CRITERION 3—

# Chapter 7. A Revised Sudden Oak Death Risk Map to Facilitate National Surveys

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## Introduction

The impact of sudden oak death on Pacific Coast wildlands has received much attention from scientists, popular media, and the public. Disease symptoms were first observed in Marin County, in California, in 1994 on tanoak (*Lithocarpus densiflorus*) and, in 1995, on coast live oak (*Quercus agrifolia*) and California black oak (*Q. kelloggii*) (McPherson and others 2003). The crown foliage of affected trees appeared to die over several weeks, while bleeding cankers appeared on the lower trunks of larger trees (Rizzo and others 2002). During the next several years, sudden oak death reached epidemic levels in central and northern California (Frankel 2008, Garbelotto and others 2003, Rizzo and others 2005), with tree mortality estimated in one study to be three to four times the historic rate for tanoak and two times the historic rate for susceptible oak species (Swiecki and Bernhardt 2002). In 2001, the disease was discovered in Curry County, OR, likely having arrived there 3 or 4 years earlier (Frankel 2008, Goheen and others 2002, Hansen and others 2005). In addition to a now-quarantined portion of Curry County, sudden oak death outbreaks have so far been recorded in fourteen counties in California, extending from Monterey County northward to Humboldt County (Frankel 2008).

In 2000, sudden oak death was positively linked to the pathogen *Phytophthora ramorum*, which had been isolated from the leaves of ornamental *Viburnum* and *Rhododendron* plants in Germany and the Netherlands (Garbelotto and others 2003, Rizzo and others 2002, Werres and others 2001). This linkage highlights that there are actually two distinct diseases caused by *P. ramorum*: (1) lethal cankers on the trunks and/or branches of host trees such as coast live oak and tanoak, and (2) nonlethal foliage and twig infections on a wide variety of host species, especially ericaceous trees and shrubs such as California bay laurel (*Umbellularia californica*) (Rizzo and Garbelotto 2003, Tooley and others 2004). In natural stands, these "foliar" hosts are key to the persistence and spread of the pathogen because they serve as a source of inoculum and yield large numbers of aerially dispersed *P. ramorum* spores following rainfall (Rizzo and others 2005). In contrast, susceptible oak species represent an epidemiological endpoint, although tanoak also behaves as a foliar host (Rizzo and Garbelotto 2003, Rizzo and others 2005). Spores of *P. ramorum* may be dispersed from foliar hosts by rain splash or wind-driven rain, and have been found in watercourses downstream from infected areas as well as in soil on the shoes of hikers traveling through these areas (Davidson and others 2005, Webber and Rose 2008). Moreover, the discontinuous distribution of the pathogen across a large geographic area of California and Oregon suggests the presence of additional long-distance dispersal mechanisms that likely involve humans, who historically have been responsible for the global-scale spread of numerous *Phytophthora* species (Davidson and Shaw 2003, Ristaino and Gumpertz 2000).

Indeed, the potential and, in some cases, actual movement of infected plants via the commercial nursery trade has raised *P. ramorum* from a regional forest health issue to one of global concern. A number of confirmed host species, particularly in genera from the family Ericaceae (e.g., *Rhododendron*), are grown in nurseries and sold in large quantities for planting as ornamentals. In 2001, the pathogen was detected on containerized *Rhododendron* plants in a nursery in Santa Cruz County, CA, as well as in waterways surrounding the nursery (Frankel 2008). Although this discovery was followed by the issuance of an interim regulation by the Animal and Plant Health Inspection Service (APHIS) (of the U.S. Department of Agriculture) and related quarantine efforts, the ramifications of *P. ramorum* having been detected in the commercial nursery network in the United States were not fully realized until 2004, when two large wholesale nurseries in California were found to be infected. Prior to detection of the pathogen, these nurseries had shipped millions of potentially infected ornamental plants to outlets in 39 States (Frankel 2008, Stokstad 2004). Trace-forward inspections of the receiving nurseries revealed 110 infected locations across 20 States (Suslow 2008). An APHIS 2005 emergency order broadened the quarantine on nursery stock shipments and stepped up inspection and eradication efforts, and although a small number of nurseries nationwide have been found positive for *P. ramorum* in the years since, the pathogen is not believed to be established in any wildlands or semi-natural environments outside of California and Oregon. However, the pathogen was detected in southern England in 2002, and subsequently at least 160 outbreaks have been confirmed in woodlands or semi-natural environments of the United Kingdom, along with several hundred nurseries (Webber and Rose 2008). Evidence also suggests that *P. ramorum* was introduced to several other European countries via nursery stock (Brasier and others 2004a). There is general consensus that the pathogen is native to neither North America nor Europe, and the presence of three distinct clades in some nurseries in the United States further underlines the contribution of the commercial nursery plant trade to the pathogen's introduction and dispersal (Brasier and others 2004a, Ivors and others 2006).

In 2002, motivated in part by the discoveries of *P. ramorum* in California and European nurseries as well as the economic threat posed to oak forests in the United States, the Forest Service, U.S. Department of Agriculture, initiated a national survey to detect *P. ramorum* in wildland environments. The survey was intended as a companion to the APHIS nursery inspection program (USDA Forest Service 2004). To aid the detection effort, a team of Forest Service scientists created a risk map to serve as a national sampling frame. Their approach involved spatial overlay of data sets representing three factors: (1) distributions of host species; (2) suitable climatic conditions for the pathogen's persistence and spread; and (3) probable pathways of introduction into previously uninfected areas (Smith and others 2002). The resulting map of the conterminous United States (fig. 7.1) consisted of hexagons for three ordinal levels of risk (high/moderate/low), with the high-risk hexagons falling in areas where all three factors coincided. Although

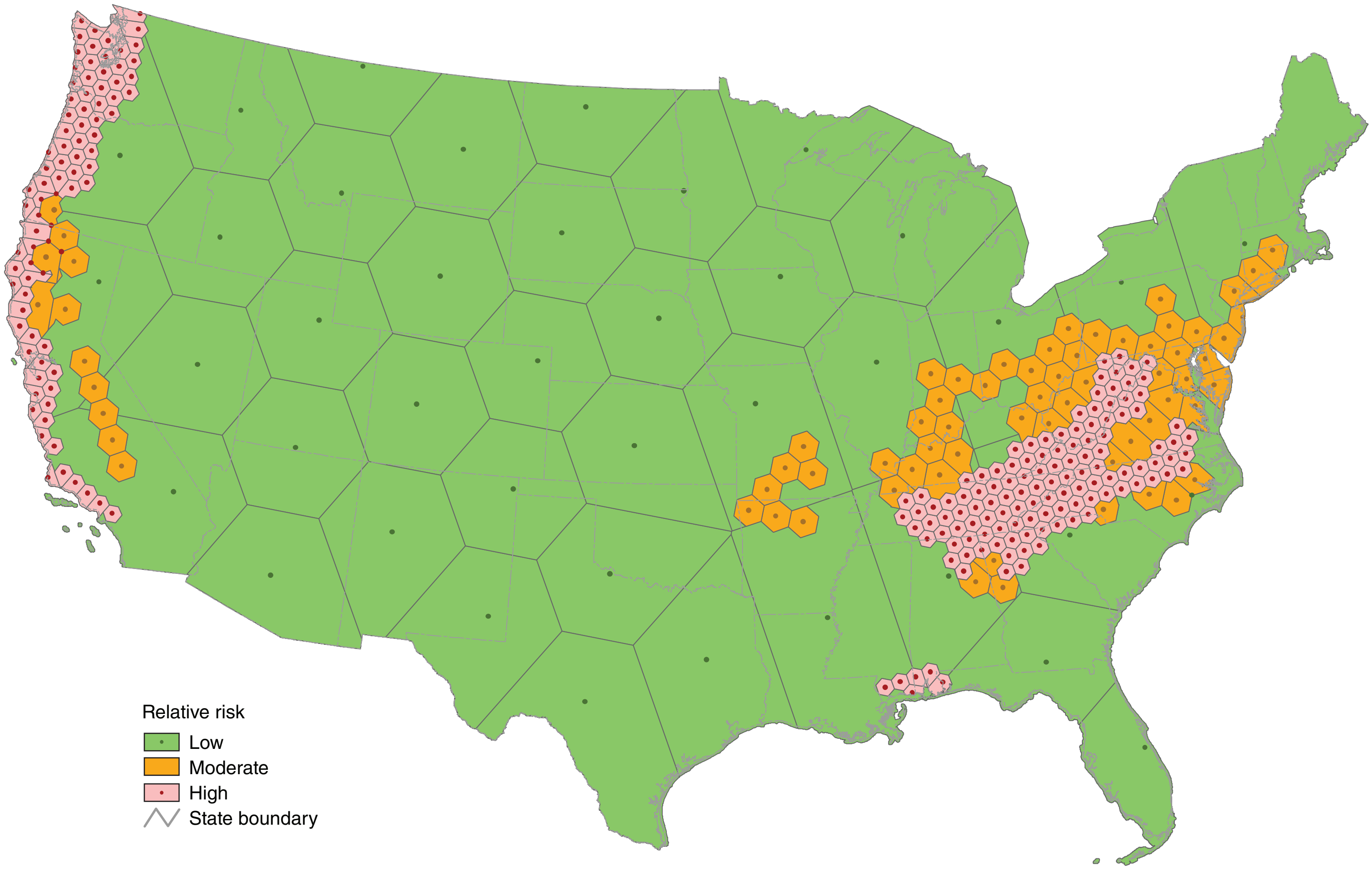


*Figure 7.1—2002 national sudden oak death (*Phytophthora ramorum*) risk map, designed to facilitate surveys of forested environments. State boundaries are included for reference.*

the methodology of the *P. ramorum* national detection survey has changed over the past several years—now emphasizing stream baiting techniques rather than vegetation surveys—the 2002 risk map has continued to serve as a guide in prioritizing sample placement (Oak and others 2008a, Oak and others 2008b). Nevertheless, in subsequent years the list of susceptible hosts has expanded, the climatic factors favoring the pathogen are better understood, and much more is known about basic epidemiology of *P. ramorum*. Therefore, the objective of this analysis was to create a new national risk map utilizing the most current information and also incorporating data sources and analytical techniques not employed for the 2002 map.

