

Mapping Sudden Oak Death Risk Nationally Using Host, Climate, and Pathways Data¹

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Abstract

In 2002, a team of United States Department of Agriculture-Forest Service (USDA-FS) scientists developed a preliminary risk map to serve as the foundation for an efficient, cost-effective sample design for the national sudden oak death detection survey. At the time, a need to initiate rapid detection in the face of limited information on *Phytophthora ramorum* necessitated a simple spatial intersection of factors traditionally used in risk mapping: (1) distribution of hosts known or likely to be susceptible to the pathogen, (2) climatic conditions adequate for survival and propagation of the pathogen, and (3) pathways for introduction of the disease outside the currently infected region. The resulting map consisted of hexagons indicating three ordinal levels of risk (high, moderate, low) covering the conterminous U.S. Beyond aiding prioritization of sampling effort, the map has facilitated the dissemination of information about the potential threat of the disease to the public. However, additional information about the pathogen has emerged in the last few years, so we created a new map by incorporating current data and approaches to better depict principal factors of *P. ramorum* risk. The new risk map will be used to improve sampling procedures for detecting the pathogen's potential movement into wildland areas. In addition, it will serve as the basis for analysis of the potential economic costs if *P. ramorum* were to become established in eastern U.S. forests.

Key words: *Phytophthora ramorum*, sudden oak death, risk map, detection survey.

Introduction

By early 2002, *Phytophthora ramorum* had been detected on nursery stock in California and Europe, in addition to infesting forests in California and Oregon (COMTF 2007). This suggested the potential for *P. ramorum* to be dispersed long distances by infected plants. While the United States Department of Agriculture-Animal and Plant Health Inspection Service (APHIS) began efforts to regulate movement of nursery stock, concerns regarding the potential economic risk to the nation's oak forests led to the development of a national sudden oak death detection survey, managed by the USDA-FS. To facilitate this detection effort, a team of Forest Service researchers developed a risk map in 2002 that could serve as a national sampling frame. Their approach was based on three factors: 1) climatic conditions affecting the pathogen's distribution where it was established, or as determined from laboratory studies; 2) likely host species based on their distribution in areas where the pathogen was established, or as determined from laboratory inoculations; and 3) likely pathways of introduction into new areas (Smith and others 2002; U.S.

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Department of Agriculture Forest Service 2004). Areas at greatest risk for new introductions occurred where these three factors spatially coincided.

This preliminary risk map (fig. 1) has served its purpose of prioritizing sample placement, but after five years, more has become known about the pathogen in terms of basic epidemiology, suitable hosts, and suitable environmental conditions. Our primary objective was to create a new national risk map for *P. ramorum* incorporating current knowledge about the pathogen as well as additional data sources and techniques not utilized for the preliminary map. Recently, there have been several publications presenting national-scale maps related to *P. ramorum* risk. Venette and Cohen (2006) employed CLIMEX software to model suitability for establishment based on climatic variables, calculating parameter values from laboratory studies of *P. ramorum* and *P. cinnamomi*. Fowler and others (2006) similarly modeled infection risk using climatic variables and laboratory-based parameter estimates. Kluza and others (2007) modeled the ecological niche of *P. ramorum* from the known occurrences in Oregon and California, applying a genetic algorithm to topographic, climatic, and remotely sensed variables. Kelly and others (2007) compared the results of several different niche models developed from the known occurrences. These studies focused primarily on environmental constraints for *P. ramorum* and included, if at all, limited data on host species distribution. They also did not address potential pathways of introduction of the pathogen into forested landscapes. Our map is intended to provide a comprehensive depiction of risk that incorporates detailed host and pathways variables in addition to climatic constraints, thus making it useful for optimizing the national detection survey.

