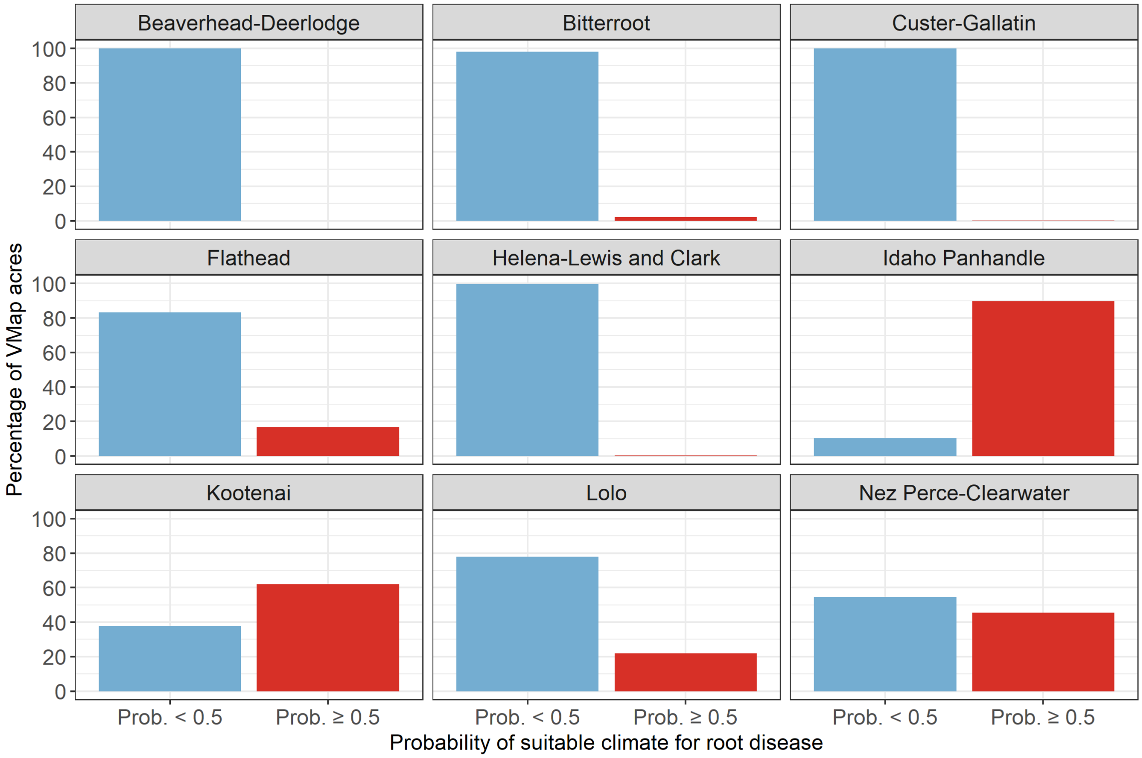


Figure 3. Probability of suitable climate for root disease by National Forest based on model outputs from the Holden et al. (2020) climatic suitability model. Values reflect the percentage of acres for all VMap polygons (or portions of polygons) within National Forest boundaries for which LIFEFORM = 4000 (TREE).

Relationship between existing vegetation dominance classes and root disease

The most abundant DomMid40 class in the FIA plot network was MX-PSME (*Pseudotsuga menziesii*), with 3,515 subplots representing over 5.3 million acres (Table 6). Root disease impacts were observed on 1,389 of those subplots. This suggests that root disease may be present on up to 2.1 million acres (approx. 39%) of the Forest Service land on which Douglas-fir represents at least a 40% plurality of the stand composition (Table 6, Fig. 4). MX-PSME was also the most abundant class in the regional VMap dataset, with approximately 5.7 million acres. The Holden et al. (2020) climatic suitability model predicted that the climate would be suitable for root disease on over 1.8 million (approx. 32%) of those acres (Table 7, Fig. 5). According to the FIA summary database, root disease was present on about 57% of the forested area with an MX-ABGR, *Abies grandis*) DomMid40 class, and approximately 40% of the forested area with an MX-ABLA (*A. lasiocarpa*) class (Table 6, Fig. 4). The climatic suitability model estimated suitable climate for root disease on 77% and 9% of the MX-ABGR and MX-ABLA classes, respectively (Table 7; Fig. 5).

The MX-LAOC (*Larix occidentalis*) class had higher proportions of acres with root disease present than the MX-ABLA class in both the observed and modeled datasets. Even though the early seral species *L. occidentalis* is generally considered more root disease tolerant than Douglas-fir and true firs, including *A. lasiocarpa*, this does not mean that the MX-LAOC class should be expected to have lower root disease. The MX-LAOC stands may also contain other, more susceptible species, such as *P. menziesii* and *A. grandis*, and conditions in these sites are favorable to root disease.

In interpreting the occurrence or predicted suitability for root disease on different dominance classes, it must be remembered that the dominance class represents a mixture of species that may vary in their susceptibility to root disease and that species representation may change over time. Highly susceptible species may dominate early and succumb early under some environmental conditions, to be replaced by more root-disease tolerant climax species such as western redcedar and western hemlock, while the susceptible species may persist as climax species under drier conditions that are less favorable to many of the root diseases prevalent in Region 1.

The same consideration—that presence of any susceptible species in a stand mix under favorable environmental conditions can foster suitability for root disease to develop--applies to stand types categorized as having a plurality of later-seral species. *Thuja plicata* is an example of a later-seral species considered less susceptible to root disease, however it is susceptible as a seedling and sapling, then becomes more able to resist root disease infections over time. The MX-THPL (*Thuja plicata*) class had the greatest proportion of acres with root disease of any DomMid40 class in the FIA summary database. Of the 312 MX-THPL subplots, 216 were given a Hagle rating greater than zero, representing over 330,000 acres (70%) of the National Forest land on which western red cedar has at least a 40% plurality of the stand composition (Table 6, Fig. 4). The Holden et al. (2020) climatic suitability model predicted that the climate would be suitable for root disease on over 430,000 (90%) of the MX-THPL acres from VMap (Table 7; Fig. 5). The DomMid40 class with the greatest proportion of acres predicted by the climatic suitability model to be suitable for root disease was MX-TSHE (western hemlock) with 99.98% of nearly 65,000 acres predicted as having probability of suitable climate ≥ 0.5 (Table 7, Fig. 5). The FIA database estimates indicated that root disease was present on 63% of FIA subplots in the MX-TSHE (*Tsuga heterophylla*) dominance type (Table 6, Fig. 4). The DomMid40 classes indicating a plurality of pines, including MX-PIFL2 (*Pinus flexilis*), MX-PIAL (*Pinus albicaulis*), and MX-PIPO (*Pinus ponderosa*) had some of the lowest rates of root disease occurrence of any of the conifer-dominated forest types in the FIA database (Table 6, Fig. 4). These DomMid40 classes also had some of the lowest percentages of VMap acres with climate predicted from the model to be suitable for root disease (Table 7, Fig. 5). The MX-PICO (*P. contorta*) class had overall low climatic suitability for root disease according to the climatic suitability model, with only 10% of VMap acres having probability of suitable climate ≥ 0.5 (Table 7, Fig. 5). However, FIA crews observed root disease impacts on approximately 22% of subplots with the MX-PICO DomMid40 class (Table 6).

Western redcedar and hemlocks are major shade tolerant species, and root disease was observed more frequently on FIA subplots with the DomMid40 class TMIX (57%) than on IMIX (50%), though the 95% confidence intervals for the acres and percentage of acres overlap indicating that they are not statistically different (Table 6, Fig. 4). The climatic suitability model predicted that suitable climate for root disease was more likely to occur on TMIX (47% of VMap acres with probability ≥ 0.5) than on IMIX (33% of VMap acres with probability ≥ 0.5) (Table 7, Fig. 5).

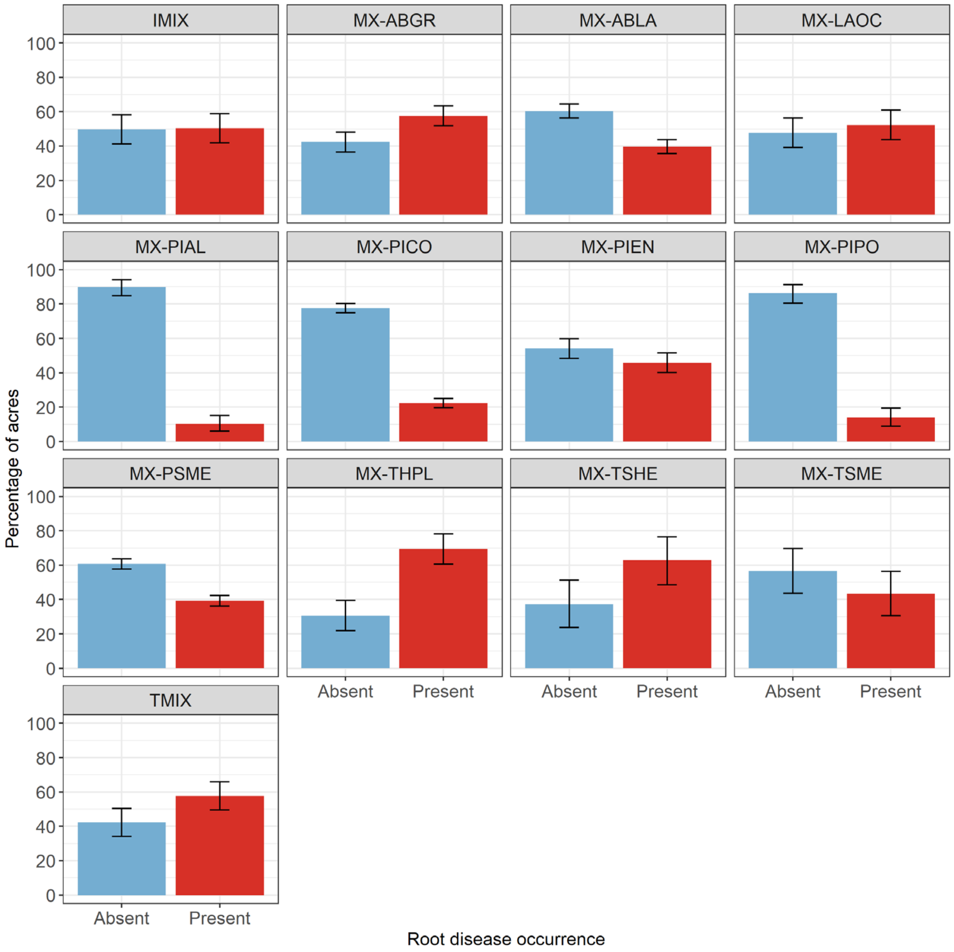


Figure 4. Root disease occurrence (percentage of acres) by dominance 40% plurality (DomMid40) class on Region 1 FIA subplots. The DomMid40 classes shown here are the conifer-dominated forest types with the most FIA plot data available. All DomMid40 types are shown in Table 6. See Barber et al. (2011) for detailed descriptions of DomMid40 classes. Error bars represent 95% confidence intervals from 40,000 bootstraps.

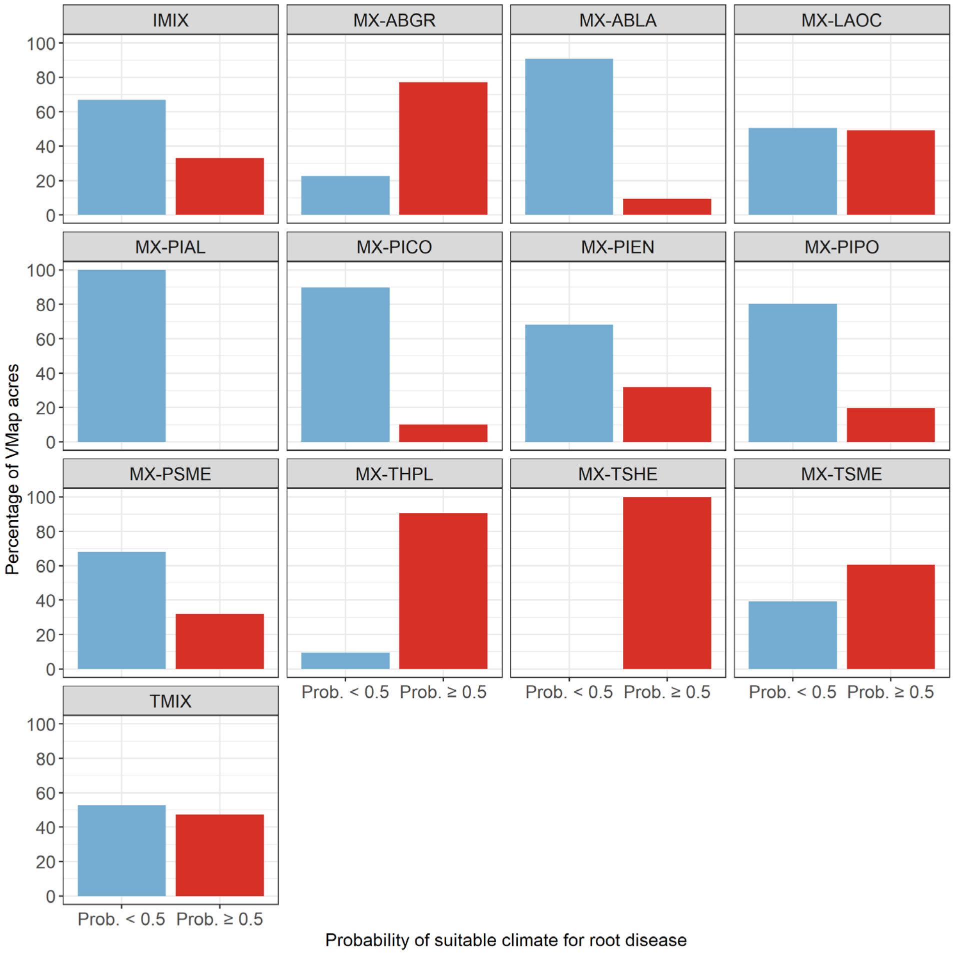


Figure 5. Probability of suitable climate for root disease by dominance 40% plurality (DomMid40) classes based on model outputs from the Holden et al. (2020) climatic suitability model. All VMap polygons (or portions of polygons) were within National Forest boundaries and had LIFEFORM = 4000 (TREE). All DomMid40 types are shown in Table 7. See Barber et al. (2011) for detailed descriptions of DomMid40 classes.

Table 6. Root disease occurrence by dominance 40% plurality (DomMid40) class for all Region 1 forests from the R1 FIA summary database. See Barber et al. (2011) for detailed descriptions of DomMid40 classes.

DomMid40 Class	Root disease occurrence	FIA subplots	Acres	Acres [95% C.I.][a]	Percentage of acres	Percentage of acres [95% C.I.][a]
HMIX	Absent	2	3,047	[0 – 5,332]	50.0	[0.0 – 87.5]
	Present	2	3,047	[0 – 5,332]	50.0	[0.0 – 87.5]
IMIX	Absent	226	345,080	[283,551 – 401,108]	49.7	[41.2 – 58.2]
	Present	225	343,553	[288,675 – 405,040]	50.3	[41.9 – 58.8]
MX-ABGR	Absent	412	635,505	[543,305 – 716,000]	42.4	[36.5 – 48.2]
	Present	552	851,453	[770,378 – 943,029]	57.6	[51.8 – 63.4]
MX-ABLA	Absent	1147	1748410	[1612843 – 1846421]	60.3	[56.3 – 64.5]
	Present	732	1,115,812	[1,017,687 – 1,252,553]	39.7	[35.5 – 43.7]
MX-BEPA	Absent	4	6,094	-	100.0	-
	Present	0	0	-	0.0	-
MX-CELE3	Absent	4	6,094	-	100.0	-
	Present	0	0	-	0.0	-
MX-FRPE	Absent	1	6,094	-	100.0	-
	Present	0	0	-	0.0	-
MX-JUNIP	Absent	51	79,223	-	100.0	-
	Present	0	0	-	0.0	-
MX-LALY	Absent	25	42,028	[27,859 – 48,753]	87.5	[57.1 – 100.0]
	Present	4	6,725	[0 – 21,668]	12.5	[0.0 – 44.4]
MX-LAOC	Absent	212	319,291	[258,065 – 371,091]	47.7	[39.2 – 56.4]
	Present	225	338,870	[286,965 – 400,761]	52.3	[43.6 – 60.9]
MX-PIAL	Absent	493	759,290	[719,093 – 797,287]	89.8	[84.9 – 94.1]
	Present	57	87,788	[50,003 – 127,875]	10.2	[5.9 – 15.1]
MX-PICO	Absent	2371	3,556,625	[3,425,860 – 3,679,681]	77.7	[74.9 – 80.4]
	Present	680	1,020,036	[895,058 – 1,150,161]	22.3	[19.6 – 25.1]
MX-PIEN	Absent	549	833,951	[748,873 – 925,256]	54.2	[48.4 – 59.8]
	Present	470	713,947	[621,110 – 798,963]	45.8	[40.1 – 51.6]
MX-PIFL2	Absent	114	173,682	[158,447 – 182,823]	95.0	[86.7 – 100]
	Present	6	9,141	[0 – 24,758]	5.0	[0.0 – 13.5]
MX-PIMO3	Absent	8	12,188	[0 – 24,376]	50.0	[0.0 – 100.0]
	Present	8	12,188	[0 – 24,376]	50.0	[0.0 – 100.0]
MX-PIPO	Absent	487	755,064	[707,383 – 800,711]	86.2	[80.6 – 91.2]
	Present	79	122,485	[77,338 – 170,297]	13.8	[8.8 – 19.4]
MX-POPUL	Absent	6	10,447	[0 – 12,188]	87.5	[0.0 – 100.0]
	Present	1	1,741	[0 – 6,094]	12.5	[0.0 – 50.0]
MX-POTR5	Absent	47	80,198	[67,938 – 85,317]	93.5	[79.6 – 100.0]
	Present	3	5,119	[0 – 17,379]	6.5	[0.0 – 20.4]
MX-PSME	Absent	2126	3,228,872	[3,081,498 – 3,403,191]	60.8	[57.7 – 63.7]
	Present	1389	2,109,550	[1,935,552 – 2,258,153]	39.2	[36.3 – 42.3]
MX-THPL	Absent	96	148,133	[105,313 – 189,940]	30.5	[21.9 – 39.5]
	Present	216	333,300	[291,320 – 376,707]	69.5	[60.5 – 78.2]
MX-TSHE	Absent	61	91,181	[56,206 – 121,962]	37.2	[23.6 – 51.3]
	Present	98	146,488	[115,534 – 181,648]	62.8	[48.6 – 76.4]
MX-TSME	Absent	116	174,979	[132,821 – 212,464]	56.7	[43.6 – 69.7]
	Present	86	129,726	[92,898 – 171,802]	43.3	[30.5 – 56.4]
None	Absent	765	1,325,350	[1,284,326 – 1,358,301]	95.3	[92.4 – 97.8]
	Present	37	64,102	[31,096 – 105,362]	4.7	[2.2 – 7.6]
TMIX	Absent	204	317,790	[259,837 – 383,288]	42.3	[34.1 – 50.3]
	Present	285	443,971	[377,834 – 501,605]	57.7	[549.6 – 65.8]

[a] 95% confidence intervals calculated from 40,000 bootstraps.

