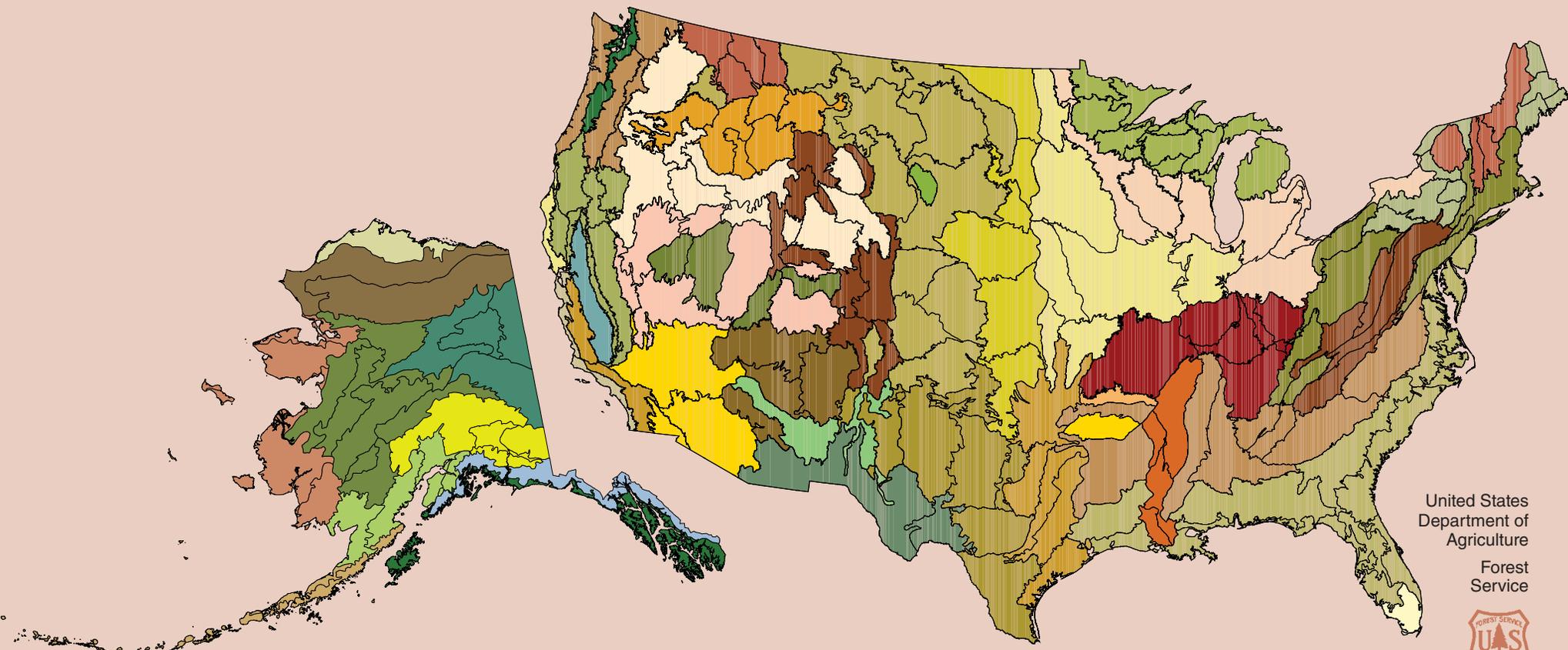


Forest Health Monitoring: 2008 National Technical Report

Editors Kevin M. Potter Barbara L. Conkling



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Front cover map: Bailey's ecoregion provinces and ecoregion sections for the conterminous United States (Cleland and others 2007) and for Alaska (Nowacki and Brock 1995).

Back cover map: Forest land (green) backdrop derived from Advanced Very High Resolution Radiometer satellite imagery (Zhu and Evans 1994).

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Forest Health Monitoring: 2008 National Technical Report

Editors

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Abstract

The Forest Health Monitoring (FHM) Program's annual national technical report has three objectives: (1) to present forest health status and trends from a national or a multi-State regional perspective using a variety of sources, (2) to introduce new techniques for analyzing forest health data, and (3) to report results of recently completed evaluation monitoring projects funded through the FHM national program. The first section of the report, which addresses the first two objectives, is organized according to the Criteria and Indicators for the Conservation and Sustainable Management of Temperate and Boreal Forests. A new phylogenetic approach is described for assessing the health of forest communities from an evolutionary perspective. Also depicted are new tools that allow the public to retrieve high-resolution maps of land cover patterns for specific locations. A methodology is described for the comparison of moisture conditions between different geographical areas and time periods. Aerial survey data are used to identify hotspots of insect and disease activity based on the relative exposure to defoliation- and mortality-causing agents. Satellite data are employed to detect geographic clusters of forest fire occurrence. Forest Inventory and Analysis data from 17 States are employed to detect regional differences in tree mortality.

Phytophthora kernoviae is described as a developing threat to forest health, and a national map of *P. kernoviae* establishment risk is presented. Soil quality indicator data are analyzed to determine regional trends in soil chemistry characteristics that play an important role in the growth of forest trees. Finally, annual change in woody carbon stocks is presented in an initial assessment of down woody material carbon flux in the North Central United States. In the second section of the report, seven recently completed evaluation monitoring projects are summarized, addressing a variety of forest health concerns at smaller scales. These projects include an evaluation of exotic plant invasion vulnerability in Pennsylvania, a description of black ash decline in Minnesota, an assessment of white pine blister rust in Washington State, an evaluation of alder dieback impact on ecosystem nitrogen balance in Alaska, an assessment of the impact of Swiss needle cast on Douglas-fir in Oregon, an examination of the effect of Minnesota winter temperatures on eastern larch beetle, and an evaluation of native bunchgrass communities in Oregon and Idaho following fire.

Keywords—Drought, evaluation monitoring, fire, forest health, forest insects and disease, soil, tree mortality.

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Healthy ecosystems are stable and sustainable, able to maintain their organization and autonomy over time while remaining resilient to stress (Costanza 1992). The national Forest Health Monitoring (FHM) Program of the Forest Service, U.S. Department of Agriculture, with its cooperating researchers within and outside the Forest Service, quantifies the health of U.S. forests within the context of the sustainable forest management criteria and indicators outlined in the Criteria and Indicators for the Conservation and Sustainable Management of Temperate and Boreal Forests (Montréal Process Working Group 2007). The analyses and results outlined in this FHM annual national technical report offer a snapshot of the current condition of U.S. forests from a national or a multi-State regional perspective, incorporating baseline investigations of forest ecosystem health, examination of change over time in forest health metrics, and the assessment of developing threats to forest stability and sustainability. Several chapters also describe new techniques for analyzing forest health data as well as new applications of established techniques. Finally, this report presents results from recently completed evaluation monitoring (EM) projects that have been funded through the FHM national program to determine the extent, severity, and causes of forest health problems (Forest Health Monitoring 2008).

The conservation of evolutionary diversity is an important biological criterion for judging the sustainability of forests because it is necessary for the adaptation of species and the resistance of communities to changes in environmental conditions (chapter 2). Community phylogenetic analysis is a new approach that quantifies evolutionary variation across communities of species. As such, it represents a potential tool for assessing the health of forest communities, both in terms of biodiversity and community resilience to stress. Regional patterns of phylogenetic diversity in forest tree species, calculated from more than 100,000 plots maintained by the Forest Inventory and Analysis (FIA) Program of the Forest Service, are similar to those of species richness across the conterminous United States, but important differences exist. Additionally, measures of phylogenetic structure suggest that forest tree communities may possess differing levels of susceptibility to generalist forest threats, and that such threats may have differing effects on the ecological functionality of these communities.

Forest fragmentation, landscape mosaics, and other land cover patterns are important indicators of forest health, but their reporting has been limited to regional statistical summaries and relatively coarse-scale maps (chapter 3). New tools, however, have made it possible

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to prepare such national maps as online databases through which readers can retrieve high-resolution maps for specific locations. Specifically, national maps derived from the 2001 National Land Cover Database (Homer and others 2007) are now available, portraying three land cover indices at very fine scales: forest area density, land cover mosaic, and forest spatial pattern. The forest area density index shows the proportion of area surrounding a 0.09-ha pixel, within a 15-ha neighborhood that is forest; the land cover mosaic index shows the mixture of developed, agriculture, and seminatural land cover in the surrounding 15-ha neighborhood; and the forest spatial pattern index describes the physical structure of the forest in which the pixel is located.

Drought conditions can affect forest health both directly and indirectly, so an appropriate regional index of drought is necessary to gain important insights about the health of forests (chapter 4). A newly developed moisture index difference (*MID*) methodology allows for the reasonable comparison of moisture conditions between different geographical areas and time periods. This approach is computationally simple and repeatable, requiring only climate variables and omitting soil or other environmental factors that are unavailable nationally at fine scales. The

MID technique yields effective 1-year snapshots of drought conditions as demonstrated by its ability to capture several significant drought events from recent decades. Using more recent data from 2007, the *MID* methodology mapped severe to extreme drought conditions in several heavily forested ecoregion sections in the Southeastern United States, as well as parts of southern California and the Intermountain West.

Monitoring the occurrence of forest pest and pathogen outbreaks is also important at regional scales because of the significant impact insects and disease can have on forest health across landscapes (chapter 5). Hotspot analysis of Forest Service Forest Health Protection low-altitude aerial survey and ground survey data from 2006 detected significant clusters of forest mortality associated with mountain pine beetle in the West, emerald ash borer in Michigan, and balsam woolly adelgid in Maine. Forest tent caterpillar and gypsy moth were responsible for several hotspots of defoliation in the Northeast and the Southeast, while western spruce budworm and a handful of other insects were the main causes of defoliation in the Northern Rockies and the Northwest. Spruce beetle was the most significant cause of mortality in Alaska, where the aspen leafminer was the most important defoliation agent.

Forest fire occurrence outside the historic range of frequency and intensity can result in extensive economic and ecological impacts. The detection of geographic clusters of fire occurrences should allow for the identification of areas at greatest risk of significant impact and for the selection of locations for more intensive analysis (chapter 6). The ecoregion sections with the greatest number of fire occurrences from 2005 to 2007, per 100 km² of forested area, were located in southern California and the Northern Rockies. Hotspots of fire occurrence generally differed by year, with the exception of a highly clustered and extensive hotspot that appeared each year in central Idaho and western Montana. Other hotspots were detected in the Northern Cascades, northern California, east Texas, western Louisiana, Arkansas, east central Arizona, and southern Georgia.

Tree mortality is a natural process in all forested ecosystems, but high levels of mortality at large scales may indicate that forest health is declining. FIA phase 2 data offers tree mortality information at a more spatially intense sample than the FHM and FIA phase 3 data used in past forest health annual technical reports (chapter 7). An analysis of FIA plots from 17 States found that the highest ratios of annual mortality to gross growth occurred in ecoregion sections

of the High Plains, northern Minnesota, and Pennsylvania. The species experiencing mortality varied across ecoregion sections, while the ratio of average dead tree diameter to live tree diameter varied within ecoregion sections.

A developing threat to forest health is *Phytophthora kernoviae*, a fungus-like pathogen of trees and shrubs, which was identified in the United Kingdom in 2003 (chapter 8). Its epidemiological and host similarity with *P. ramorum*, the sudden oak death pathogen that has caused significant tree damage and mortality in California and Oregon, has raised concerns about the possibility of *P. kernoviae* introduction and establishment in the United States. Ecoregion sections facing the greatest risk of introduction and establishment of *P. kernoviae* are located in the Central Appalachian Mountains and adjacent plateaus.

Concentrations of calcium (Ca) and aluminum (Al) are soil chemistry characteristics that play an important role in the growth of forest trees and the maintenance of forest ecosystem health and vitality (chapter 9). Soil quality indicator data were collected from FIA phase 3 plots across the conterminous United States to calculate the spatial distribution of Ca:Al molar ratios in two sampled soil layers.

Preliminary results indicate that Midwestern and northern soils are subjected to significant acid deposition, that western soils are often rich in Ca, and that southern soils are more highly weathered than soils in the North and West, with high precipitation transporting mobile cations such as Ca from the soil. The data also indicate what Ca:Al conditions are associated with different forest types and allow for the inference that certain forest groups will not tolerate or cannot compete in conditions of soil Ca depletion and associated high exchangeable Al.

Down woody materials (DWM) encompass a detrital forest ecosystem component offsetting approximately 1 percent of annual CO₂ emissions in the United States. To provide an initial assessment of DWM carbon (C) flux across large scales, the annual change in fine and coarse woody C stocks and other attributes were assessed for forests in the North Central United States using FIA DWM data (chapter 10). Flux rates varied both in their amount and status (emission/sequestration) by forest type, latitude, and DWM component size. Specifically, initial evidence exists that higher latitudes are experiencing coarse woody debris C emission

while fine woody debris C stocks remain relatively static, suggesting that DWM C stocks are at a greater threat of becoming net C emitters because of the possibility of increased decay rates.

Finally, seven recently completed EM projects address a wide variety of forest health concerns at a smaller scale. These projects, funded by the FHM Program:

- Evaluate the ability of coarse-scale FIA data to predict vulnerability to invasion by exotic plant species in the Allegheny National Forest of Pennsylvania (chapter 11).
- Determine the pattern and extent of black ash (*Fraxinus nigra*) decline in Minnesota, and relate these to climatic, physiographic, and edaphic data (chapter 12).
- Assess the development of white pine blister rust in young plantations of western white pine (*Pinus monticola*), genetically enhanced in breeding programs for resistance to blister rust, in Washington State (chapter 13).
- Evaluate the impact of alder (*Alnus tenuifolia*) dieback on ecosystem nitrogen balance in Alaska, and establish transects to monitor alder dieback and mortality (chapter 14).

- Assess the impact of Swiss needle cast on Douglas-fir (*Pseudotsuga menziesii*) diameter and height growth in the Cascade Mountains of northern Oregon (chapter 15).
- Examine the effect of winter temperatures in Minnesota on the overwintering success of the eastern larch beetle, a pest affecting the health of eastern larch (*Larix laricina*) (chapter 16).
- Monitor how native bunchgrass communities in the Wallowa-Whitman National Forest of eastern Oregon and western Idaho change after fire, particularly in relationship to invasive plants (chapter 17).

The FHM program, in cooperation with researchers inside and outside the Forest Service, continues to investigate a wide variety of issues relating to forest health using a wide variety of data and techniques. This report presents some of the latest results from ongoing

national-scale detection monitoring and smaller scale environmental monitoring efforts by FHM and its cooperators. For more information about efforts to determine the status, changes, and trends in indicators of the condition of U.S. forests, please visit the FHM Web site at <http://www.fs.fed.us/foresthealth/fhm/>.

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SECTION 1.
Forest Health
Monitoring
Research

Forests cover a vast area of the United States, 303.1 million ha (749 million acres) or approximately one-third of the Nation's land area (Smith and others 2004). These forests are of substantial ecological, economic, and social importance. Both their ecological integrity and their capacity to provide goods and services are of considerable concern in the face of a long list of threats, including insect and disease infestation, fragmentation, catastrophic fire, invasive species, and the effects of global climate change.

Assessing and monitoring the health of these forests is, therefore, a critical and challenging task. While there is no universally accepted definition of forest health, a healthy forest ecosystem is likely to possess four characteristics (Kolb and others 1994):

- The physical environment, biotic resources, and energy consumption networks to support productive forests during at least some successional stages
- Resistance to catastrophic change and/or the ability to recover from catastrophic change at the landscape level

- A functional equilibrium between supply and demand of essential resources (water, nutrients, light, growing space) for major portions of the vegetation
- A diversity of seral stages and stand structures that provide habitat for many native species and all essential ecosystem processes

The national Forest Health Monitoring (FHM) Program of the Forest Service, U.S. Department of Agriculture, produces this annual national technical report on the health of U.S. forests, using the Criteria and Indicators for the Conservation and Sustainable Management of Temperate and Boreal Forests (Montréal Process Working Group 2007) as an organizing framework.

The FHM national technical report has three specific objectives. The first is to present information about forest health from a national perspective, or from a multi-State regional perspective when appropriate, using data collected by the Forest Health Protection (FHP) and Forest Inventory and Analysis (FIA) programs of the Forest Service, in addition to data from other sources. The chapters in the first

Chapter 1. Introduction

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section of the report achieve this objective, in chapters organized according to the Criteria and Indicators for the Conservation and Sustainable Management of Temperate and Boreal Forests (Montréal Process Working Group 2007). These results stem from the ongoing national scale detection monitoring efforts from FHM and its cooperators, using a wide variety of regional-scale data and analysis techniques. While in-depth interpretation and analysis of specific geographic or ecological regions are beyond the scope of this report, the report presents information for the identification of areas that may require investigation at a finer scale.

