Climate-Host Mapping of *Phytophthora ramorum*, Causal Agent of Sudden Oak Death[1]

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Abstract

We modeled *Phytophthora ramorum* infection using the North Carolina State University-Animal and Plant Health Inspection Service Plant Pest Forecasting System (NAPPFAST) for the conterminous United States. Our infection model is based on a temperature-moisture response function. The model parameters were: leaf wetness, minimum temperature, optimum temperature and maximum temperature over a specified number of accumulated days. The NAPPFAST weather database, which involves approximately 2,000 weather stations across North America, was used to generate a spatially interpolated climate match for *P. ramorum* infection at a 10 km^2 resolution. The model was used to create maps showing the frequency of favorable years for infection, which were validated by comparison with historical *P. ramorum* observations from California in urban and natural settings. We then overlaid climate match areas for *P. ramorum* infection with hardwood forest density and understory host density to generate a composite risk map. We further increased the precision of the maps by applying masks that removed areas where: 1) no climate match occurred, 2) lethal cold soil temperatures for *P. ramorum* occurred, 3) no hardwood hosts occurred and 4) no understory hosts occurred. These maps are designed to improve the efficacy and economy of survey and detection activities for *P. ramorum* by federal, state and local regulatory agencies. We also generated global maps using the NAPPFAST system at a 55 km^2 monthly resolution. Parameters used in the global model were: minimum average monthly temperature, maximum average monthly temperature and monthly precipitation. We used an air temperature lethal cold mask as a surrogate for soil temperature in the global model. These maps may assist in the search for the origin of *P. ramorum*.

Key words: Infection, validation, climate, hosts, risk map.

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Introduction

Phytophthora ramorum, the causal agent of sudden oak death, is currently found in localized areas of California and Oregon (USDA-APHIS 2007). *Phytophthora ramorum* has caused considerable oak mortality in California and is undergoing eradication in Oregon. There are concerns that *P. ramorum* could be introduced into the eastern United States where it could threaten indigenous hardwoods.

To assist in activities like early detection, survey, mitigation and formation of regulatory policy, we generated risk maps that visualize areas at risk for *P. ramorum* infection for the conterminous United States. Our maps were generated from models incorporating climatology and host presence. We also generated global maps for frequency of infection occurrence to assist in the search for *P. ramorum's* origin.

Materials and Methods

Conterminous United States Model

Climatology—

We used the North Carolina State University-Animal and Plant Health Inspection Service Plant Pest Forecasting System (NAPPFAST) to simulate the climatology models (Borchert and Magarey 2004, Magarey and others 2007). NAPPFAST is an internet-based modeling tool with flexible templates for model creation. Our models are based on historical climate data for the past 10 years. We generated both monthly and annual maps for frequency of infection occurrence. In constructing our models, we assumed that *P. ramorum* would be climatically limited by moisture and temperature requirements for zoosporic infection.

We generated a North American *P. ramorum* infection model at a 10 km^2 spatial and daily temporal resolution. The spatial interpolation is based upon a weighted average (Barnes, 1964) and generated from commercial and government weather station data utilizing approximately 2,000 weather stations in North America (Russo, 1999). Daily leaf wetness hours and soil temperature are derived using proprietary algorithms. Validation of the leaf wetness algorithm has been published (Magarey *et al*., 2005). The weather data undergoes quality control prior to archiving.

The infection model is based on a temperature response function that is scaled to a daily leaf wetness requirement (Magarey *et al*., 2005). The model inputs were daily average temperature and daily total hours of leaf wetness for each of the past 10 years. The model parameters were: 1) minimum daily temperature ≥ 3 °C, 2) optimum daily temperature of 20 °C, 3) maximum daily temperature ≤ 28 °C and 4) ≥ 12 hours of accumulated leaf wetness per day (Hüberli *et al*., 2003, Orlikowski and Szkuta 2002, Tooley and Kyde 2005, Werres *et al*., 2001). For each day the model returns a value between zero and one. These values are then accumulated over time. We used a threshold of ≥ 10 accumulated days for the monthly maps and ≥ 60 accumulated days for the annual map (Jones personal communication, 2004). The climate risk map represents the frequency of years in 10 meeting these conditions.