Table 7. Probability of suitable climate for root disease by dominance 40% plurality (DomMid40) class. See Barber et al. (2011) for detailed descriptions of DomMid40 classes.

DomMid40 Class	Probability of suitable climate for root disease	VMap tree acres[a]	Percentage of VMap tree acres
HMIX	Prob. < 0.5	10,576	66.2
	Prob. ≥ 0.5	5,410	33.8
IMIX	Prob. < 0.5	322,329	67.0
	Prob. ≥ 0.5	159,009	33.0
MX-ABGR	Prob. < 0.5	405,140	22.7
	Prob. ≥ 0.5	1,380,977	77.3
MX-ABLA	Prob. < 0.5	2,167,583	90.7
	Prob. ≥ 0.5	222,243	9.3
MX-JUNIP	Prob. < 0.5	13,745	100.0
	Prob. ≥ 0.5	0	0.0
MX-LALY	Prob. < 0.5	37,999	100.0
	Prob. ≥ 0.5	0	0.0
MX-LAOC	Prob. < 0.5	592,386	50.6
	Prob. ≥ 0.5	577,621	49.4
MX-PIAL	Prob. < 0.5	460,255	100.0
	Prob. ≥ 0.5	21	0.0
MX-PICO	Prob. < 0.5	3,793,675	89.9
	Prob. ≥ 0.5	428,495	10.1
MX-PIEN	Prob. < 0.5	907,428	68.1
	Prob. ≥ 0.5	424,431	31.9
MX-PIFL2	Prob. < 0.5	58,683	100.0
	Prob. ≥ 0.5	7	0.0
MX-PIMO3	Prob. < 0.5	49	1.7
	Prob. ≥ 0.5	2,865	98.3
MX-PIPO	Prob. < 0.5	1,062,738	80.3
	Prob. ≥ 0.5	261,329	19.7
MX-POPUL	Prob. < 0.5	4,931	62.9
	Prob. ≥ 0.5	2,904	37.1
MX-POTR5	Prob. < 0.5	264	98.9
	Prob. ≥ 0.5	3	1.1
MX-PSME	Prob. < 0.5	3,886,628	68.0
	Prob. ≥ 0.5	1,830,926	32.0
MX-THPL	Prob. < 0.5	45,007	9.4
	Prob. ≥ 0.5	431,753	90.6
MX-TSHE	Prob. < 0.5	13	0.0
	Prob. ≥ 0.5	64,750	100.0
MX-TSME	Prob. < 0.5	137,448	39.4
	Prob. ≥ 0.5	211,676	60.6
TMIX	Prob. < 0.5	212,236	52.8
	Prob. ≥ 0.5	190,097	47.3

[a] All VMap polygons (or portions of polygons) were within National Forest boundaries and had LIFEFORM = 4000 (TREE).

Comparisons of root disease severity on FIA plots with predicted root disease severity from the root disease severity model

Of the estimated 7.9 million forested acres in Region 1 affected by root disease, FIA crews identified low-severity root disease (Hagle ratings 1-3) on 4,223 subplots representing nearly 6.5 million acres, or 29% of the total forested area in the region (Table 8, Fig. 6). Moderate-to-high severity root disease (Hagle ratings 4-9) was observed on 932 FIA subplots, representing an estimated 1.4 million acres, or 6% of the total forested area in the region (Table 8, Fig. 6). The root disease severity model outputs represent mean FIA plot severity values, and the maximum root disease severity rating was only 3.26, while the Hagle severity values assigned to the FIA subplots range from 0 to 9. This makes it particularly difficult to directly compare the observed severity and modeled severity values. The root disease severity model predicted that approximately 9.5 million acres, nearly 47% of the total forested acres on National Forest lands, had the potential for low-severity root disease (Table 9, Fig. 6).

Table 8. Root disease severity for Region 1 based on estimates from the FIA summary database (2011 hybrid).

Root disease severity class[a]	FIA subplots	Acres	Acres [95% C.I.][b]	Percentage of acres	Percentage of acres [95% C.I.][b]
None	9,527	14,611,480	[14,301,642 – 14,948,574]	65.0	[63.5 – 66.4]
L	4,223	6,476,780	[6,165,786 – 6,758,225]	28.7	[27.4 – 30.0]
MH	932	1,429,401	[1,279,904 – 1,578,488]	6.3	[5.7 – 7.0]
Total	14,682	22,517,661		100.0	

[a] None = 0; L (low) = 1- 3; MH (moderate-to-high) = 4- 9. Root disease severity ratings are those described by Hagle (1992).
[b] confidence intervals were calculated from 40,000 bootstraps.

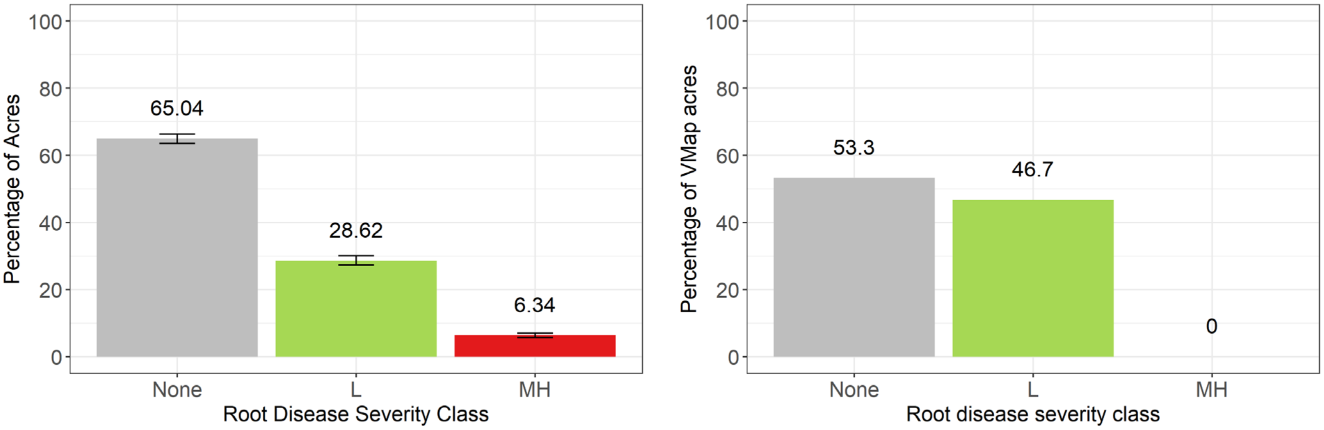


Figure 6. Left: Root disease severity on forested acres in Region 1 from the 2011 hybrid FIA summary database, expressed as percentage of total acres. Error bars represent 95% confidence intervals for the estimate calculated from 40,000 bootstraps. All FIA subplots occurred on forested potential vegetation type (PVT) and were associated with National Forests in Region 1. Right: Root disease severity predicted from the Holden et al. (2020) root disease severity model. Estimated percentage of acres. Values reflect the percentage of total VMap acres for all VMap polygons (or portions of polygons) within National Forest boundaries for which LIFEFORM = 4000 (TREE).

Table 9. Root disease severity for all forested VMap acres in Region 1 based on model outputs from the Holden et al. (2020) severity model.

Root disease severity class[a]	VMap tree acres[b]	Percentage of VMap tree acres
None	10,826,746	53.3
L	9,486,882	46.7
MH	0	0.0
Total	20,313,628	100.0

[a] None = 0; L (low) = 1- 3; MH (moderate-to-high) = 4- 9. Root disease severity ratings are those described by Hagle (1992).
[b] Acreage values reflect the sum of VMap polygons within National Forest boundaries for which LIFEFORM = 4000 (TREE).

According to the Forest-level estimates from the FIA summary database, the area with significant root disease impacts (moderate-to-high severity) ranged from 32,628 acres (1%) on the BDNF to 356,000 acres (nearly 15%) on the IPNF (Table 10, Fig. 7). The Holden et al. (2020) root disease severity model also identified the IPNF as having the most root disease, though the model outputs did not yield any values exceeding the threshold for moderate-to-high severity (i.e. Hagle rating of 4). The model predicted that nearly 2.5 million acres (approx. 94%) of national forest land in the IPNF would have low-severity root disease (Table 11, Fig. 8), compared to the total of 1.5 million acres affected by root disease (approx. 62%) estimated from the FIA summary database (Table 10, Fig. 7). Low-severity root disease was observed on 748 FIA subplots on the IPNF representing approximately 1.15 million acres (47%) (Table 10, Fig. 7).

In Montana, the Flathead National Forest (FNF) had the greatest root disease impacts with over 1.1 million acres (nearly 50% of the forest) affected by root disease, and an estimated 231,000 acres (approx. 10% of the forest) having moderate-to-high severity based on FIA estimates (Table 10, Fig. 7). Root disease was also present on about 50% of the KNF, but many fewer acres were in the moderate-to-high severity category. The root disease severity model predicted nearly 1.6 million acres of low-severity root disease on the FNF, approximately 79% of the total forested area within the FNF boundary (Table 11, Fig. 8). The model yielded similar results for the KNF, with nearly 1.9 million acres of low-severity root disease representing nearly 80% of the forested area within the KNF boundary (Table 11, Fig. 8).

The estimates of root disease from the severity model for forests east of the Continental Divide were much lower than the observed values from the FIA summary database. For the BDNF, the root disease severity model predicted 0 acres in the each of the low and moderate-to-high severity categories (Table 11, Fig. 8), while the estimates from the FIA database indicated that almost 9% of the total forested area on the BDNF had root disease, with just over 225,000 acres having low severity and nearly 33,000 acres having moderate-to-high severity (Table 10, Fig. 7). The Custer-Gallatin National Forest (CGNF) was predicted by the root disease severity model to have only 2,900 acres (0.16%) of forest with low-severity root disease (Table 11, Fig. 8), while the FIA database estimates showed nearly 15% of that forest as having root disease, with over 326,000 acres of low severity impacts, and nearly 49,000 acres of moderate-to-high severity impacts observed (Table 10, Fig. 7).

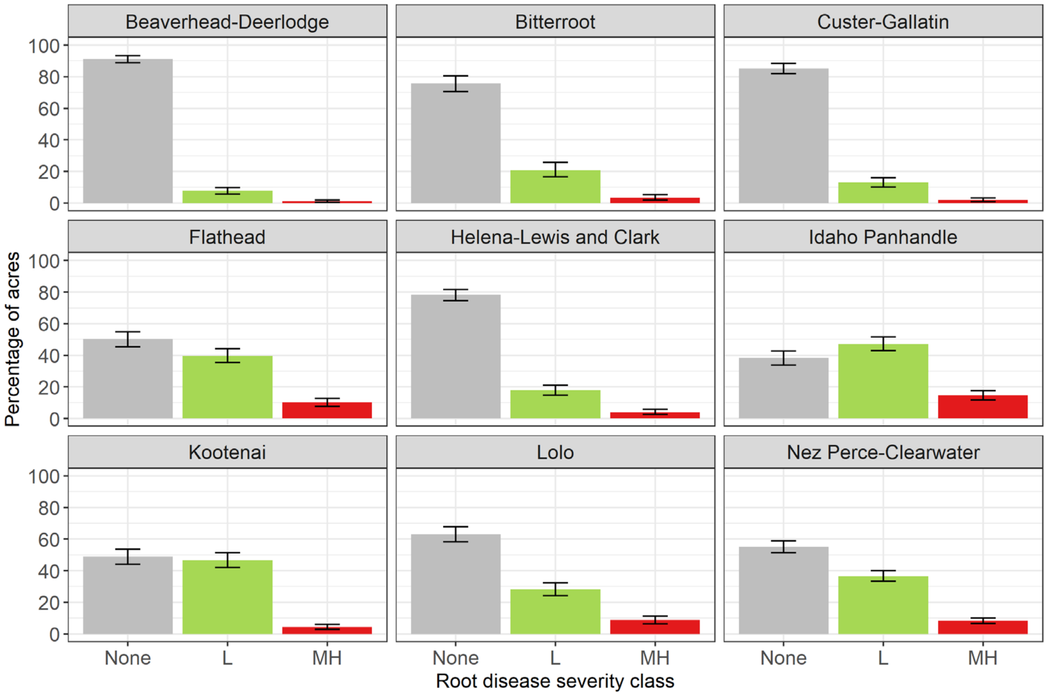


Figure 7. Estimated percentage of forested area in three root disease severity classes for Region 1 National Forests from Region 1 FIA summary database. Error bars represent 95% confidence intervals calculated from 40,000 bootstraps.

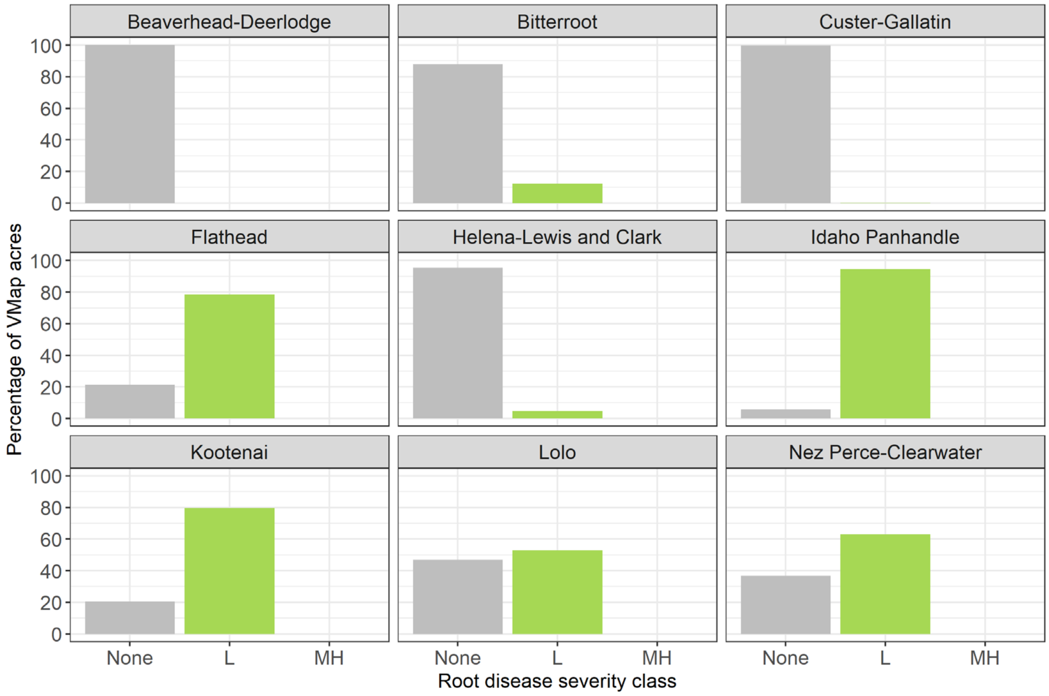


Figure 8. Bottom: Estimated percentage of VMap acres per forest based on model outputs from the Holden et al. (2020) root disease severity model. Acreage values reflect the percentage of acres for all VMap polygons (or portions of polygons) within National Forest boundaries for which LIFEFORM = 4000 (TREE). Root disease severity classes are as follows: None = 0, L (low) = 1-3; MH (moderate-to-high) = 4-9.

Table 10. Summary of root disease severity in FIA subplots on nine national forests in Region 1, including estimates of acres and percentage of acres in three root disease severity classes.

Forest	Root disease severity class[a]	FIA subplots	Acres	Acres [95% C.I.][b]	Percentage of acres	Percentage of acres [95% C.I.][b]
Beaverhead-Deerlodge	None	1693	2,630,439	[2,564,138 – 2,696,743]	91.1	[88.8 – 93.4]
	L	145	225,289	[164,607 – 286,409]	7.7	[5.7 – 9.9]
	MH	21	32,628	[14,297 – 54,677]	1.1	[0.5 – 1.9]
Bitterroot	None	746	1,136,871	[1,064,188 – 1,214,758]	75.7	[70.5 – 80.5]
	L	210	320,031	[247,671 – 385,794]	20.8	[16.4 – 25.6]
	MH	34	51,814	[27,534 – 82,014]	3.5	[1.8 – 5.4]
Custer-Gallatin	None	1331	2,088,167	[2,018,311 – 2,174,547]	85.2	[81.9 – 88.3]
	L	208	326,325	[248,628 – 393,583]	13.0	[10.1 – 16.0]
	MH	31	48,635	[21,010 – 75,987]	1.9	[0.9 – 3.1]
Flathead	None	812	1,203,407	[1,066,286 – 1,285,574]	50.3	[45.5 – 54.8]
	L	614	909,965	[831,314 – 1,034,025]	39.6	[35.5 – 44.1]
	MH	156	231,196	[179,031 – 298,417]	10.1	[7.6 – 12.7]
Helena-Lewis and Clark	None	1377	2,109,240	[2,016,276 – 2,209,800]	78.2	[74.5 – 81.6]
	L	318	487,101	[399,525 – 570,205]	17.8	[14.8 – 21.1]
	MH	72	110,287	[69,642 – 151,679]	4.0	[2.6 – 5.6]
Idaho Panhandle	None	602	928,015	[824,357 – 1,042,145]	38.4	[33.8 – 42.8]
	L	748	1,153,082	[1,043,656 – 1,254,717]	47.1	[42.8 – 51.5]
	MH	231	356,099	[283,738 – 430,019]	14.6	[11.6 – 17.6]
Kootenai	None	767	1,095,710	[959,831 – 1,170,912]	49.0	[44.1 – 53.7]
	L	691	987,139	[917,022 – 1,119,128]	46.6	[42.1 – 51.4]
	MH	67	95,714	[60,368 – 134,330]	4.4	[2.8 – 6.2]
Lolo	None	860	1,336,563	[1,241,680 – 1,440,761]	63.0	[58.4 – 67.7]
	L	393	610,778	[514,884 – 688,456]	28.1	[24.2 – 32.4]
	MH	116	180,281	[134,678 – 239,230]	8.8	[6.3 – 11.2]

Forest	Root disease severity class[a]	FIA subplots	Acres	Acres [95% C.I.][b]	Percentage of acres	Percentage of acres [95% C.I.][b]
Nez Perce-Clearwater	None	1339	2,207,258	[2,070,578 – 2,363,595]	55.2	[51.5 – 58.8]
	L	896	1,477,000	[1,340,166 – 1,605,482]	36.6	[33.3 – 39.9]
	MH	204	336,281	[261,255 – 407,321]	8.2	[6.5 – 10.1]

[a]None = 0; L (low) = 1- 3; MH (moderate-to-high) = 4- 9. Root disease severity ratings are those described by Hagle (1992).
[b]confidence intervals were calculated from 40,000 bootstraps.

Table 11. Root disease severity on forested VMap acres in Region 1 based on model outputs from the Holden et al. (2020) severity model.