## Methods

We adopted a decision rule-based approach for assembling the host, climate, and pathways datasets used in our map. To construct our final map of ordinal risk hexagons, we first combined the host and climate layers into a single hazard map and then analyzed its spatial intersection with the corresponding pathways map. The hazard map may be basically interpreted as a representation of the risk of *P. ramorum* establishment, while the pathways map may be seen as a representation of the risk of introduction. These two gridded maps (1-km$^2$ spatial resolution) are also intended to serve as stand-alone reference products that may be suited to a given user's specific objectives (e.g., a State forest health specialist who is attempting to survey residential landscapes for infected ornamental plants).

**Host sub-layers—**Our host layer was designed to reflect the particular epidemiology (i.e., the two distinct diseases and diverse suite of hosts) of *P. ramorum*. It is a combination of five sub-layers, each corresponding to a particular category of hosts for the pathogen:

***(1) Overstory hosts with high predicted mortality levels (fig. 7.2A)*—**Tanoak (*L. densiflorus*) exhibits the highest mortality rates in the infected areas

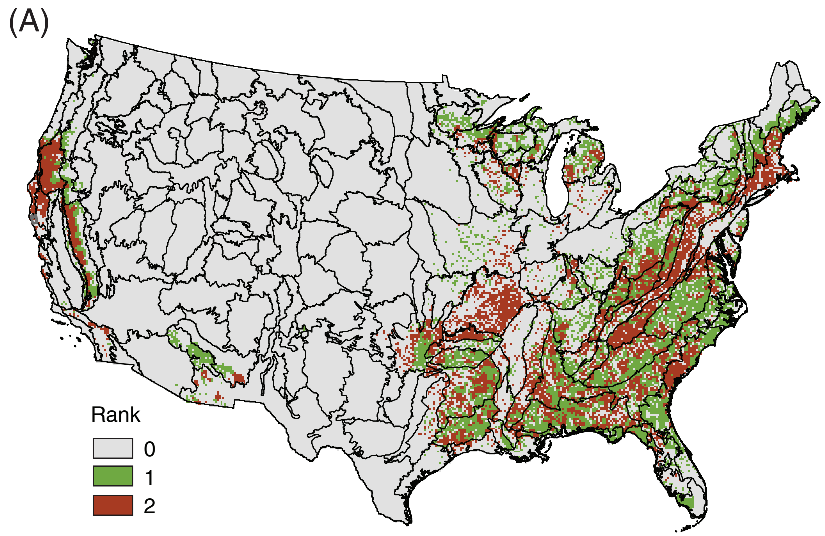


*Figure 7.2—Host sub-layers used in the construction of the combined host layer: (A) overstory hosts with high predicted mortality levels; (B) evergreen midstory foliar hosts; (C) deciduous midstory foliar hosts; (D) evergreen background hosts; and (E) deciduous background hosts. The rank scoring criteria for (A), (B), and (C) are described in tables 7.2, 7.3, and 7.4, respectively. For (D) and (E), a rank of 1 indicates the presence of at least one species listed in table 7.5 or table 7.6, respectively, while a rank of 0 indicates absence of listed species. See text regarding data sources for each sub-layer. Ecoregion section boundaries (Cleland and others 2007) are included for reference.* *(continued on next page)*

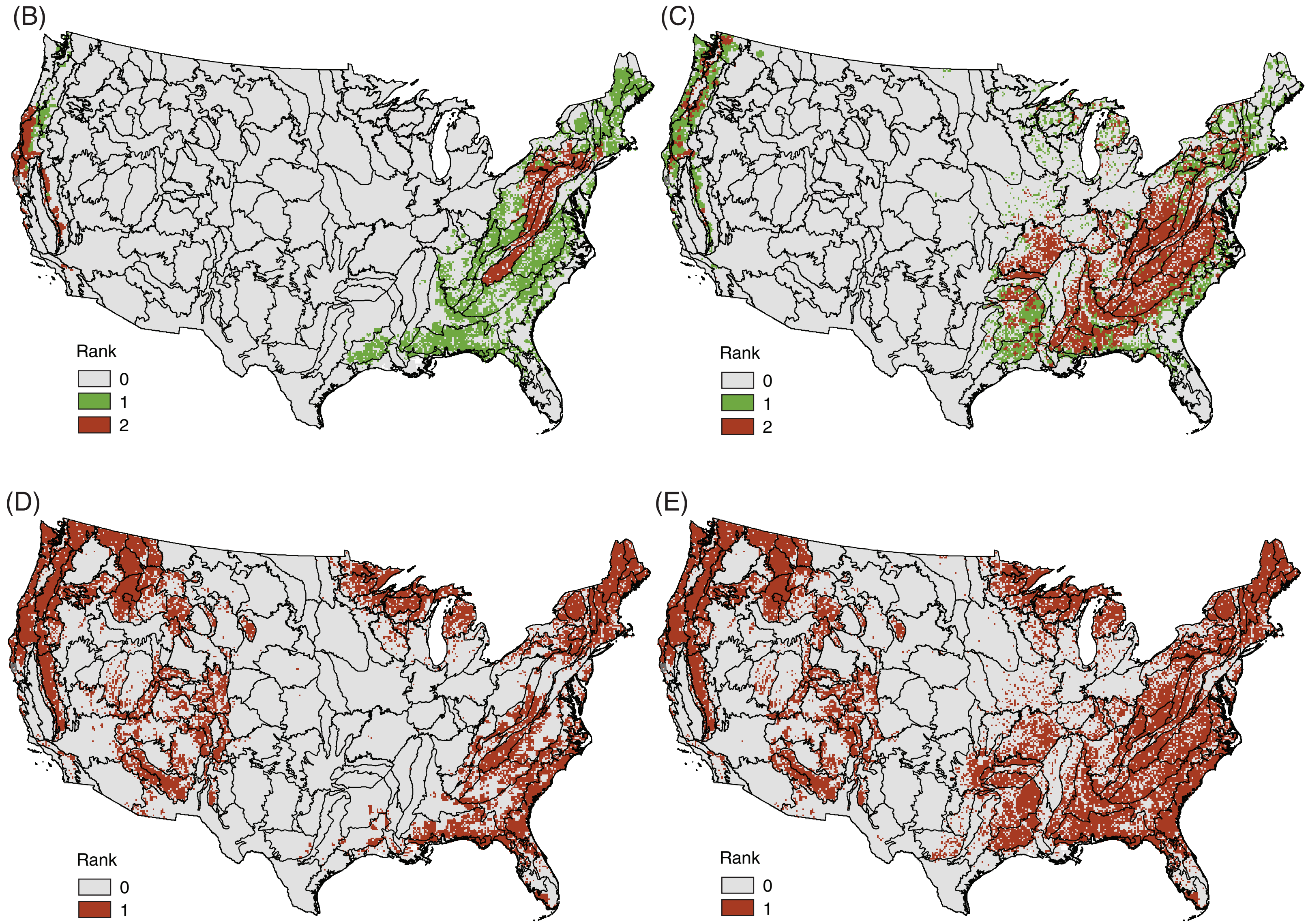


*Figure 7.2 (continued)—Host sub-layers used in the construction of the combined host layer: (B) evergreen midstory foliar hosts; (C) deciduous midstory foliar hosts; (D) evergreen background hosts; and (E) deciduous background hosts. The rank scoring criteria for (A), (B), and (C) are described in tables 7.2, 7.3, and 7.4, respectively. For (D) and (E), a rank of 1 indicates the presence of at least one species listed in table 7.5 or table 7.6, respectively, while a rank of 0 indicates absence of listed species. See text regarding data sources for each sub-layer. Ecoregion section boundaries (Cleland and others 2007) are included for reference.*

of California and Oregon (Rizzo and others 2005). Four oak species have also displayed high mortality due to the pathogen (Murphy and Rizzo 2003, Rizzo and Garbelotto 2003, Rizzo and others 2002): coast live oak (*Q. agrifolia*), California black oak (*Q. kelloggii*), canyon live oak (*Q. chrysolepis*), and Shreve's oak (*Q. shrevei*), although the latter has a limited geographic distribution and is not recorded in the database of the Forest Inventory and Analysis (FIA) Program of the Forest Service. The affected species are from the red/black oak (*Quercus* section *Lobatae*) and intermediate oak (*Quercus* section *Protobalanus*) groups; notably, white oaks do not appear to be affected by *P. ramorum* in natural stands (Rizzo and Garbelotto 2003). Although relatively few North American oak species have been tested for susceptibility to the pathogen, southern red oak (*Q. falcata*) was the first tree discovered to have *P. ramorum* cankers in the United Kingdom, while northern red oak (*Q. rubra*) trees were found naturally infected in the Netherlands (Brasier and others 2004a, Brasier and others 2004b). Based on these observations as well as the general taxonomy of North American oaks (Dodd and others 2005, Jensen 1997, Nixon 1993, 2002), we included a group of oak species from the Eastern and Southwestern United States for which we predict high mortality in our overstory host layer for *P. ramorum* (table 7.1). In addition, research has demonstrated fairly high mortality rates in Pacific madrone (*Arbutus menziesii*) due to the pathogen (Maloney and others 2004), so we also included that species in the overstory layer.