The second objective of the report, also covered in section 1, is to present new techniques and new applications of established techniques for analyzing forest health data. Examples in this report are chapter 2, which presents a new set of statistical techniques for quantifying evolutionary variation among tree communities; chapter 3, which describes new tools that allow for the fine-scale display of national land cover mosaic maps; chapter 4, which introduces a newly developed drought index methodology that allows for the comparison of moisture conditions between geographical areas and across periods of time;

and chapters 5 and 6, which use a Geographical Information System hotspot analysis to, respectively, detect significant clusters of forest mortality and defoliation and detect significant clusters of forest fire occurrences.

The third objective of the national technical report, addressed in its second section, is to present results of recently completed evaluation monitoring (EM) projects that have been funded through the FHM national program. These projects are funded by FHM to determine the extent, severity, and/or causes of forest health problems (Forest Health Monitoring 2009), generally at a finer scale than that addressed in the first section of the report. Each chapter in the second section of the report contains an overview of the EM project, key results, and contacts for more information. This objective is new to the national technical report, and these EM project summaries are included for the first time.

Organization of the Report

The Forest Service has adopted the Santiago Declaration and accompanying Criteria and Indicators for the Conservation and Sustainable Management of Temperate and Boreal Forests (Montréal Process Working Group 2007) as

a forest sustainability assessment framework (Smith and others 2001, U.S. Department of Agriculture Forest Service 2004). It is appropriate, therefore, to note which criterion is addressed by each of the chapters in the first section of this FHM national technical report. The seven criteria are:

Criterion 1—conservation of biological diversity

Criterion 2—maintenance of productive capacity of forest ecosystems

Criterion 3—maintenance of forest ecosystem health and vitality

Criterion 4—conservation and maintenance of soil and water resources

Criterion 5—maintenance of forest contribution to global carbon cycles

Criterion 6—maintenance and enhancement of long-term multiple socioeconomic benefits to meet the needs of societies

Criterion 7—legal, institutional, and economic framework for forest conservation and sustainable management

While a complete evaluation of all the sustainability criteria is not appropriate in this report, it contains chapters associated with four criteria: criterion 1 (chapters 2 and 3); criterion 3 (chapters 4, 5, 6, 7, and 8); criterion 4 (chapter 9); and criterion 5 (chapter 10).

When appropriate throughout this report, authors used Bailey's revised ecoregion provinces and sections (Cleland and others 2007) as a common ecologically based spatial framework for their forest health assessments (fig. 1.1). Specifically, when the spatial scale of the data and the expectation of an identifiable pattern in the data were appropriate, authors used ecoregion sections as assessment units for their analyses. In Bailey's hierarchical system, the two broadest ecoregion scales, domains and divisions, are based on large ecological climate zones, while each division is broken into provinces based on vegetation macrofeatures (Bailey 1995). Provinces are further divided into sections, which may be thousands of square miles in extent and are expected to encompass regions similar in their geology, climate, soils, potential natural vegetation, and potential natural communities (Cleland and others 1997).

Alaska ecoregion provinces

-  Alaska Mixed Forest (213)
-  Alaska Range Taiga (135)
-  Aleutian Meadow (271)
-  Arctic Tundra (121)
-  Bering Sea Tundra (129)
-  Brooks Range Tundra (125)
-  Pacific Coastal Icefields (244)
-  Pacific Gulf Coastal Forest (245)
-  Upper Yukon Taiga (139)
-  Yukon Intermontaine Taiga (131)

Eastern ecoregion provinces

-  Adirondack—New England Mixed Forest—Coniferous Forest—Alpine Meadow (M211)
-  Central Appalachian Broadleaf Forest—Coniferous Forest—Meadow (M221)
-  Central Interior Broadleaf Forest (223)
-  Eastern Broadleaf Forest (221)
-  Everglades (411)
-  Laurentian Mixed Forest (212)
-  Lower Mississippi Riverine Forest (234)
-  Midwest Broadleaf Forest (222)
-  Northeastern Mixed Forest (211)
-  Ouachita Mixed Forest—Meadow (M231)
-  Outer Coastal Plain Mixed Forest (232)
-  Ozark Broadleaf Forest (M223)
-  Prairie Parkland (Subtropical) (255)
-  Prairie Parkland (Temperate) (251)
-  Southeastern Mixed Forest (231)

Western ecoregion provinces

-  American Semi-Desert and Desert (322)
-  Arizona—New Mexico Mountains Semi-Desert—Open Woodland—Coniferous Forest—Alpine Meadow (M313)
-  Black Hills Coniferous Forest (M334)
-  California Coastal Chaparral Forest and Shrub (261)
-  California Coastal Range Open Woodland—Shrub—Coniferous Forest—Meadow (M262)
-  California Coastal Steppe—Mixed Forest—Redwood Forest (263)
-  California Dry Steppe (262)
-  Cascade Mixed Forest—Coniferous Forest—Alpine Meadow (M242)
-  Chihuahuan Semi-Desert (321)
-  Colorado Plateau Semi-Desert (313)
-  Great Plains—Palouse Dry Steppe (331)
-  Great Plains Steppe (332)
-  Intermountain Semi-Desert (342)
-  Intermountain Semi-Desert and Desert (341)
-  Middle Rocky Mountain Steppe—Coniferous Forest—Alpine Meadow (M332)
-  Nevada—Utah Mountains Semi-Desert—Coniferous Forest—Alpine Meadow (M341)
-  Northern Rocky Mountains Forest—Steppe—Coniferous Forest—Alpine Meadow (M333)
-  Pacific Lowland Mixed Forest (242)
-  Sierran Steppe—Mixed Forest—Coniferous Forest—Alpine Meadow (M261)
-  Southern Rocky Mountains Steppe—Open Woodland—Coniferous Forest—Alpine Meadow (M331)
-  Southwest Plateau and Plains Dry Steppe and Shrub (315)

Data Sources

A major source of data in FHM national technical reports has been the FIA program, which collects forest inventory information across all forest land ownerships in the United States. FIA maintains a network of more than 100,000 permanent ground plots across the conterminous United States, with a sampling intensity of approximately 1 plot per 2428.11 ha (6,000 acres). The FIA Program's phase 2 encompasses the annualized inventory measured on plots at regular intervals, with each plot surveyed every 5 years in most Eastern States, but with plots in the Rocky Mountain and Pacific Northwest regions surveyed once every 10 years (Reams and others 2005). The standard one-sixth-acre plot (fig. 1.2) consists of four 24-foot-radius subplots (approximately 0.0415 or 1/24 acre), on which field crews measure trees at least 5 inches in diameter. Within each of these subplots is nested a 6.8-foot-radius microplot (approximately 1/300th acre), on which crews measure trees smaller than 5 inches in diameter. A core-optional variant of the standard design includes four "macroplots," each with a radius of

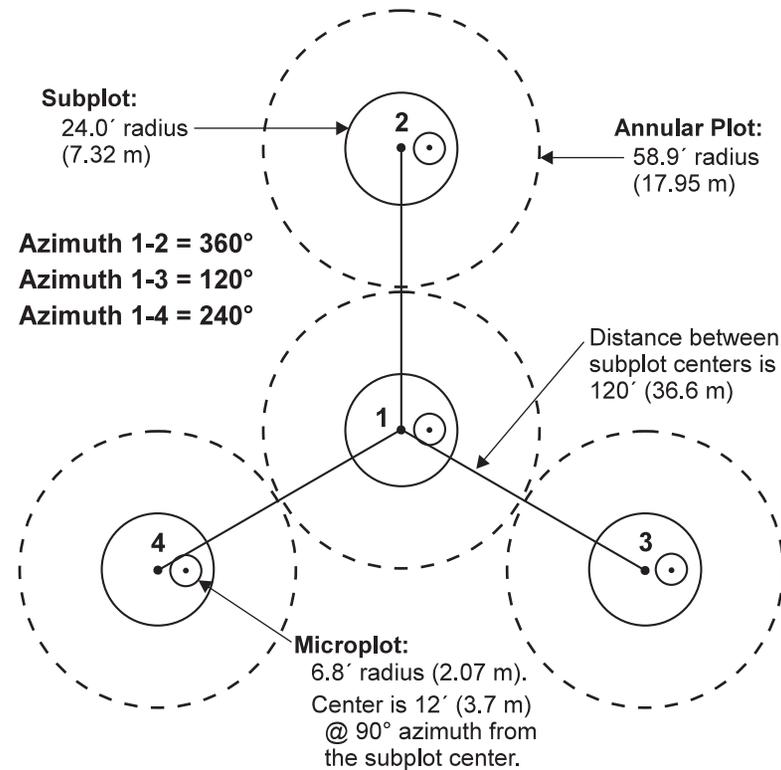


Figure 1.2—The FIA mapped plot design. Subplot 1 is the center of the cluster with subplots 2, 3, and 4 located 120 feet away at azimuths of 360°, 120°, and 240°, respectively (Forest Inventory and Analysis 2009).

58.9 feet (approximately one-fourth acre), that originate at the center of each subplot (Forest Inventory and Analysis 2009).

FIA phase 3 plots are a subset of the phase 2 plots, with 1 phase 3 plot for every 16 standard phase 2 plots. In addition to traditional forest inventory measurements, data for a variety of important ecological indicators are collected from phase 3 plots, including tree crown condition, lichen communities, down woody material (DWM), soil condition, and vegetation structure and diversity. Additionally, data on ozone bioindicator plants are collected on a separate grid of plots. Prior to 2000¹, these additional forest health indicators were measured as part of the FHM detection monitoring ground plot system (Palmer and others 1991).

Forest Service data sources in this edition of the FHM national technical report include: FIA annualized phase 2 survey data, FIA phase 3

DWM data (2001–06), FIA phase 3 soil quality data (2001–05), FHP low-altitude aerial survey forest mortality and defoliation data (2006), Moderate Resolution Imaging Spectroradiometer (MODIS) active fire detections for the U.S. database (2005–07), and forest cover data developed from MODIS satellite imagery by the Forest Service, Remote Sensing Applications Center. Other sources of data were: the 2001 high-resolution National Land Cover Database map (Homer and others 2007), the Parameter-Elevation Regression on Independent Slopes climate mapping system data (PRISM Group 2008), the NCSU-APHIS Plant Pest Forecasting System climatic and environmental variable data for pest and pathogen geographical distribution modeling (Magarey and others 2007), the Biota of North America county-level plant species distribution data (Kartesz 2008), and the wildland-urban interface data (Radeloff and others 2005).

¹ U.S. Department of Agriculture Forest Service. 1998. Forest health monitoring 1998 field methods guide. Research Triangle Park, NC: U.S. Department of Agriculture Forest Service, National Forest Health Monitoring Program. 473 p. On file with: Forest Health Monitoring Program, 3041 Cornwallis Road, Research Triangle Park, NC 27709.

The Forest Health Monitoring Program

Forest Health Monitoring is a national program designed to determine the status, changes, and trends in indicators of forest condition on an annual basis. The program covers all forested lands through a partnership encompassing the Forest Service, State foresters, and other State and Federal Agencies and academic groups (Forest Health Monitoring 2008). The FHM program utilizes data from a wide variety of data sources, both inside and outside the Forest Service, and develops analytical approaches for addressing forest health issues that affect the sustainability of forest ecosystems. It has five major activities (fig. 1.3):

- Detection monitoring—nationally standardized aerial and ground surveys to evaluate status and change in condition of forest ecosystems
- Evaluation monitoring—projects to determine extent, severity, and causes of undesirable changes in forest health identified through detection monitoring

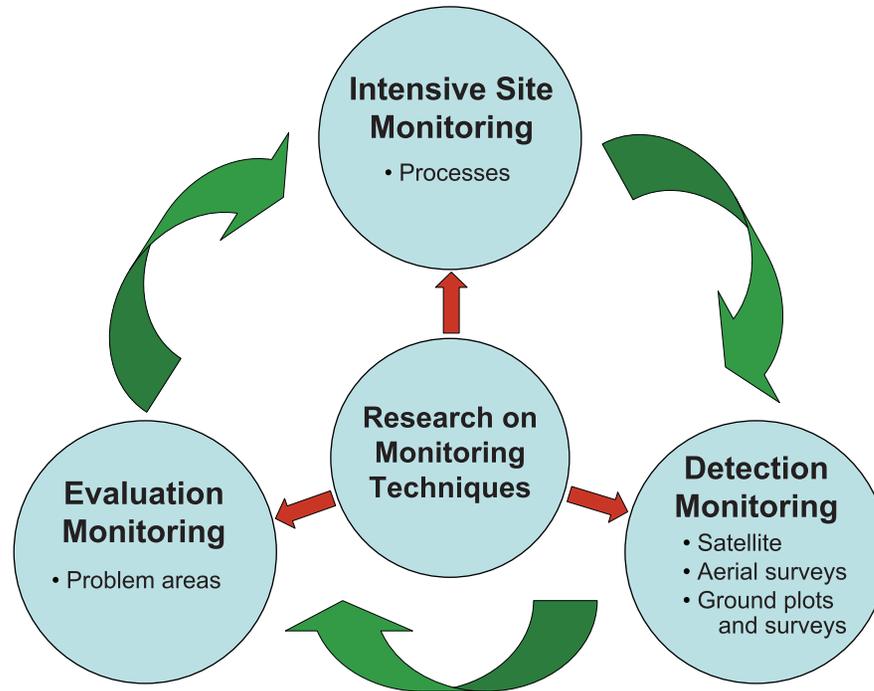


Figure 1.3—The design of the FHM Program (Forest Health Monitoring 2003). A fifth component, analysis and reporting of results, draws from the four FHM components shown here and provides timely information to help support land management policies and decisions.

- Intensive site monitoring—to enhance understanding of cause and effect relationships by linking detection monitoring to ecosystem process studies and to assess specific issues, such as calcium depletion and carbon sequestration, at multiple spatial scales
- Research on monitoring techniques—to develop or improve indicators, monitoring systems, and analytical techniques, such as urban and riparian forest health monitoring, early detection of invasive species, multivariate analyses of forest health indicators, and spatial scan statistics
- Analysis and reporting—synthesis of information from various data sources within and external to the Forest Service to produce issue-driven reports on the status of and change in forest health at national, regional, and State levels

In addition to its national reporting efforts, FHM generates regional and State reports. These reports may be produced with FHM partners, both within the Forest Service and in State forestry and agricultural departments. Some examples are Keyes and others (2003), Laustsen

and others (2003), Neitlich and others (2003), Steinman (2004), Lake and others (2006), Morin and others (2006), and Cumming and others (2006, 2007). The Forest Health Highlights series, available on the FHM Web site at www.fs.fed.us/foresthealth/fhm/, is produced by the FHM regions in cooperation with their respective State partners. FHM and its partners also produce reports on monitoring techniques and analytical methods, such as Smith and Conkling (2004) and O'Neill and others (2005).

For more information about efforts to determine the status, changes, and trends in indicators of the condition of U.S. forests, please visit the FHM Web site at www.fs.fed.us/foresthealth/fhm/. This FHM national technical report is produced by the National Forest Health Monitoring Research Team, which is a part of the Eastern Forest Environmental Threat Assessment Center established under the Healthy Forest Restoration Act as part of a nationwide network of early warning activities about threats to forest health. For more information about the research team, and about threats to U.S. forests, please visit www.forestthreats.org/about.

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Introduction

The facilitation of evolutionary processes is a necessary biological criterion for judging the sustainability of forests because these processes allow for the adaptation of species and resilience of communities to changes in environmental conditions. Levels and patterns of genetic diversity within species are the result of evolutionary and ecological processes, and therefore reflect the integrity and functioning of these processes (Brown and others 1997). The fundamental importance of genetic variation is recognized by its incorporation into criteria and indicators of forest sustainability, including the Criteria and Indicators for the Conservation and Sustainable Management of Temperate and Boreal Forests (Montréal Process Working Group 2007).

The Montréal Process, as amended in 2007, incorporates three indicators of genetic diversity under criterion 1 (conservation of biological diversity): (1) number and geographic distribution of forest-associated species at risk of losing genetic variation and locally adapted genotypes, (2) population levels of selected representative forest associated species to describe genetic diversity, and (3) status of onsite and offsite efforts focused on conservation of genetic diversity (Montréal Process Working Group 2007). While these indicators address population characteristics that affect the maintenance of genetic variability within individual species, they are necessarily limited

to a handful of indicator species inhabiting forest ecosystems, rather than to entire communities of flora and fauna.

Community phylogenetic analysis (Webb and others 2002) is a new approach that quantifies genetic diversity for communities of species and can easily be used to describe the spatial distribution of such genetic variation across landscapes. This synthesis of evolutionary biology and landscape ecology has potential as a tool for assessing the health of forest communities, both in terms of biodiversity and community resistance to stress (Potter 2009). Specifically, it should shed light on the effects of ongoing environmental changes on the evolutionary potential and biological distinctiveness of biotic communities at a range of temporal and spatial scales.