Forest	Root disease severity class	VMap tree acres[a]	Percentage of VMap tree acres
Beaverhead-Deerlodge	None	2,303,837	100.0
	L	0	0.0
	MH	0	0.0
Bitterroot	None	1,037,969	87.8
	L	144,544	12.2
	MH	0	0.0
Custer-Gallatin	None	1,861,054	99.8
	L	2,898	0.2
	MH	0	0.0
Flathead	None	428,423	21.4
	L	1,576,680	78.6
	MH	0	0.0
Helena-Lewis and Clark	None	2,272,929	95.3
	L	111,073	4.7
	MH	0	0.0
Idaho Panhandle	None	147,581	5.7
	L	2,459,794	94.3
	MH	0	0.0
Kootenai	None	481,339	20.3
	L	1,884,961	79.7
	MH	0	0.0
Lolo	None	1,064,334	47.0
	L	1,198,897	53.0
	MH	0	0.0
Nez Perce-Clearwater	None	1,229,280	36.8
	L	2,108,036	63.2
	MH	0	0.0

[a]Acreage values reflect the sum of VMap polygons within National Forest boundaries for which LIFEFORM = 4000 (TREE).

According to the FIA summary database, root disease was present on an estimated 2.1 million acres in the MX-PSME class (Table 12), compared with the approximately 2.6 million acres predicted from the Holden et al. root disease severity model (Table 13, Fig. 10). The MX-PSME class had the most total area (over 400,000 acres) with moderate-to-high root disease severity of any DomMid40 class in the FIA database (Table 12). This accounted for approximately 7.6% of the total area in that DomMid40 class (Table 12, Fig. 9). In the MX-ABGR class, over 850,000 acres (57.6%) had root disease present, with over 660,000 acres having low severity and 190,000 acres having moderate-to-high severity (Table 12, Fig. 9). The MX-ABGR class had the highest proportion of acres (nearly 13%) in the moderate-to-high severity category of any DomMid40 class in the FIA database (Table 12, Fig. 9). Of the approximately 1.1 million acres (39%) of MX-ABLA with root disease present, about 913,000 had low-severity root disease and 200,000 acres had moderate-to-high severity based on FIA database estimates (Table 12, Fig. 9). The root disease severity model predicted just over 720,000 acres with the potential for low-severity root disease in the MX-ABLA class (30%), and nearly 1.6 million acres (88%) in the MX-ABGR class (Table 13, Fig. 10).

From both the observed and modeled values for root disease severity, the forest types with a plurality of pines have the lowest overall root disease occurrence and the lowest root disease severity (Tables 12, 13; Figs. 9, 10). Root disease was virtually absent on the high-elevation five-needle pine (MX-PIAL and MX-PIFL2) DomMid40 classes in both the FIA database and the root disease severity model outputs. However, there was some disagreement between observed and modeled values about the occurrence and severity of root disease in stands with the MX-PIPO class. An estimated 99,928 acres (11%) of MX-PIPO had low-severity root disease based on FIA plot data (Table 12), while the root disease severity model predicted that approximately 470,000 acres (35%) in the MX-PIPO class would have root disease (Table 13). Estimates from the FIA database suggested that 23,257 acres of MX-PIPO forest had moderate-to-high root disease that was not represented in the root disease severity model outputs.

There was also agreement between the observed and modeled values for the MX-PICO class. The estimate of total area affected by root disease from the FIA database was 1.02 million acres (22%), whereas the root disease severity model predicted 1.01 million acres (24%) (Tables 12, 13; Figs. 9, 10). The values for the total area in the low root disease severity category for MX-PICO were also close, as the FIA database did not have many subplots for which there was moderate-to-high root disease severity in the MX-PICO DomMid40 class. Thus, most of the FIA subplots in MX-PICO with root disease present were in the low-severity category (Table 12). The DomMid40 classes MX-TSHE and MX-THPL had the greatest overall estimated proportions of area with root disease from the FIA database, with approximately 63% and 70%, respectively (Table 12, Fig. 9). These classes also had the highest percentage of acres of root disease from the root disease severity model outputs, but the values were much higher, with MX-TSHE and MX-THPL predicted to have 99.9% and 97% of acres with low-severity root disease, respectively (Table 13, Fig. 10).

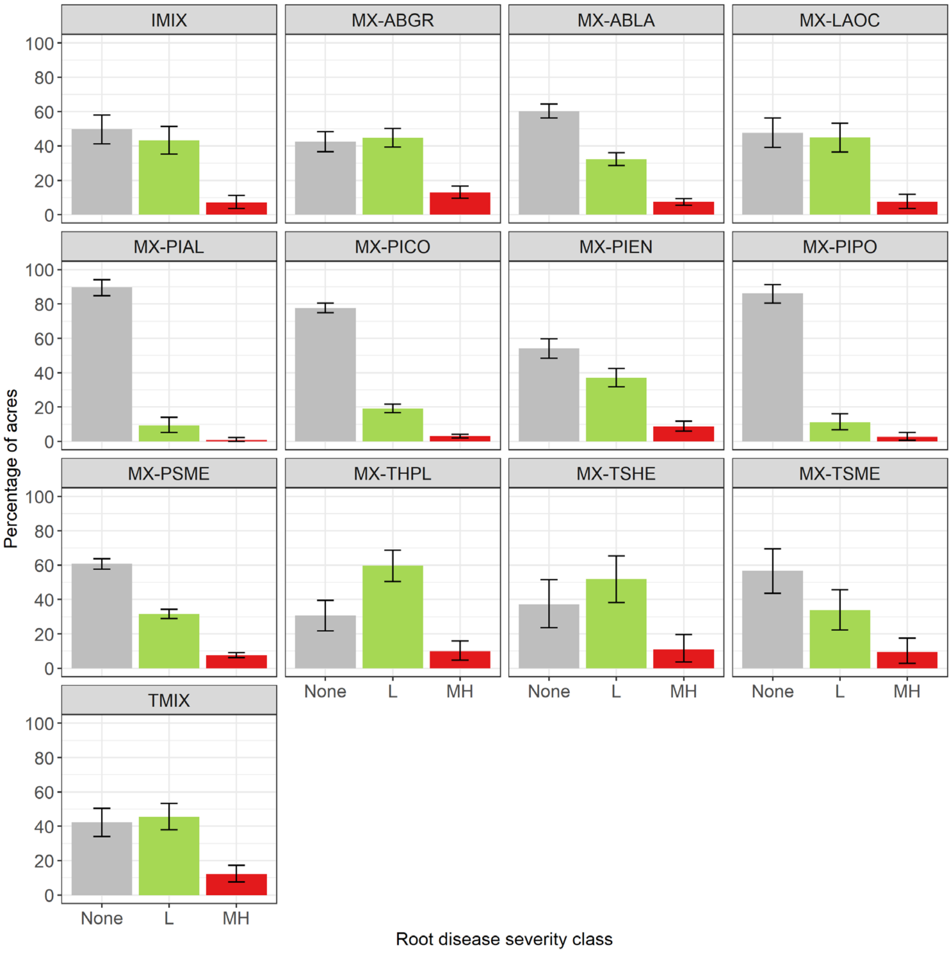


Figure 9. Root disease severity (percentage of acres) in selected dominance 40% plurality (DomMid40) classes for Region 1 National Forests from the R1 FIA summary database. Error bars represent 95% confidence intervals calculated from 40,000 bootstraps. All DomMid40 types are shown in Table 12. Root disease severity classes are as follows: None = 0, L (low) = 1-3; MH (moderate-to-high) = 4-9. See Barber et al. (2011) for detailed descriptions of DomMid40 classes.

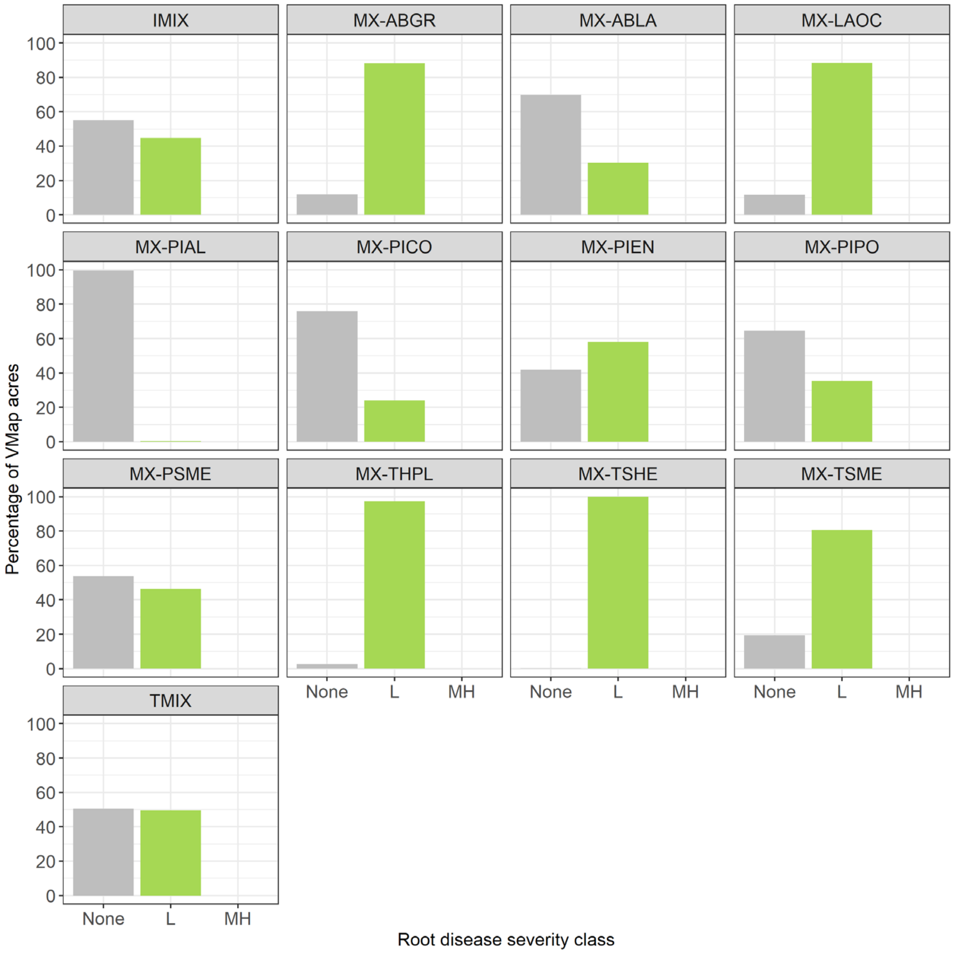


Figure 10. Root disease severity (percentage of acres) in selected dominance 40% plurality (DomMid40) classes for Region 1 VMap polygons (or portions of polygons) within National Forest boundaries. Root disease data are from Holden et al. (2020) root disease severity model outputs. All DomMid40 types are shown in Table 13. Acreage values reflect the percentage of acres for all VMap polygons (or portions of polygons) within National Forest boundaries for which LIFEFORM = 4000 (TREE). Root disease severity classes are as follows: None = 0, L (low) = 1-3; MH (moderate-to-high) = 4-9. See Barber et al. (2011) for detailed descriptions of DomMid40 classes.

Table 12. Root disease severity by dominance 40% plurality (DomMid40) class for all Region 1 forests from the R1 FIA summary database. See Barber et al. (2011) for detailed descriptions of DomMid40 classes.

DomMid40 class	Root Disease Severity Class[a]	FIA subplots	Acres	Acres [95% C.I.][b]	Percentage of acres	Percentage of acres [95% C.I.][b]
HMIX	None	2	3,047	[0 – 5,332]	50.0	[0 – 87.5]
	L	2	3,047	[0 – 5,332]	50.0	[0 – 87.5]
	MH	0	0	-	0.0	-
IMIX	None	226	345,080	[283,592 – 399,958]	49.7	[41.2 – 58.1]
	L	193	294,692	[242,708 – 353,241]	43.2	[35.2 – 51.3]
	MH	32	48,861	[24,378 – 77,175]	7.1	[3.5 – 11.2]
MX-ABGR	None	412	635,505	[543,929 – 716,580]	42.4	[36.6 – 48.2]
	L	429	661,727	[585,029 – 746,378]	44.7	[39.3 – 50.2]
	MH	123	189,726	[141,841 – 245,987]	12.9	[9.5 – 16.5]
MX-ABLA	None	1147	1,748,410	[1,611,669 – 1,846,535]	60.3	[56.3 – 64.5]
	L	599	913,076	[819,511 – 1,033,383]	32.2	[28.6 – 36.1]
	MH	133	202,736	[153,408 – 269,609]	7.4	[5.4 – 9.4]
MX-BEPA	None	4	6,094	-	100.0	-
	L	0	0	-	0.0	-
	MH	0	0	-	0.0	-
MX-CELE3	None	4	6,094	-	100.0	-
	L	0	0	-	0.0	-
	MH	0	0	-	0.0	-
MX-FRPE	None	1	6,094	-	100.0	-
	L	0	0	-	0.0	-
	MH	0	0	-	0.0	-
MX-JUNIP	None	51	79,223	-	100.0	-
	L	0	0	-	0.0	-
	MH	0	0	-	0.0	-
MX-LALY	None	25	42,028	[27,085 – 48,753]	87.5	[55.6 – 100]
	L	4	6,725	[0 – 20,894]	12.5	[0 – 42.9]
	MH	0	0	-	0.0	-
MX-LAOC	None	212	319,291	[257,400 – 371,197]	47.7	[39.1 – 56.4]
	L	193	290,676	[240,591 – 350,247]	44.9	[36.6 – 53.2]
	MH	32	48,195	[23,858 – 77,992]	7.4	[3.6 – 11.9]
MX-PIAL	None	493	759,290	[719,203 – 797,075]	89.8	[84.9 – 94.1]
	L	52	80,087	[44,057 – 118,591]	9.3	[5.2 – 14.0]
	MH	5	7,701	[0 – 19,762]	0.9	[0.0 – 2.3]
MX-PICO	None	2371	3,556,625	[3,426,500 – 3,681,604]	77.7	[74.9 – 80.4]
	L	583	874,531	[766,179 – 998,627]	19.2	[16.7 – 21.8]
	MH	97	145,505	[96,156 – 192,311]	3.1	[2.1 – 4.2]
MX-PIEN	None	549	833,951	[748,935 – 926,789]	54.2	[48.4 – 59.9]
	L	380	577,234	[493,842 – 656,634]	37.1	[31.9 – 42.4]
	MH	90	136,713	[92,564 – 182,482]	8.7	[6.0 – 11.8]
MX-PIFL2	None	114	173,682	[158,065 – 182,823]	95.0	[86.5 – 100]
	L	6	9,141	[0 – 24,376]	5.0	[0 – 13.3]
	MH	0	0	-	0.0	-
MX-PIMO3	None	8	12,188	[0 – 24,376]	50.0	[0 – 100]
	L	4	6,094	[0 – 24,376]	25.0	[0 – 100]
	MH	4	6,094	[0 – 24,376]	25.0	[0 – 100]
MX-PIPO	None	487	755,064	[707,252 – 800,210]	86.2	[80.6 – 91.2]
	L	64	99,228	[59,419 – 140,908]	11.1	[6.8 – 16.1]
	MH	15	23,257	[6,178 – 45,782]	2.7	[0.7 – 5.2]
MX-POPUL	None	6	10,447	[0 – 12,188]	87.5	[0 – 100]
	L	1	1,741	[0 – 6,094]	12.5	[0 – 50]
	MH	0	0	-	0.0	-
MX-POTR5	None	47	80,198	[67,938 – 85,317]	93.5	[79.6 – 100]
	L	2	3,413	[0 – 12,087]	4.2	[0 – 14.2]
	MH	1	1,706	[0 – 9,480]	2.4	[0 – 11.1]

DomMid40 class	Root Disease Severity Class[a]	FIA subplots	Acres	Acres [95% C.I.][b]	Percentage of acres	Percentage of acres [95% C.I.][b]
MX-PSME	None	2126	3,228,872	[3,080,270 – 3,402,871]	60.8	[57.7 – 63.7]
	L	1123	1,705,561	[1,546,114 – 1,836,791]	31.6	[29.0 – 34.4]
	MH	266	403,989	[328,153 – 484,142]	7.6	[6.1 – 9.1]
MX-THPL	None	96	148,133	[104,726 – 190,113]	30.5	[21.8 – 39.5]
	L	185	285,465	[243,321 – 330,586]	59.7	[50.5 – 68.7]
	MH	31	47,835	[22,468 – 76,177]	9.8	[4.7 – 15.8]
MX-TSHE	None	61	91,181	[56,021 – 122,136]	37.2	[23.6 – 51.4]
	L	81	121,077	[90,690 – 155,400]	51.9	[38.2 – 65.4]
	MH	17	25,411	[8,737 – 46,500]	10.9	[3.7 – 19.6]
MX-TSME	None	116	174,979	[132,903 – 211,806]	56.7	[43.6 – 69.5]
	L	67	101,065	[68,184 – 139,433]	33.8	[22.4 – 45.8]
	MH	19	28,660	[8,858 – 53,147]	9.5	[2.9 – 17.4]
none	None	765	1,325,350	[1,284,090 – 1,358,356]	95.3	[92.4 – 97.8]
	L	31	53,707	[24,163 – 91,162]	4.0	[1.7 – 6.6]
	MH	6	10,395	[0 – 28,192]	0.7	[0 – 2.0]
TMIX	None	204	317,790	[260,157 – 383,928]	42.3	[34.2 – 50.4]
	L	224	348,946	[289,424 – 405,859]	45.5	[38.0 – 53.3]
	MH	61	95,025	[57,437 – 131,945]	12.2	[7.5 – 17.3]

[a] None = 0; L (low) = 1- 3; MH (moderate-to-high) = 4- 9. Root disease severity ratings are those described by Hagle (1992).
[b] confidence intervals were calculated from 40,000 bootstraps.

Table 13. Root disease severity by dominance 40% plurality (DomMid40) class. DomMid40 data are from R1 VMap, and root disease severity data are from Holden et al. (2020) root disease severity model outputs. See Barber et al. (2011) for detailed descriptions of DomMid40 classes.