We constructed the layer via ordinary kriging of FIA phase 2 plot data. We first identified all ecoregion sections (Cleland and others 2007) containing FIA plots where the species of interest were present, and then assembled all plots that fell within these sections into geographically referenced samples of basal area values. We fit spherical semivariogram models to each section-level sample using weighted least squares (Cressie 1993). To predict basal area values for unknown locations, we used the 30 nearest neighboring FIA plots or, if fewer plots were available within a 60-km radius of the unknown location, we included all plots within this distance threshold. We performed separate interpolations for each ecoregion section containing the species of interest and then mosaiced the kriged sections into 1-km$^2$ resolution grids for the conterminous United States, masking the results using a forest cover map developed from Moderate Resolution Imaging Spectroradiometer (MODIS) satellite imagery by the USDA Forest Service Remote Sensing Applications Center.

We added together the grids for all overstory species using map algebra, and then re-classed the total overstory basal area grid according to a three-level ordinal risk ranking (table 7.2). The

**Table 7.1—Oak species included in the overstory host layer for *P. ramorum*. All species listed are classified as red or black oaks (*Quercus* sect. *Lobatae*) except for canyon live oak (*Quercus chrysolepis*), which is an intermediate oak (*Quercus* sect. *Protobalanus*)**

| Species | Common name | Regional distribution |
|---|---|---|
| *Q. agrifolia* | Coast live oak | California |
| *Q. buckleyi*[a] | Nuttall oak | Oklahoma and Texas |
| *Q. chrysolepis* | Canyon live oak | West Coast and Southwestern United States |
| *Q. coccinea* | Scarlet oak | Eastern United States |
| *Q. ellipsoidalis* | Northern pin oak | Great Lakes |
| *Q. emoryi* | Emory oak | Southwestern United States |
| *Q. falcata* | Southern red oak | Southeastern United States |
| *Q. hypoleucoides* | Silverleaf oak | Southwestern United States |
| *Q. ilicifolia* | Bear oak, scrub oak | Northeastern United States |
| *Q. imbricaria* | Shingle oak | Eastern United States |
| *Q. incana* | Bluejack oak | Southeastern United States |
| *Q. kelloggii* | California black oak | West Coast United States |
| *Q. laevis* | Turkey oak | Southeastern United States |
| *Q. laurifolia* | Laurel oak | Southeastern United States |
| *Q. marilandica* | Blackjack oak | Eastern United States (esp. SE) |
| *Q. nigra* | Water oak | Southeastern United States |
| *Q. pagoda* | Cherrybark oak | Southeastern United States |
| *Q. palustris* | Pin oak | Eastern United States (esp. NE) |
| *Q. phellos* | Willow oak | Eastern United States (esp. SE) |
| *Q. rubra* | Northern red oak | Eastern United States |
| *Q. shumardii* | Shumard oak | Eastern United States |
| *Q. velutina* | Black oak | Eastern United States |
| *Q. wizlenii* | Interior live oak | California |

Note: Data for all species were compiled from the Forest Inventory and Analysis FIADB 3.0 database. Species distributions are based on Kartesz (2008) and Stein and others (2003).
[a] Species re-named *Q. texana*.

**Table 7.2—Decision rules used to reclassify overstory host basal area (BA) values into an ordinal ranking**

| Decision rule | Overstory host rank |
|---|---|
| BA ≥ 10.43 $ft^2$/ac | 2 |
| 0.7 $ft^2$/ac ≥ BA < 10.43 $ft^2$/ac | 1 |
| BA < 0.7 $ft^2$/ac | 0 |

ranking is built upon an estimate of the basal area (per acre) necessary to achieve average spacing of 60 feet or less between overstory host trees. Davidson and others (2005) suggested that rain splash, the most likely mode by which *P. ramorum* spores are dispersed locally, may commonly disperse spores up to distances of 32.8 feet (10 m) from infected foliar hosts, and more rarely distances of 49.2 feet (15 m) or more. At an average overstory spacing of 60 feet or less, it is likely that one or more overstory host trees in an area of interest falls within the potential rain splash dispersal range of relevant foliar hosts. The average diameter at breast height (d.b.h.) of a host tree from the FIA data is 11.3 inches, with a corresponding basal area of 0.7 square feet. If we assume, for simplicity, that host trees are all of average size and are uniformly distributed over a hexagonal lattice, then a basal area of 10.43 square feet per acre will yield an approximate overstory host tree spacing of 60 feet.

*(2) Evergreen midstory foliar hosts (fig. 7.2B)*—Foliar hosts that grow into the midstory of forest stands have the potential to support *P. ramorum* sporulation and, hence, spore dispersal over relatively large areas. Furthermore, species that are evergreen may serve as year-round sources of inoculum. In the currently infected zone, the evergreen California bay laurel (*U. californica*) is probably the single most important host because it supports high levels of spore production; quite simply, infection levels tend to be high in areas wherever the species is dominant (Condeso and Meentemeyer 2007, Maloney and others 2005, Rizzo and others 2005). Midstory tanoaks—also an evergreen species—are similarly important, especially on sites where California bay laurel is less common (Maloney and others 2005). Furthermore, based on their known level of susceptibility, potential for supporting sporulation, growth habit, and wide distributions, two evergreen species seem likely to serve similar epidemiological roles in the Eastern United States (Rizzo and others 2005, Tooley and Browning 2009, Tooley and others 2004): mountain laurel (*Kalmia latifolia*) and great rhododendron (*R. maximum*). These species grow densely in many Eastern United States forests and can reach heights of 20–35 feet (Preston and Braham 2002).

We developed a ranking for evergreen midstory hosts (table 7.3) that highlights the presence of these species in their respective regions. In addition, for the Western United States, the ranking assigns a moderate level of risk to Pacific madrone, which exhibits both stem and foliar symptoms (Hansen and others 2005, Maloney and others 2004) but is believed to support only low levels of sporulation. For the Eastern United States, the ranking assigns a moderate risk level to southern magnolia (*Magnolia grandiflora*), a foliar host that can grow to heights of 100 feet or more, but which is sparsely distributed relative to mountain laurel or great rhododendron.

**Table 7.3—Decision rules used to develop ordinal rankings for important evergreen midstory hosts found in the Eastern and Western United States**

| Decision rule | Evergreen midstory host rank |
|---|---|
| Eastern United States | |
| *Rhododendron maximum* and/or *Kalmia latifolia* present | 2 |
| *Magnolia grandiflora* present but neither *R. maximum* nor *K. latifolia* present | 1 |
| None of these three species present | 0 |
| Western United States | |
| *Umbellularia californica* and/or *Lithocarpus densiflorus* present | 2 |
| *Arbutus menziesii* present, but neither *U. californica* nor *L. densiflorus* present | 1 |
| None of these three species present | 0 |

We derived distribution maps for these species in two different ways. First, to supplement the existing basal area maps for tanoak and

Pacific madrone, we created basal area maps for California bay laurel and southern magnolia through spatial interpolation of FIA phase 2 plot data (see overstory host layer description). For each species, we then created a presence-absence map by labeling any grid cell with a basal area > 0 as having the species present. Second, because neither mountain laurel nor great rhododendron is recorded in the FIA database, we created presence-absence maps based on county-level distribution data (Kartesz 2008), masking the results using the previously described forest cover map.

***(3) Deciduous midstory foliar hosts (fig. 7.2C)—*** Although not year-round sources of inoculum, deciduous hosts growing in the midstory may still support sporulation and spore dispersal over relatively large areas. On the West Coast, three proven or associated host species of *P. ramorum* grow to moderate heights in forests (Preston and Braham 2002, USDA Animal and Plant Health Inspection Service 2008): bigleaf maple (*Acer macrophyllum*), California buckeye (*Aesculus californica*), and Oregon ash (*Fraxinus latifolia*). Furthermore, recent research (Tooley and Browning 2009) suggests that a number of deciduous species from the Eastern United States also exhibit high susceptibility and potential to support sporulation, perhaps most notably serviceberry (*Amelanchier* species), dogwood (*Cornus florida*), and black locust (*Robinia pseudoacacia*).

We created a deciduous midstory layer in a similar fashion to our overstory host layer. For each of the species named above, we interpolated density maps, in trees per acre, from FIA phase 2 plot data for all relevant ecoregion sections, which were then mosaiced and masked using the previously described forest cover map. We next added the individual species layers together using map algebra, resulting in one combined grid of midstory deciduous host density in trees per acre, which we reclassified according to a three-level ordinal ranking (table 7.4). The ranking is based on the density necessary to provide complete coverage of a forest area in terms of potential rain splash dispersal of spores (Davidson and others 2005) from deciduous midstory foliar hosts. A density of 12.1 trees per acre translates to a mean spacing of 30 feet between host trees in this category (Pielou 1977), a distance that would potentially facilitate transmission of *P. ramorum* from one deciduous midstory foliar host tree to another as well as to overstory hosts.