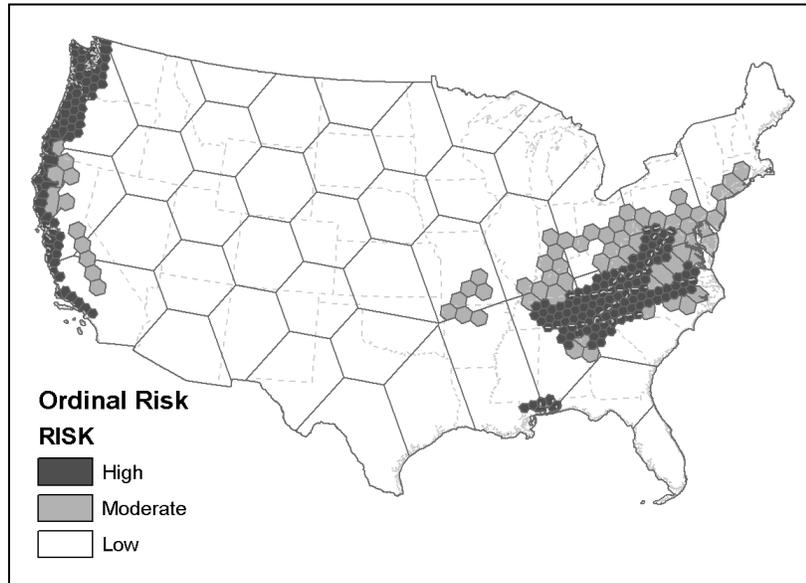


Figure 1—Preliminary national risk map (2002) for *P. ramorum*.

Methods

To construct a new map, we adopted a decision-rule-based approach with three basic steps. First, we assembled input data into three “surfaces” representing (1) host species distribution, (2) climatic suitability, and (3) potential pathways of *P. ramorum* introduction into natural forests. Second, we combined the host and climate surfaces into a surface that we have termed “hazard”. In this context, hazard represents the relative likelihood of significant forest damage given a successful introduction. Third, we created a risk map composed of sampling hexagons in low, moderate and high risk size classes. We determined where to place the high and moderate risk hexagons based on threshold values for the hazard and introduction potential surfaces; in other words, the risk rating represents a combination of these two factors.

Host Surface

Only 14 forest species were known to be affected by *P. ramorum* in 2002. The new map’s host surface incorporates the distribution of the several dozen species currently on the proven and associated host lists managed by APHIS (APHIS 2007). Another significant change from the 2002 map is the removal of certain oak (*Quercus*) species from the list of susceptible eastern U.S. hosts. Examination of infrageneric relationships between oak species revealed that western live oaks (including coast live oak, *Quercus agrifolia*) belong to the red oak group, while eastern live oaks (*Quercus virginiana* and other species) are members of the white oak group and thus apparently unsuitable hosts (Nixon 1993, 2002).

We constructed the host surface from three components: a background host layer, a midstory sporulators layer, and an overstory layer. The background host layer depicts areas of the U.S. with at least some hosts present, enabling propagation of *P. ramorum*. To build the layer, we used Floristic Synthesis of North America software (Kartesz 2007), which provides county-level distribution data for most plant species, both native and exotic, found in U.S. forests. For each county, we tallied occurrences of all non-oak host species on the APHIS lists into a total abundance score. When scoring, we assigned two species, California bay laurel (*Umbellularia californica*) and tanoak (*Lithocarpus densiflorus*), and one genus (*Rhododendron* spp.) multipliers of ten, five, and five, respectively, to reflect their importance to *P. ramorum* spread. To minimize the effect of any individual counties with incomplete records, we generalized the map at the ecoregion subsection level (McNab and others 2005).

California bay laurel and tanoak are common in forest midstories. Compared to other understory hosts, they can disperse *P. ramorum* spores over a larger area and may expose some mature hosts to potential infection. Based on preliminary data (Paul Tooley, unpublished data), we also identified four eastern U.S. forest species with high sporulation potential that commonly grow into the midstory: dogwood (*Cornus florida*), black locust (*Robinia pseudoacacia*), serviceberry (*Amelanchier canadensis*), and southern magnolia (*Magnolia grandiflora*). We used ordinary kriging to interpolate USDA-FS Forest Inventory and Analysis (FIA) Phase Two plot data into a national map depicting percentage of the total susceptible-species basal area composed of these midstory sporulators.