Community phylogenetics has been made possible by the recently improved ability to create well-supported phylogenies of plant species. These hypothesized phylogenetic “family trees” of species are generated following surveys of existing molecular systematic studies that use gene sequencing to determine the relationships among species and to estimate the amount of time since their common ancestors diverged. Fossil evidence from paleobotanical studies is further used to calibrate the age of the nodes at which species or species groups diverged. The lengths of all the branches within these phylogenetic trees are calculated in millions of years, with the branch lengths used to compute

CRITERION 1—

Chapter 2. Evolutionary Diversity and Phylogenetic Community Structure of Forest Trees Across the Conterminous United States

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a variety of statistics. No new gene sequencing work is required to construct these phylogenetic trees because, in recent years, molecular systematic studies have been published for a wide variety of plant groups, including those of most North American tree species.

Phylogenetic diversity (PD) statistics (Faith 1992, Webb and others 2006), which rely on such phylogenetic trees, may be more meaningful measures of biodiversity than traditional metrics such as species richness, abundance, and evenness because they measure the cumulative evolutionary age and evolutionary potential of all the species in the community of interest, rather than weighting all species equally regardless of their relatedness. This is of particular interest in the context of conservation because existing evolutionary lineages will generate future biodiversity, and as such are the cornerstone of natural environmental health (Erwin 1991). Therefore, conserving the evolutionary potential of individual lineages, species, and groups of species, as measured by PD statistics, has become an increasingly important goal (Rodrigues and Gaston 2002, Sechrest and others 2002, Soltis and Gitzendanner 1999).

Additionally, it is possible to use species phylogenies to determine whether the species within a specific community are more clustered or dispersed across the overall phylogenetic tree (of all the tree species in North America, for example) than expected by chance (Webb 2000). These measures of phylogenetic clustering or

dispersion may serve as useful community-level measures of potential genetic resilience to pests, pathogens, climate change, and other stressors. This is because communities of species that are more evenly dispersed on the phylogenetic tree—that is, less closely related than expected by random chance—possess greater-than-expected evolutionary diversity, and may, therefore, encompass a higher proportion of species unaffected by a given stressor or able to adapt to it. Phylogenetically clustered communities, in contrast, contain less evolutionary diversity and are more closely related than a random set of species, and may therefore be more vulnerable to stressors such as pests, pathogens, and climate change.

Methods

I used the software package Phylocom 3.41 (Webb and others 2008) to examine forest tree community phylogenetics across the 48 conterminous United States, quantifying forest tree PD and phylogenetic community structure for each of 102,304 one-sixth-acre Forest Inventory and Analysis (FIA) plots. These plots represented the latest available FIA phase 2 tree and sapling inventory data (trees ≥ 1 inch d.b.h.) as of November 2007 (Forest Inventory and Analysis Program 2007). They encompassed the latest annualized data available or periodic data when a full cycle of annualized data was unavailable.

This analysis required the construction of a phylogenetic reference supertree (fig. 2.1) encompassing the 311 forest tree species

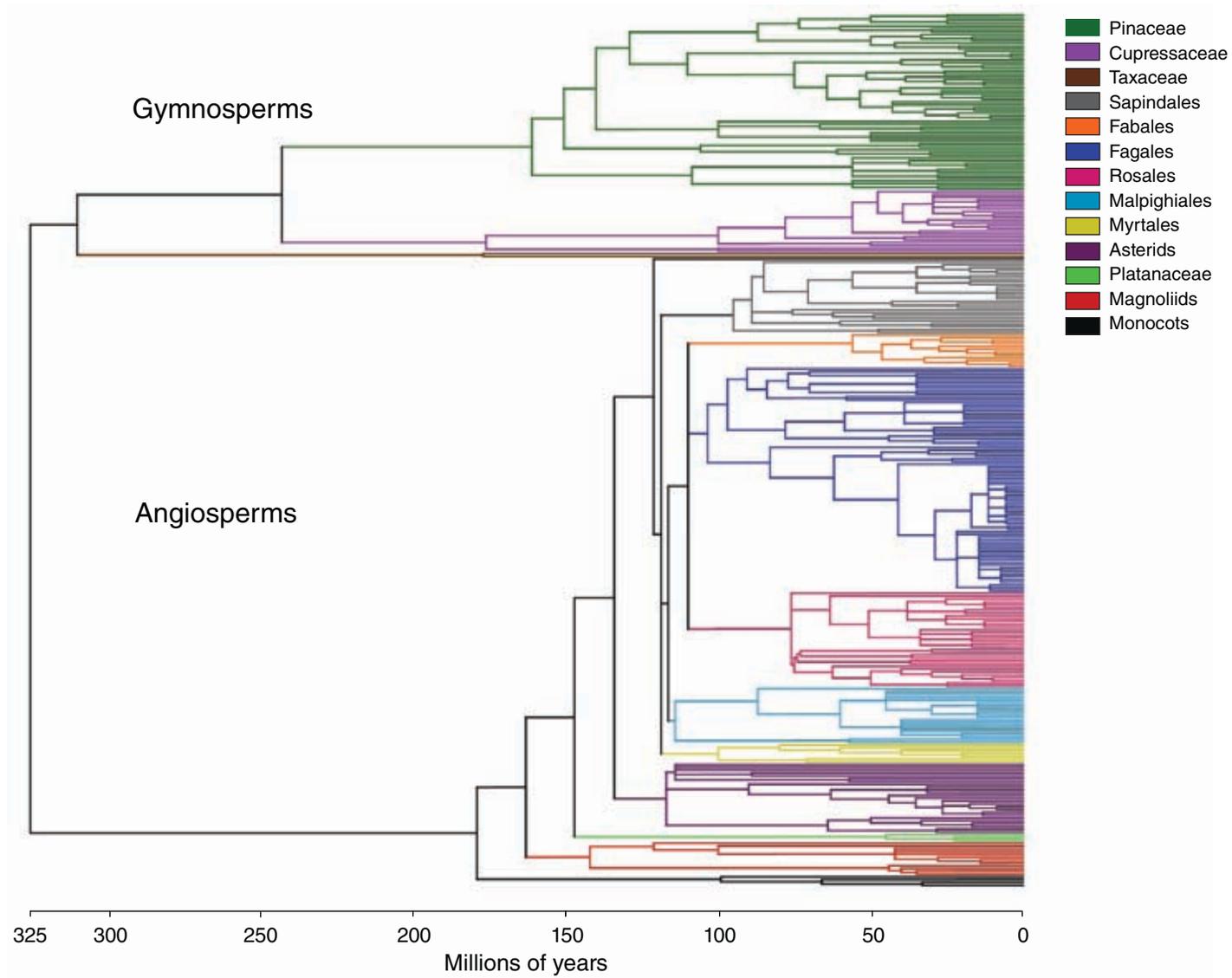


Figure 2.1—The phylogenetic supertree of the 311 forest tree species of the conterminous United States inventoried by FIA, with branch lengths measured in millions of years (Potter and Woodall 2012). Evolutionary relationships and branch lengths were based on a survey of recent molecular systematic and paleobotanical studies, except for basal angiosperm relationships, which were from Wikström and others (2001).

inventoried by FIA (Potter and Woodall 2012). This reference phylogeny, which can be used to estimate phylogenetic distance among species in units of millions of years, approximates the actual evolutionary relationships among species. (See appendix A for additional details about the construction of the reference phylogeny.)

Three sets of analyses were conducted for differing groups of species: all species, angiosperm (flowering) species, and gymnosperm (cone-bearing) species. In addition to plot-level species richness (the number of species present on a plot), I calculated three measures of PD:

1. Faith's (1992) index of PD measures the total evolutionary history represented by the species on a plot. This is done by generating a phylogenetic tree encompassing the species on the plot [taken from the phylogenetic reference tree (fig. 2.1)] and then summing the branch lengths of that plot-level phylogenetic tree, measured in millions of years of evolutionary time (Potter 2009). I calculated mean PD and species richness values for ecoregion sections, after excluding sections containing fewer than 25 plots.
2. The Nearest Taxon Index (NTI) is a standardized measure of the branch-tip phylogenetic structure of species in a community (Webb and others 2006). This statistic measures whether evolutionary diversity among the species on a plot is greater (dispersed) or less (clustered) than

expected by chance, as compared to the pool of species present in the ecoregion section in which the plot is located.

3. The Net Relatedness Index (NRI) is a standardized measurement of basal phylogenetic structure of species in a community (Webb and others 2006). This statistic measures whether evolutionary diversity among the deeper phylogenetic ranks (families, orders, classes, and divisions) on a plot is greater (dispersed) or less (clustered) than expected by chance, again as compared to the pool of species present in the ecoregion section.

NTI and NRI values are positive when species occur with other closely related species (clustered), and are negative when species do not occur together with closely related species (dispersed) (Kembel and Hubbell 2006). These statistics measure different evolutionary characteristics of communities, so it is, therefore, possible for a community to be considered clustered by one metric and overdispersed by the other (table 2.1). Because the data were not normally distributed, I used a Wilcoxon signed rank test to determine whether section-level median NTI and NRI scores were significantly different from zero, with positive values significantly clustered and negative values significantly overdispersed. Sections with fewer than 25 plots were not included in the analysis. (See appendix A for additional details about the calculation of these statistics.)

Table 2.1—Interpretation of the evolutionary characteristics of forest communities based on their phylogenetic structure as measured by the Net Related Index and Nearest Taxon Index

		Clustered	Neither	Dispersed
Net Related Index—Treewide Phylogenetic Structure				
Nearest Taxon Index—Branch-Tip Phylogenetic Structure	Clustered	Low overall diversity/evenness, including higher order groups (angiosperms vs. gymnosperms, etc.)	Moderate overall diversity/evenness including higher order groups	High overall diversity/evenness, including higher order groups (angiosperms vs. gymnosperms, etc.)
		Low diversity/evenness across lower order groups (families, genera, etc.)	Low diversity/evenness across lower order groups	Low diversity/evenness across lower order groups (families, genera, etc.)
	Neither	Low overall diversity/evenness, including higher order groups	Moderate overall diversity/evenness including higher order groups	High overall diversity, including higher order groups
		Moderate diversity/evenness across lower order groups	Moderate diversity/evenness across lower order groups	Moderate diversity/evenness across lower order groups
	Dispersed	Low overall diversity/evenness, including higher order groups (angiosperms vs. gymnosperms, etc.)	Moderate overall diversity/evenness including higher order groups	High overall diversity/evenness, including higher order groups (angiosperms vs. gymnosperms, etc.)
		High diversity/evenness across lower order groups (families, genera, etc.)	High diversity/evenness across lower order groups	High diversity/evenness across lower order groups (families, genera, etc.)

Results and Discussion

The two metrics of biodiversity, species richness and PD (a measure of evolutionary history), were highly correlated at the plot level ($r = 0.89$). As expected, a similar general pattern appeared between the metrics at the

ecoregion section scale (fig. 2.2). For each, mean plot species richness and PD are higher in the Eastern United States than in the West, with the lowest values located in the interior West. At the same time, some important differences existed between these measures of biodiversity. For

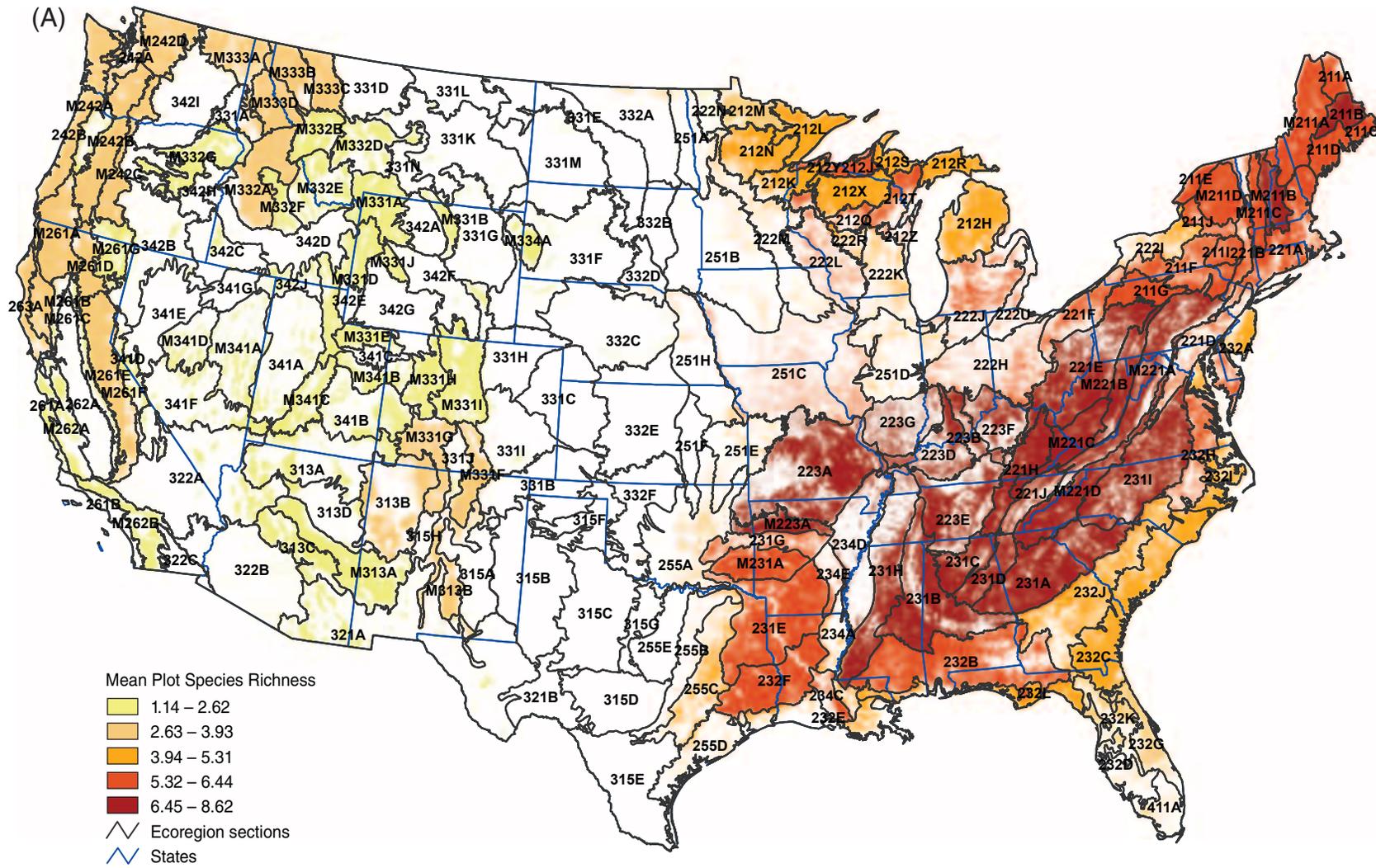


Figure 2.2—Mean forest tree (A) species richness and (B) Faith's index of phylogenetic diversity for FIA plots across ecoregion sections (Cleland and others 2007). The two statistics were divided into five equal interval classes for comparison purposes. Forest cover is derived from MODIS imagery by the Forest Service, Remote Sensing Applications Center. (Data source: Forest Service, Forest Inventory and Analysis Program) (continued on next page)