***(4) Evergreen and (5) Deciduous background host layers (figs. 7.2D and 7.2E)—***We created two additional map layers depicting the distributions of hosts not included in the overstory or midstory layers. Because these "background" hosts are low in stature and/or sparsely distributed, they are not especially important in an epidemiological sense, yet

**Table 7.4—Decision rules used to reclassify deciduous midstory host trees per acre (TPA) values into an ordinal ranking**

| Decision rule | Deciduous midstory host rank |
|---|---|
| TPA ≥ 12.1 trees/acre | 2 |
| 0 trees/acre > TPA < 12.1 trees/acre | 1 |
| TPA = 0 trees/acre | 0 |

they may allow *P. ramorum* to persist in a site where no overstory or midstory hosts occur. Using county-level plant distribution data for the conterminous United States (Kartesz 2008), we mapped counties containing at least one evergreen (table 7.5) and/or deciduous (table 7.6) host species on the APHIS list of proven and associated hosts for *P. ramorum* (USDA Animal and Plant Health Inspection Service 2008). We omitted species already included in the overstory and midstory layers from these lists. As with all other host layers, we masked the results using the forest cover map developed by the Remote Sensing Applications Center.

**Combined host layer—**To create a single host layer for *P. ramorum* (fig. 7.3), we first combined the midstory and background host layers into a single layer according to a simple set of decision rules (table 7.7). These rules emphasize the important midstory foliar hosts over background hosts, as well as evergreen over deciduous host species. We then combined this midstory/background host layer with our overstory, high-mortality host layer using a

**Table 7.5—List of species used in constructing the evergreen background host layer**

| Species or genus name |
|---|
| *Abies* species *(A. concolor, A. grandis, A. magnifica)* |
| *Arbutus unedo*[a] |
| *Arctostaphylos* species (*A. columbiana, A. manzanita, A. uva-ursi*) |
| *Calluna vulgaris*[a] |
| *Ceanothus thyrsiflorus* |
| *Cinnamomum camphora*[a] |
| *Dryopteris arguta* |
| *Euonymus kiautschovicus*[a] |
| *Frangula californica* |
| *Garrya elliptica* |
| *Gaultheria shallon* |
| *Heteromeles arbutifolia* |
| *Kalmia* species (all species in U.S.) |
| *Laurus nobilis*[a] |
| *Leucothoe* species *(L. axillaris, L. fontanesiana)* |
| *Mahonia aquifolium* |
| *Nerium oleander*[a] |
| *Pieris* species |
| *Pittosporum undulatum*[a] |
| *Prunus* species (*P. laurocerasus*[a], *P. lusitanica*[a]) |
| *Quercus ilex*[a] |
| *Quercus parvula* var. *shrevei* |
| *Pseudotsuga menziesii* var. *menziesii* |
| *Pyracantha koidzumii*[a] |
| *Rhododendron* species (evergreen) |
| *Rosa rugosa*[a] |
| *Sequoia sempervirens* |
| *Taxus* species (*T. baccata*[a], *T. brevifolia*) |
| *Torreya californica* |
| *Vaccinium* species (evergreen) |

[a] Nonnative species confirmed as host, but with very limited distribution in the United States.

**Table 7.6—List of species used in constructing the deciduous background host layer**

| Species or genus name |
|---|
| *Acer* species (*A. pseudoplatanus*[a], *A. circinatum*) |
| *Adiantum* species (*A. aleuticum, A. jordanii*) |
| *Aesculus hippocastanum*[a] |
| *Calycanthus occidentalis* |
| *Castanea sativa*[a] |
| *Corylus cornuta* (var. *californica*, var. *cornuta*) |
| *Fagus sylvatica*[a] |
| *Frangula purshiana* |
| *Fraxinus excelsior*[a] |
| *Hamamelis virginiana* |
| *Lonicera hispidula* |
| *Maianthemum racemosum* |
| *Magnolia* species (*M. kobus*[a], *M. stellata*[a], *M. ×soulangiana*[a]) |
| *Osmorhiza berteroi* |
| *Physocarpus opulifolius* |
| *Quercus cerris*[a] |
| *Rhododendron* species (deciduous) |
| *Rosa gymnocarpa* |
| *Rubus spectabilis* |
| *Salix caprea*[a] |
| *Syringa vulgaris*[a] |
| *Toxicodendron diversilobum* |
| *Trientalis borealis* ssp. *latifolia* |
| *Vaccinium* species (deciduous) |
| *Vancouveria planipetala* |
| *Viburnum* species (all species in U.S.) |

[a] Nonnative species confirmed as host, but with very limited distribution in the United States.

second set of rules (table 7.8) that assigned ranks on a six-point scale. The rules emphasize the midstory/background host rank, under the assumption that the occurrence of any midstory or background foliar hosts translates to some degree of *P. ramorum* establishment risk, whether overstory hosts are present or not. In the latter case, however, the rules assign a very low combined host rank (rank = 1) except when the midstory/background host rank is relatively high (rank ≥ 4).

**Climatic suitability layer**—Laboratory evidence indicates that *P. ramorum* has high infection potential during periods of persistent precipitation and relatively mild temperatures (DEFRA-UK 2004, Moralejo and others 2006, Rizzo and Garbelotto 2003, Werres and others 2001). Based on this evidence, we used daily weather station data from the National Climatic Data Center (NCDC) to create annual grid maps (4-km$^2$ spatial resolution) of the longest string of consecutive days where two conditions occurred simultaneously: (1) a temperature between 15.56 and 26.67 °C (60 and 80 °F) during the day and (2) some precipitation, fog, or mist during the day, or alternatively, mean relative humidity during the day of > 90 percent. We created the maps for each year in the 10-year period 1997–2006; typically for any given year, between 4,000 and 5,000 NCDC station points were available nationwide after initial filtering (i.e., after removing any stations with lengthy data gaps). While all of the stations record precipitation amount and temperature, only a small percentage (typically < 10 percent)

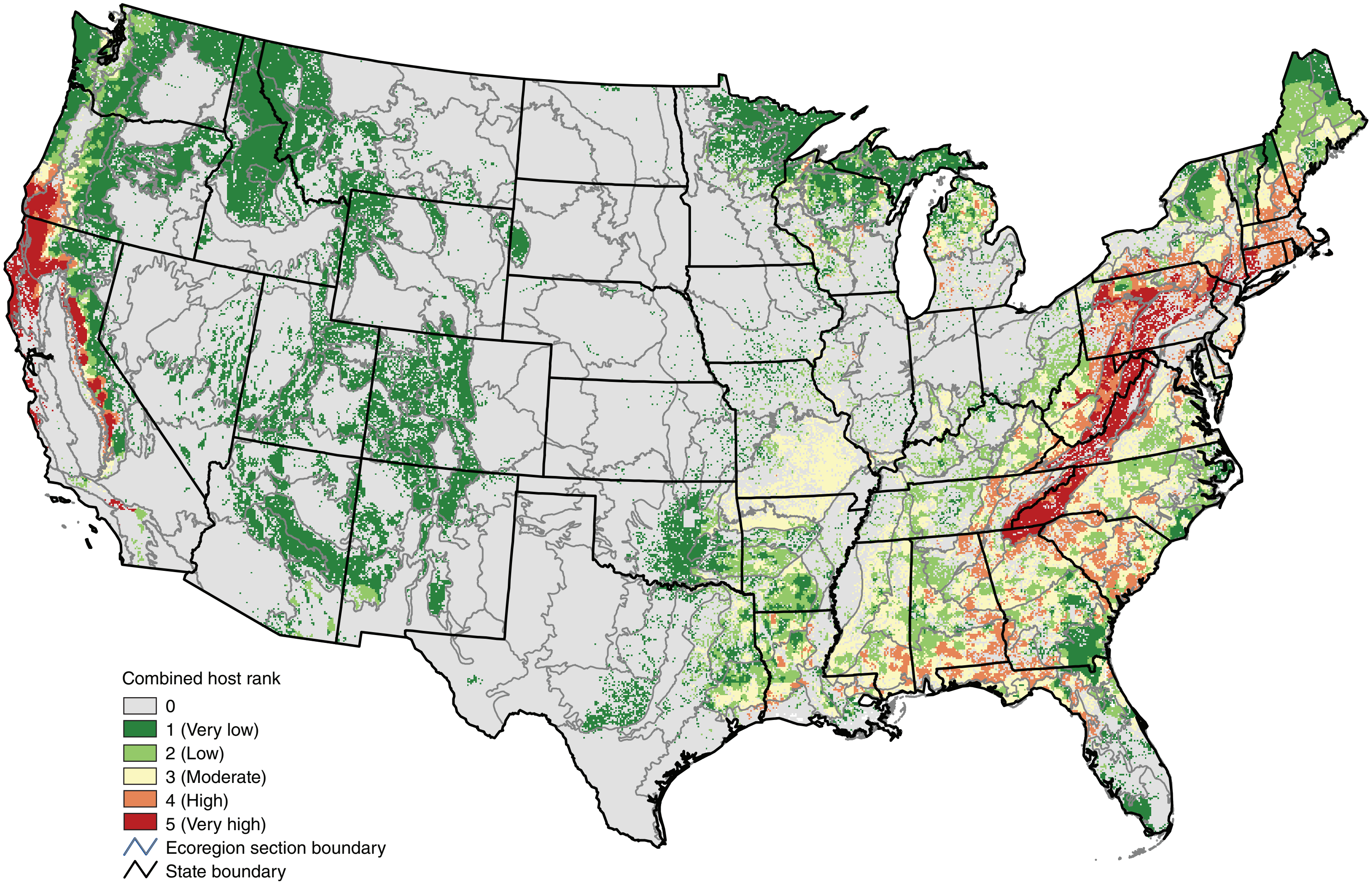


*Figure 7.3—Host layer created by combining the host sub-layers. Please see text regarding the determination of rank scores. Ecoregion section (Cleland and others 2007) and State boundaries are included for reference.*