The overstory layer represents the distribution of hosts with potentially significant mortality due to *P. ramorum*. In addition to tanoak, this included all oak species from the true red and black oak group, the willow oak group, and the western live oak group, as well as canyon live oak (*Q. chrysolepis*) from the intermediate oak group (Nixon 1993, 2002). We also included Pacific madrone (*Arbutus menziesii*) due to recent observation of mortality in the species due to *P. ramorum* (Ellen Goheen, personal communication). We used ordinary kriging to interpolate FIA plot data into a national grid of basal area.

We combined these three components into a single 1 km² resolution host surface by rescaling the background layer abundance scores and by evaluating where the midstory and overstory layers met thresholds of 10 percent and 3.44 m²/ha (15 ft²/ac) in basal area, respectively. The final surface had a four-point rating scale (table 1).

Table 1—Rating scale for final host surface

Rating	General Description
0	Oak hosts but no other host species
1	Limited (<3.44 m ² /ha basal area) oaks with some other hosts OR abundant (≥3.44 m ² /ha basal area) oaks with only non-sporulating hosts
2	Limited oaks with midstory sporulators comprising >10 percent of susceptible-species basal area OR abundant oaks with sporulating hosts, but no midstory sporulators
3	Abundant oaks, midstory sporulators, and additional sporulating hosts

Climate Surface

In the 2002 map, climatic limits for *P. ramorum* were defined using maps from the Climate Atlas of the United States. Climate Atlas maps are monthly or annual summaries, so they cannot capture the fine-temporal-scale, simultaneous occurrence of temperature and moisture conditions that may promote the pathogen's persistence (Garbelotto and others 2003, Rizzo and Garbelotto 2003). We used daily weather station data from the National Climatic Data Center (NCDC) to create annual grids (4 km² resolution) of the longest string of consecutive days where two conditions occurred simultaneously: (1) temperature between 15.56 and 26.67 °C during the day and (2) some precipitation, fog, or mist during the day OR mean relative humidity during the day of greater than 90 percent. We defined these conditions based on results of laboratory studies (Werres and others 2001, Rizzo and Garbelotto 2003, DEFRA 2004). We averaged 10 years (1997 to 2006) of annual grids into a single consecutive-day grid. We then divided the consecutive-day grid into two parts by ecoregion domain, placing the Humid Temperate and Humid Tropical Domains (Eastern U.S., Pacific Coast) in one super-region and the Dry Domain (Interior West, northern Great Plains) in another (McNab and others 2005). We reclassified the two super-regions using different rating scales (table 2)—accounting for factors such as the general moisture deficit in the Dry Domain (Bailey 1998)—and then recombined them into a single grid.

Table 2—Rating scales for climate variable, the largest number of consecutive days with co-occurrence of optimum temperatures and moisture, in two U.S. super-regions

Humid Super-region		Dry Super-region	
# Consecutive Days	Rating	# Consecutive Days	Rating
< 3.5	0	< 3.5	0
3.5 – 7	3	3.5 – 5	1
7 – 14	4	5 – 7	2
14 – 28	5	7 – 14	3
> 28	6	> 14	4

In the 2002 map, any areas with more than one winter month where the maximum temperature was below 0 °C or more than one summer where the maximum temperature was above 32.22 °C were considered unsuitable for long-term persistence of *P. ramorum* (David Rizzo, personal communication). For the new map, based on laboratory observation of infection after prolonged time periods at 0 °C (DEFRA 2004), we applied a cold temperature mask excluding areas where the minimum temperature was below 0 °C for 150 or more days. We did not use a high temperature mask because, as evidence from the Southern Appalachian region suggests (James Vose, unpublished data), areas under forest canopies may be as much as 3 to 4 °C cooler in the summer than non-forested areas, mitigating the deleterious effect of heat on pathogen survival.