Climate Model Validation

We used two confirmation data sets to validate the climate model. The first was California OakMapper, which reported detections in California as of December 20, 2006 (UC Berkeley, 2006). The second consisted of field confirmations in Sonoma County, California (Meentemeyer personal communication, 2006).

Hosts

We obtained the hardwood host layer from the National Land Cover Dataset (NLCD) for the conterminous United States (Vogelmann *et al*., 2001). This data layer expresses forest composition in percentages. We assumed that mixed forests would have an equal distribution of hardwoods and softwoods. We queried the NLCD data set for all hardwoods plus 50 percent of mixed forests to generate the hardwood host layer. This raster was visualized at a one km^2 resolution.

We obtained the understory host layer from NatureServe (2002). We estimated the distribution of seven Ericaceae hosts of *P. ramorum* and combined them as a shapefile that was demarcated based on frequency of occurrence. This was then converted to a raster at a one km^2 resolution. We converted this raster to percentages by dividing it by seven and multiplying by 100 using the raster calculator in ArcGIS.

Masks

We used four masks in our climate-host risk map for the conterminous United States at a one km^2 resolution. We masked out areas where: 1) no climate match occurred, 2) no hardwood hosts occurred, 3) no understory hosts occurred and 4) a lethal cold soil temperature of –25 °C occurred for at least one day during January (DEFRA, 2004).

For the global infection model we cannot currently map soil temperature. Consequently, we used an average minimum monthly air temperature of –10 °C as a surrogate for the –25 °C lethal cold soil temperature mask that was used in the map for the conterminous United States. We masked areas where the average minimum monthly temperature was less than –10 °C for at least one month during the year.

The NAPPFAST one-year climate-match frequency band identifies areas that have a match of one and below. Consequently, this band is visualizing areas that are not at risk for *P. ramorum* infection. To account for this, we used the zero and one-year bands to mask areas where no climate-match occurred.

Risk Model

We generated the risk map by summing the percentage values for climate frequency, hardwood hosts and understory hosts and dividing the total by three. We then applied the four masks to remove areas where infection could not occur.

Global Climate Model

The global infection model was generated at a 55 km^2 spatial and monthly temporal resolution (Climate Research Unit, Norwich, U.K.) (New *et al*., 1999). The model parameters were: 1) average minimum temperature ≥ 3°C, 2) average maximum temperature ≤ 28 °C, 3) ≥ 10 days of precipitation during the month and 4) ≥ 2 months meeting these conditions. The risk map represents the frequency of years in ten meeting these conditions.

Results and Discussion

All of the *P. ramorum* confirmations for both validation data sets occurred in the highest climate frequency of occurrence band (figs. 1 and 2). Although the validation is based on confirmation data from one state, it suggests that our model is accurately predicting where infection will occur.

The risk maps indicate that both the west coast and the eastern third of the conterminous United States, especially the Appalachian Mountains, are at similar risk for infection (fig. 3). The relative risk maps also allowed for precise visualization of at-risk areas for infection and establishment (fig. 4). This information can aid in surveys, early detection and eradication of the disease should it move east.

Our global prediction model identified areas at greatest risk for infection on each continent, though at a coarse resolution (fig. 5). Future iterations of the NAPPFAST system will generate global predictive maps at a 10 km^2 daily resolution. These higher resolution maps will be of greater use in the search for *P. ramorum's* origin and also provide a means for additional validation by comparing our model's predictions with known disease occurrence in other countries.