**Table 7.7—Decision rules for combining the midstory and background host layers into a single ordinal ranking. See tables 7.3 and 7.4, respectively, regarding the evergreen and deciduous midstory host ranks**

| Decision rule | Midstory/background host rank |
|---|---|
| Evergreen midstory host rank = 2 | 5 |
| Evergreen midstory host rank = 1 and evergreen background host rank = 1 | 4 |
| Deciduous midstory host rank = 2 and evergreen background host rank = 1 (evergreen midstory host rank = 0) | 4 |
| Evergreen midstory host rank = 1 and evergreen background host rank = 0 | 3 |
| Deciduous midstory host rank = 2 and evergreen background host rank = 0 (evergreen midstory host rank = 0) | 3 |
| Deciduous midstory host rank = 1 and evergreen background host rank = 1 (evergreen midstory host rank = 0) | 3 |
| Deciduous midstory host rank = 1 and evergreen background host rank = 0 (evergreen midstory host rank = 0) | 2 |
| Evergreen background host rank = 1 and deciduous background host rank = 0 or 1 | 2 |
| Deciduous background host rank = 1 and no other component ranked > 0 | 1 |
| No component ranked > 0 | 0 |



record observations of foggy or misty conditions. Because this latter group of stations tends to exhibit longer strings of consecutive days with suitable conditions, we used co-kriging (Cressie 1993) to interpolate our grids, treating the stations that record fog and mist as our primary dataset and the remaining stations as our covariate or supporting dataset. We then averaged the ten annual co-kriged grids into a single consecutive-day grid using map algebra.

According to laboratory and field evidence, *P. ramorum* spores do not survive well at low relative humidity levels (Davidson and others 2002, Venette and Cohen 2006). Therefore, we masked out areas on our consecutive-day map where mean annual relative humidity fell below 60 percent; this excluded much of the Interior West and northern Great Plains. In addition, based on laboratory observation of high spore mortality at a temperature of -25 °C (DEFRA-UK 2004), we applied a mask that excluded areas where the annual extreme minimum temperature fell below this threshold. We did not use a high-temperature mask because evidence suggests that *P. ramorum* is relatively heat-tolerant (Tooley and others

2008) and, furthermore, because forest canopy structure may have a significant cooling effect that mitigates the deleterious impact of heat on pathogen survival (Potter and others 2001). We used Parameter-elevation Regression on Independent Slopes (PRISM) climate data (Daly and others 2002) to generate both the relative humidity and cold-temperature masks; cell values in the PRISM data sets (4-km$^2$ spatial resolution) were calculated for the 30-year period 1971–2000.

We modified our consecutive-day map in order to account for the seasonal (i.e., month-to-month) distribution of precipitation across the conterminous United States. Using 30-year PRISM climate data, we created two national grids, the first depicting, for each cell, the number of wet days per month averaged across the 12 months of the year, and the second depicting the number of wet days in the wettest month of the year. We subsequently created a ratio map by dividing the wettest-month grid by the 12-month mean grid using map algebra, then divided the result by the maximum value (3.07692) to scale it between 0 and 1. This ratio map represents an approximation of the precipitation distribution throughout the year using a method of moments approach. To create our final climatic suitability layer (fig. 7.4), we multiplied our consecutive-day and precipitation ratio maps using map algebra, then reclassified the resulting map of adjusted climate scores into five ordinal levels of climatic suitability (table 7.9).

**Table 7.8—Decision rules for the final combined host layer ranking**

| Overstory host rank (see table 7.2) | Midstory/background host rank (see table 7.7) | Combined host layer rank |
|---|---|---|
| 2 | 5 | 5 (very high) |
| | 4 | 4 (high) |
| | 3 | 3 (moderate) |
| | 2 | 2 (low) |
| | 1 | 1 (very low) |
| | 0 | 0 |
| 1 | 5 | 4 |
| | 4 | 3 |
| | 3 | 2 |
| | 2 | 1 |
| | 1 | 1 |
| | 0 | 0 |
| 0 | 5 | 3 |
| | 4 | 2 |
| | 3 | 1 |
| | 2 | 1 |
| | 1 | 1 |
| | 0 | 0 |

**Hazard layer—**We created a national hazard layer (fig. 7.5) by combining our host and climate layers according to a set of decision rules (table 7.10). The hazard layer is intended to portray the risk of *P. ramorum* establishment were the pathogen to be introduced to an area of interest. The assigned hazard rank (from 0 to 5) depends on both the optimality of climatic conditions for the pathogen's persistence and the presence of sufficient host to facilitate sporulation and dispersal (i.e., to provide

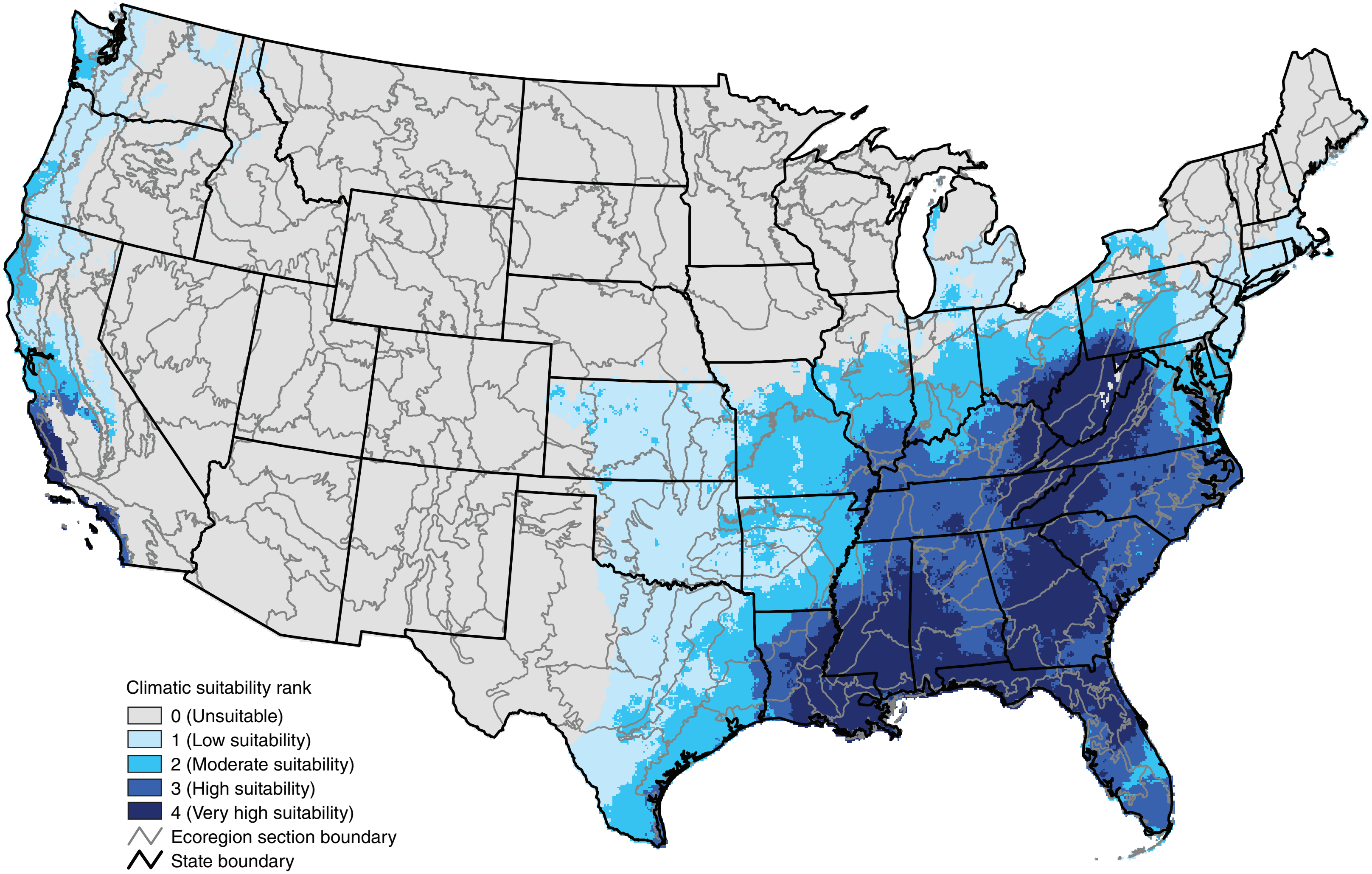


*Figure 7.4—Climatic suitability layer. Please see text regarding the determination of rank scores. Ecoregion section (Cleland and others 2007) and State boundaries are included for reference.*

**Table 7.9—Ordinal ranking of climatic suitability derived by reclassifying adjusted climate scores**

| Adjusted climate score | Climatic suitability rank |
|---|---|
| ≥ 10 | 4 (very high suitability) |
| 7.5 – 9.99 | 3 (high suitability) |
| 5 – 7.49 | 2 (moderate suitability) |
| 2.5 – 4.99 | 1 (low suitability) |
| < 2.5 | 0 (unsuitable) |

functional connectivity for further spread). In practice, the decision rules place greater emphasis on the combined host rank than on the climatic suitability rank; basically, the hazard rank is equivalent to the host rank unless the suitability rank is simultaneously very high (which typically increases the hazard rank) or very low (which typically decreases the hazard rank). This reflects our view that host presence is more critical to the long-term establishment of *P. ramorum* than climate, given that the pathogen can persist in far less than optimal climatic conditions (Browning and others 2008, Tooley and others 2008) if appropriate hosts are available.