Introduction Surface

In 2002, *P. ramorum* had been detected on nursery stock in a few instances, but the nursery industry had not yet experienced widespread impacts. The 2002 map did incorporate locations of rhododendron nurseries based on a national growers’ association listing, but it has since been documented that infected nursery stock has been shipped from California, Oregon, and Washington to roughly 40 states in the past few years (Stokstad 2004), and that some of this stock was sold to customers before it could be destroyed. This emphasizes the possibility that *P. ramorum* could escape from ornamental plantings in residential landscapes into natural forests. To represent this possibility, we constructed an introduction surface from maps of wildland-urban interface. These maps, developed at the census block level, combine housing density information, land cover percentages, and forest proximity measurements to classify areas into one of thirteen classes according to the level of interspersed between residential areas and natural vegetation. We reclassified these maps for the entire U.S. to emphasize areas with moderate levels of intermix (table 3). We used a neighborhood function to define “edge” zones, areas where high-risk intermix and contiguous areas of natural vegetation are adjacent (table 3).

Table 3—Rating scale for introduction surface

Rating	Description
0	Excluded areas (highly urban, water, or natural vegetation not included in an edge zone)
1	Low risk (housing densities greater than 741.3 units/km ²)
2	Moderate risk (interface ^a with housing densities less than 741.3 units/km ²)
3	High risk (intermix ^b with housing densities less than 741.3 units/km ²)
4	Edge zone (high-risk intermix and natural vegetation immediately adjacent)

^a natural vegetation occupies < 50 percent of area, but areas with > 75 percent natural vegetation are within 2.4 km

^b natural vegetation occupies > 50 percent of area

Risk Map Construction

We created a national hazard surface by combining our host and climate surfaces using a simple equation: hazard score = host surface score * 10 + climate surface score. We then reclassified the result on a four-point scale (table 4). For the 2002 map, three hexagonal tessellations covering the conterminous U.S., with hexagon sizes increasing from low to high relative risk, were generated via intensification of the North American hexagon of the global Environmental Monitoring and Assessment (EMAP) sampling grid (White and others 1992); we used these same tessellations in the new map. To select which moderate and high risk hexagons were retained, we calculated mean hazard surface and mean introduction surface scores for each hexagon. For the high risk stratum, we retained any hexagon with a mean hazard score greater than 1.5 or a mean hazard score greater than 1.0 and a mean introduction score greater than 2.0. For the moderate risk stratum, we retained any hexagon with a mean hazard score greater than 1.0. In addition, we used the locations of positive nurseries from APHIS trace forwards to indicate potential introduction hotspots. These data served to promote hexagons in terms of risk; for example, if a hexagon had inadequate hazard or pathways scores to be considered high risk, but did contain one or more positive nurseries, it was retained in the high risk stratum. We overlaid the selected high and moderate risk hexagons on the background low risk hexagons to create our map.

Table 4—Rating scale for hazard surface

Rating	Hazard Score Range ^a	Description
0	n/a	Non-forested areas
1	0-21, 30	Poor climatic conditions and/or low host levels
2	22-26	Moderate host levels and adequate to good climatic conditions
3	33-36	High host levels and adequate to good climatic conditions

^a Two possible scores from the hazard equation, 31 and 32, did not occur within the conterminous U.S.