DomMid40 class	Root disease severity class	VMap acres[a]	Percentage of VMap acres
HMIX	None	1,218	7.6
	L	14,768	92.4
	MH	0	0.0
IMIX	None	265,514	55.2
	L	215,825	44.8
	MH	0	0.0
MX-ABGR	None	209,562	11.7
	L	1,576,555	88.3
	MH	0	0.0
MX-ABLA	None	1,668,239	69.8
	L	721,588	30.2
	MH	0	0.0
MX-JUNIP	None	13,743	100
	L	2	0.0
	MH	0	0.0
MX-LALY	None	37,878	99.7
	L	121	0.3
	MH	0	0.0
MX-LAOC	None	134,927	11.5
	L	1,035,080	88.5
	MH	0	0.0
MX-PIAL	None	458,307	99.6
	L	1,968	0.4
	MH	0	0.0
MX-PICO	None	3,209,890	76.0
	L	1,012,282	24.0
	MH	0	0.0
MX-PIEN	None	556,386	41.8
	L	775,472	58.2

DomMid40 class	Root disease severity class	VMap acres[a]	Percentage of VMap acres
	MH	0	0.0
MX-PIFL2	None	58,612	99.9
	L	78	0.1
	MH	0	0.0
MX-PIMO3	None	0	0.0
	L	2,913	100.0
	MH	0	0.0
MX-PIPO	None	855,203	64.6
	L	468,863	35.4
	MH	0	0.0
MX-POPUL	None	637	8.1
	L	7,199	91.9
	MH	0	0.0
MX-POTR5	None	0	0.0
	L	267	100.0
	MH	0	0.0
MX-PSME	None	3,073,592	53.8
	L	2,643,963	46.2
	MH	0	0.0
MX-THPL	None	12,206	2.6
	L	464,554	97.4
	MH	0	0.0
MX-TSHE	None	62	0.1
	L	64,701	99.9
	MH	0	0.0
MX-TSME	None	67,742	19.4
	L	281,381	80.6
	MH	0	0.0
TMIX	None	203,031	50.5
	L	199,302	49.5
	MH	0	0.0

[a]Acreage values reflect the sum of VMap polygons (or portions of polygons) within National Forest boundaries for which LIFEFORM = 4000 (TREE)

Conclusions

Root disease severity data from the 2011 hybrid version of the Region 1 FIA summary database were used as inputs for the Holden et al. (2020) climatic suitability and root disease severity models. These models estimated the probability of suitable climate for root disease and potential root disease severity over a continuous geographic extent across Region 1. Over the entire region, there is approximately one FIA plot every 6,000 acres. The FIA database uses an area expansion factor to calculate the total area accounted for by each FIA plot. This procedure also applies the FIA data to much larger area than that which is sampled. Thus, both the observed values from the FIA database and the model outputs assume that the FIA plots, which generally consist of four 1/24th acre subplots, are representative of the broader landscape. This assumption should be considered when interpreting the area estimates derived from these data sources.

Generally, the root disease data derived from the FIA summary database should be viewed as the most reliable available. It must also be recognized that root disease ratings recorded on FIA plots have limitations, such as being based on non-destructive ground observations. To estimate the Hagle root disease rating for a subplot, FIA crews are trained by Forest Health Protection personnel to recognize and evaluate above-ground symptoms such as diagnostic types of crown thinning, tree mortality, proportion of canopy loss, etc. There is likely some error associated with their root disease diagnoses and severity estimates due to subjectivity among crew members. These pathogens and the root diseases they cause have differences in their specific occurrences and expressions in different hosts and host mixtures, climates, soil textures and depths, stand histories, ages, and states of succession, and spacing among susceptible trees.

This report provides a comparison of the observed root disease occurrence and severity from FIA plots with the model outputs (climatic suitability for root disease and root disease severity) to assess the utility of the models. For land managers who are using these models to support their decision-making processes, it is important to consider the appropriate spatial scale(s) at which the root disease models are meant to be applied and interpreted. Brohman et al. (2005) define "broad-level" products as providing information used for regional, multi-state, and state-level assessments, "mid-level" products as providing support for multi-forest and forest needs such as planning and monitoring, and "base-level" products as providing the highest level of detail and being primarily used for within-forest and district needs. The climatic root disease suitability and severity models were not intended for use below the mid-level. These models are not appropriate for use at the watershed, district, or project area scales without localized data collection to verify whether model spatial output or FIA summary database estimates are representative at these levels. The differences between model results and FIA data for different National Forests in this report have indicated that the climatic suitability model, along with VMap-based predictions of the abundance of suitable hosts, may be useful for identifying general trends of areas where root disease is more likely to occur. However, local resource management knowledge along with further validation would be needed to determine whether and in what ways the model might be useful for deciding where to target ground surveys for root disease.

At the broad-level, the climatic suitability model has some utility for deriving numerical estimates of the acres with suitable climate for root disease. The relative proportion of area in Region 1 with climate predicted to be suitable for root disease to occur was close to the FIA database estimates of area with root disease present (Tables 1, 2), as was expected due to the fact that the climatic suitability model was developed using presence/absence data from the FIA summary database (Holden et al. 2020). It is the nature of such models to provide outputs that reflect broad overall trends. However, there were inconsistencies in the spatial distribution of modeled suitable climate for root disease and observed root disease occurrence. These indicate that model outputs should not be interpreted as being equivalent to the probability of root disease occurrence, rather they reflect the probability of suitable climate for root disease to potentially occur. The outputs of the climatic suitability model cannot be used to assess presence or absence of root disease on the ground, and while it may provide reasonable numerical estimates of the area with suitable climate, it may not provide reliable estimates of precise locations where the suitable climate occurs.

The incidence and severity of root disease in Region 1 appeared strongly influenced by an east-west gradient, with much greater impacts west of the Continental Divide. Overall, the modeled spatial distribution (i.e., geographic location) of suitable climate had much greater representation in forests west of the Continental Divide where root disease was more common (i.e. Nez Perce-Clearwater NF, Idaho Panhandle NF) than in forests east of the Divide. At the forest level, the climatic suitability model appeared to slightly overestimate the area with climate suitable for root disease west of the Divide and slightly underestimate the area with climate suitable for root disease east of the Divide, compared to the FIA data. The Flathead National Forest is an exception to this characterization, as this forest—the easternmost of the National Forests west of the Divide—had numerical estimates of area with suitable climate for root disease that were very low compared to the area with root disease present based on FIA observations. The greatest evidence of spatial inaccuracy of the climatic suitability model was the observed prevalence of root disease on FIA plots in locations where the model predicted low climatic suitability for root disease development (Appendix B).

The root disease severity values from the root disease severity model are much lower than the values observed on FIA subplots, due to averaging of subplot values to produce whole-plot FIA values for modeling. While the Hagle root disease severity rating system ranges from 0 to 9, the outputs from the root disease severity model range from 0 to 3.26, resulting in a very conservative estimate of root disease severity from the model. At the broad-level, there were 1.43 million acres estimated to have moderate-to-high root disease severity from the FIA database while the model predicted none. While the rankings of National Forests and DomMid40 classes by root disease severity were generally consistent between the model and the FIA summary database estimates, the area estimates and spatial distribution of root disease severity derived from the model were not consistent with those from the FIA database (Appendix B), and thus were deemed too unreliable for use in management planning and analysis. Holden et al. (2020) found that only a small proportion (about 20%) of the variation in root disease severity was explained by the climatic and biophysical variables in the root disease severity model, indicating the model had relatively low predictive accuracy. The authors also noted that the distribution of FIA plots is not well suited for predicting spatial variation in root disease severity in Region 1 (Holden et al. 2020). There is also an inherent difficulty in modeling stochastic ecological systems. Many of the factors influencing the occurrence and severity of root disease are not well described, and models such as these are not intended to incorporate all possible influencing factors.

The climatic suitability and root disease severity models were developed by associating the observed spatial variation in root disease data from the FIA database with climatic and biophysical variables. These associations were then used to predict climatic suitability and root disease severity over a continuous spatial distribution across the landscape. This suggests that the models may be biased towards providing more accurate predictions where root disease was most abundant and/or where there were greater numbers or densities of FIA plots. For instance, the model predictions for climatic suitability on the Nez Perce-Clearwater NF were very close to the observed root disease occurrence values from the FIA database, and this forest had the most FIA plots and some of the highest root disease occurrence and severity values in the FIA database. On the other hand, some forests east of the Continental Divide (e.g. Beaverhead-Deerlodge and Custer Gallatin) where there is lower root disease occurrence and the climate is less suitable for root disease to occur were predicted by the models to have little or no root disease despite the fact that the FIA database estimates showed hundreds of thousands of acres with root disease on those forests.

Land managers should consider the relative reliability of each of the data sources presented here. The FIA observations are the most reliable source of root disease data and thus should carry the most weight when considering root disease occurrence and severity in the decision-making process. Despite its limitations and potential errors in individual readings, assessment of numbers of acres of root disease that are derived directly from proportions of affected FIA plots, as summarized herein, appear more likely to be useful than the models based on the same data. The climatic suitability model may provide reasonable estimates of the spatial distribution of suitable climate for forests west of the Continental Divide. This model is less useful for predicting the spatial distribution of suitable climate for the Flathead National Forest and for forests east of the Continental Divide, and thus will have much less utility for land managers on those forests. The root disease severity model is the least reliable of the three data sources and should not be used for any planning or monitoring purposes.

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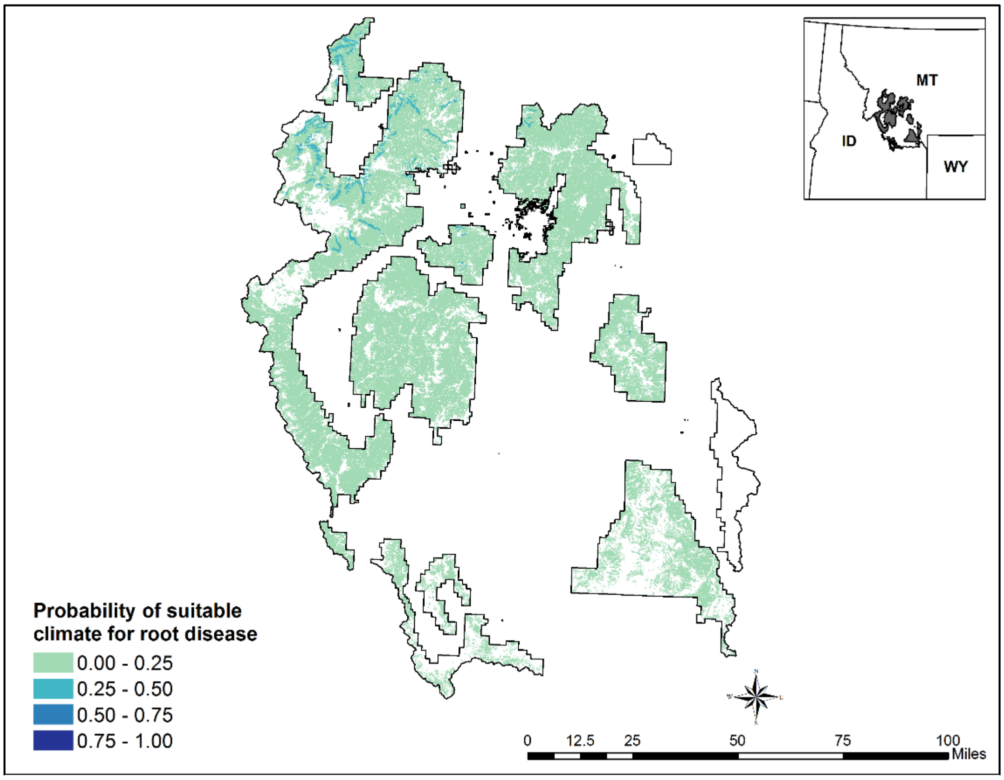
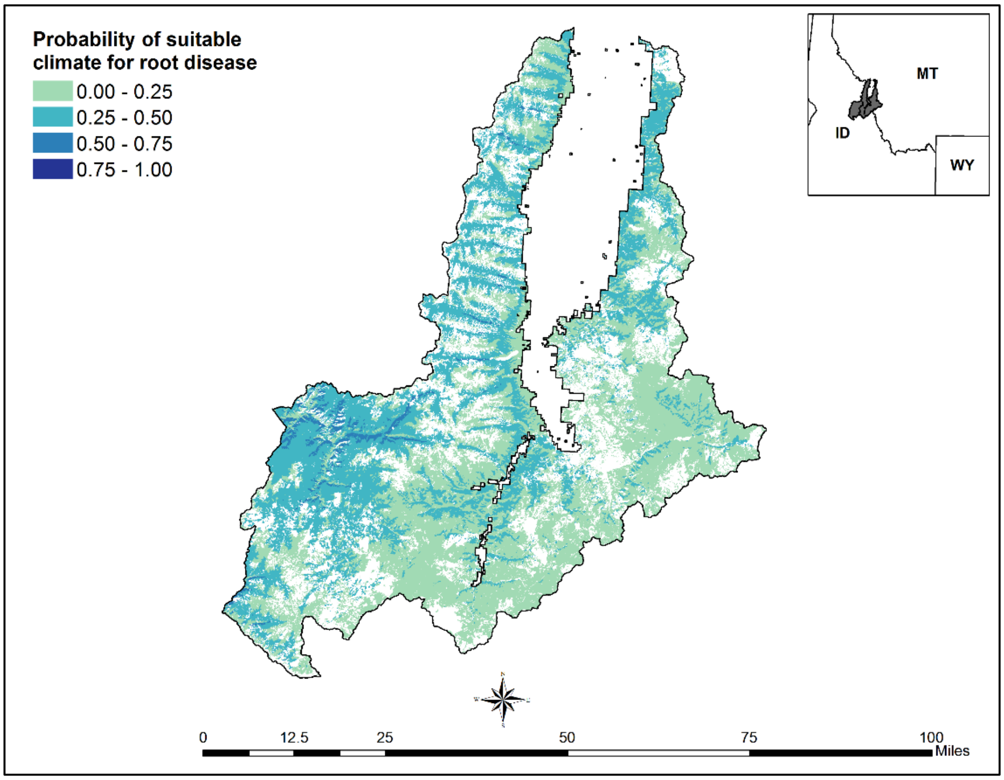
Appendix A: Maps showing modelled probability of suitable climate for root disease on all National Forest lands in Region 1