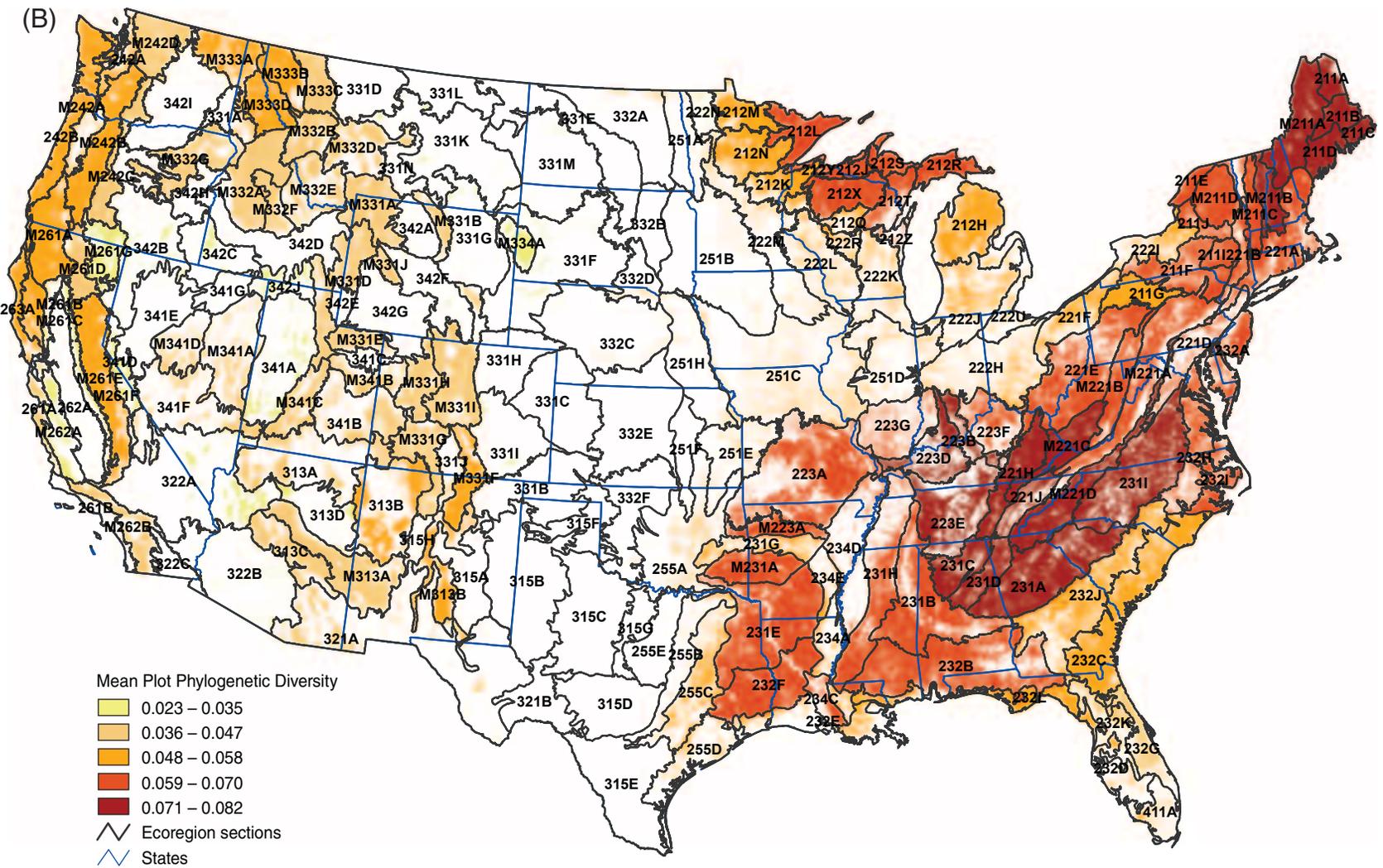


Figure 2.2 (continued)—Mean forest tree (B) Faith's index of phylogenetic diversity for FIA plots across ecoregion sections (Cleland and others 2007). The two statistics were divided into five equal interval classes for comparison purposes. Forest cover is derived from MODIS imagery by the Forest Service, Remote Sensing Applications Center. (Data source: Forest Service, Forest Inventory and Analysis Program)

example, the 10 sections with the highest species richness were all located in the Southeast, while four of the sections with the highest PD were in the Northeast, in addition to six from the Southeast (table 2.2). Additionally, PD was higher relative to species richness in several sections along the Pacific coast and in the northern and southern Rocky Mountains.

Interestingly, some of the regions with higher PD values relative to species richness are regions that contain a combination of relatively high angiosperm (flowering) and gymnosperm (cone-bearing) forest tree PD, particularly in the Lake States and New England (fig. 2.3). In general, angiosperm PD is high in the East and very low in the West (fig. 2.3A). Gymnosperm PD was highest in the West and in parts of the Upper Midwest and Northeast (fig. 2.3B). The Southeast generally had low gymnosperm PD, except for three ecoregion sections with moderate PD [the Central Ridge and Valley (221J), the Central Appalachian Piedmont (231I), and the Blue Ridge Mountains (M221D)].

Meanwhile, the analysis of phylogenetic structure (fig. 2.4) found strong regional differences in phylogenetic dispersion and clustering. Because the two calculations of phylogenetic structure measure different evolutionary characteristics of communities

Table 2.2—Ecoregion sections with the highest species richness and phylogenetic diversity

Section	Species richness
M221C—Northern Cumberland Mountains	8.62
M221D—Blue Ridge Mountains	8.36
221H—Northern Cumberland Plateau	8.33
223E—Interior Low Plateau-Highland Rim	8.20
221J—Central Ridge and Valley	8.15
231I—Central Appalachian Piedmont	8.08
231C—Southern Cumberland Plateau	8.03
223D—Interior Low Plateau-Shawnee Hills	7.79
223B – Interior Low Plateau – Transition Hills	7.75
M223A—Boston Mountains	7.46

Section	Phylogenetic diversity
231I—Central Appalachian Piedmont	0.0816
211B—Maine-New Brunswick Foothills and Lowlands	0.0812
M221D—Blue Ridge Mountains	0.0799
221J—Central Ridge and Valley	0.0768
211D—Central Maine Coastal and Embayment	0.0757
M221C—Northern Cumberland Mountains	0.0749
221H—Northern Cumberland Plateau	0.0748
231C—Southern Cumberland Plateau	0.0743
M211B—New England Piedmont	0.0737
211A—Aroostook Hills and Lowlands	0.0731

(table 2.1), they may lead to different predictions about the susceptibility of forest communities to threats. A community consisting of species evenly dispersed across the phylogenetic tree (e.g., consisting of both flowering trees and conifers), but clustered toward the branch tips (e.g., consisting of mostly pines and oaks), may contain more species adapted or simply not susceptible to a given threat, but may be more likely to lose important ecological functions provided by the species eliminated by that agent. Meanwhile, a community of species clustered across the phylogenetic tree (e.g., dominated by only conifers), but evenly dispersed at the tips (e.g., consisting of several conifer genera, such as spruces, firs, and pines), may better retain its ecological functionality in that situation, but might encompass more species at risk of elimination.

The two measures of phylogenetic structure showed similar general patterns, with moderate to high phylogenetic clustering in the Upper Midwest and Northeast, slight to moderate clustering near the Pacific coast and along the Appalachian Mountains, and slight to moderate dispersion in the Interior West. However, some differences were apparent between the two measures. Using the NTL, which quantifies clustering at the tips of the phylogenetic tree, portions of the Southeast were slightly or moderately dispersed (fig. 2.4A). With the NRI, however, these same areas were slightly to moderately clustered (fig. 2.4B). This may be the result of low gymnosperm diversity in

the region (fig. 2.3B), resulting in tree-wide phylogenetic clustering, combined with moderate angiosperm diversity (fig. 2.3A).

Also interesting is the patchwork of dispersion and clustering in ecoregion sections across the Interior West. In this region of low angiosperm diversity (fig. 2.3A), section-level differences in phylogenetic structure are likely the result of the interaction between differences in conifer richness (the number of different conifer species) and differences in the degree of relatedness among the conifer species present (how phylogenetically related the species are).

The phylogenetic structure of a community or region reveals something about the ecological processes that predominate there. For example, when the species present are more closely related than chance would dictate (phylogenetic clustering), this suggests a pattern of environmental filtering. Environmental filtering occurs when closely related species share similar tolerances to the abiotic environment, and where, as a result, habitat use is a conserved trait among the species in the community (Cavender-Bares and others 2004, Tofts and Silvertown 2000). Because such plant communities share a great deal of evolutionary history as well as an affinity for similar environmental conditions, they may be particularly susceptible to a variety of threats, such as generalist insects and diseases and shifting conditions associated with global climate change.

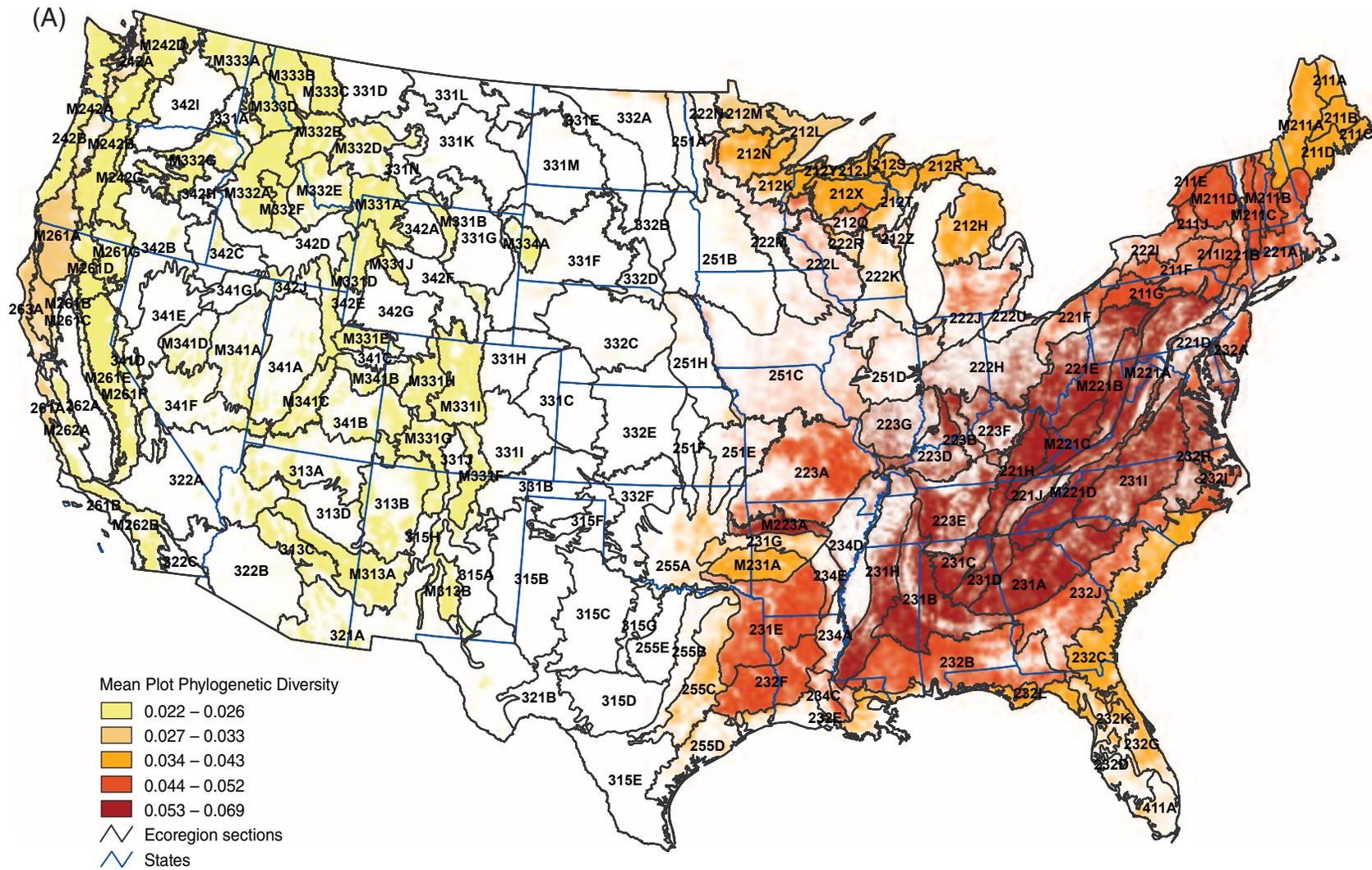


Figure 2.3—Mean forest tree phylogenetic diversity for (A) angiosperm (flowering) tree species and (B) gymnosperm (cone-bearing) tree species from FIA plots across ecoregion sections (Cleland and others 2007). The results were divided into five equal interval classes for comparison purposes. Forest cover is derived from MODIS imagery by the Forest Service, Remote Sensing Applications Center. (Data source: Forest Service, Forest Inventory and Analysis Program) (continued on next page)

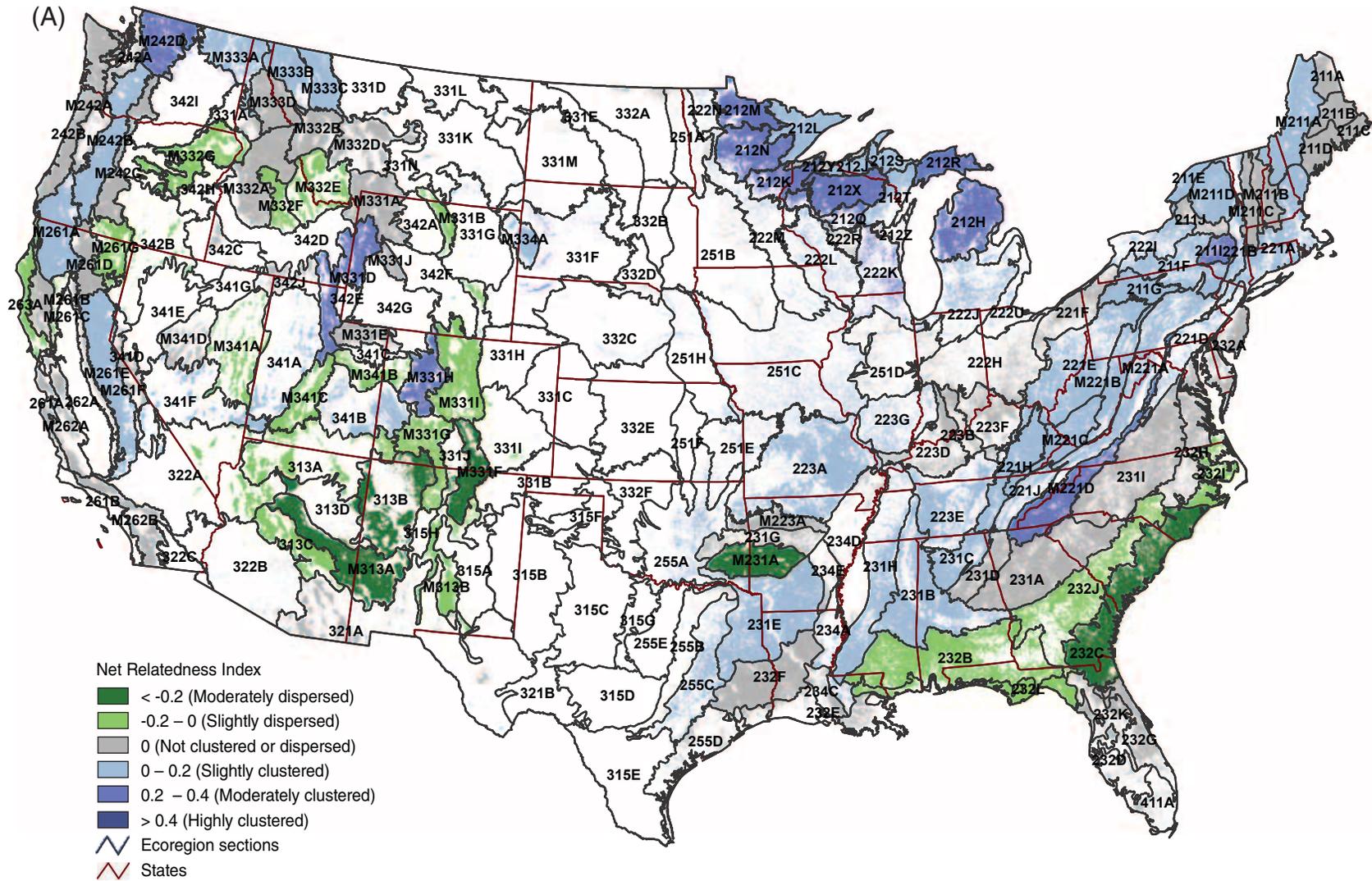


Figure 2.4—Mean FIA plot-level measures of phylogenetic clustering across ecoregion sections (Cleland and others 2007) using (A) the Nearest Taxon Index, a measure of clustering at the branch tips of the phylogenetic tree, and (B) the Net Relatedness Index, a measure of clustering throughout the phylogenetic tree. A Wilcoxon signed rank test was used to determine whether index values were significantly different from zero, with negative index values dispersed and positive values clustered compared to random. Forest cover is derived from MODIS imagery by the Forest Service, Remote Sensing Applications Center. (Data source: Forest Service, Forest Inventory and Analysis Program) (continued on next page)