**Pathways layer**—We developed a pathways map layer by re-categorizing wildland-urban interface (WUI) spatial datasets for the conterminous United States. Since 2004, *P. ramorum* has been periodically detected at nurseries in various parts of the country (Frankel 2008, Suslow 2008). Notably, plants brought in from wholesalers or other sources typically remain in nurseries only briefly before they are sold to homeowners or other customers. We believe that the epidemiological risk of *P. ramorum* moving unbeknownst from an infected ornamental plant in a developed (e.g., residential) landscape to host plants in a nearby, naturally vegetated landscape can be reasonably represented through re-categorization of data primarily intended to characterize interface areas according to their degree of fire risk. Once re-categorized, these data, developed by the University of Wisconsin-Madison and the Northern Research Station of the Forest Service, allowed us to highlight geographic areas where *P. ramorum* seems most likely to be introduced and subsequently spread into naturally vegetated environments (Radeloff and others 2005).

We started with polygon WUI coverages for each State and the District of Columbia. The coverages are composed of U.S. Census blocks, each of which has been assigned a housing density value according to data from the 2000 Census. In addition, 1992 National Land Cover Data (NLCD) were used to determine percentages of various land cover classes in each block (Radeloff and others 2005). Based on the calculated housing density and landcover percentage values, each census block polygon was assigned to one of 14 wildland-urban interface categories (table 7.11).

We reclassified the original WUI categories to emphasize those we believe present the greatest risk in terms of facilitating the spread of *P. ramorum* (table 7.11). We assigned our highest risk ranking of 3 to the Low and Medium Density Intermix categories, because

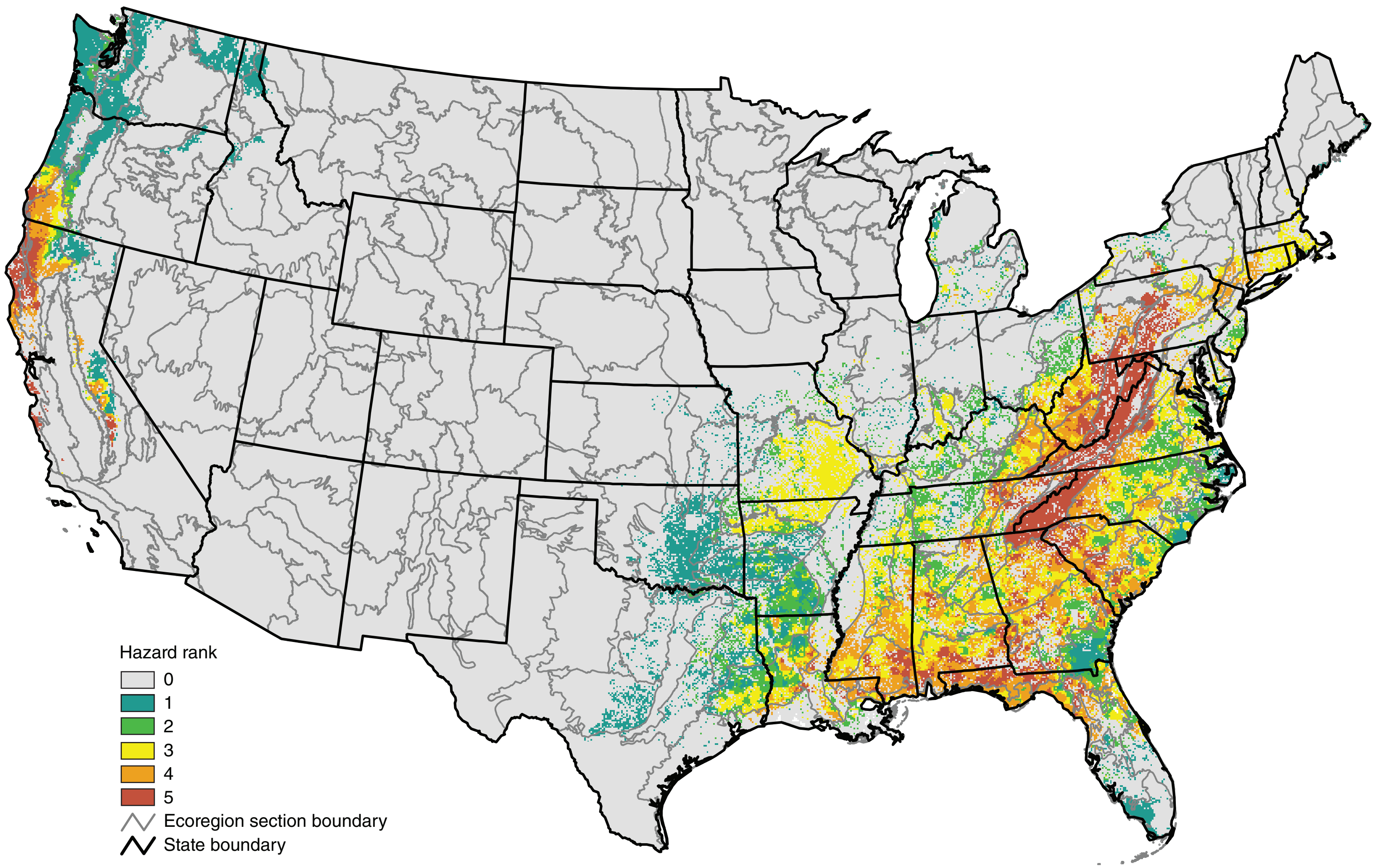


*Figure 7.5—Hazard layer generated by combining the host and climatic suitability layers. Please see text regarding the determination of rank scores. Ecoregion section (Cleland and others 2007) and State boundaries are included for reference.*

**Table 7.10—Decision rules for the final hazard layer ranking**

| Combined host layer rank (see table 7.8) | Climatic suitability rank (see table 7.9) | Hazard rank |
|---|---|---|
| 5 (very high) | 4 (very high suitability) | 5 (very high) |
| | 3 (high suitability) | 5 |
| | 2 (moderate suitability) | 5 |
| | 1 (low suitability) | 4 (high) |
| | 0 (unsuitable) | 0 |
| 4 (high) | 4 | 5 |
| | 3 | 4 |
| | 2 | 4 |
| | 1 | 3 (moderate) |
| | 0 | 0 |
| 3 (moderate) | 4 | 4 |
| | 3 | 3 |
| | 2 | 3 |
| | 1 | 2 (low) |
| | 0 | 0 |
| 2 (low) | 4 | 3 |
| | 3 | 2 |
| | 2 | 2 |
| | 1 | 1 (very low) |
| | 0 | 0 |
| 1 (very low) | 4 | 2 |
| | 3 | 1 |
| | 2 | 1 |
| | 1 | 1 |
| | 0 | 0 |
| 0 | 4 | 0 |
| | 3 | 0 |
| | 2 | 0 |
| | 1 | 0 |
| | 0 | 0 |

**Table 7.11—Original wildland-urban interface categories, with brief descriptions, and their new ranking values for the introduction pathways layer**

| Category | Description | Pathways rank |
|---|---|---|
| Low Density Interface | Housing density ≥ 6.177635 and < 49.42108 units/km$^2$, Vegetation[a] ≤ 50%, within 2.414 km of area with ≥ 75% Vegetation | 2 (moderate) |
| Medium Density Interface | Housing density ≥ 49.42108 and < 741.3162 units/km$^2$, Vegetation ≤ 50%, within 2.414 km of area with ≥ 75% Vegetation | 2 |
| High Density Interface | Housing density ≥741.3162 units/km$^2$, Vegetation ≤ 50%, within 2.414 km of area with ≥ 75% Vegetation | 1 (low) |
| Low Density Intermix | Housing density ≥ 6.177635 and < 49.42108 units/km$^2$, Vegetation > 50% | 3 (high) |
| Medium Density Intermix | Housing density ≥ 49.42108 and < 741.3162 units/km$^2$, Vegetation > 50% | 3 |
| High Density Intermix | Housing density ≥ 741.3162 units/km$^2$, Vegetation > 50% | 1 |
| Uninhabited, Low Vegetation | Housing density = 0, Vegetation ≤ 50% | -1[b] |
| Very Low Density, Low Vegetation | Housing density > 0 and < 6.177635 units/km$^2$, Vegetation ≤ 50% | -1[b] |
| Low Density, Low Vegetation | Housing density ≥ 6.177635 and < 49.42108 units/km$^2$, Vegetation ≤ 50% | -1[b] |
| Medium Density, Low Vegetation | Housing density ≥ 49.42108 and < 741.3162 units/km$^2$, Vegetation ≤ 50% | -1[b] |
| High Density, Low Vegetation | Housing density ≥ 741.3162 units/km$^2$, Vegetation ≤ 50% | -1[b] |
| Uninhabited, High Vegetation | Housing density = 0, Vegetation > 50% | 0 |
| Very Low Density, High Vegetation | Housing density > 0 and < 6.177635 units/km$^2$, Vegetation > 50% | 0 |
| Water | Water | -2[b] |

[a] "Vegetation" is the percentage of an area of interest that falls within one or more of the following landcover types: deciduous, evergreen, or mixed forest; shrubland; grassland/herbaceous; woody or emergent wetlands; or transitional land.
[b] Negative ranking values for sparsely vegetated categories and water served as temporary placeholders during the edge zone analysis (see text), after which all negative values were set to zero.

census blocks in these categories typically contain large inclusions of natural vegetation. We assigned our next highest ranking of 2 to the Low and Medium Density Interface categories because, while census blocks in these categories usually have fewer inclusions, areas dominated by natural vegetation can be found in close proximity (within less than 2.5 km). We assigned a risk ranking of 1 to census blocks in the High Density Intermix and High Density Interface categories because they contain numerous residential parcels distributed throughout, likely resulting in smaller (although not necessarily fewer) inclusions of natural vegetation. Negative values for sparsely vegetated areas and water served as placeholders that were set to zero after we performed an additional "edge zone" analysis, which is described below.