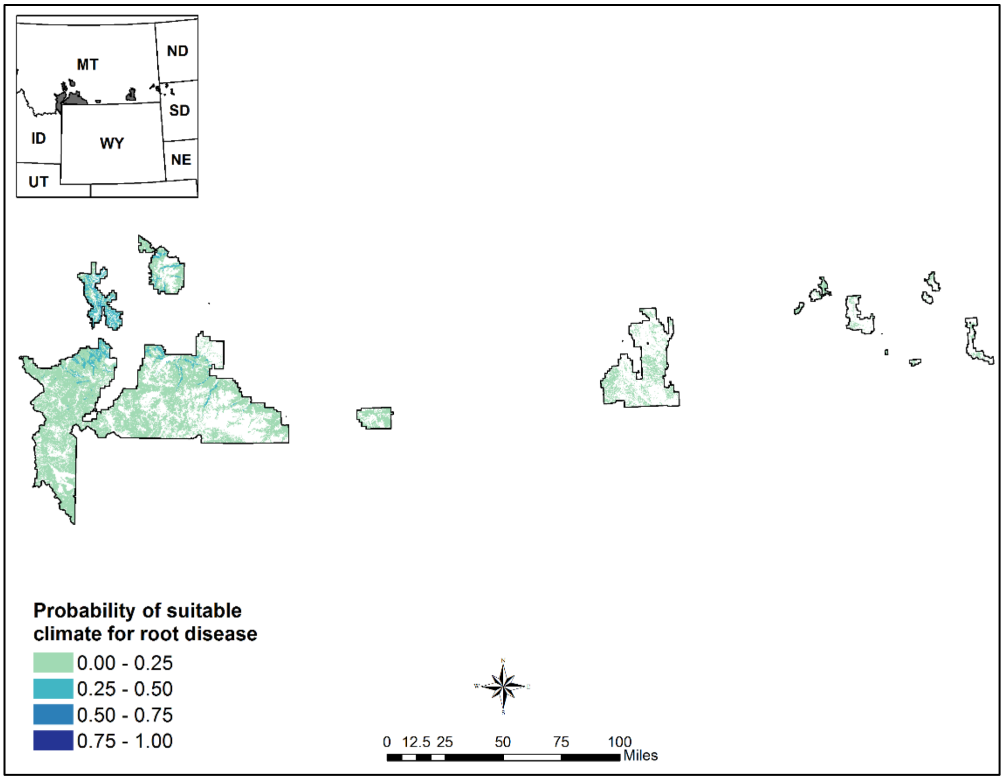
Beaverhead-Deerlodge National Forest



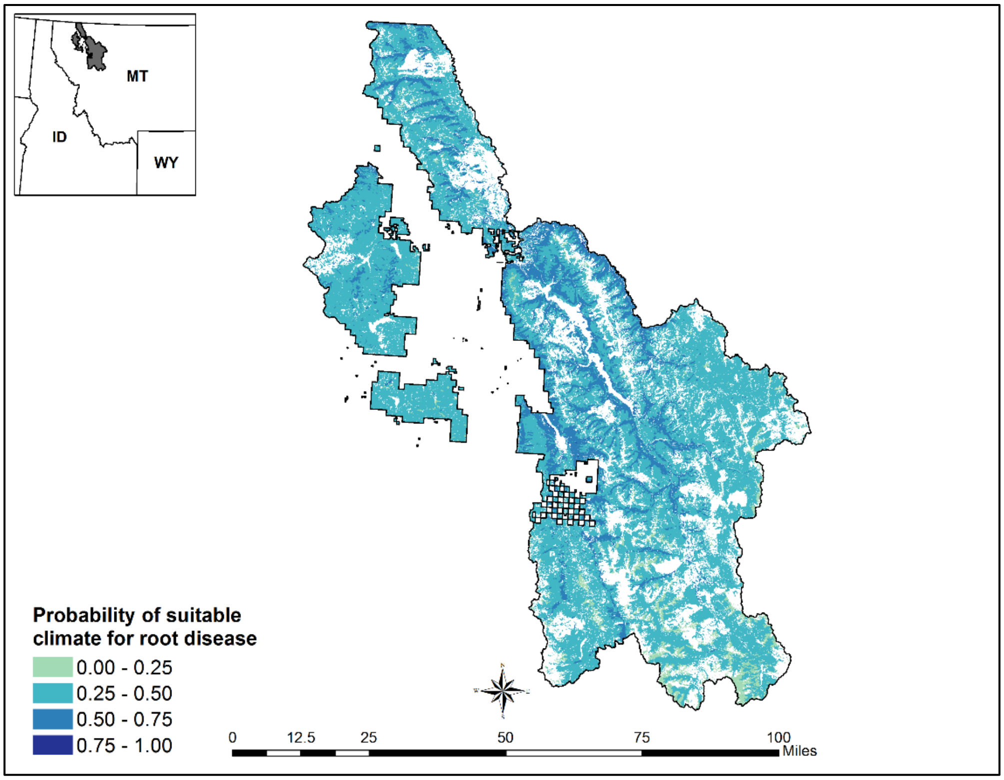
Bitterroot National Forest



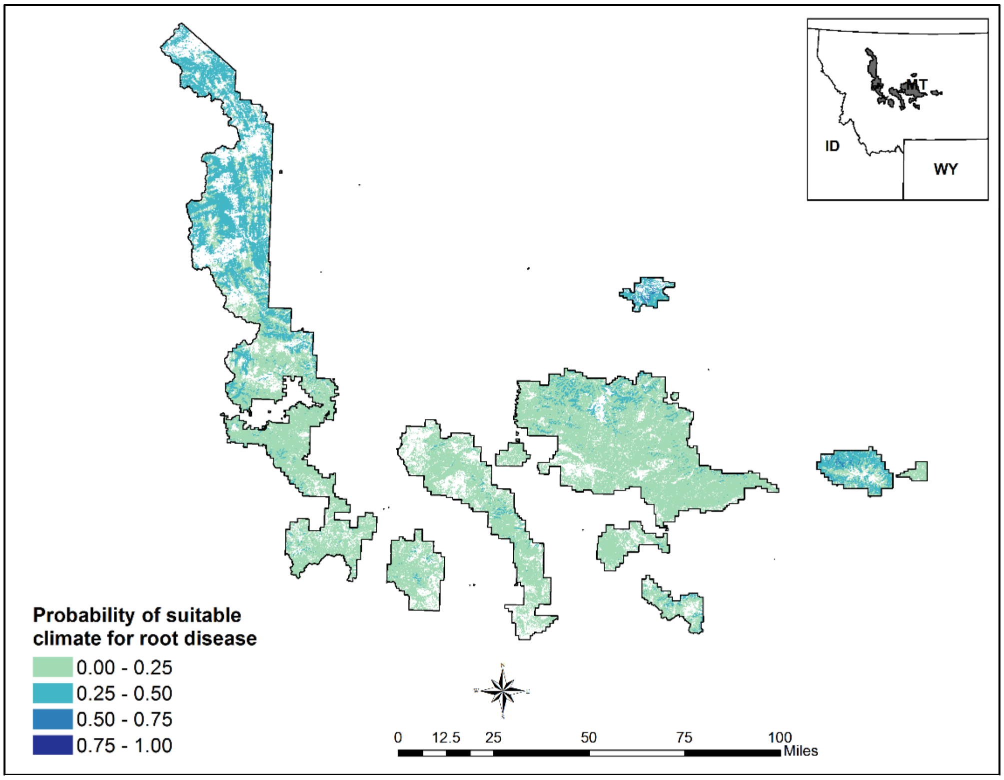
Custer-Gallatin National Forest



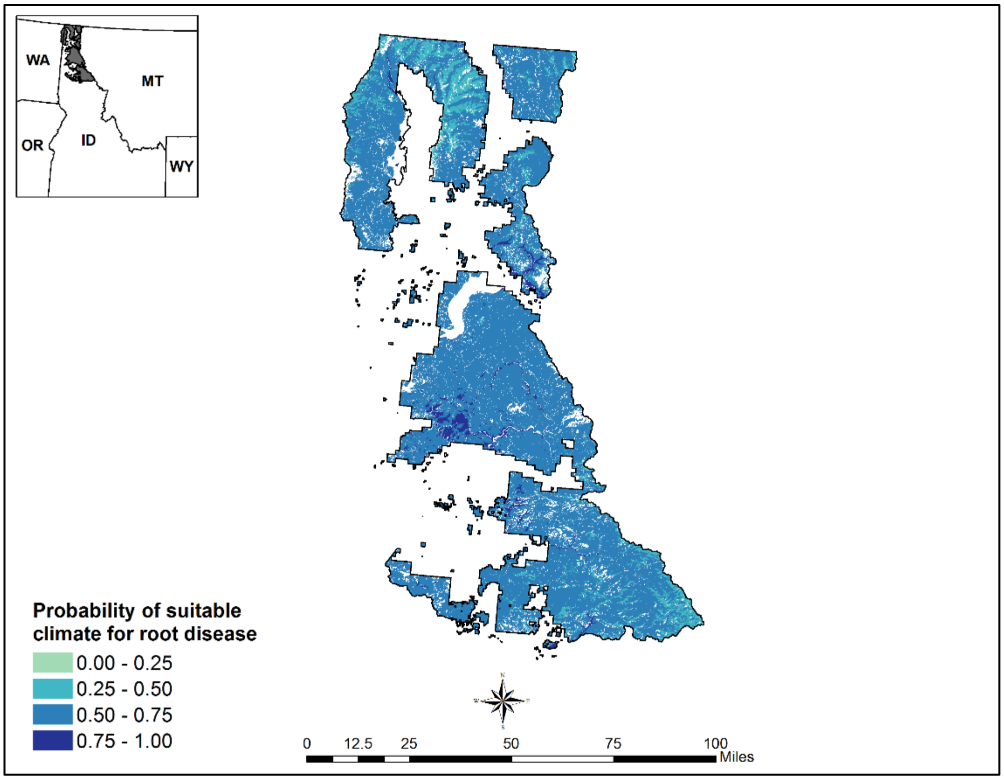
Flathead National Forest



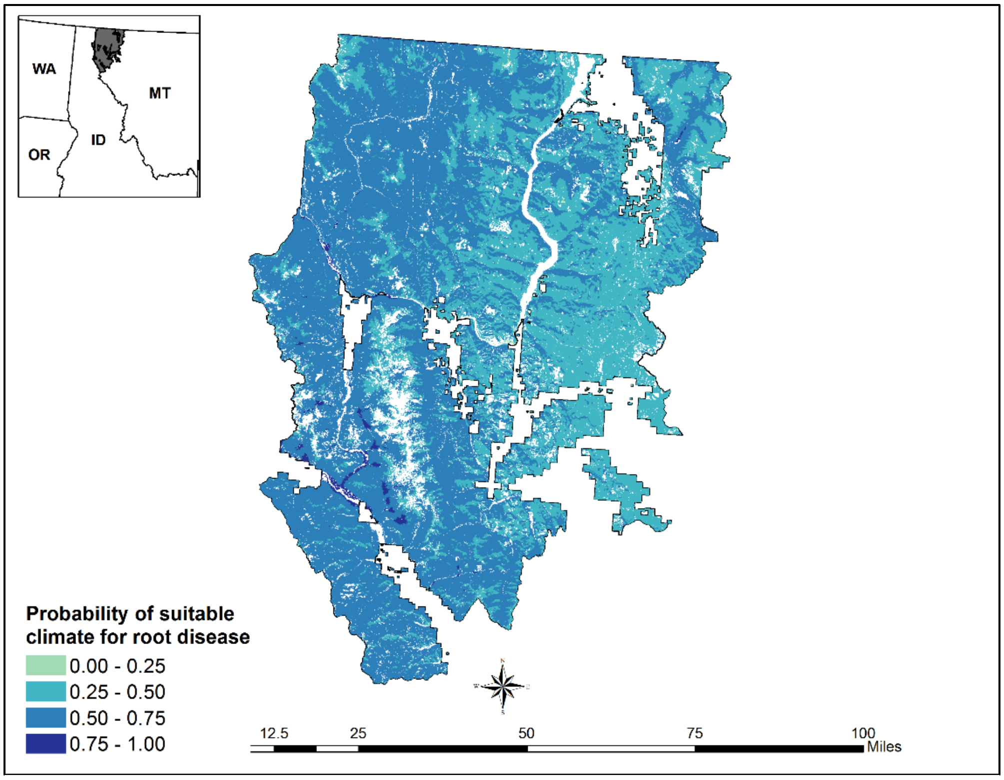
Helena-Lewis and Clark National Forest



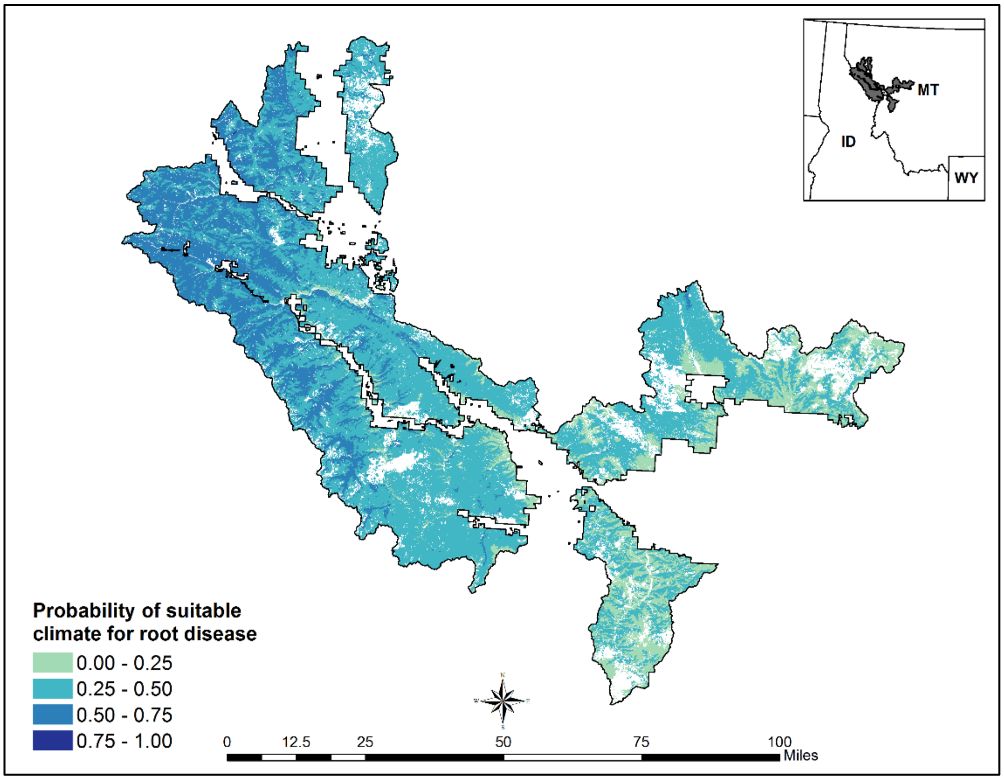
Idaho Panhandle National Forest



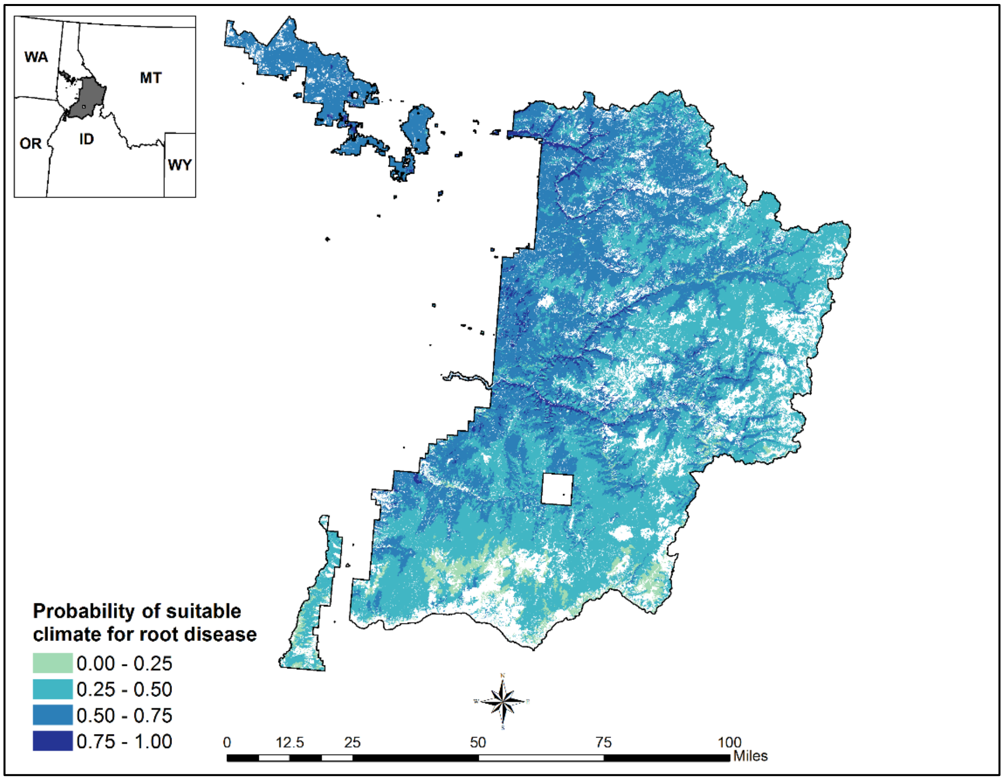
Kootenai National Forest



Lolo National Forest

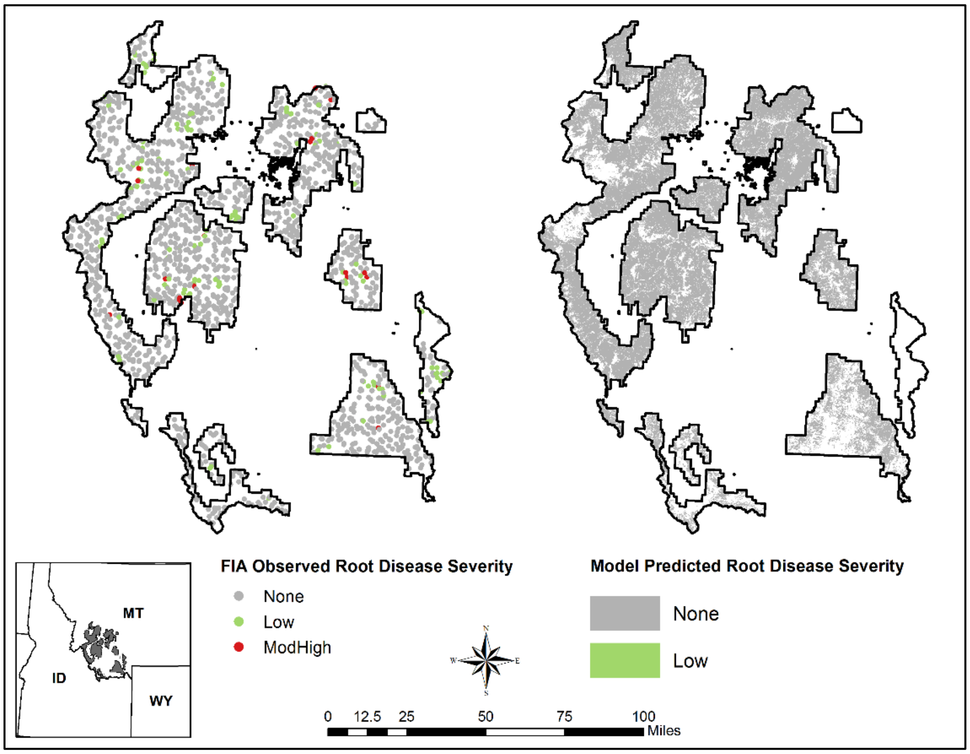


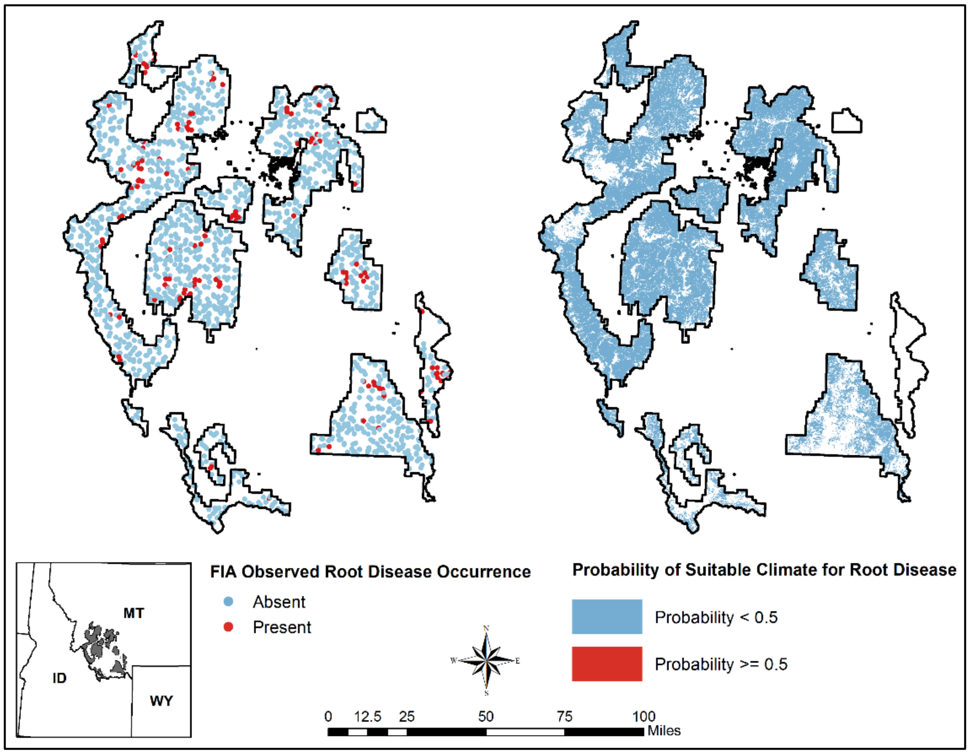
Nez Perce-Clearwater National Forest



Appendix B: Maps showing spatial distributions of root disease on FIA subplots* and R1 VMap polygons for all National Forest lands in Region 1