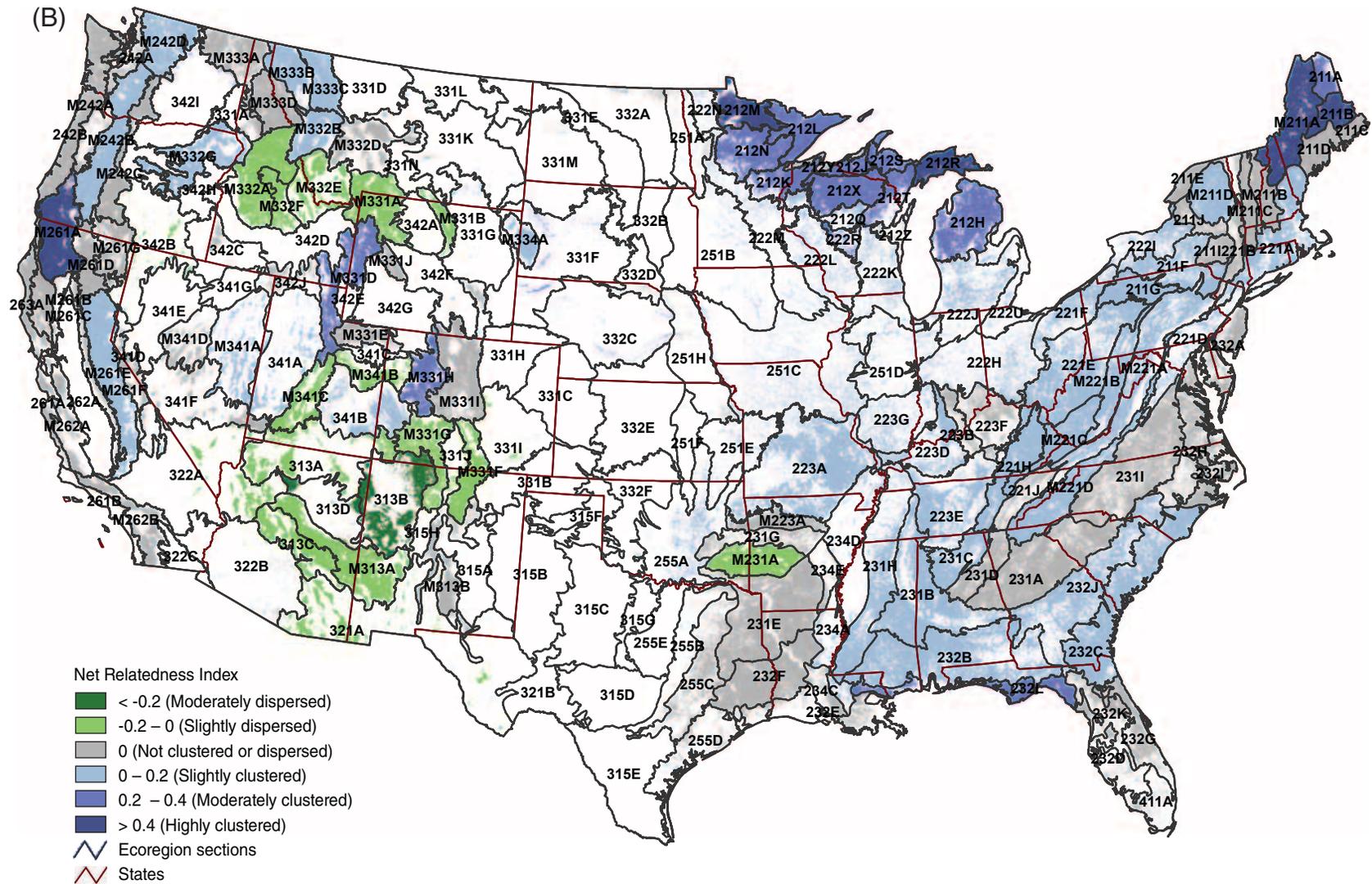


Figure 2.4 (continued)—Mean FIA plot-level measures of phylogenetic clustering across ecoregion sections (Cleland and others 2007) using (B) the Net Relatedness Index, a measure of clustering throughout the phylogenetic tree. A Wilcoxon signed rank test was used to determine whether index values were significantly different from zero, with negative index values dispersed and positive values clustered compared to random. Forest cover is derived from MODIS imagery by the Forest Service, Remote Sensing Applications Center. (Data source: Forest Service, Forest Inventory and Analysis Program)

On the other hand, a pattern of phylogenetic dispersion, where the species in a community are less closely related than chance, may indicate the existence of competitive exclusion among closely related species. This occurs when closely related species are competing for similar environmental niches within the community, and are excluding each other when they share limiting resources (Cavender-Bares and others 2004, Tofts and Silvertown 2000). The ecological integrity of such communities may be less at risk from changing conditions because they may encompass a wider variety of evolutionary adaptations to respond to those changes, and because these communities may encompass a wider variety of niches than communities where environmental filtering is a more dominant ecological process.

The pattern of forest tree phylogenetic structure in this study suggests that competitive exclusion for resources among related species is an important process in certain warmer and drier ecoregion sections, while niche conservatism may be a more common occurrence in moister and more temperate areas. Additionally, broad-scale historical patterns, such as the plant migrations associated with the series of ice ages occurring during the Pleistocene epoch, may also contribute to the patterns of phylogenetic clustering and dispersion. Historic

outbreaks of invasive insects or pathogens, such as the chestnut blight fungus (*Cryphonectria parasitica*), hemlock woolly adelgid (*Adelges tsugae*), and white pine blister rust (*Cronartium ribicola*), have eliminated individual species or groups of species and may also have left a phylogenetic signature—increased phylogenetic clustering when the eliminated species are relatively distinct evolutionarily and increased phylogenetic dispersion when the eliminated species are more closely related to other species in their community.

Generating PD and community structure statistics at large scales is one approach for investigating the role evolutionary biology plays in shaping the processes and patterns in the natural world. Similar approaches that consider the evolution of forest species within the community context also have the potential to improve our understanding of important forest health issues. Future analyses could include:

- Assessments of whether nonnative invasive species are more or less phylogenetically related than expected by chance, compared to nonnative species that are not invasive (Strauss and others 2006). Results could help identify evolutionary groups of species most at risk of becoming invasive.

- Incorporation of phylogenetic relationships among forest tree species in assessments of risk from imported pathogens, including mapping likely pathogen host ranges (Gilbert and Webb 2007). This approach may be useful because the likelihood that a pathogen can infect two plant species decreases continuously with phylogenetic distance, and because the phylogenetic structure of forest communities is likely to impact the rate of spread and the ecological impacts of a disease through a natural plant community (Gilbert and Webb 2007).
- Research aiming to detect the phylogenetic signal (e.g., Silvertown and others 2006) of forest tree traits relating to forest health, such as susceptibility to insect and disease infestation. This would be particularly helpful in identifying evolutionary groups of tree species at risk from insects and pathogens with multiple hosts, such as sudden oak death (*Phytophthora ramorum*), and at risk from broad environmental changes such as those associated with global climate change.
- Studies that investigate which local environmental characteristics, such as climate and soil factors; and historical elements, such as Pleistocene species migration patterns or selective mortality caused by invasive forest pests, are associated with PD and phylogenetic structure measures within forest tree communities.

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Reference Tree Construction

I built the reference phylogeny (Potter and Woodall 2012) in part by using the online phylogenetic database and toolkit Phylomatic (Webb and Donoghue 2005) to generate a backbone phylogenetic supertree topology based on the Angiosperm Phylogeny Group II classification of flowering plant families (Angiosperm Phylogeny Group 2003). I then used the Branch Length ADJustment module in Phylocom 3.41 (Webb and others 2008) to assign ages to nodes in this supertree based on the fossil and molecular estimates reported by Wikström and others (2001), with undated nodes spaced evenly between dated nodes to minimize variance in branch lengths. To extend the resolution of this supertree from the family and genus level to the species level and to include gymnosperms in addition to angiosperms, I incorporated the results of approximately 80 recent molecular systematic and paleobotanical studies.

Calculating Nearest Taxon Index and Net Relatedness Index Values

The NTI and NRI are calculated using two other statistics that measure different aspects of phylogenetic relatedness among the species in a community or plot.

Mean nearest neighbor distance is the mean minimum phylogenetic distance between each species on the plot and the most closely related species also on the plot, measured in millions of years (Webb and others 2006). This statistic quantifies how closely related, on average, each species in a community is to the most closely related species. It is used to determine the NTI, a standardized measure of the terminal (branch-tip) clustering of co-occurring taxa regardless of the clustering of the higher level groups in the phylogenetic tree:

$$NTI = -(MNND - MNND_{NULL}) / \sigma MNND_{NULL}$$

where

$MNND_{NULL}$ = mean nearest neighbor phylogenetic distance from 1,000 randomly generated null communities, drawn from the pool of species present in the plot's ecoregion section

$\sigma MNND_{NULL}$ = the standard deviation of the null community scores

To generate null communities, I used the independent swap algorithm, which randomizes patterns of species co-occurrence on the plots.

Appendix, cont.

The algorithm does not introduce species from the reference phylogeny tree into the null community plots (Webb and others 2008). Rather, the null communities for each plot were drawn from species contained within plots in the same ecoregion section.

Meanwhile, mean phylogenetic distance is the mean evolutionary distance, again measured in millions of years, between each species on a plot and all of the other species on the plot (Webb and others 2006). This statistic quantifies how closely related, on average, each species in a community is to every other species in the community. It is used to ascertain the NRI, a standardized measurement of phylogenetic

structure across the phylogenetic tree. It is calculated as:

$$\text{NRI} = -(\text{MPD} - \text{MPD}_{\text{NULL}}) / \sigma\text{MPD}_{\text{NULL}}$$

where

MPD_{NULL} = mean nearest neighbor phylogenetic distance from 1,000 null communities, drawn from the pool of species present in the plot's ecoregion section

$\sigma\text{MPD}_{\text{NULL}}$ = the standard deviation of the null community scores

Again, null communities for each plot were drawn from species across plots within the same ecoregion section.

Introduction

As development introduces competing land uses into forest and grassland landscapes, the public expresses concern for landscape patterns through headline issues such as urban sprawl and fragmentation. Resource managers need a deeper understanding of the causes and consequences of landscape patterns, to know if, where, and how to take any needed actions. The spatial arrangement of the environment affects all ecological processes within that environment; the task for resource managers is to arrange a forest or grassland in an appropriate way to provide the desired balance of biodiversity, water quality, and other amenities. National assessments of landscape patterns can help to inform those decisions by documenting the status and trends of the landscape context of natural resources.

Forest fragmentation, landscape mosaics, and other land cover patterns have been assessed in previous national technical reports by the national Forest Health Monitoring (FHM) Program of the Forest Service, U.S. Department of Agriculture. However, because of the size and complexity of the databases, the reporting has necessarily been limited to regional statistical

summaries, and the relatively coarse-scale maps that have been presented could not portray the wealth of local detail contained in the databases. As a result, it has been difficult for readers to visualize land cover patterns in specific locations or to interpret their meaning in relation to other geographic features. To alleviate that problem, national maps have been prepared as an online database, which permits readers to see high-resolution maps of land cover patterns for any specific location. All that is required is an Internet connection, a geographic browser, and the keyhole markup language (KML) documents, which serve as the user interface for the online databases. Now, readers can access the national results in full spatial resolution for any specific location and can overlay the land cover pattern maps with other online databases such as aerial photography and road maps to better interpret the meaning and implications of land cover patterns. The objectives of this chapter are to describe the available online databases of land cover patterns and the use of the KML documents with a freely available geographic browser. Visualization examples are provided for three of the landscape pattern maps that have been used in forest assessments.

CRITERION 1—

Chapter 3. Online Maps for Visualizing Landscape Patterns at High Spatial Resolution

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Overview

The online database currently comprises three national maps that were derived from the 2001 version of the National Land Cover Database (Homer and others 2007), a national map that portrays 16 types of land cover at a spatial resolution of 0.09 ha per pixel. The derived maps portray three land cover pattern indices at a spatial resolution of 0.09 ha per pixel—forest area density, land cover mosaic, and forest spatial pattern—which have been selected for reporting in various Forest Service assessments including those by FHM, the Resource Planning Act group, and the Montreal Process Criteria and Indicators group. On each map, the color of a 0.09-ha pixel indicates the land cover pattern in a surrounding fixed-area neighborhood, and the maps can, therefore, be interpreted as maps of land cover pattern context for each pixel.

The map of the forest area density index (FDEN) shows the proportion of the surrounding 15-ha neighborhood that is forest. In previous assessments, FDEN has been used to answer the question “how much forest is surrounded by how much other forest” (Riitters and others 2002). The map of the land cover mosaic index shows the mixture of three major land cover types (developed, agriculture, seminatural) in the surrounding 15-ha neighborhood. That

index has been used in previous assessments to answer the question “what is the anthropogenic land cover context of forest” (Riitters and others 2008). The forest morphological spatial pattern index (MSPA) shows the physical structure of which a forest pixel is part (Vogt and others 2007). The MSPA will be used in upcoming assessments to report on, for example, the amount and location of forest and grassland which exists as part of “core,” “corridor,” and “edge” structures. The three indices are described in more detail at the World Wide Web sites listed in table 3.1.

Table 3.1—Online sources for the geographic browser and keyhole markup language (KML) documents mentioned in the text

Google Earth geographic browser download page:
<http://earth.google.com/>

Note: Version 4 or later of Google Earth is required.

Land cover mosaic index information page and KML download page:
<http://forestthreats.org/tools/landcover-maps/lcm>
http://data.forestthreats.org/fhm/us-mosaic_v1_1-NEMAC_EDIT.kml

Forest spatial pattern index information page and KML download page:
<http://forestthreats.org/tools/landcover-maps/mspa>
http://data.forestthreats.org/fhm/us-mspa_v1_1-NEMAC_EDIT.kml

Forest area density index information page and KML download page:
<http://forestthreats.org/tools/landcover-maps/fden>
http://data.forestthreats.org/fhm/us-fden_v1_1.kmz

A geographic browser and a KML document are required to access an online map. An example of a freely available geographic browser for popular computing platforms is Google Earth, which can be obtained at the URL shown in table 3.1, but any other geographic browser that supports KML should work as well. The locations of the three KML documents for the three land cover pattern indices are also shown in table 3.1. After starting the geographic browser application, a KML document is opened from that application, and a national map of that landscape pattern index is initialized. The user is then free to navigate the maps with built-in browser functions such as “pan” and “zoom.”

Some geographic browsers automatically provide a background of recent aerial photographs, and that capability can be used to help interpret the land cover pattern maps. One approach is to open two copies of the geographic browser, displaying the background photography in one copy and a map of land

cover pattern in the other copy (fig. 3.1). Some geographic browsers also support user-controlled transparency, which permits the overlay of a land cover pattern map upon the background aerial photography within one copy of the browser. The transparency of the overlaid land cover pattern map can be adjusted so that the background aerial photography can be seen “through” the land cover pattern map (fig. 3.2).

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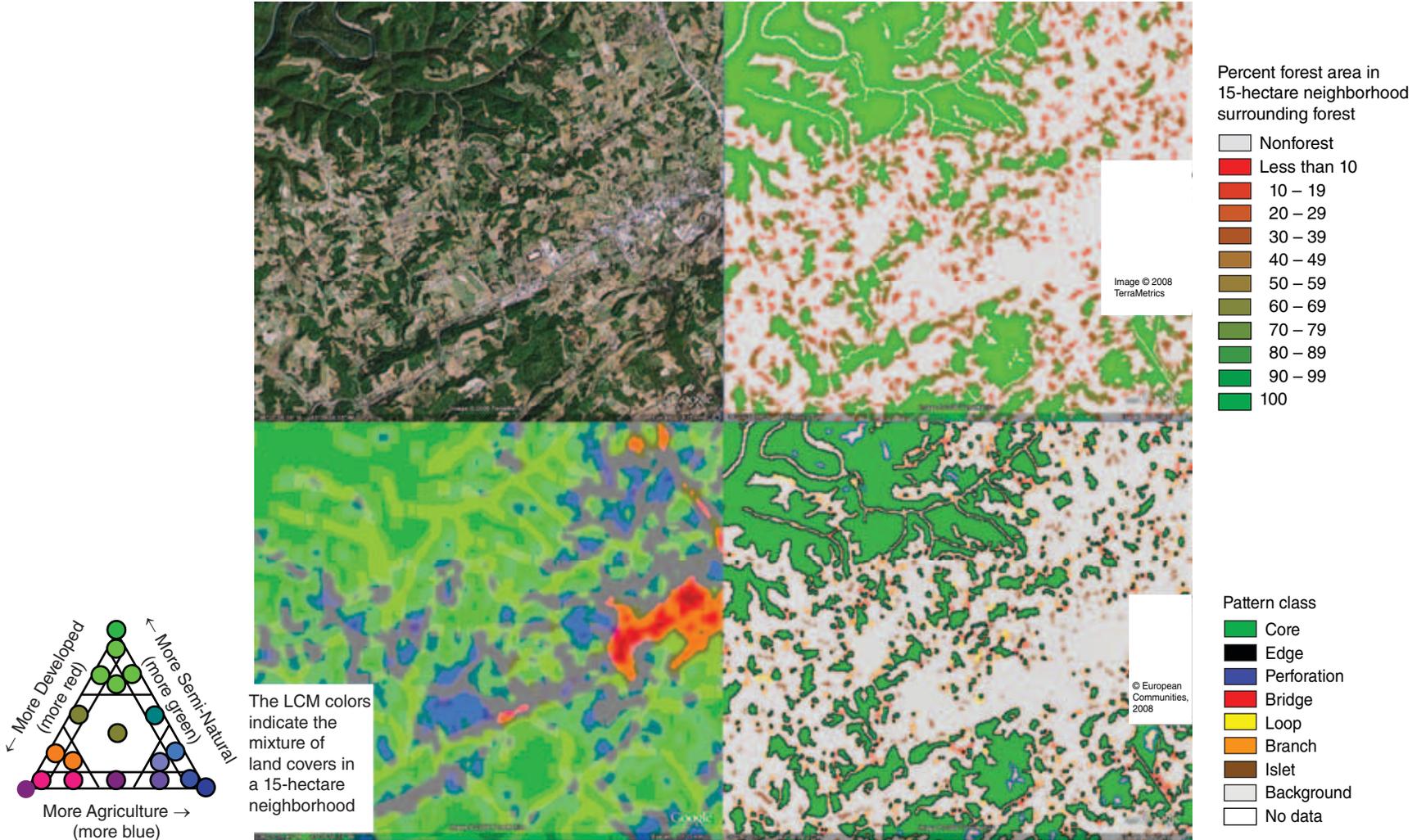