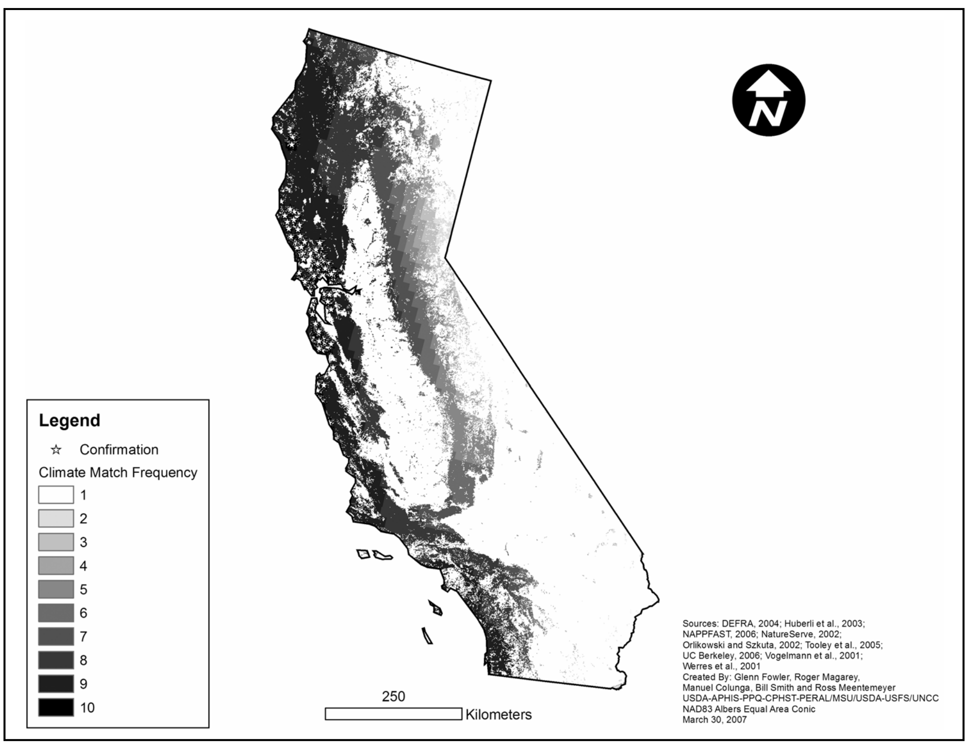

Figure 1—Infection model validation using the OakMapper data set.

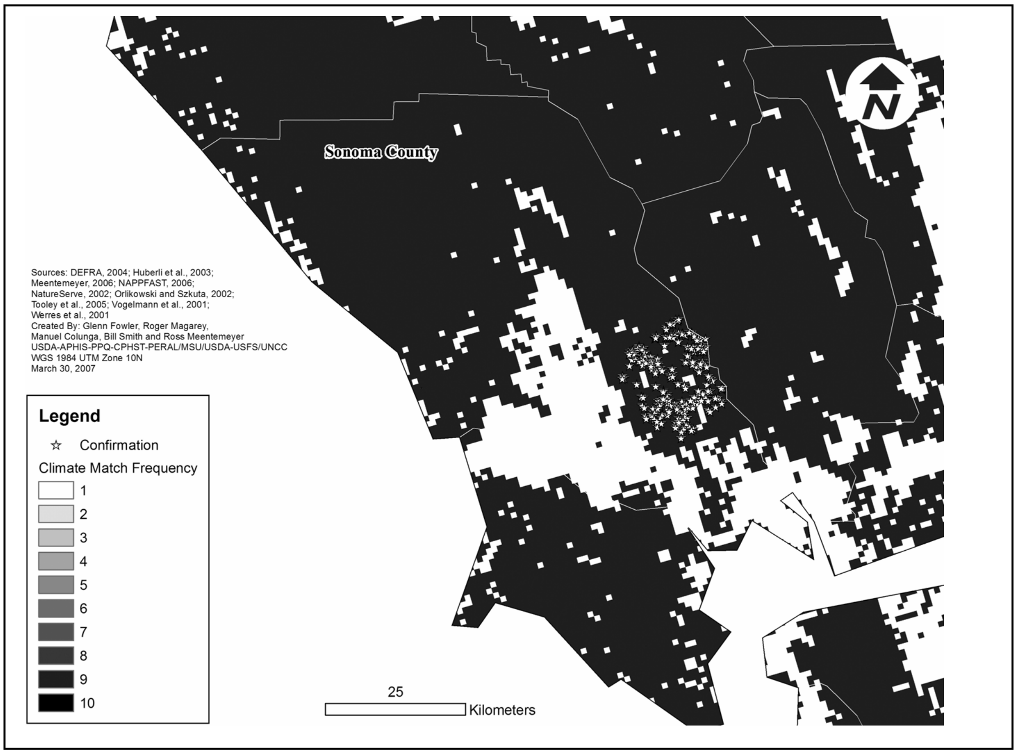

Figure 2—Infection model validation using the Meentemeyer (2006) data set in Sonoma County, California.