We joined the reclassified State WUI coverages into a single national coverage, converted it to grid format at a 0.625-$km^2$ spatial resolution, and then resampled to a 1-$km^2$ grid using block majority filtering. As a last step, we defined an edge zone composed of grid cells that were classified as either "high" natural vegetation (risk ranking = 0) or high-risk intermix (risk ranking = 3) and were also adjacent to at least one grid cell in the other category based on an eight-neighbor rule. We assigned grid cells in this zone a ranking of 4, thus expanding our risk scale (fig. 7.5).

**Final risk map—**For the 2002 *P. ramorum* map, three hexagonal tessellations covering the conterminous United States, with hexagon sizes increasing from low to high relative risk, were generated through 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 constructing our new map; hence, our final risk map is composed of high-, moderate-, and low-risk polygons with typical areas of ~2600 $km^2$, ~7900 $km^2$, and ~166,000 $km^2$, respectively. Because each tessellation was wall-to-wall (i.e., covered the entire conterminous United States), we developed a set of rules for selecting which individual hexes would be retained for each risk category. These rules (table 7.12) dictate

**Table 7.12—Rules for selecting the high-, moderate-, and low-risk hexagons that were retained in the final composite risk map**

| Risk rating | Rule |
|---|---|
| High | { IF ≥ 5% of the hex is forested<br>AND ≥ 10% of the hex's forested area is "in hazard" (hazard score > 0)<br>AND ≥ 10% of the forest area in hazard has a score = 5<br>AND ≥ 40% of the forest area in hazard has a score ≥ 4<br>AND ≥ 10% of the hex's area is "in pathways" (pathways score > 0)<br>AND ≥ 60% of the hex area in pathways has a score = 4 }<br>OR<br>{ IF ≥ 5% of the hex is forested<br>AND ≥ 10% of the hex's forested area is "in hazard" (hazard score > 0)<br>AND any portion of the forest area in hazard has a score = 5<br>AND ≥ 60% of the forest area in hazard has a score ≥ 4<br>AND any portion of the hex has a pathways score > 0 }<br>OR<br>{ IF ≥ 10% of the hex's forested area is "in hazard" (hazard score > 0)<br>AND ≥ 99% of the forest area in hazard has a score ≥ 4 } |
| Moderate | { IF ≥ 5% of the hex is forested<br>AND ≥ 10% of the forested area is "in hazard" (hazard score > 0)<br>AND ≥ 50% of the forest area in hazard has a score ≥ 3 } |
| Low | All remaining areas |

requirements for the high- and moderate-risk categories with respect to the percentage of a hex that is forested, the percentage of a hex's forested area that is at-risk (i.e., "in hazard" according to our combined hazard map; see fig. 7.5), and/or the percentage of forested area that falls in one of the higher hazard classes. In addition, the three rules defining the high-risk category include tiered requirements for the presence of pathway areas (see fig. 7.6); briefly, as the percentage of a hex's forested area falling within a higher hazard class increases, then the importance of pathways within the hex decreases (to zero in the case of the third high-risk rule). In our view, if virtually all of a hex's forested area falls in a higher hazard class, then the hex should be considered high-risk, regardless of its pathways status.

We removed a small number (< 15) of hexes from our chosen high-risk set that either did not share an edge with any other hex in the set or were in an isolated cluster of two (i.e., they only shared a single edge with each other and no other hex in the set). The areas associated with these hexes were subsequently assigned to the moderate-risk category (i.e., were assigned to moderate-risk hexes). Finally, any areas that did not meet the requirements for either the high- or moderate-risk categories were assigned to low-risk hexes.

## Results and Discussion

A number of recent studies (Fowler and others 2006, Kelly and others 2007, Kluza and others 2007, Magarey and others 2008, Venette and Cohen 2006) have presented national- or global-scale map products related to *P. ramorum* risk. These studies typically focused on identifying environments where *P. ramorum* would be likely to persist and subsequently become established were it to be introduced, although most also included a limited representation of the pathogen's host species (e.g., the spatial distributions of overstory hosts but not those of foliar hosts that support sporulation). The aforementioned studies suggest broadly similar areas of suitability for *P. ramorum* in the conterminous United States, as does the climatic suitability layer we generated for our analysis (fig. 7.4). Indeed, some of these studies (Kluza and others 2007, Venette and Cohen 2006) indicated, as did our analysis, that large areas of the Eastern United States are highly suitable for the pathogen, while areas in California and Oregon where the pathogen is currently established exhibit only moderate suitability. These findings may seem counterintuitive, until one considers that many parts of the East experience long periods of persistent moisture and moderate temperatures; regardless, the findings emphasize the importance of adopting a suitably broad-scale perspective with respect to *P. ramorum* risk. Towards this end, another goal for our analysis was the creation of a comprehensive, nationwide representation of host spatial distribution that reflected key aspects of *P. ramorum* epidemiology, such as the co-occurrence of critical host species at the landscape level (Holdenrieder and others 2004). We were additionally interested in depicting the pathways by which introductions are likely to occur. Including this

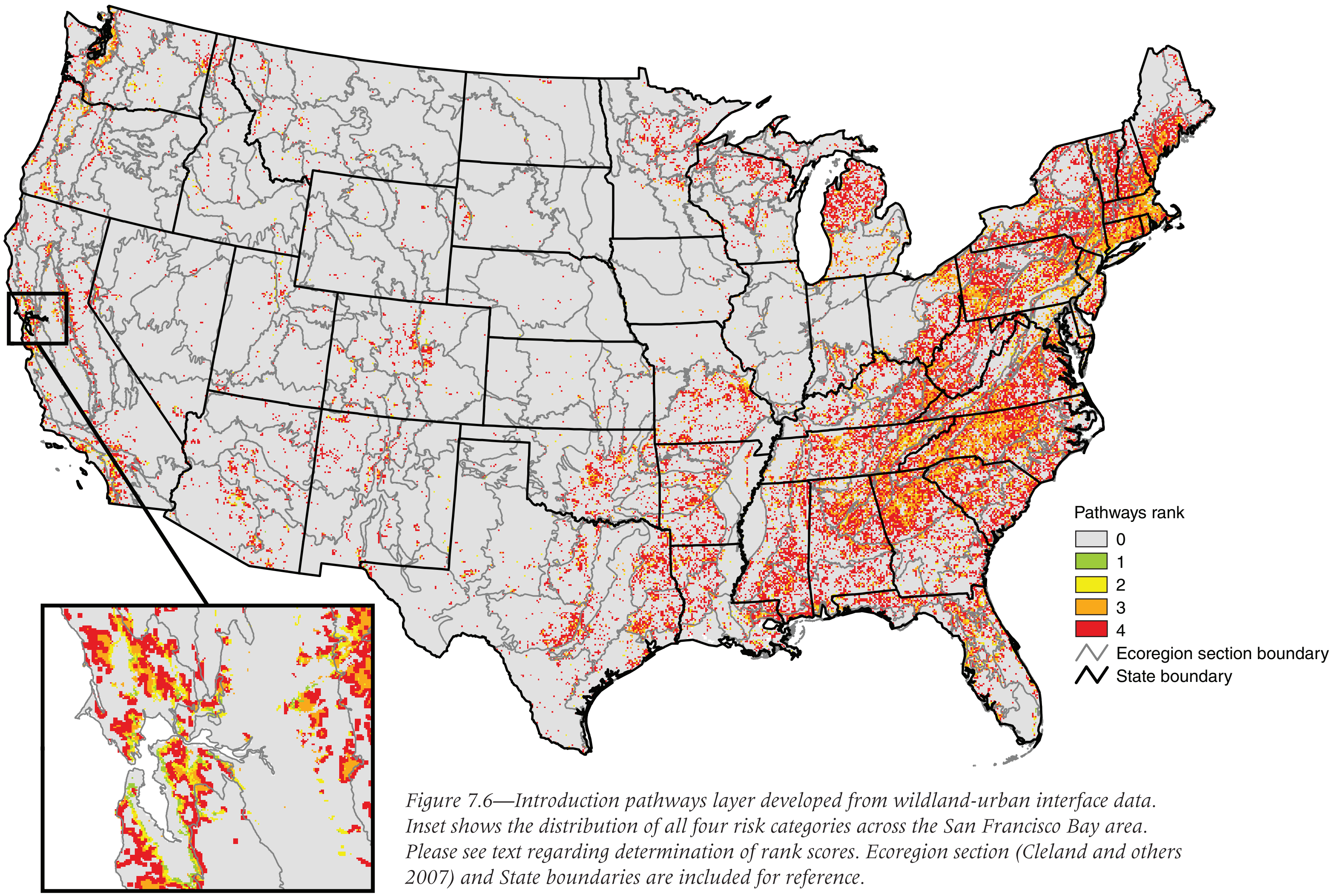


*Figure 7.6—Introduction pathways layer developed from wildland-urban interface data. Inset shows the distribution of all four risk categories across the San Francisco Bay area. Please see text regarding determination of rank scores. Ecoregion section (Cleland and others 2007) and State boundaries are included for reference.*

pathways component was intended to yield a more integrated picture of *P. ramorum* risk, thus making the map more useful for optimizing the national detection survey.