Figure 3.1—Online browsing of national land cover pattern maps is illustrated for a landscape near New Tazewell (Claiborne County), TN. Clockwise from top left: background aerial photography provided by the geographic browser service; the forest area density index (FDEN); the forest spatial pattern index (MSPA); and the land cover mosaic index (LCM). (Data sources: Google, TerraMetrics, Forest Service, U.S. Geological Survey)

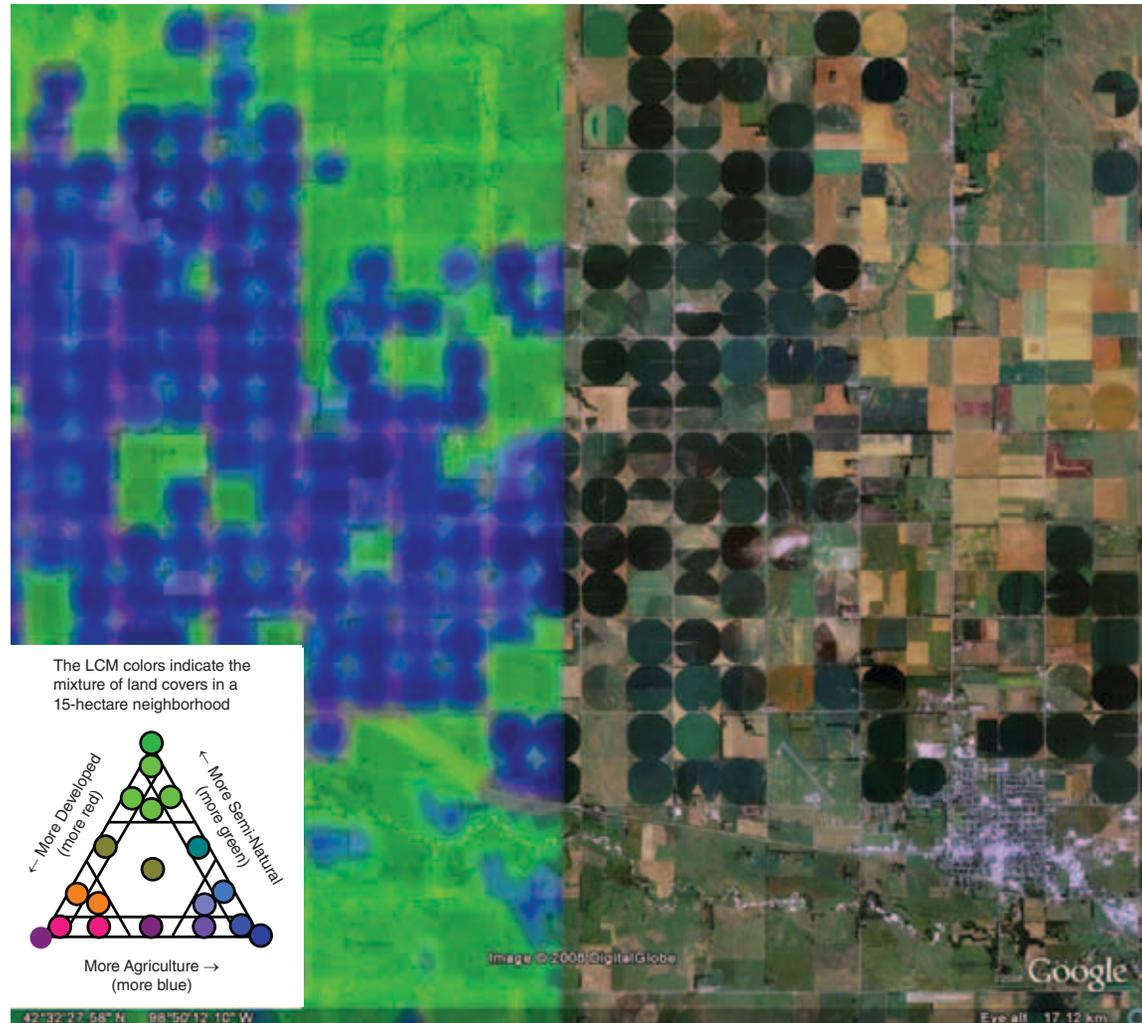


Figure 3.2—Utilizing the transparency option provided by some geographic browsers to explore the land cover mosaic index (LCM) in relation to background aerial photography. In this landscape near O’Neill, NE, the dominant land cover patterns are created by the center-pivot crop irrigation systems, which are visible in aerial photography (right) as dark-green circles separated by a road network. In the adjacent region (left), the LCM portrays the continuation of that pattern as blue circles representing concentrations of agriculture land cover separated by cyan regions representing the road network. Note that the LCM map (left) has been made partially transparent to enable inspection of LCM in relation to the background aerial photography. (Data sources: Google, TerraMetrics, Forest Service, U.S. Geological Survey)

Introduction

Drought has significant direct and indirect impacts on forest health. In direct terms, low-to-moderate drought stress limits plant growth, while more severe drought stress reduces both growth and photosynthetic activity (Kareiva and others 1993, Mattson and Haack 1987). Indirectly, drought stress in forest communities may predispose trees to insect infestation, in some cases leading to major outbreaks (Mattson and Haack 1987). In addition, drought slows organic matter decomposition and reduces the moisture content of woody debris and other fuels, greatly increasing fire risk in wildland areas (Clark 1989, Keetch and Byram 1968, Schoennagel and others 2004).

Several indices have been developed for regional drought monitoring. The most commonly used of these indices is the Palmer Drought Severity Index (PDSI), which is derived from data on total precipitation, precipitation periodicity, and soil characteristics related to moisture supply (Heim 2002). Despite its continued popularity, the PDSI has been criticized for many reasons, including the complexity of its calculation and a lack of spatial comparability between regions of the United States and across different time periods (Alley 1984, Guttman 1998). Moreover, the PDSI is considered an index of meteorological drought,

as is the more recently derived Standardized Precipitation Index (SPI); other indices, some related to the PDSI, have been developed to instead target hydrological drought, e.g., Palmer Hydrologic Drought Severity Index, or agricultural drought, e.g., the Crop Moisture Index and the Palmer Z-Index (Keyantash and Dracup 2002).

The National Climatic Data Center (NCDC) calculates the PDSI monthly for each climate division in the conterminous United States, and provides PDSI data for every month from 1895 to present through a publicly accessible archive (National Climatic Data Center 2007). The U.S. Drought Monitor project, a collaborative effort of the National Drought Mitigation Center, the U.S. Department of Agriculture, and the National Oceanic and Atmospheric Administration, produces weekly contour maps utilizing a blend of drought indices, including the PDSI, as well as daily streamflow percentiles and a remotely sensed vegetation health index (Svoboda and others 2002). These maps may be downloaded in Geographic Information System (GIS) format (National Drought Mitigation Center 2008). Although the PDSI data available through the NCDC archive and the U.S. Drought Monitor maps may serve as adequate reference for broadscale summaries, they are not well suited for analyses involving finer scale covariates or response variables. Because these and other

CRITERION 3—

Chapter 4. High-Resolution Mapping of Drought Conditions

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similar drought monitoring tools are typically derived from point-based weather station data, they have limited spatial precision and are regionally variable in terms of spatial accuracy and detail (Brown and others 2008). Therefore, we adopted a primary objective of developing a methodology for mapping drought stress using historical, high-spatial-resolution climate data that provides complete coverage of the conterminous United States. We wanted our methodology to be computationally simple and require only limited inputs, yet still allow for reasonable comparison of moisture conditions between different geographic areas and time periods.

Methods

We used gridded data (approximately 4-km² spatial resolution) created with the Parameter-Elevation Regression on Independent Slopes (PRISM) climate mapping system to complete our analyses. The PRISM system is knowledge based, integrating a localized climate-elevation regression function with other algorithmic components: topographic facets; coastal proximity; a two-layer atmosphere, i.e., a boundary layer and the free atmosphere above it; and weighting of weather station observations based on these and other factors (Daly and

others 2002). At the time we performed our analyses, grids depicting total precipitation, mean daily minimum temperature, and mean daily maximum temperature for the conterminous United States were available monthly from 1895 to 2007 (although the December 2007 grids were preliminary rather than final datasets). All data were available for public download from the PRISM group Web site (PRISM Group 2008).

Calculating a Moisture Index— We adopted an approach, utilizing the PRISM climate grids, in which a moisture index value for a given location, i.e., a grid cell, is calculated based on both precipitation and potential evapotranspiration values for that location during the time period of interest. Potential evapotranspiration measures the loss of soil moisture through plant uptake and transpiration (Akin 1991). It does not measure actual moisture loss, but rather the loss that would occur under ideal conditions, i.e., if there were no possible shortage of moisture for plants to transpire (Akin 1991, Thornthwaite 1948). The inclusion of both precipitation and potential evapotranspiration provides a fuller accounting of the water balance of a location than precipitation alone. So, to complement the PRISM monthly precipitation grids, we

computed monthly potential evapotranspiration grids using the Thornthwaite formula (Akin 1991, Thornthwaite 1948):

$$PET_m = 1.6L(10\frac{T_m}{I})^a \quad (1)$$

where

PET_m = the potential evapotranspiration for a given month m in cm

L = a correction factor for the hours of daylight and number of days in a month for all locations at a particular latitude

T_m = the mean temperature for month m in degrees C

I = an annual heat index, calculated as $I = \sum_{i=1}^{12} \left(\frac{T_i}{5}\right)^{1.514}$, where T_i is the mean temperature for each month i of the year

a = an arbitrary exponent calculated by $a = 6.75 \times 10^{-7}I^3 - 7.71 \times 10^{-5}I^2 + 1.792 \times 10^{-2}I + 0.49239$

To implement equation 1 spatially, we created a grid of latitude values for determining the L adjustment for any given 4-km² grid cell in the conterminous United States [see Thornthwaite (1948) for a table of L correction factors]. We calculated the mean

monthly temperature grids as the mean of the corresponding PRISM daily minimum and maximum monthly temperature grids.

Thornthwaite also proposed an equation for calculating a moisture index based on precipitation and potential evapotranspiration (Akin 1991):

$$MI = 100 \frac{P - PET}{PET}$$

where

MI = moisture index

P = precipitation

PET = potential evapotranspiration

(P and PET must be in equivalent measurement units, e.g., mm)

Thornthwaite's MI can be calculated for any time period of interest by totaling precipitation and potential evapotranspiration during the period and entering these two quantities into the equation. It has a lower bound of -100 , but does not have an upper bound; if precipitation during the time period is very high and/or potential evapotranspiration is very low, the index value can be over 100. Willmott and Feddema (1992) argued that a better index would be bounded meaningfully at both ends of the scale and

would also be symmetric around zero. They proposed a modified version of Thornthwaite's index with the following form:

$$MI' = \begin{cases} P/PET - 1 & , P < PET \\ 1 - PET/P & , P \geq PET \\ 0 & , P = PET = 0 \end{cases}$$

This set of equations yields a dimensionless index scaled between -1 and 1 . As with Thornthwaite's formulation, MI' can be calculated for any time period but is typically calculated on an annual basis (Willmott and Feddema 1992). An alternative to the annual summation approach, which we adopted for these analyses, is to calculate MI' from monthly precipitation and potential evapotranspiration values and then, for a given year, calculate the annual MI' as the mean of the 12 monthly MI' values. This "mean-of-months" approach limits the ability of short-term peaks in either precipitation or potential evapotranspiration to negate corresponding short-term deficits, as would happen under an annual summation approach.

100-Year Normal Moisture Index Map—

Applying the modified equations of Willmott and Feddema (1992) to the gridded precipitation and potential evapotranspiration data, we calculated

annual MI' grid maps for each year from 1907 to 2006. We then calculated a normal annual MI' grid as the mean of these 100 MI' grids. Although we also calculated a 2007 MI' grid, we did not include it in this normal calculation because the December 2007 PRISM data were preliminary at the time of analysis.

Drought Category Thresholds and Probabilities Based on Moisture Index Difference—

We calculated moisture index difference (MID) grids for each year, including 2007, by subtracting the 100-year normal annual MI' from the year's MI' grid. The resulting MID grids are scaled from 2 to -2 , although actual values rarely approach either endpoint; a positive value in a grid cell indicates the relative amount of moisture surplus that the cell exhibited for the year of interest when compared to the 100-year mean, while a negative value indicates the relative amount of moisture deficit exhibited by the cell.

To make the MID useful as a drought index, we had to identify meaningful threshold values that distinguish between moisture deficit, i.e., drought, categories. Drought may be viewed as a random phenomenon (Weber and Nkemdirim 1998). Thus, assuming the MID to be a temporally random variable with an approximately normal distribution and a mean

of zero, we selected a set of four threshold values related to the average standard deviation across the 100 annual *MID* grids: *MID* values from 0.5 to <1 standard deviation below the mean, i.e., zero, indicate a mild drought; from 1 to <1.5 standard deviations, a moderate drought; from 1.5 to <2 standard deviations, a severe drought; and values 2 or more standard deviations below the mean indicate extreme drought conditions. Mild, moderate, severe, and extreme wetness may be defined similarly by corresponding standard deviations above the mean, while values between 0.5 and -0.5 standard deviations indicate near normal conditions. To provide additional context regarding our selected thresholds, we created a series of four empirical probability grids by overlaying the annual *MID* grids and subsequently determining, for each grid cell, the proportion of years out of 100 that the cell exhibited: (1) at least a mild drought, (2) at least a moderate drought, (3) at least a severe drought, and (4) an extreme drought.

Historic and Current (2007) Drought Maps Based On Moisture Index Difference—

To illustrate how the *MID* approach depicts significant drought events, we identified 4 years from the latter part of the 20th century during which notable regional droughts had been documented in scientific literature: the Northeastern United States in 1964; the Great

Plains region (Central United States) in 1980; the Northwestern United States to the Great Plains in 1988; and the Southwestern United States in 1996 (Andreadis and others 2005, Groisman and Knight 2008, Karl and Quayle 1981, Mueller and others 2005, Namias 1983, Trenberth and Branstator 1992, Trenberth and others 1988). We also examined the *MID* grid for 2007, a year in which the Southeastern United States experienced unusually harsh drought conditions, while a prolonged drought extended into an eighth year in parts of the Western United States (Goodman 2007, Boxall and Powers 2007).

