Mapping the Risk of Sudden Oak Death in Oregon: Prioritizing Locations for Early Detection and Eradication[1]

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Abstract

Phytophthora ramorum was first discovered in forests of southwestern Oregon in 2001. Despite intense eradication efforts, disease continues to spread from initially infested sites because of the late discovery of disease outbreaks and incomplete detection. Here we present two GIS predictive models of sudden oak death (SOD) establishment and spread risk that can be used to target monitoring and eradication activities in western Oregon. Model predictions were based on three primary parameters: weather and climate variability, host vegetation susceptibility and distribution, and dispersal (force of infection). First, a heuristic model using multi-criteria evaluation (MCE) method was developed to identify the areas at *potential* risk. We mapped and ranked host susceptibility using new geospatial vegetation data available from the U.S. Department of Agriculture, Forest Service (USDA FS)/Oregon State University (OSU) Landscape, Ecology, Modeling, Mapping, and Analysis project (LEMMA). Precipitation and temperature conditions derived from PRISM climate database were parameterized in accordance to their epidemiological importance in the SOD disease system. The final appraisal scores were calculated and summarized to represent a cumulative spread risk index, standardized into five risk categories from very low risk to very high risk. Second, we used the machine-learning method, maximum entropy (MAXENT) to predict the current distribution of SOD infections. Here, probability of infection was calibrated based on the correlation between 500 field observations of disease occurrence and several predictor variables including climate variability, host susceptibility and abundance, topographic variables, and a dispersal constraint. The dispersal constraint estimates the force of infection at all locations and thus predicts the actual or current distribution of the pathogen rather than its potential distribution. Numerous forests across the western region of Oregon appear to be susceptible to SOD. Areas at greatest risk of disease spread are concentrated in the southwest region of Oregon where the highest densities of susceptible host species exist, in particular tanoak (*Lithocarpus densiflorus*). These models provide a better picture of threatened forest resources across the state and are being actively used to prioritize early detection and eradication efforts.

Introduction

Phytophthora ramorum was first discovered in forests of southwestern Oregon in 2001. In contrast to the pathogen's relatively wide distribution throughout coastal California, in Oregon, it occurs only in one small area in Curry County near the town of Brookings. Despite intense eradication efforts, consisting of clearcuts, burns, and herbicide applications, disease continues to spread from the initially infested sites. It is believed that the major reason why control activities have been partially effective is the late discovery of disease outbreaks and incomplete detection. Since field and aerial surveys are labor intensive and costly methods, predictive risk models can be effective alternatives for prioritizing areas for early detection and eradication treatments. Predictive risk models have been developed and used in California (for example, Meentemeyer and others 2004, 2008), but similar modeling has been limited in Oregon due to unavailable vegetation data. Using new data available from the U.S. Department of Agriculture, Forest Service (USDA FS)/Oregon State University (OSU) Landscape, Ecology, Modeling, Mapping, and Analysis project (LEMMA) we present two GIS predictive models of sudden oak death (SOD) potential spread risk and actual distribution that can be used to target monitoring and eradication activities throughout six forest ecoregions in western Oregon.

Methods

Model predictions were based on three primary parameters: weather and climate variability, host vegetation susceptibility and distribution, and force of infection. First, we developed a heuristic (rule-based) model using multi-criteria evaluation (MCE) method to identify the areas at potential risk of SOD establishment and spread. Following methods described in Meentemeyer and others (2004) for California, we mapped and ranked host susceptibility using new geospatial vegetation data from the LEMMA project. These vegetation data were developed based on extensive sample-based field inventories and combination of multivariate statistics and gradient nearest-neighbor (GNN) imputation resulting in maps of detailed vegetation composition and structure in forest and woodland areas (Ohmann and Gregory 2002). We compiled these vegetation data to create a host index calculated as a product of abundance scores and species spread scores. We followed the scoring scheme in Meentemeyer and others (2004), ranking each host's potential to produce inoculum and spread the disease to other hosts (table 1). However, we assigned tanoak, *Lithocarpus densiflorus*, (instead of myrtlewood, *Umbellularia californica*) the highest score because tanoak appears to play a more important epidemiological role in Oregon than myrtlewood.