Our new risk map is shown in figure 7.7. The map includes 241 high-risk hexes, 177 moderate-risk hexes, and 70 low-risk hexes. (In the current version, sliver polygons—portions of some hexes that remain after eliminating any overlap between different risk categories—have not been reassigned to a neighboring hex.) The new map departs from the 2002 version (fig. 7.1) in a couple of key ways. Foremost, instead of labeling nearly all of the Pacific Coast from Los Angeles to Seattle as uniformly high risk, the new map highlights a more limited coastal region extending from central California (near the city of San Luis Obispo) to southern Oregon. We believe this smaller region represents a more optimal target area for the implementation of surveys focused on forest (or more broadly, wildland) environments. Although much of the Pacific Coast appears to be climatically suitable for *P. ramorum* (fig. 7.4), the most epidemiologically important host species (tanoak and California bay laurel) reach their greatest densities in our smaller highlighted region, as do the known susceptible oak species (see figs. 7.2 and 7.3). Areas to the south of this region are only sparsely forested, and thus have limited, and disconnected, host presence. Furthermore, areas to the north of this region feature only one notable host, Pacific madrone, but this species is considered a relatively minor foliar host (i.e., it supports only limited sporulation by *P. ramorum*).

With respect to the Eastern portion of the country, our new risk map emphasizes the Southeastern United States to a greater degree (i.e., has more high- and moderate-risk hexes in this region) than the 2002 map. This difference is due to a combination of factors operating at a regional scale. For instance, our analysis indicates a generally higher level of climatic suitability for this region than estimated in the previous map, which instead emphasized an area encompassing the Central and Southern Appalachian Mountains. The discrepancy can be attributed in part to the data used to portray suitability in each map. In particular, the 2002 map defined climatic limits for *P. ramorum* using maps from the Climate Atlas of the United States. Because Climate Atlas maps are monthly or annual summaries, they cannot capture the fine-temporal-scale, simultaneous occurrence of temperature and moisture conditions that appear to promote the pathogen's persistence (Garbelotto and others 2003, Rizzo and Garbelotto 2003); for this reason, we believe our new map is more realistic in portraying suitability in the Eastern United States (Venette and Cohen 2006). Furthermore, because of evidence that the pathogen is able to tolerate fairly high temperatures (Tooley and others 2008), we did not mask out some areas of the East that were deemed unsuitable in the 2002 map. Another major factor in the difference between the two maps relates to the representation of host species. Our new map depicts, in some detail, the epidemiological status of the several dozen species that have been linked to *P. ramorum* in some fashion; only 14

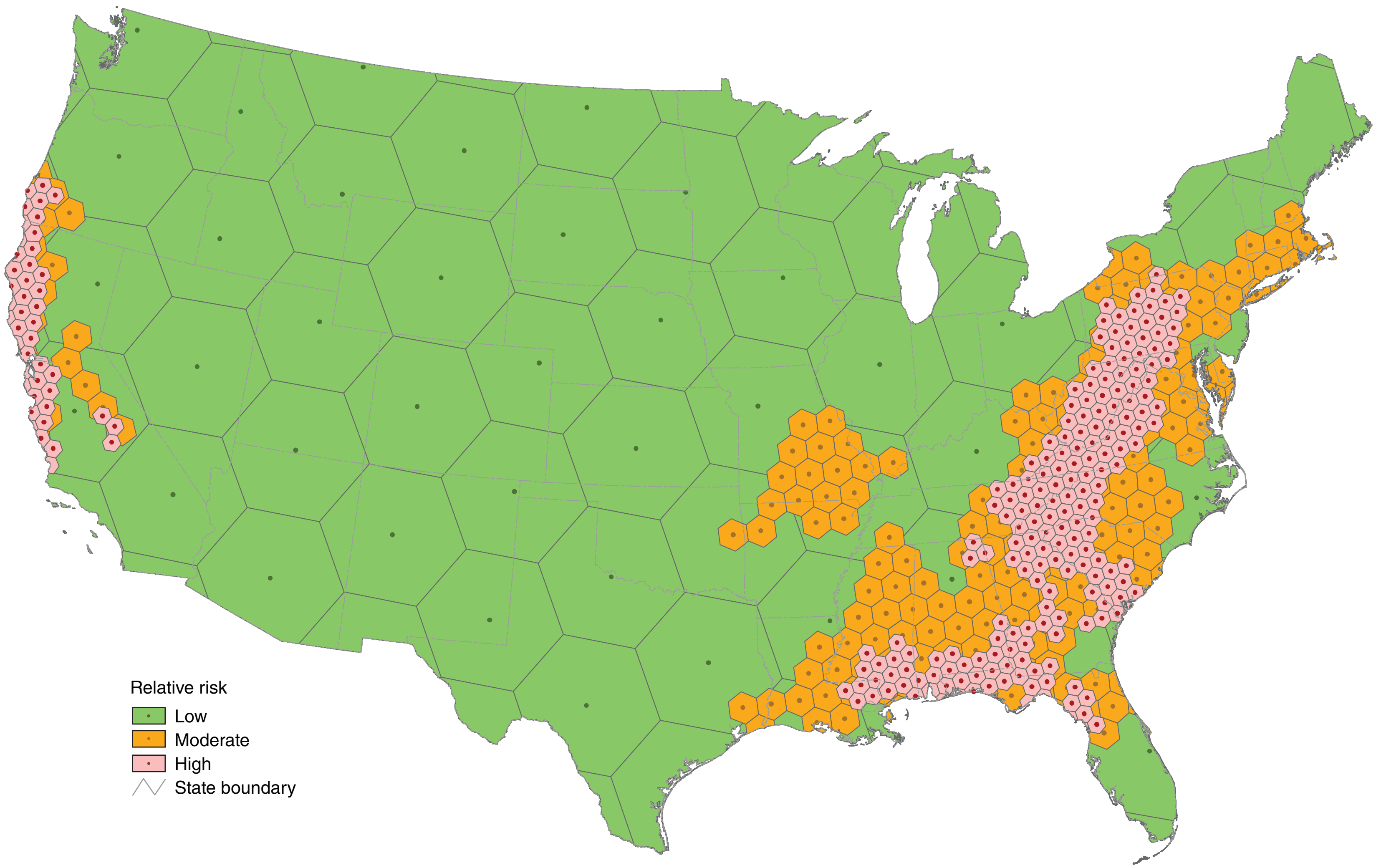


*Figure 7.7—New national risk map for sudden oak death* (Phytophthora ramorum). *State boundaries are included for reference.*

forest species were even known to be affected by the pathogen in 2002, and virtually nothing was known about the susceptibility of Eastern United States species.

Another distinction between the 2002 map and the new map is our inclusion of a pathways layer adapted from wildland-urban interface data. However, as previously noted, the pathways layer played only a relatively minor role in our selection of high-risk hexes. Furthermore, we did not consider the pathways layer during our selection of moderate- or low-risk hexes. Given the absence of good information regarding the likelihood that *P. ramorum* could move from developed to natural environments, we did not feel justified in choosing especially restrictive pathway thresholds for our current analysis. Nevertheless, we believe that the pathways layer could serve a greater role as a discriminatory factor in future risk mapping efforts, either for *P. ramorum* or other invasive organisms of interest.

We recognize that numerous unknowns remain regarding the behavior and potential impact of *P. ramorum* in the conterminous United States. Perhaps most significantly, because the pathogen has not been detected in natural environments outside of Oregon and California, the roles of many potential host species in enabling the persistence and spread of *P. ramorum* remain uncertain, particularly for the Eastern United States. This forced us to make a number of simplifying assumptions regarding hosts in our current analysis. Indeed, it is possible that we omitted some potentially significant host species. For example, Tooley and Kyde (2007) found that chestnut oak (*Q. prinus*), a white oak (*Quercus* section *Quercus*) species that is widely distributed in parts of the East, was highly susceptible to foliar inoculations of *P. ramorum* during laboratory trials; however, those authors also acknowledged that they do not know how foliar infection of oaks fits into the overall epidemiology of the pathogen. There is also uncertainty regarding the amount of inoculum that may be necessary for *P. ramorum* to become established upon arriving in a new location. Thus, while our pathways layer may highlight where spread of inoculum from anthropogenic to natural landscapes is most likely, the absolute likelihood that such spread will result in long-term establishment of the pathogen is still unknown.

In short, our new risk map should only be interpreted as a representation of a set of current hypotheses regarding *P. ramorum*. It is possible that additional information will necessitate changes to these hypotheses or, alternatively, will identify new factors that must be considered when characterizing introduction and/or establishment risk. An advantageous feature of our approach is that, as new information about the pathogen comes to light, it is relatively straightforward to alter the decision rules or replace an individual input layer with a revised version. In any case, we believe that our map, in its current form, can serve as a useful guide for national surveys. We hope that this strategy will continue to prevent *P. ramorum* from becoming a forest health issue in parts of the United States where the pathogen is not currently established.

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