Results and Discussion

100-Year Normal Moisture Index Map—

In addition to serving as the base of reference for our drought analyses, the map of the 100-year mean annual *MI'* for the conterminous United States (fig. 4.1A) may be considered a rough depiction of the country's climatic regimes. Wet climates ($MI' > 0$) are common throughout the Eastern United States, particularly the Northeast, with the wettest ($MI' > 0.5$) generally limited to mountainous ecoregion sections or adjacent plateaus, such as sections 211F—Northern Glaciated Allegheny Plateau; 211G—Northern Unglaciated Allegheny Plateau; M211C—Green, Taconic, Berkshire

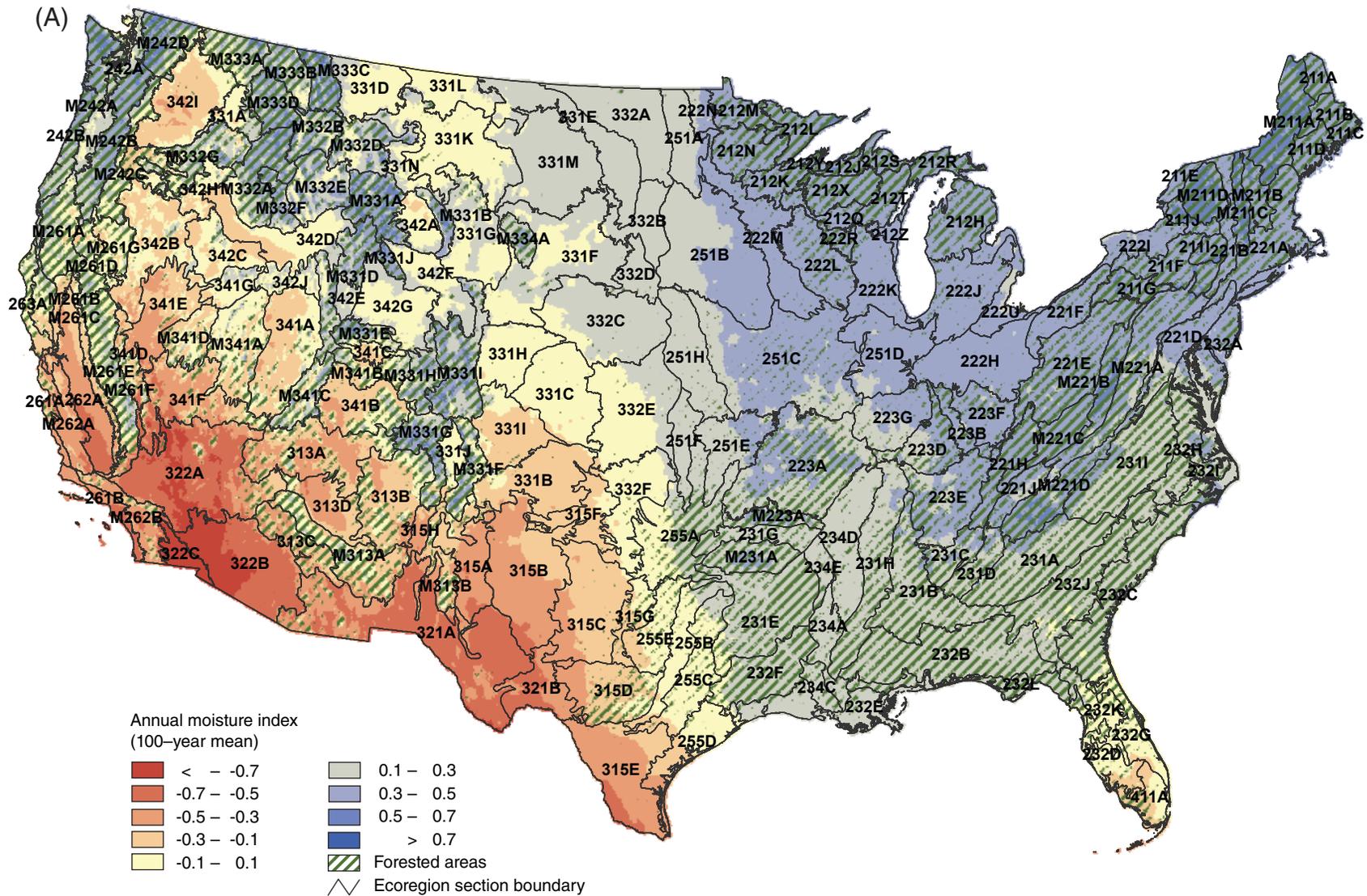


Figure 4.1—The 100-year (1907–2006) (A) mean annual moisture index or MI', (B) mean annual precipitation, and (C) mean annual potential evapotranspiration for the conterminous United States. Ecoregion section boundaries (Cleland and others 2007) and labels are included for reference. Forest cover data (overlaid green hatching) derived from MODIS imagery by the Forest Service, Remote Sensing Applications Center. (Data source: PRISM Group, Oregon State University) (continued on next page)

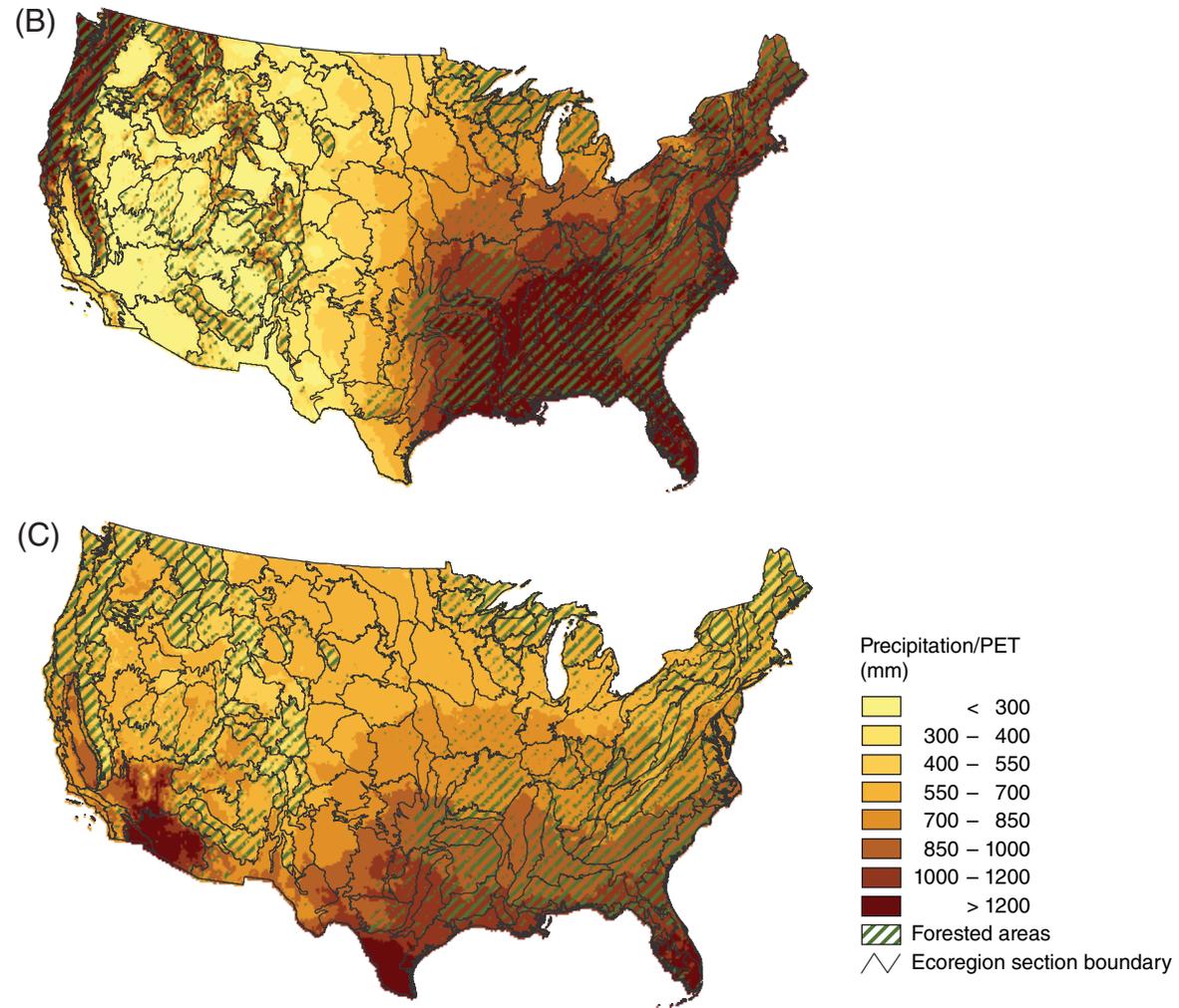


Figure 4.1 (continued)—The 100-year (1907–2006) (B) mean annual precipitation, and (C) mean annual potential evapotranspiration for the conterminous United States. Ecoregion section boundaries (Cleland and others 2007) and labels are included for reference. Forest cover data (overlaid green hatching) derived from MODIS imagery by the Forest Service, Remote Sensing Applications Center. (Data source: PRISM Group, Oregon State University)

Mountains; and M221B—Allegheny Mountains. Perhaps counterintuitively, the driest region of the Eastern United States, in terms of MI' , is southern Florida, particularly sections 232D—Florida Coastal Lowlands (Western) and 411A—Everglades in the southwestern portion of the State. This region is not dry in a traditional sense, as it typically receives a large amount of precipitation every year (fig. 4.1B). However, the region's high precipitation level is offset by an also high level of potential evapotranspiration (fig. 4.1C), resulting in negative MI' values. Interestingly, the spatial pattern of MI' in Florida as depicted in figure 4.1A echoes a recent map of the State's historical drought tendencies during the month of May, the peak of Florida's fire season (Brolley and others 2007).

Dry climates ($MI' < 0$) dominate most of the Western United States, where precipitation levels are typically much lower than in the East. Wet climates are generally confined to mountain ranges and adjacent valleys, particularly ecoregion sections in the northern Rocky Mountains and the Pacific Northwest: M242A—Oregon and Washington Coast Ranges, M242B—Western Cascades, M242D—Northern Cascades, M331A—Yellowstone Highlands, and M333C—

Northern Rockies. The driest climates extend across the Southwestern United States, where potential evapotranspiration is consistently high and precipitation is consistently low. Predictably, the lowest MI' values (< -0.7) are found across three neighboring ecoregion sections of the Southwest: 322A—Mojave Desert, 322B—Sonoran Desert, and 322C—Colorado Desert.

Drought Category Thresholds—The mean standard deviation of the MID , across all grids for the years 1907–2006, was 0.1. The value ranges we subsequently adopted for each drought or wetness category based on this standard deviation are summarized in table 4.1. The approximate theoretical frequencies, i.e., assuming a normal distribution, of MID values in each drought category are comparable to the frequencies seen with other commonly used drought indices (table 4.2); nonetheless,

Table 4.1—Moisture index difference value ranges for nine wetness and drought categories, along with the equivalent ranges in standard deviation from the mean value, i.e., zero

Category	Values	Standard deviations
Extreme wetness	≥ 0.20	≥ 2.0
Severe wetness	0.15–0.199	1.5–2.0
Moderate wetness	0.10–0.149	1.0–1.5
Mild wetness	0.05–0.099	0.5–1.0
Near normal	0.049– –0.049	0.5– –0.5
Mild drought	–0.05– –0.099	–0.5– –1.0
Moderate drought	–0.10– –0.149	–1.0– –1.5
Severe drought	–0.15– –0.199	–1.5– –2.0
Extreme drought	≤ -0.20	≤ -2.0

Table 4.2—Drought categories, with their corresponding negative value ranges and approximate theoretical frequencies of occurrence, for the moisture index difference and three commonly used drought indices: the Palmer Drought Severity Index, the Standardized Precipitation Index, and the revised Surface-Water Supply Index^a

Category	MID ^b		PDSI		SPI		Revised SWSI	
	Values	Frequency	Values	Frequency	Values	Frequency	Values	Frequency
	<i>percent</i>		<i>percent</i>		<i>percent</i>		<i>percent</i>	
Near normal	0– -0.049	19.10	0– -1.49	23	0– -0.99 ^c	34.10	0– -1.99 ^d	24
Mild drought	-0.05– -0.099	15	-1.5– -2.99 ^e	17	-1– -1.49	9.20	-2– -2.99	12
Moderate drought	-0.10– -0.149	9.20			-1.5– -1.99	4.40	-3– -3.99	12
Severe drought	-0.15– -0.199	4.40	≤ -4	4	≤ -2	2.30	≤ -4	2
Extreme drought	≤ -0.20	2.30						

MID = moisture index difference, PDSI = Palmer Drought Severity Index, SPI = Standardized Precipitation Index, SWSI = Surface-Water Supply Index.

^a The PDSI, SPI, and revised SWSI frequencies per category are adapted from previous studies (Garen 1993, Karl 1986, McKee and others 1993, Steinemann 2003).

^b The MID frequencies assume an approximately normal distribution and a mean of zero.

^c The SPI is calculated across a series of time scales. According to McKee and others (1993), a drought event for a given time scale represents a period where the SPI is continuously negative and at some point falls below -1. The drought event begins when the SPI first falls below zero, so McKee and others (1993) subsequently labeled the entire value range 0 – -0.99 as mild drought. Steinemann (2003) reinterpreted this range as near normal.

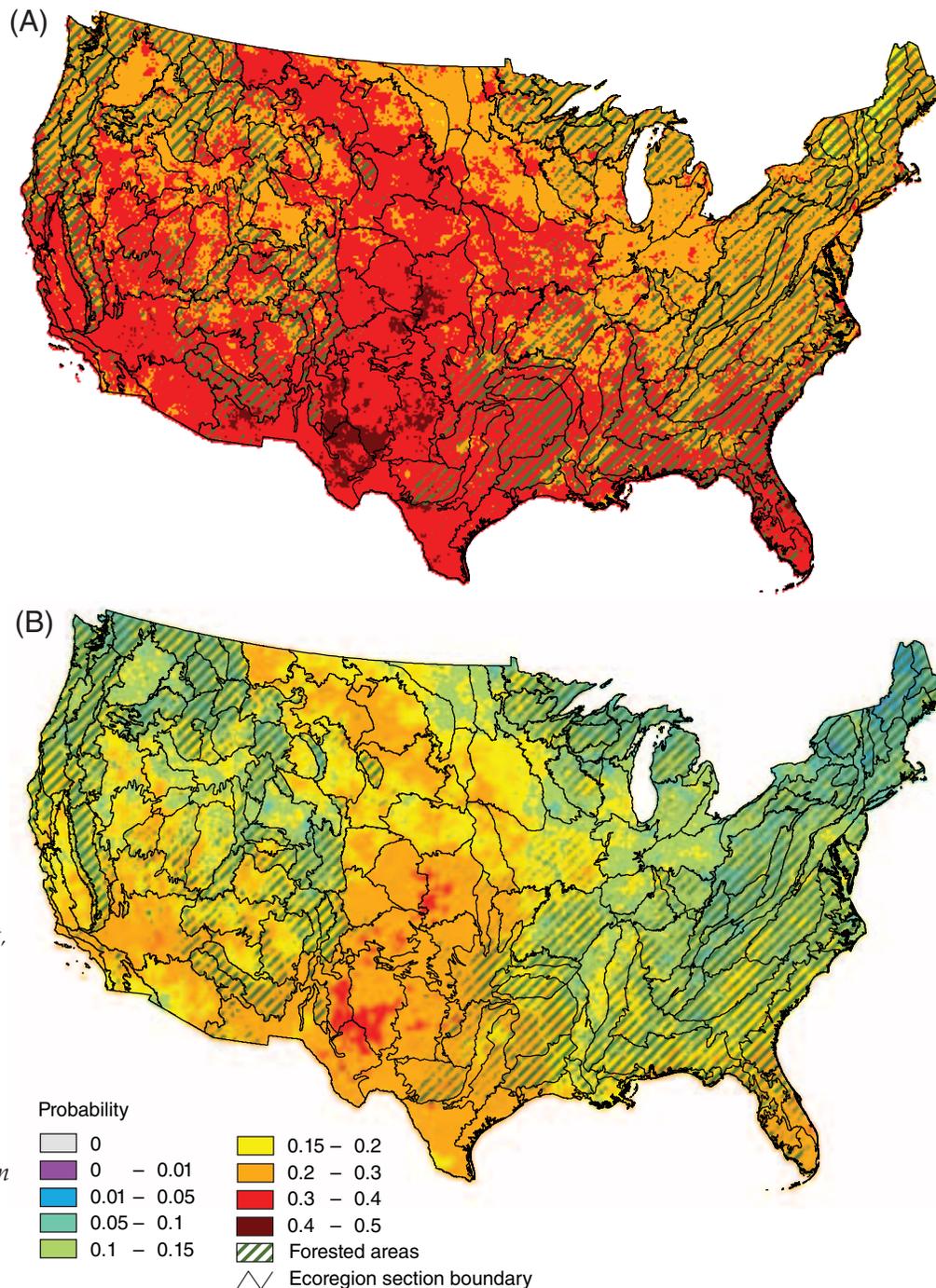
^d Garen (1993) did not include a mild drought category when reporting frequencies for the modified SWSI, but each one-unit interval of the index represents 12 percent of the theoretical probability of occurrence, e.g., values fall in the range -1 to -2 at a frequency of 12 percent.

^e Karl (1986) combined mild and moderate drought categories when reporting frequencies for the PDSI.

all of these frequencies should be interpreted cautiously since they depend upon the validity of assumptions about the value distribution and statistical properties of each index (Garen 1993, Steinemann 2003). Although the *MID* is nominally scaled between 2 and -2, actual *MID* values across all grids for the years 1907–2006 were between 0.7 and -0.7, and in most years fell between 0.5 and -0.5.