Table 1—Spread scores of host species based on their potential to spread inoculum of _P. ramorum_

Hosts	Score
Arbutus menzeisii – Pacific madrone	1
Arctostaphylos spp. – pinemat manzanita	1
Frangula californica – California buckthorn	1
Frangula purshiana – Pursh's buckthorn	1
Lithocarpus densiflorus – tanoak	10
Lonicera hispidula – pink honeysuckle	1
Pseudotsuga menziesii – Douglas-fir	1
Quercus chrysolepis – canyon live oak	0
Quercus kelloggii – California black oak	0
Rhododendron sp.	5
Rubus spectabilis – salmonberry	1
Sequoia sempervirens – coast redwood	3
Umbellularia californica – myrtlewood (California bay laurel)	5
Vaccinium ovatum – evergreen huckleberry	1

In addition to vegetation parameters, precipitation and temperature conditions derived from PRISM climate database (Daly and others 2001) were parameterized in accordance to their epidemiological importance in the SOD disease system (table 2).

Table 2—Range of values and assigned scores (_R_), ranked 0 to 5 from least to most suitable for establishment and spread of _P. ramorum_

Score (Ranks)	Precipitation (mm)	Average maximum T (ºC)	Average minimum T (ºC)
5	> 125	18-22	-
4	100-125	17-18; 22-23	-
3	75-100	16-17; 23-24	-
2	50-75	15-16; 24-25	-
1	25-50	14-15; 25-26	> 0
0	<25	< 14; > 26	< 0

The final appraisal scores were calculated and summarized for the entire area to represent a cumulative spread risk index, standardized into five risk categories from very low risk to very high risk. Each parameter was assigned a score between 0 and 5, with 5 representing the conditions that are most suitable for establishment and spread of _P. ramorum_. Weights on a scale of 1 to 6 were assigned to each variable, based on their relative importance for disease spread (table 3). Using the weights and scores of the four parameters, the final spread risk (appraisal score) was computed for each grid cell by finding the sum of the product of each scored variable and its weight:

$$\bar{S} = \sum_{i}^{n} W_i R_{ij}$$

where $\bar{S}$ is the appraisal score (spread risk) for a grid cell, W_i is the weight of the _i_th predictor variable, and R_{ij} is the rank, or score, of the _j_th value of the _i_th variable.

Table 3—Importance weights (*W*) assigned to predictor variables, ranked 1 to 6 from lowest to highest importance for *P. ramorum* (according to Meentemeyer and others 2004)

Variable	Weight
Host species index	6
Precipitation	2
Maximum temperature	2
Minimum temperature	1

Second, we used maximum entropy (MAXENT) to predict the current distribution of SOD infections within the 2008 quarantine area designed by the Oregon Department of Agriculture. MAXENT is a machine-learning method that estimates distributions of organisms by finding the probability distribution of maximum entropy (in other words, the most uniform) given the constraint that the expected value of each environmental predictor under this estimated distribution matches the empirical average of sample locations (Phillips and others 2006). We calibrated the relative likelihood of infection based on the relationship between more than 500 field observations of disease occurrence in the period 2001 to 2007 and several predictor variables including climate variability, host susceptibility and abundance, topographical variables, and a dispersal pressure. The dispersal term, calculated as the cumulative inverse distance between each target plot and other sources of infection (Allouche and others 2008), estimates the relative force of infection at all locations and thus predicts the actual or current distribution of the pathogen rather than its potential distribution. We validated the accuracy of the model by comparing its predictions with independent field observations of disease outbreaks recorded in 2008 and calculating the area under the curve (AUC) of the receiver operating characteristic (ROC).

Results

The final risk map produced by the heuristic model shows a distinct geographical pattern of *P. ramorum* establishment and spread risk in western Oregon based on the influence of host species abundance and climate parameters (fig. 1). Although there are large areas with very low and low *P. ramorum* risk in the eastern part of the area due to low host availability and unfavorable climate conditions, numerous forests across the western region of Oregon appear to be susceptible. The forests at greatest risk of disease spread are concentrated in the southwest region of Oregon where the highest densities of susceptible host species exist, in particular tanoak. From the total area of 66,000 km^2 of forest with susceptible host vegetation, over 250 km^2 were identified as very high risk, 1,870 km^2 as high risk and 4,200 km^2 as moderate risk.
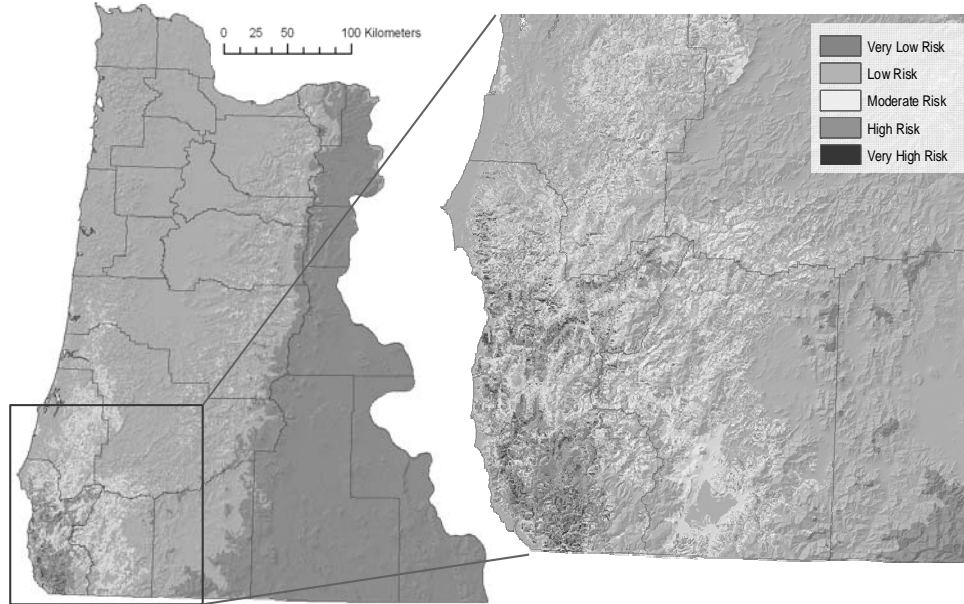
Figure 1—Predicted risk map of *P. ramorum* potential risk of establishment and spread in western Oregon.