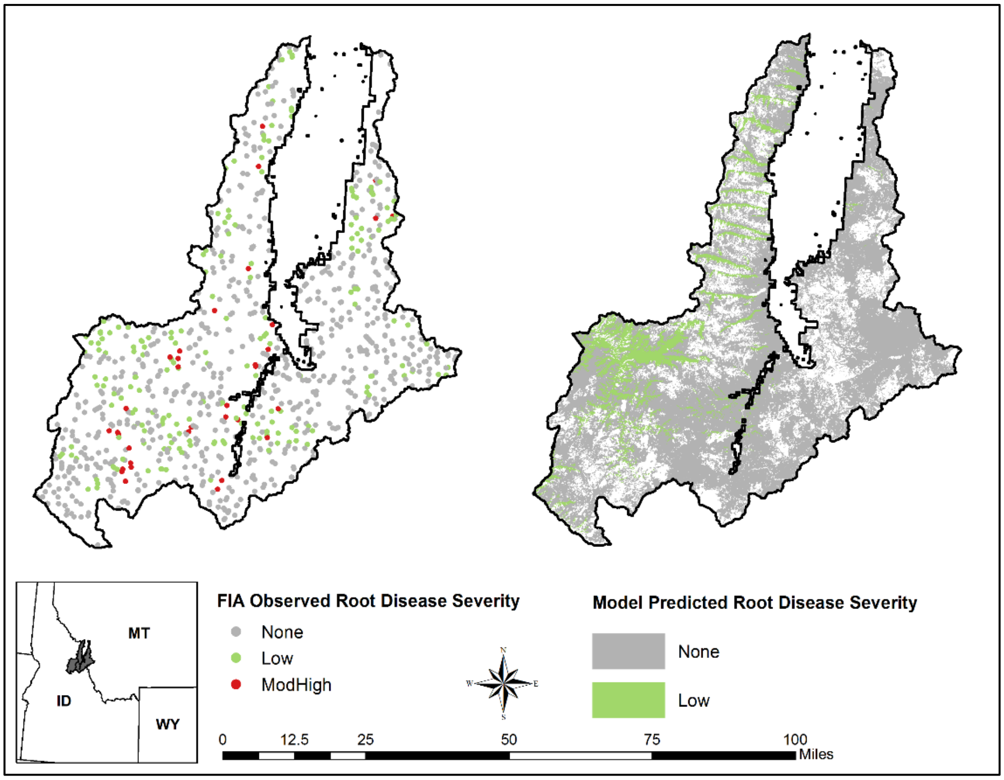
Beaverhead-Deerlodge National Forest

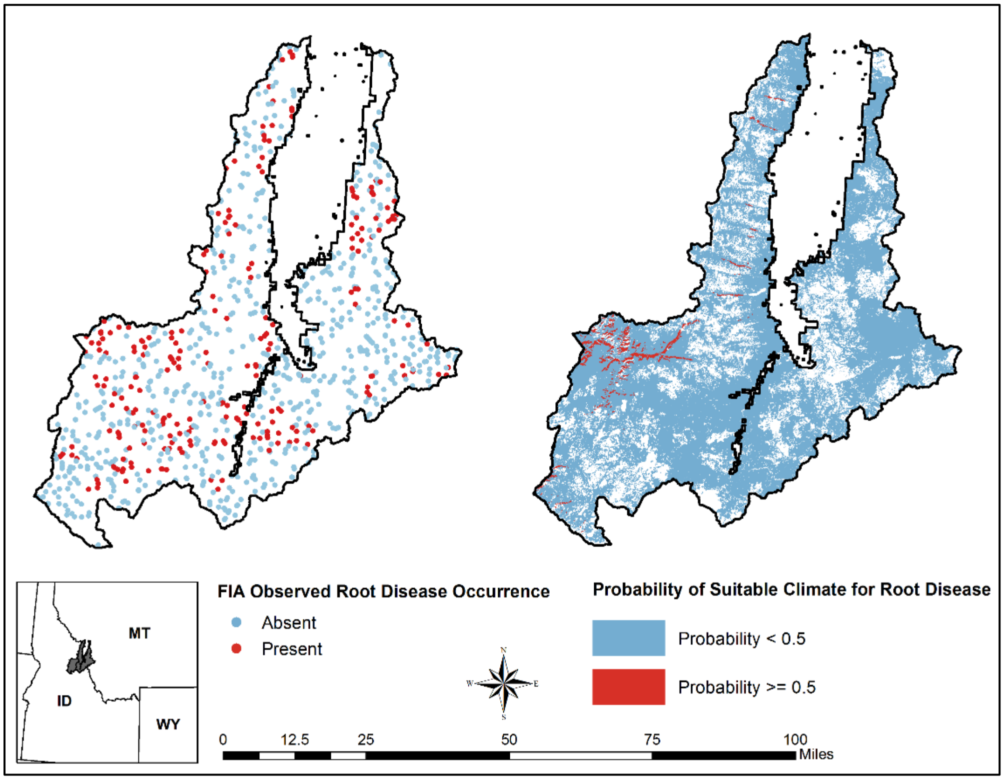




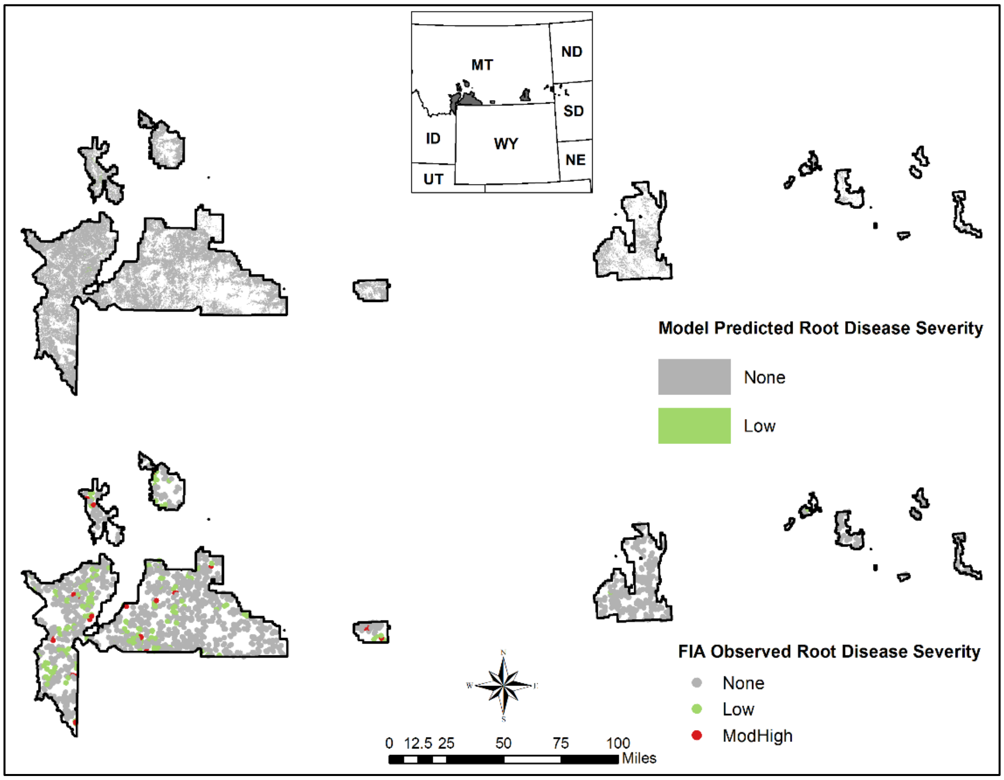
*Note: The FIA subplots shown on these maps do not reflect precise locations. The coordinates have been “fuzzed” to protect the confidentiality and integrity of FIA plots, in accordance with the Food Security Act of 1985 (reference 7 USC 2276 § 1770).