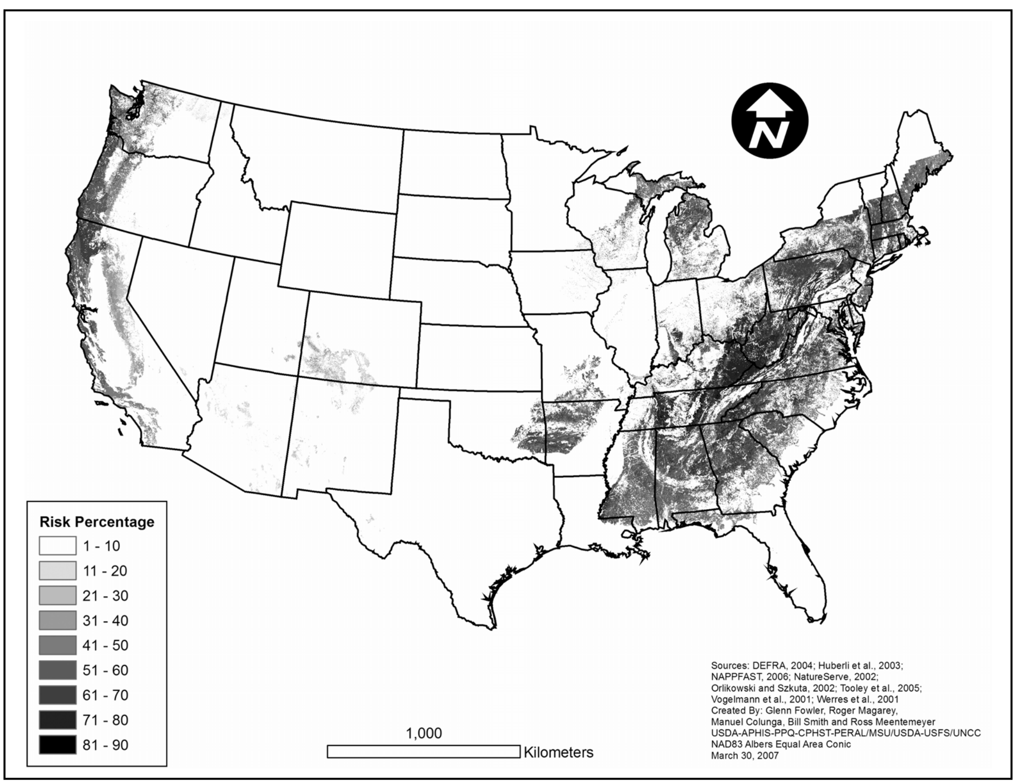

Figure 3—*Phytophthora ramorum* infection risk map for the conterminous United States based on climate and host data.