The statistical model based on maximum entropy showed that likelihood of SOD is positively associated with temperature and precipitation, and negatively associated with elevation and potential solar radiation. Tanoak abundance was strongly associated with SOD presence, followed by evergreen huckleberry (*Vaccinium ovatum*), salmonberry (*Rubus spectabilis*), Douglas-fir (*Pseudotsuga menziesii*) and myrtlewood. Application of the MAXENT model to map each of these variables predicted the current distribution of SOD (fig. 2). The highest likelihood of disease is concentrated in the southwest portion of the quarantine area and along the North Fork of the Chetco River (fig. 2). When the predicted likelihood of pathogen's presence was validated with field data from 2008, AUC of the ROC statistic was 0.95, suggesting relatively high prediction accuracy.
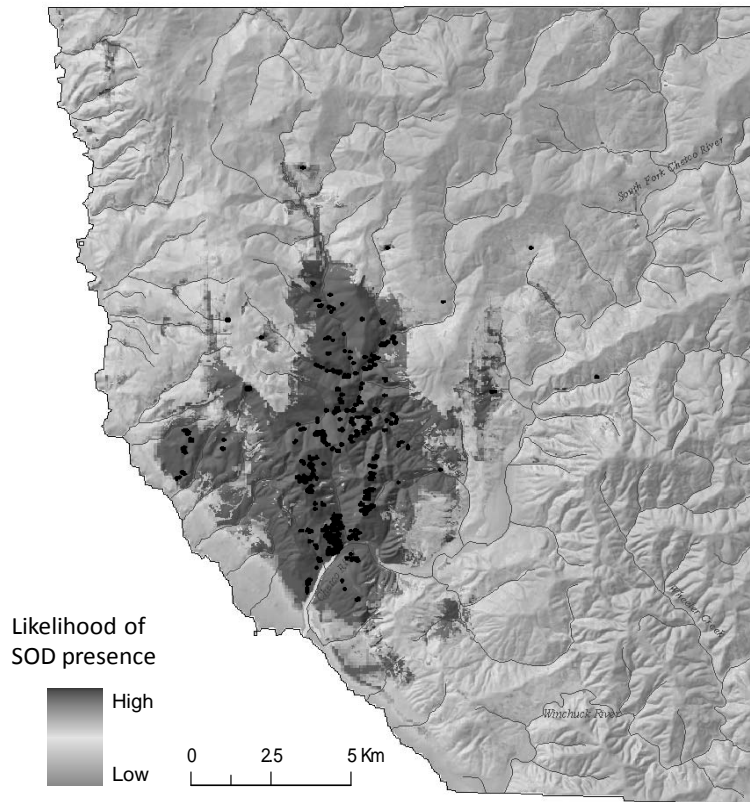
Figure 2—Predicted actual distribution of *P. ramorum* in 2008 quarantine area in southwest Oregon.

Conclusions

The two modeling approaches presented in this work build from risk modeling research previously applied in California (Meentemeyer and others 2004, 2008) and produce the first risk models of SOD specifically designed for Oregon. Although the area of current SOD infestation in Oregon is relatively small, there is more than 2,000 km^2 of forest at high and very high potential risk of disease establishment and spread. These predictive models provide a better picture of threatened forest resources across the state. As new infested sites are discovered, risk models will be updated and validated with new data, and used to prioritize locations for on-the-ground management and early detection surveys.

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