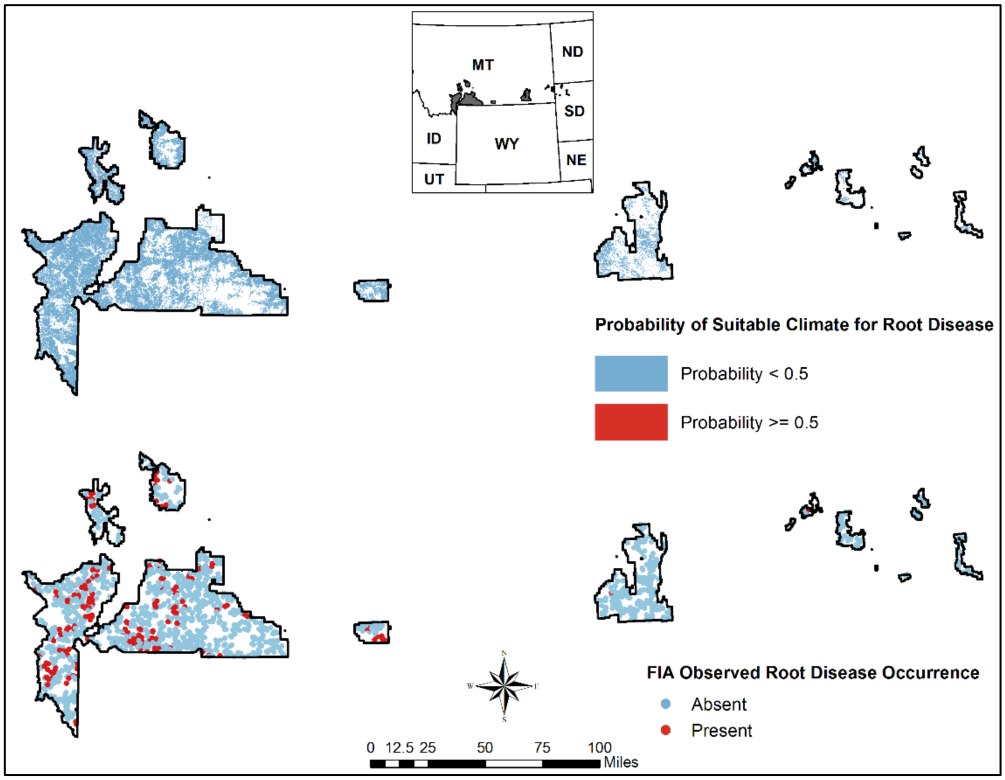
Bitterroot National Forest



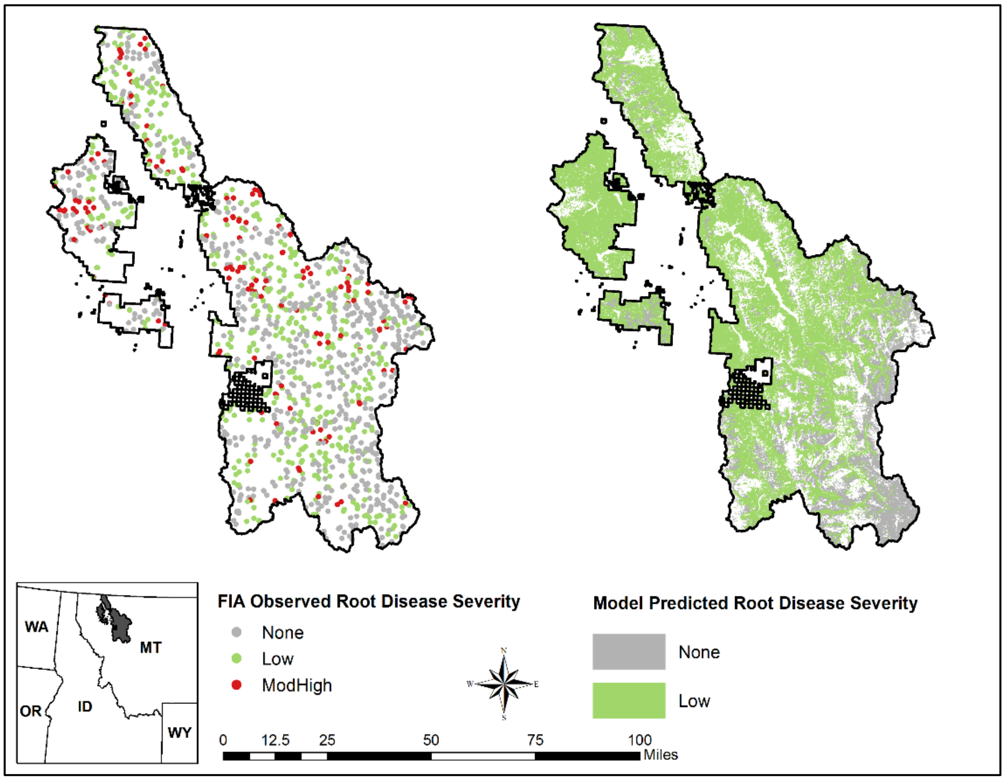


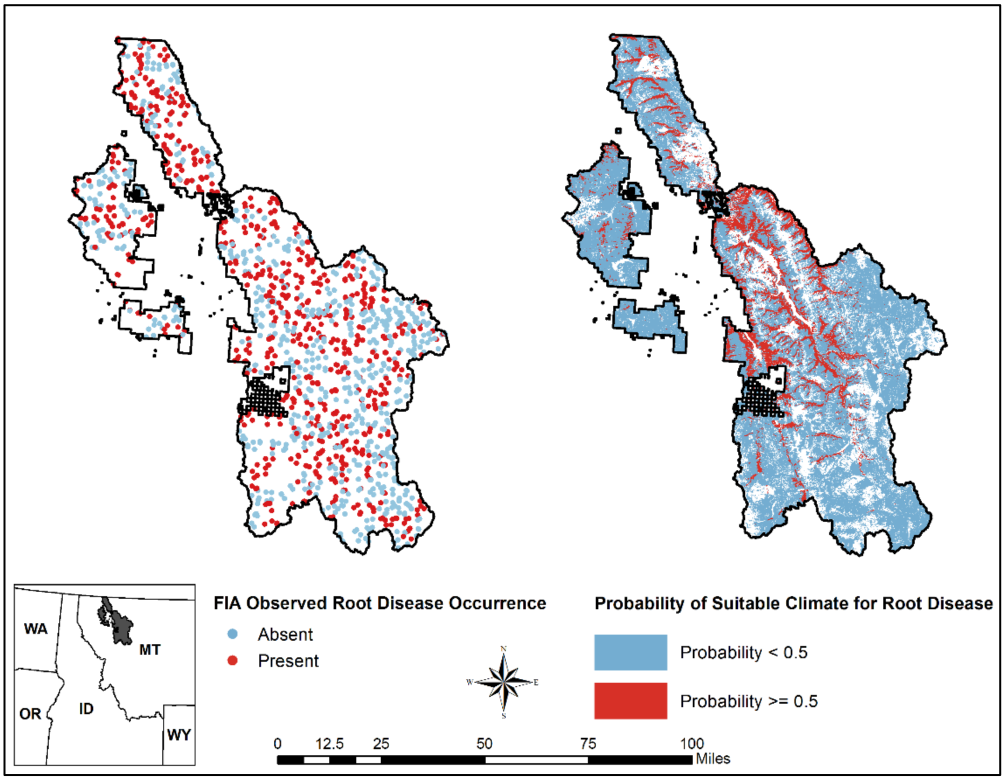
Custer-Gallatin National Forest



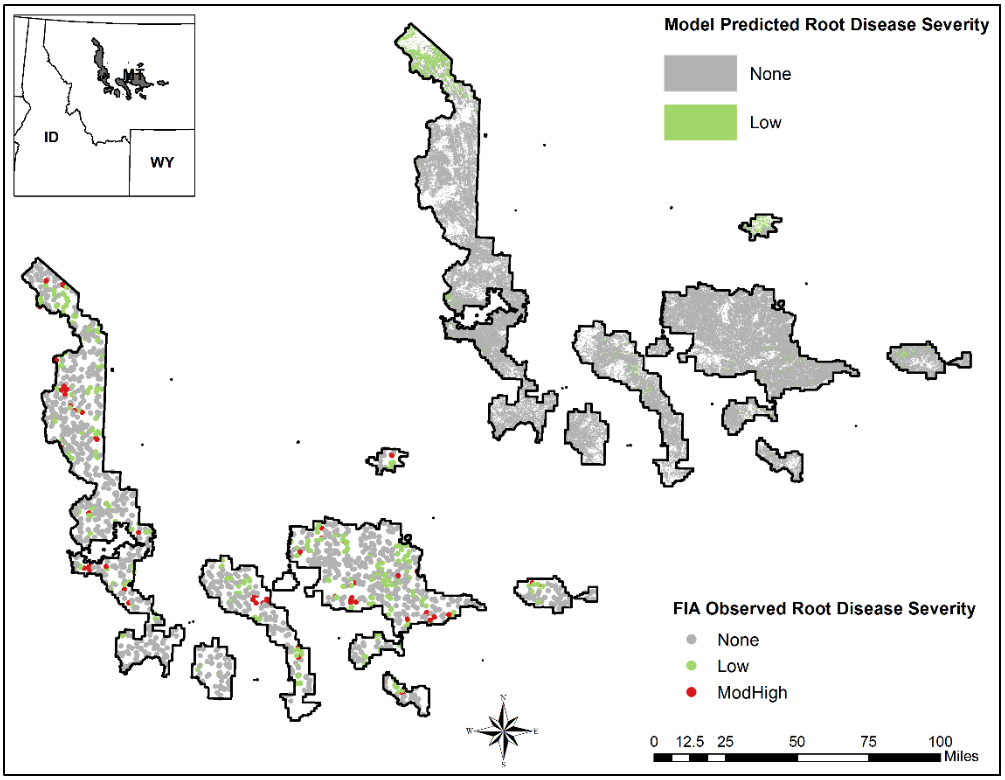


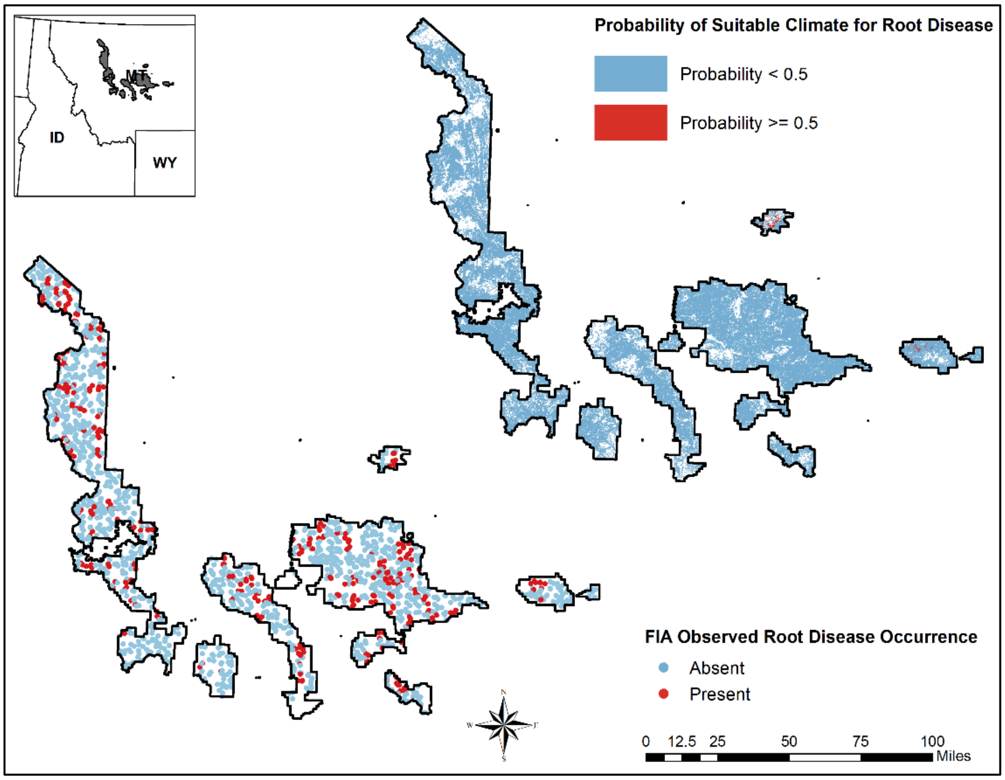
Flathead National Forest



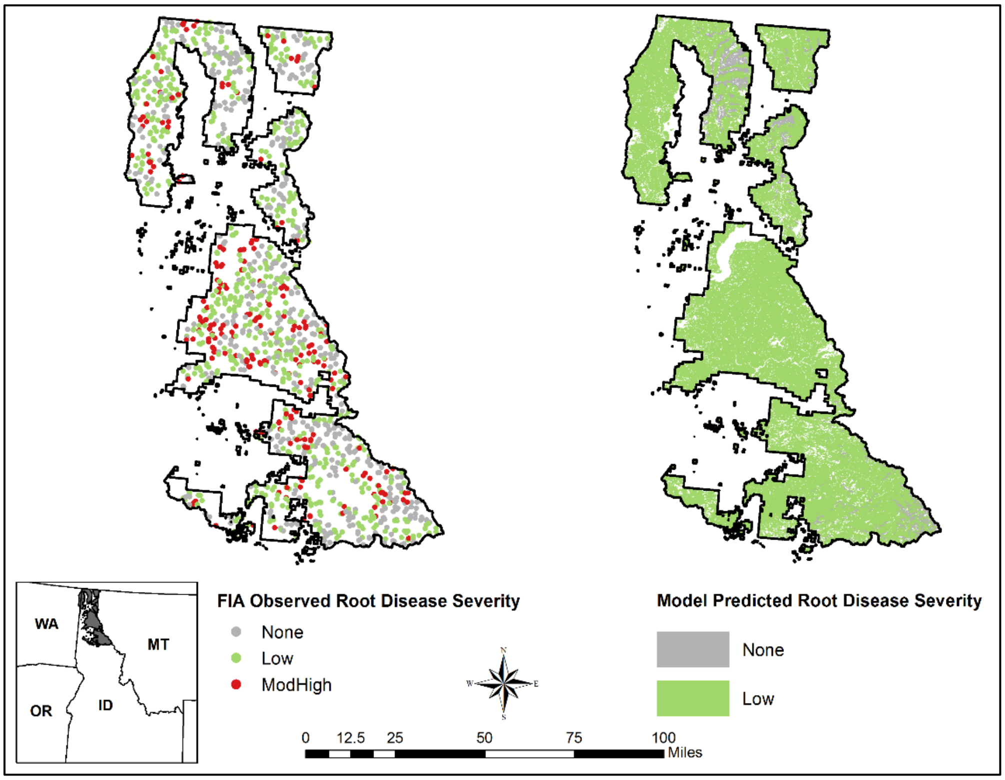


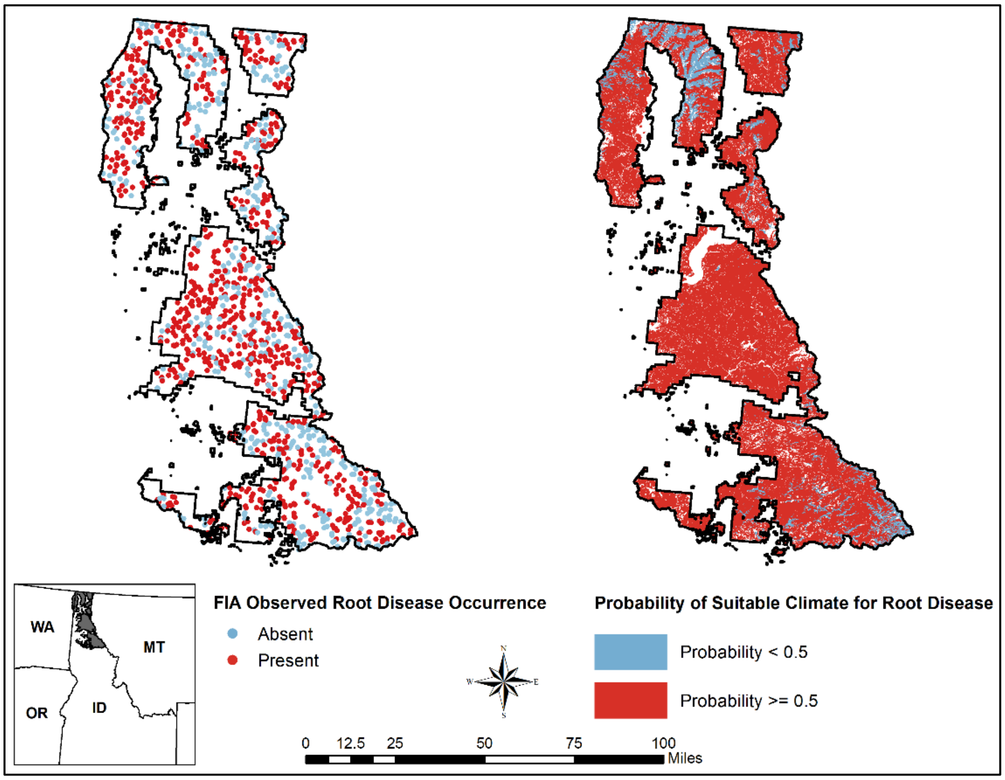
Helena-Lewis and Clark National Forest



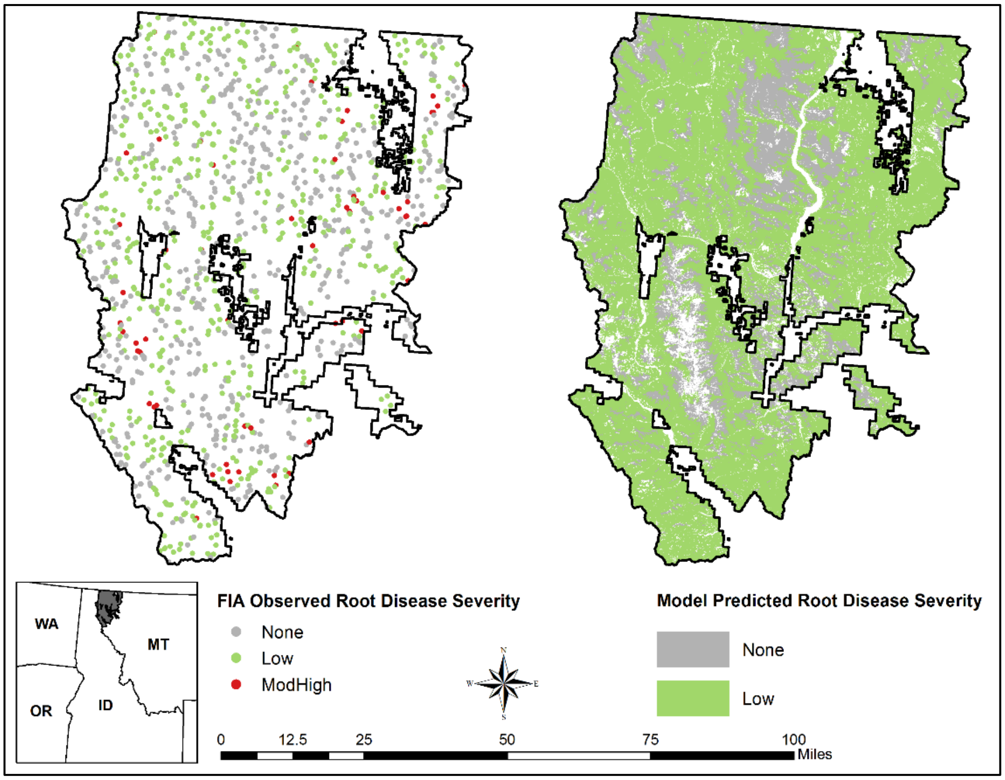


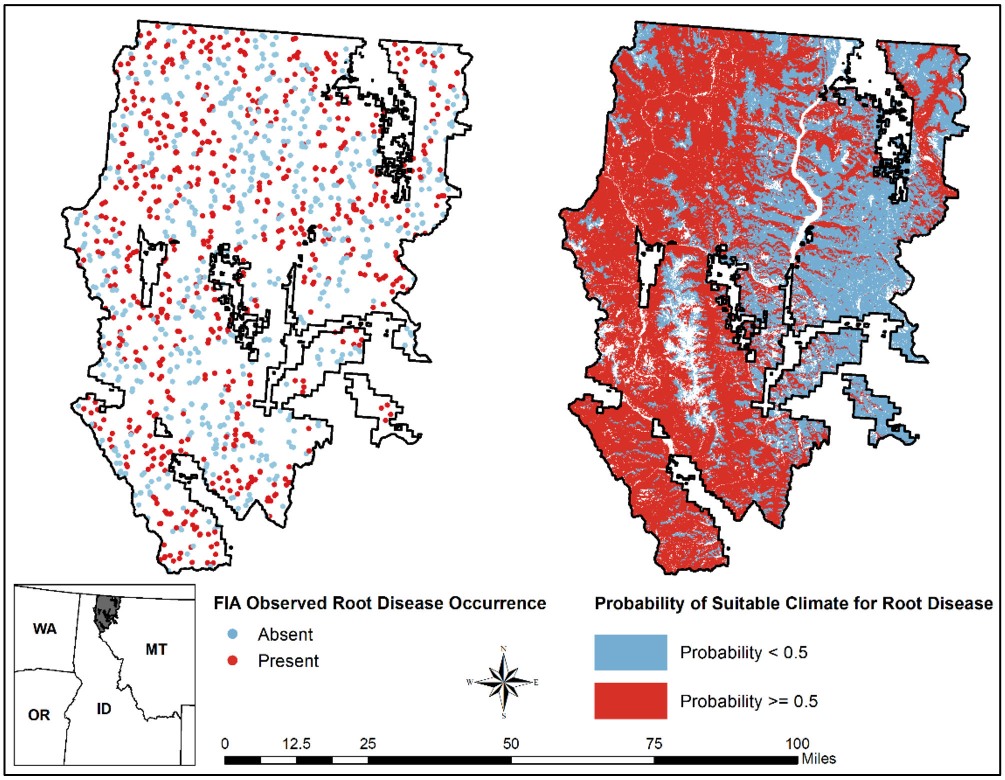
Idaho Panhandle National Forests



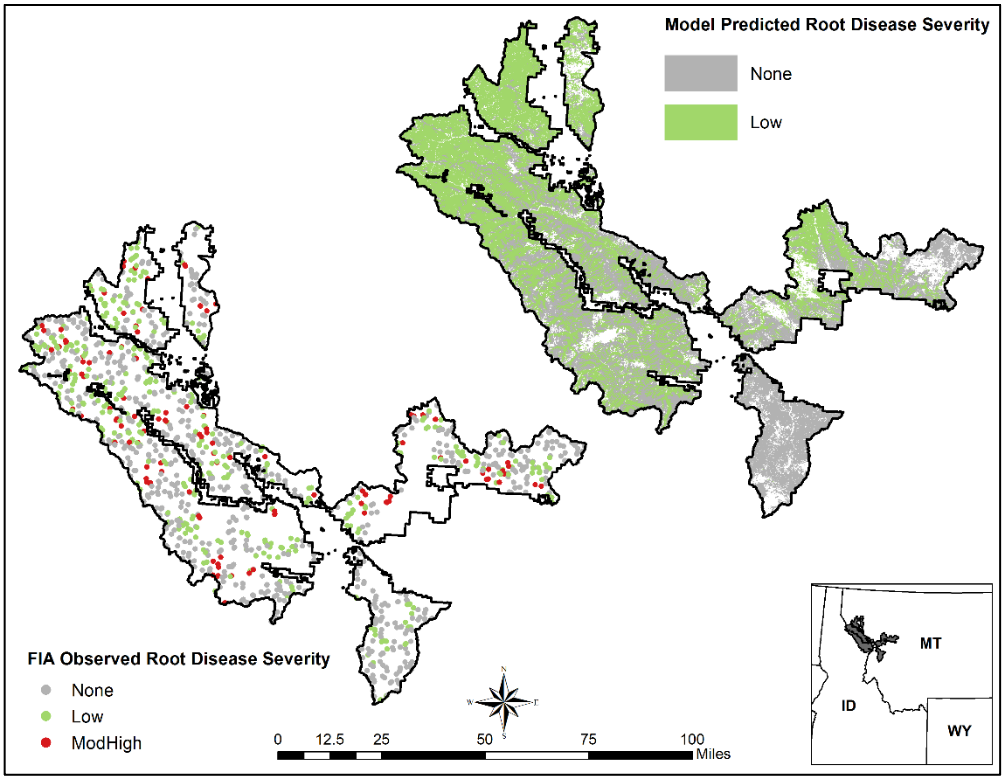


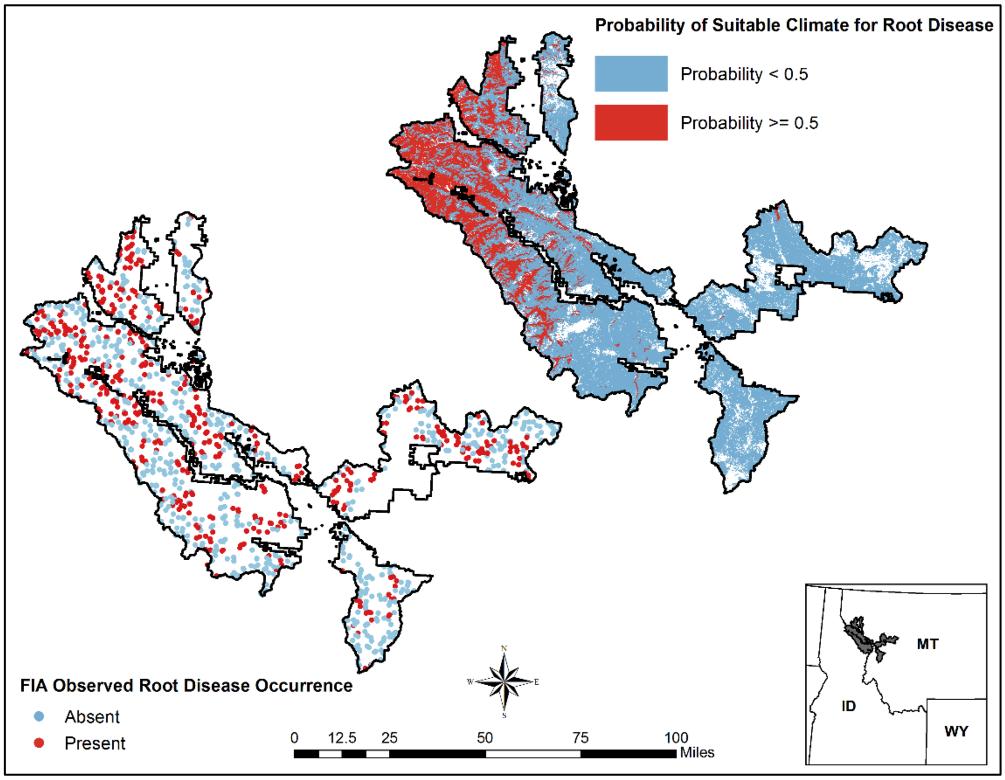
Kootenai National Forest



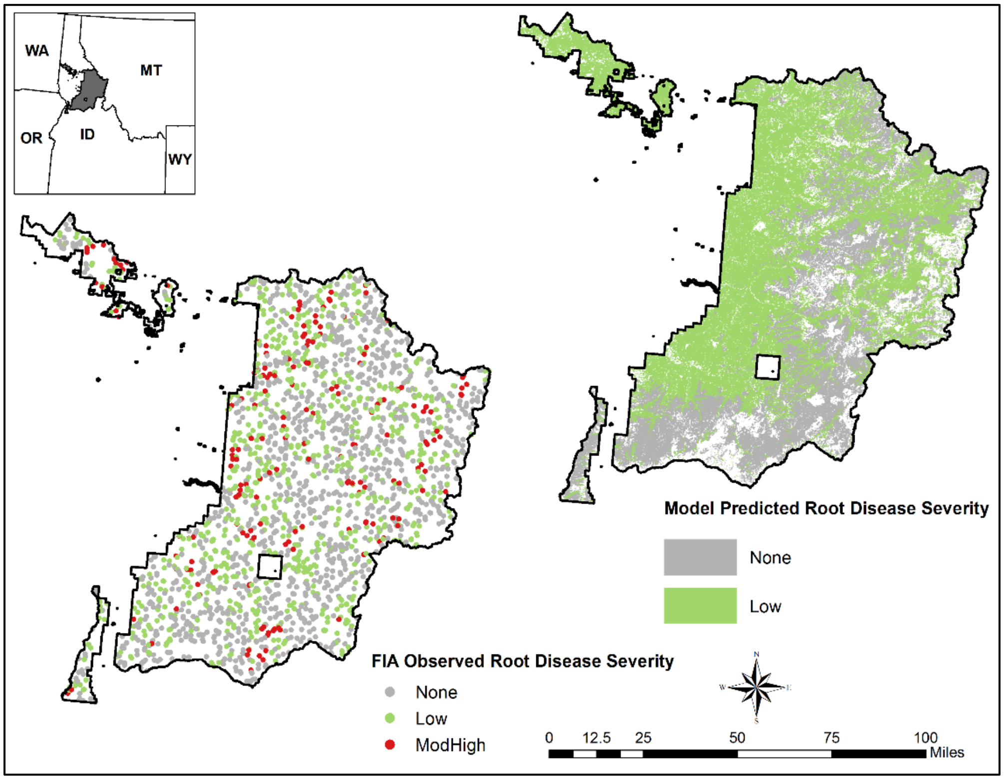


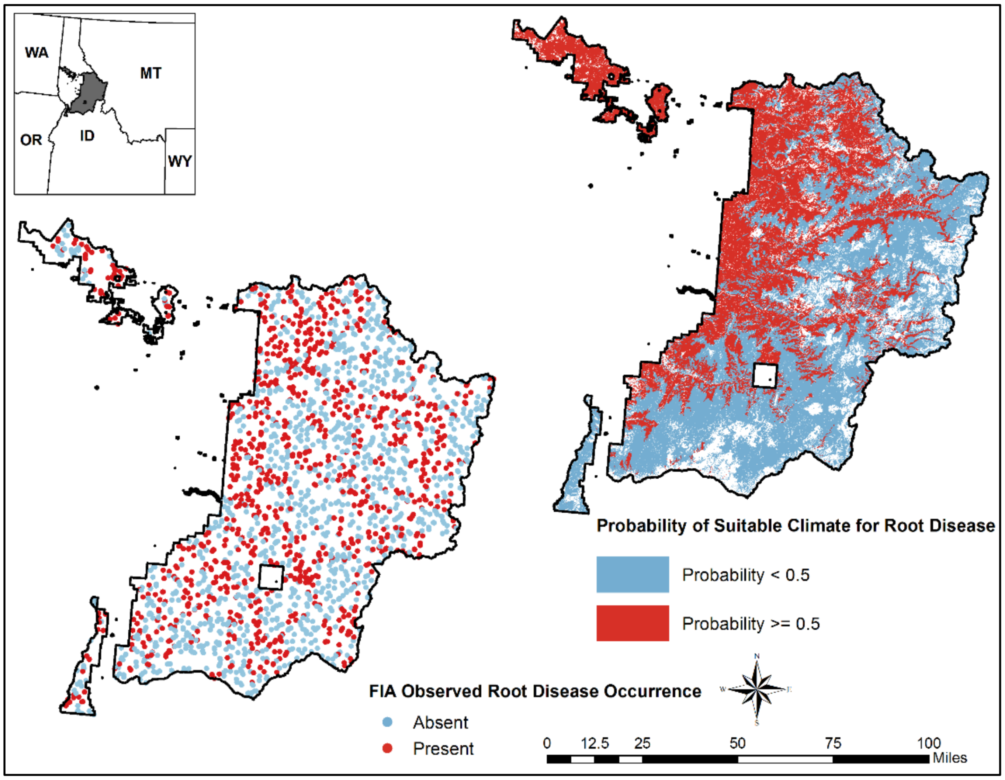
Lolo National Forest





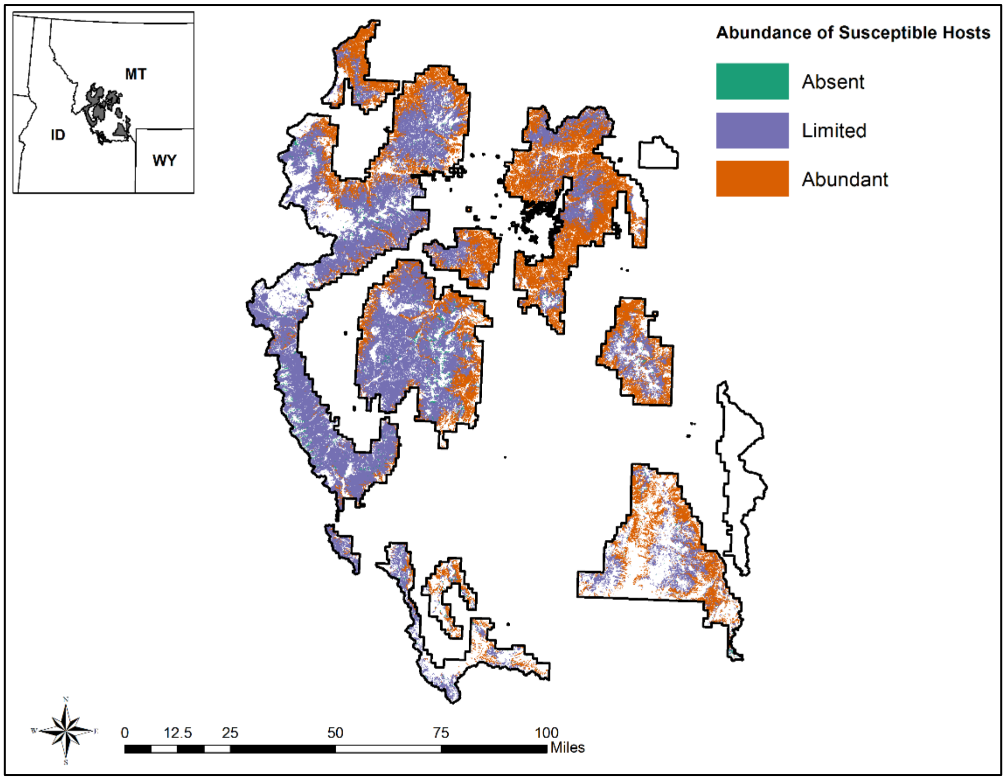
Nez Perce-Clearwater National Forest