Results and Discussion

A primary difference between the new risk map (fig. 2) and the 2002 map is an expansion of risk areas in the southeastern U.S., particularly in the Piedmont regions of North and South Carolina, Georgia, and Alabama. Coastal areas of Georgia, South Carolina, Alabama, and Mississippi have also been highlighted, as has northern Florida. Portions of the Mid-Atlantic region, along with parts of Tennessee,

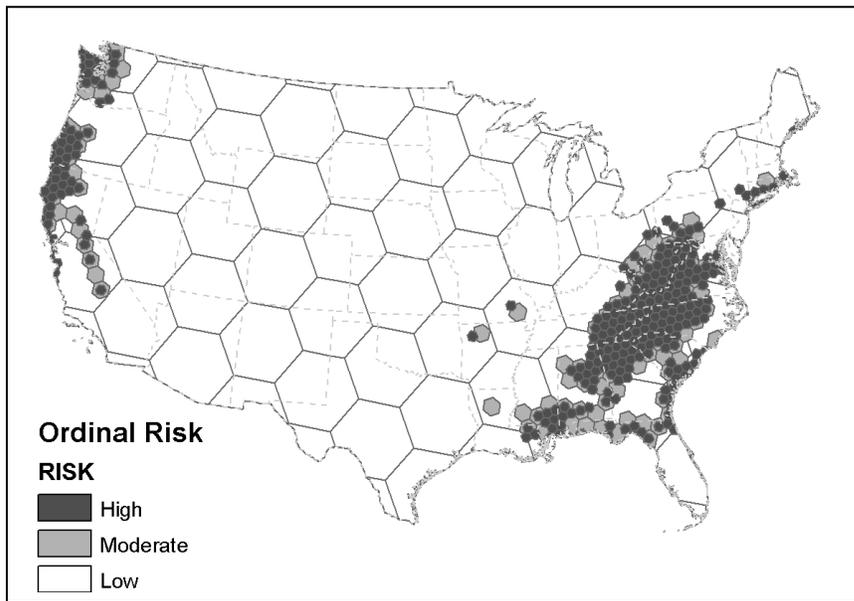


Figure 2—Revised national risk map for *P. ramorum*.

Kentucky, Indiana, and Ohio, shifted from moderate to low risk. Although we have not yet performed a planned sensitivity analysis, the appearance of moderate and high risk hexes throughout coastal areas of the Southeast appears to be largely linked to high host presence. Many of these areas were excluded by a high temperature mask in the 2002 map. How *P. ramorum* responds to extended periods of high temperatures remains an open question; as already noted, forest canopies may provide enough of a cooling effect to mitigate high summer temperatures (Geiger and others 2003). With respect to the Pacific Coast, our new map closely resembles the 2002 map, although the pattern of high and moderate risk hexes does not extend as far south along the California coast, basically ending south of the Big Sur region. Review of the input data layers suggests a lack of host species as the primary constraint. Part of this may be due to the scale and accuracy of available host data, but the extent of risk predicted in California and along the rest of the Pacific Coast appears consistent with results seen in other risk mapping efforts (for example, Meentemeyer and others 2004, Kelly and others 2007) that similarly included some representation of host species distribution.

With respect to the eastern U.S., our map is generally consistent with other studies (Venette and Cohen 2006, Kelly and others 2007, Kluza and others 2007) in locating the greatest risk in the Southeast. One major distinction is that our map ranks all of the Southern and Central Appalachian Mountain regions as high risk, while the other studies assigned lower risk ratings to at least part of these areas. This appears to be due in part to our emphasis on host dynamics, particularly the co-occurrence of critical understory species (for example, *Rhododendron* spp.) and susceptible oaks in the forested areas of these regions. However, high levels of wildland-urban intermix (in other words, introduction potential) in northern Georgia and elsewhere in the southern Appalachians contributed to the contiguity of high risk throughout the region.

We will perform sensitivity analysis to more precisely determine, for each moderate and high risk hexagon, which variables most contributed to their inclusion. We will also examine how differences from the 2002 map may have resulted from changes in methodology. After review and possible alteration, we hope to use the new map in the same fashion as the 2002 map to facilitate sampling procedures for detecting the pathogen outside its current extent. It will also serve as the basis for analysis of the potential economic costs if *P. ramorum* were to become established in eastern U.S. forests (see Holmes and Smith, this proceedings).

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