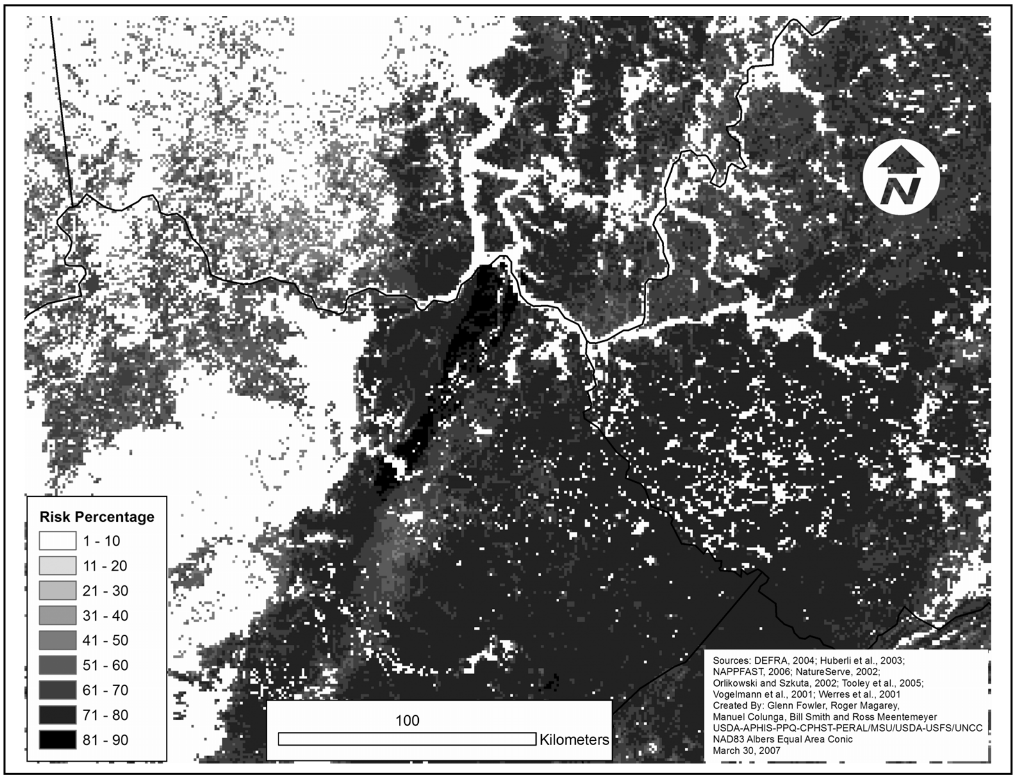

Figure 4—Precise visualization of at-risk areas for *P. ramorum* infection.

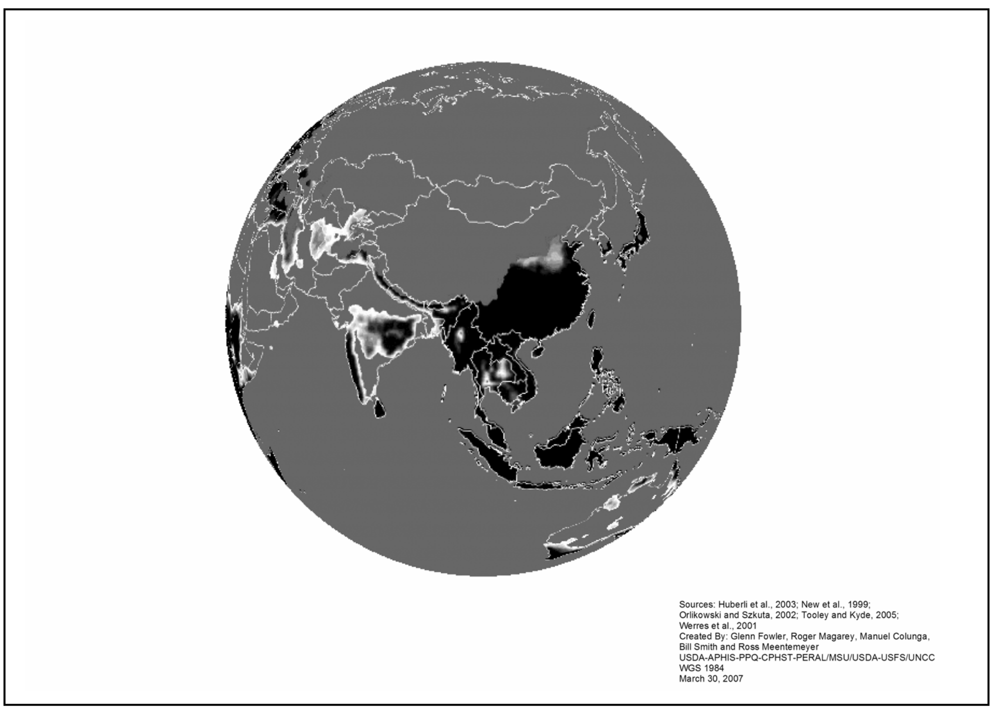

Figure 5—Sample global risk map visualizing areas with suitable climates for *P. ramorum* infection.

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