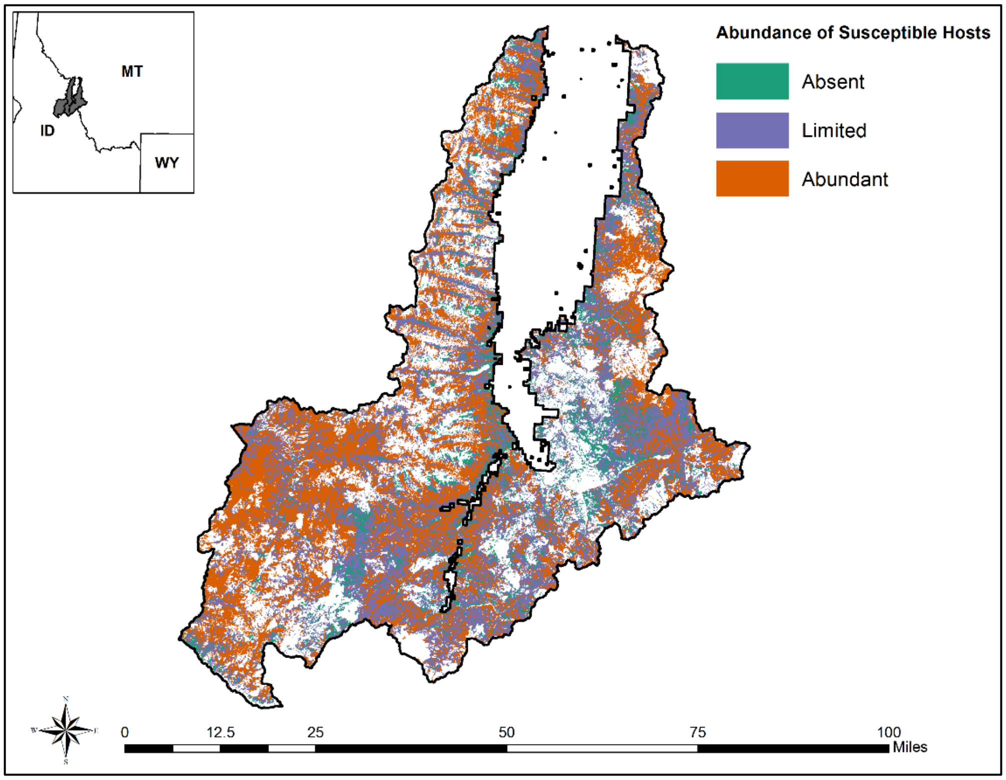


Appendix C: Maps showing spatial distributions of susceptible host species* on all National Forest lands in Region 1

Beaverhead-Deerlodge National Forest

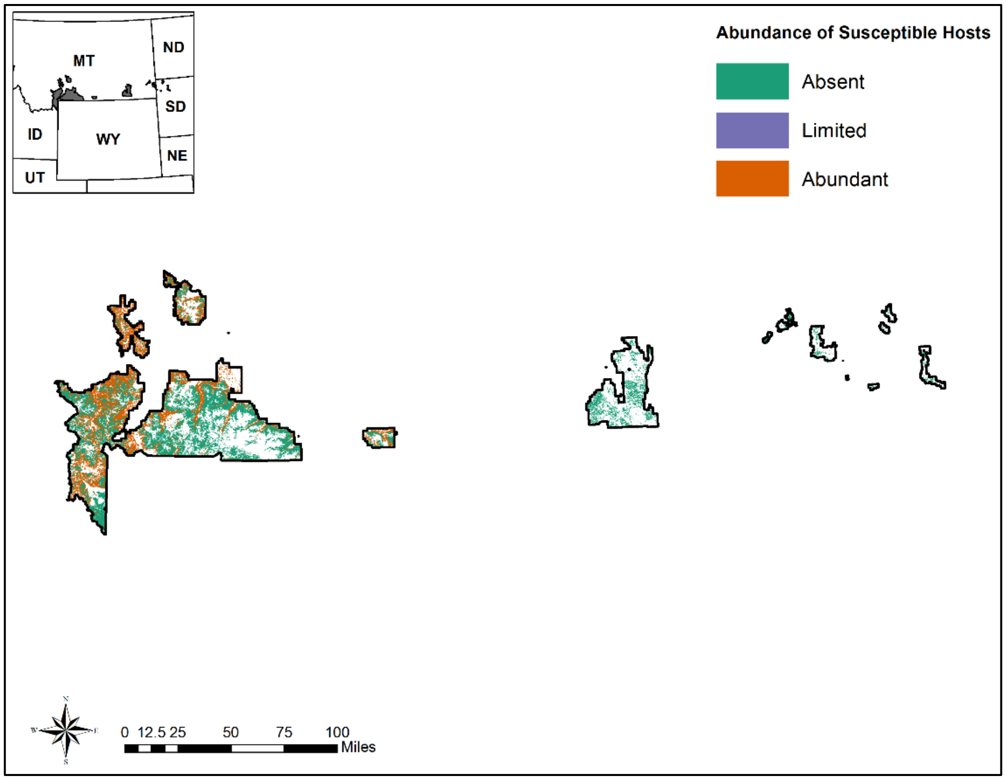


Bitterroot National Forest

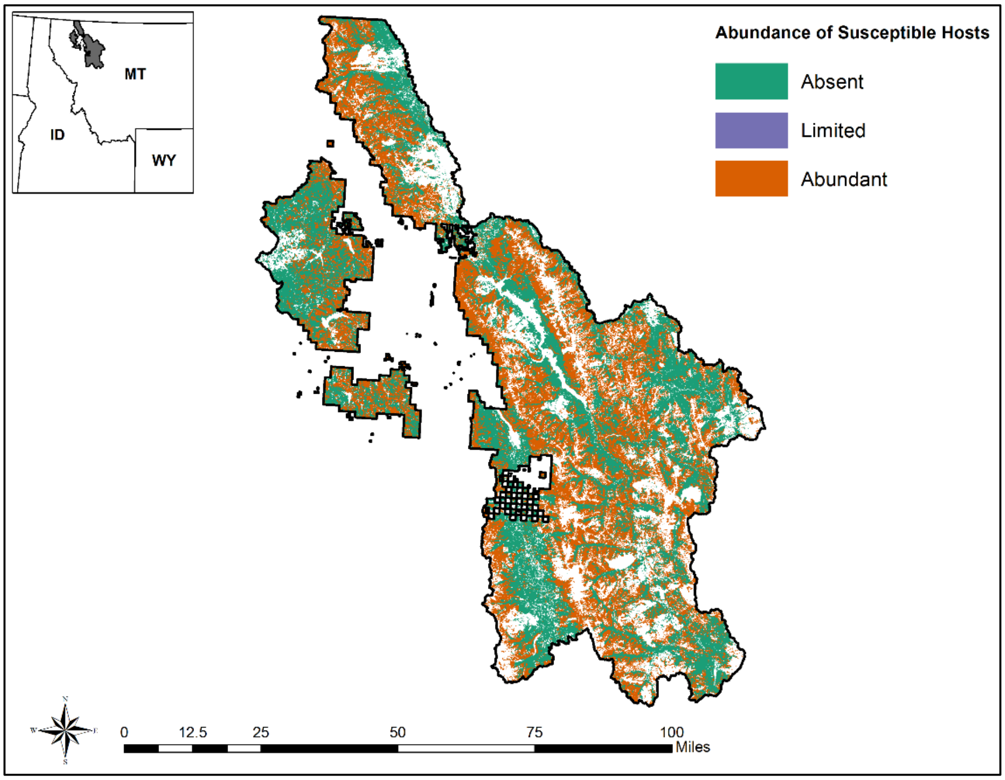


*for the purposes of these models, highly susceptible hosts species considered were Douglas-fir (*Pseudotsuga menziesii*) and true fir (*Abies* spp.).

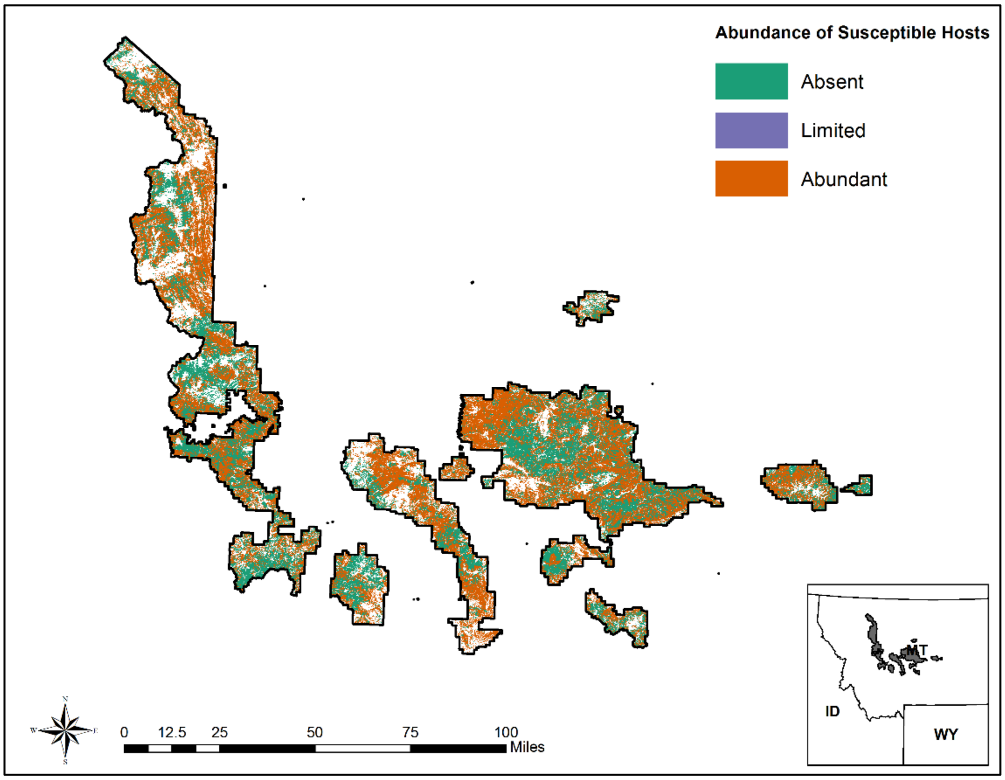
Custer-Gallatin National Forest



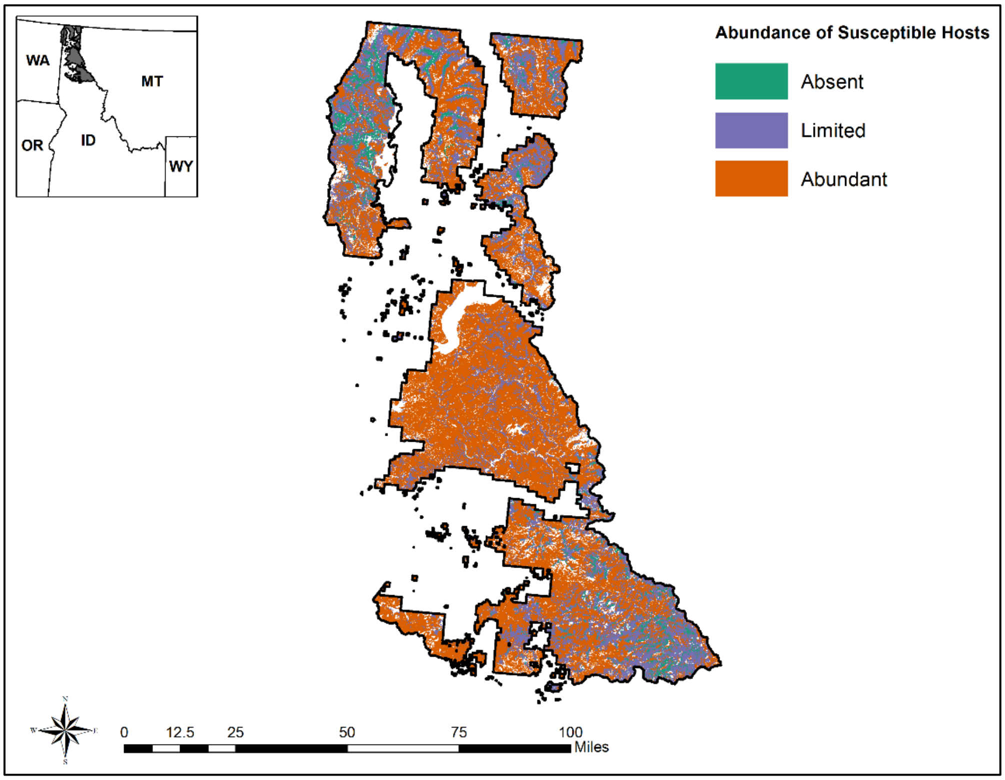
Flathead National Forest



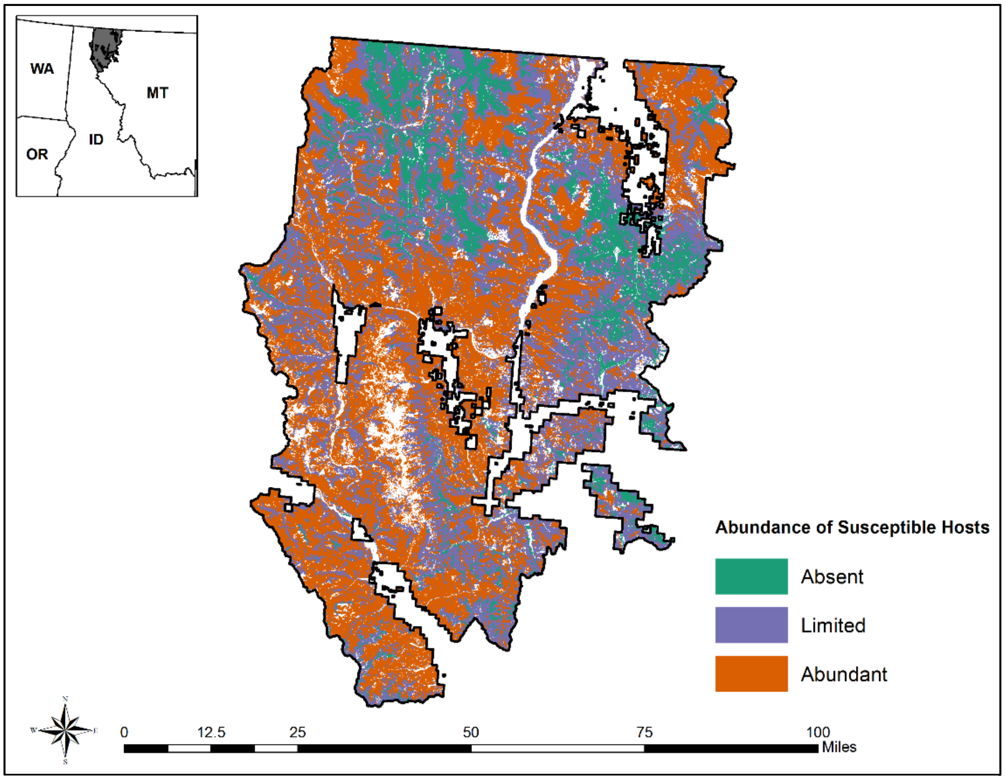
Helena-Lewis and Clark National Forest



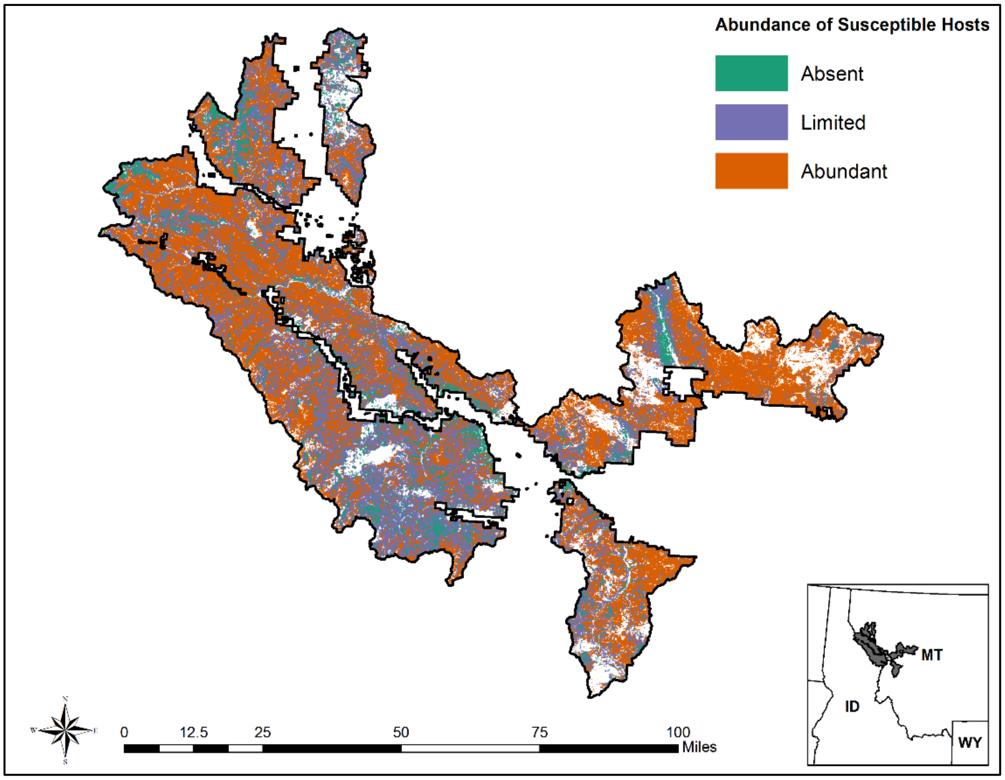
Idaho Panhandle National Forest



Kootenai National Forest



Lolo National Forest



Nez Perce-Clearwater National Forest