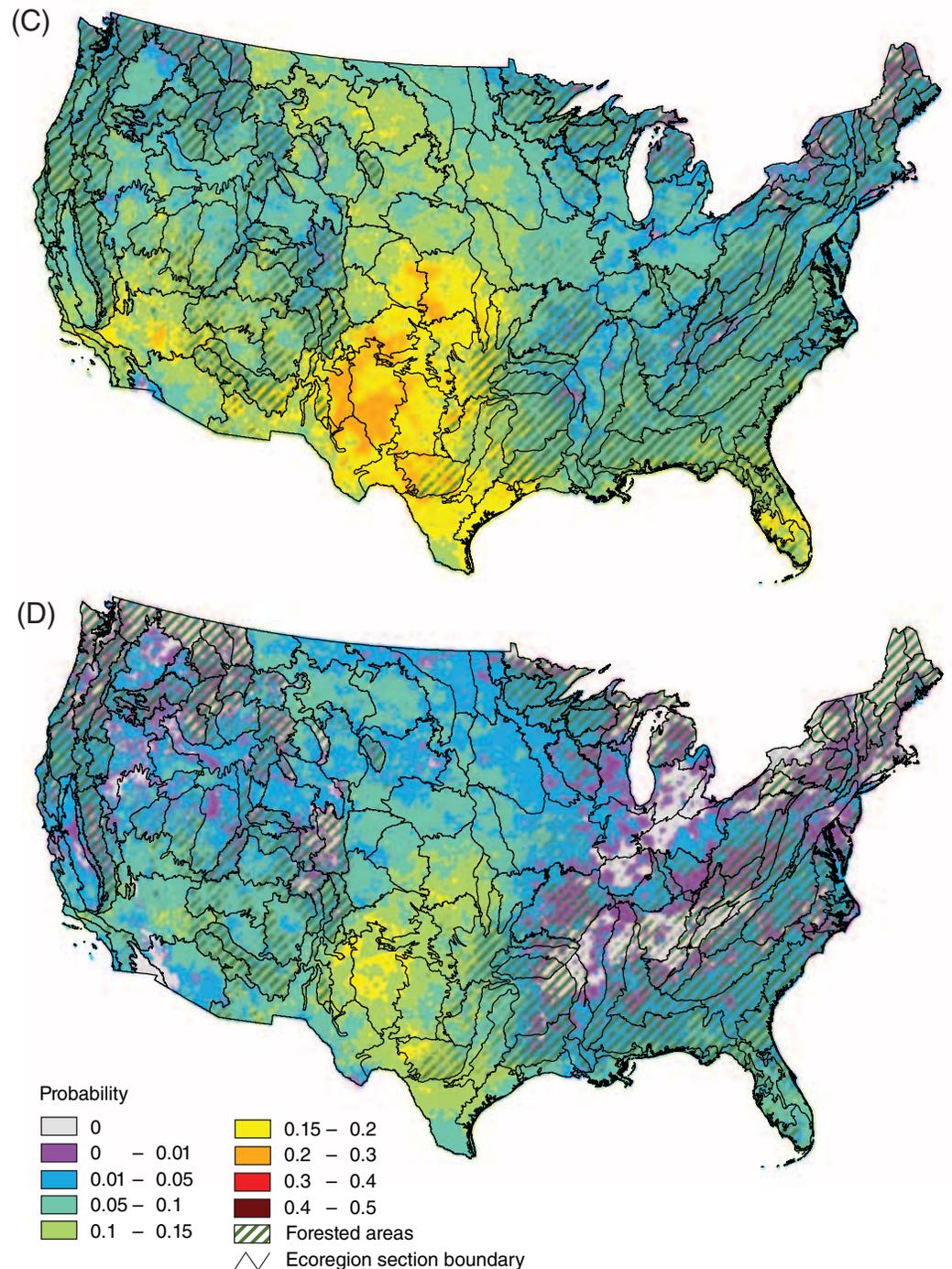
Drought Probabilities—The drought probability grid maps (fig. 4.2) provide a straightforward assessment of the *MID* due to the empirical manner in which they were constructed, i.e., simply the number of years out of 100 that the annual *MID* was less than or equal to one of the designated threshold values. In general, for all drought categories, the highest drought probabilities are found across the Southern United States (especially the Southwest) as well as the Great Plains region. Nearly the entire conterminous United States displays a moderate probability ($P \geq 0.20$) of at

Figure 4.2—Probability of (A) at least mild drought, (B) at least moderate drought, (C) at least severe drought, and (D) extreme drought for the conterminous United States. Probabilities were calculated as the number of years out of 100 (years 1907–2006) that the annual moisture index difference (*MID*) was less than or equal to corresponding drought category threshold values, specified in table 4.1. Ecoregion section boundaries (Cleland and others 2007) are included for reference. Forest cover data (overlaid green hatching) derived from MODIS imagery by the Forest Service, Remote Sensing Applications Center. (Data source: PRISM Group, Oregon State University) (continued on next page)



least mild drought conditions, i.e., annual *MID* values < -0.05 , occurring in any given year, with the exception of patches in a few ecoregion sections of the Northeast: most notably M211A—White Mountains; M211B—New England Piedmont; M211C—Green, Taconic, Berkshire Mountains; and M211D—Adirondack Highlands (fig. 4.2A). On the other hand, most of the country exhibits a low probability ($P < 0.05$) that extreme drought conditions will occur in a given year (fig. 4.2D). Indeed, some areas show a zero probability ($P = 0$) of extreme drought, although this likely reflects the limited precision of probabilities estimated using 100 years of available data. Probabilities of extreme drought are somewhat higher ($0.05 \leq P < 0.10$) in the northern Great Plains region and along the gulf coast, but the highest probabilities of extreme drought are patchily distributed throughout the Southwestern United States and the southern Great Plains region. Taking into consideration the probability grids for all four drought categories, these latter two regions appear to represent the most drought-

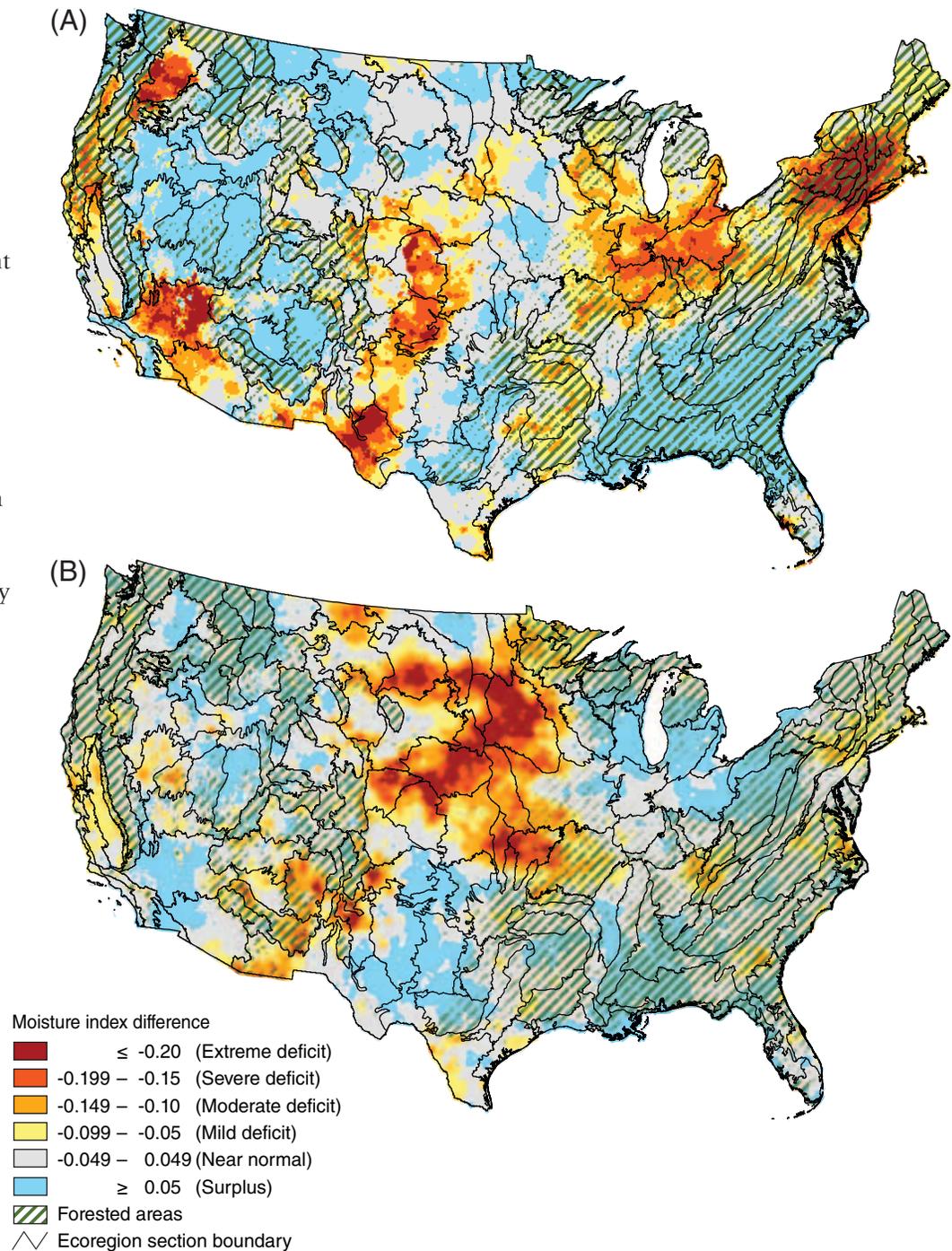
Figure 4.2 (continued)—Probability of (C) at least severe drought, and (D) extreme drought for the conterminous United States. Probabilities were calculated as the number of years out of 100 (years 1907–2006) that the annual moisture index difference (*MID*) was less than or equal to corresponding drought category threshold values, specified in table 4.1. Ecoregion section boundaries (Cleland and others 2007) are included for reference. Forest cover data (overlaid green hatching) derived from MODIS imagery by the Forest Service, Remote Sensing Applications Center. (Data source: PRISM Group, Oregon State University)



prone areas in the conterminous United States according to our analytical approach. While both regions tend to be dry climatically, they also exhibit a reasonably wide range of 100-year mean *MI'* values, i.e., they have somewhat varied climatic regimes through time. It is further worth noting that the most affected ecoregion sections are largely unforested.

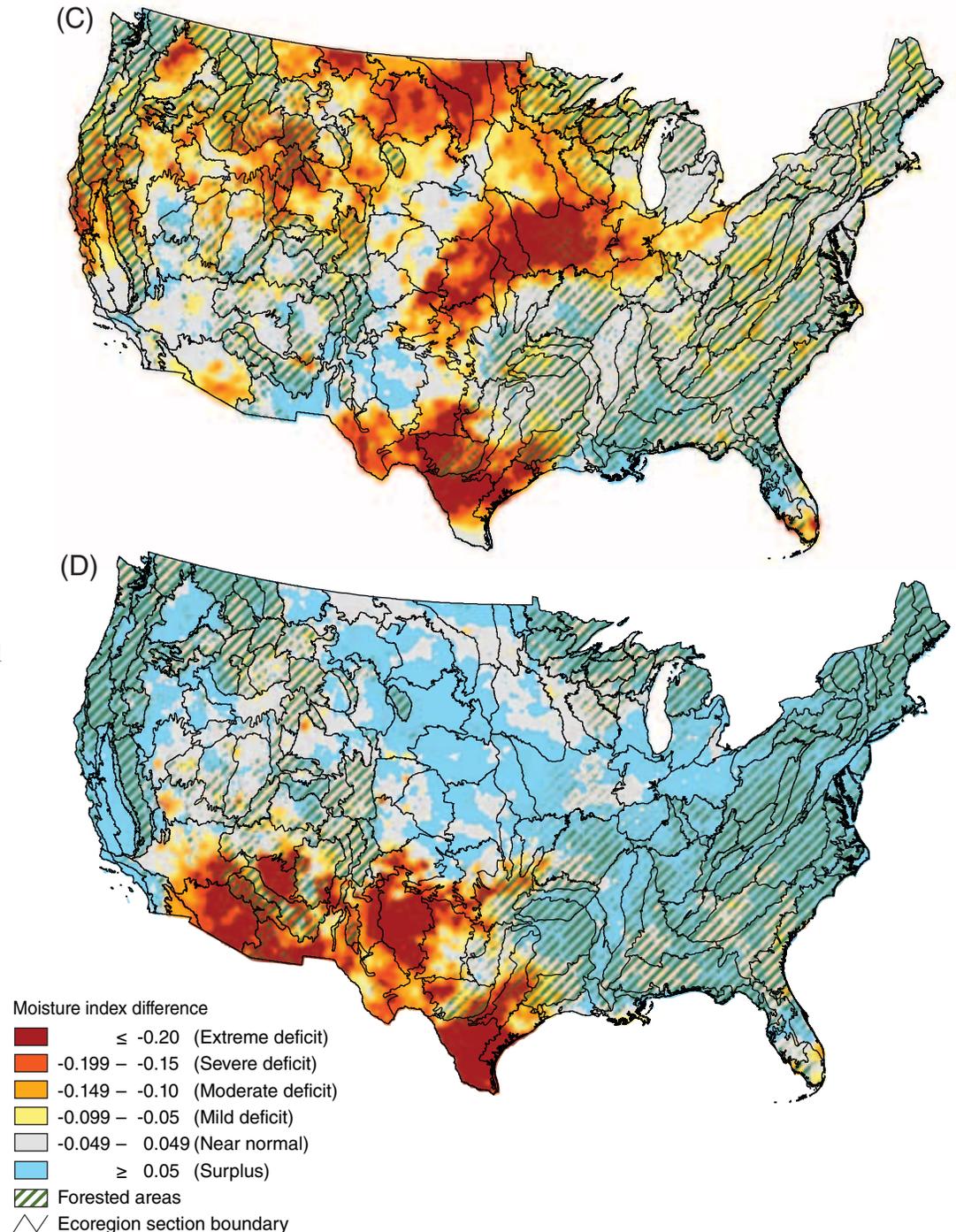
Historic Drought Maps—The *MID* approach yields effective 1-year snapshots of drought conditions, as demonstrated by its ability to capture several significant drought events from recent decades. For example, the Northeastern United States was subjected to a drought between 1962 and 1965 due to cyclonic activity off the Atlantic coast, likely caused by colder-than-normal sea surface temperatures, which led to wind anomalies and less moisture on land in New England and the Mid-Atlantic region (Namias 1983). The *MID* map for 1964 (fig. 4.3A) subsequently shows a large area of severe-to-extreme drought covering most of the Northeast. The *MID* map for 1980 (fig.

Figure 4.3—Moisture index difference (MID) maps for 4 years in which notable regional droughts occurred: (A) Northeastern United States, 1964; (B) Great Plains, 1980; (C) Northwestern United States and Great Plains, 1988; and (D) Southwestern United States, 1996. Ecoregion section boundaries (Cleland and others 2007) are included for reference. Forest cover data (overlaid green hatching) derived from MODIS imagery by the Forest Service, Remote Sensing Applications Center. (Data source: PRISM Group, Oregon State University) (continued on next page)



4.3B) shows an area of severe-to-extreme drought centered over the northern Great Plains region. While a summer heat wave eventually impacted much of the country that year, drought conditions persisted across the northern Great Plains for several months in a row (Karl and Quayle 1981). A drought that extended across much of the United States in 1988 was reported, shortly after its occurrence, as the most expensive natural disaster in the country's history (Trenberth and Branstator 1992). As illustrated by the *MID* map for 1988 (fig. 4.3C), the northern Great Plains region, southern Texas, the Northwestern United States, and the west coast were particularly affected (Andreadis and others 2005, Trenberth and others 1988). More recently, drought has deleteriously impacted vegetation in the Southwestern United States. Drought conditions occurred in 6 out of 10 years between 1995 and 2004 in this region, and extreme drought was widespread in 1996 (fig. 4.3D), precipitating extensive mortality

Figure 4.3 (continued)—Moisture index difference (*MID*) maps for 4 years in which notable regional droughts occurred: (C) Northwestern United States and Great Plains, 1988; and (D) Southwestern United States, 1996. Ecoregion section boundaries (Cleland and others 2007) are included for reference. Forest cover data (overlaid green hatching) derived from MODIS imagery by the Forest Service, Remote Sensing Applications Center. (Data source: PRISM Group, Oregon State University)



in pinyon-juniper woodlands (Mueller and others 2005). Actually, since drought conditions persisted for so long in the Southwest, a multiyear analysis could be quite informative with respect to the observed mortality patterns; this suggests a potentially fruitful area of future work with the *MID* approach.

Current (2007) Drought Map—The *MID* map for 2007 is shown in figure 4.4. In 2007, much of the Southeastern United States reached exceptional drought levels for the first time in more than 100 years, leading government officials in several States and municipalities to implement strict water restrictions (Goodman 2007). In the *MID* map, severe to extreme drought conditions covered large percentages of land area in several heavily forested ecoregion sections: 221J—Central Ridge and Valley, 223E—Interior Low Plateau-Highland Rim, 231A—Southern Appalachian Piedmont, 231B—Coastal Plains-Middle, 231C—Southern Cumberland Plateau, 231D—Southern Ridge and Valley, 231I—Central Appalachian Piedmont, 232C—Atlantic Coastal Flatwoods, and 232I—Northern Atlantic Coastal Flatwoods. Pockets of severe-to-

extreme drought were distributed across other sections in the Southeast. The *MID* map also shows extreme drought in southern Florida, especially in portions of sections 232D—Florida Coastal Lowlands-Gulf and 411A—Everglades. Lake Okeechobee, which is located in the extreme northern portion of 411A, fell to a record low in 2007, such that 12,000 acres of the lakebed were actually burned by wildfire in May of that year (O’Driscoll 2007).

Moderate-to-extreme drought covered most of central to southern California in 2007. Extreme drought also appeared in parts of the Intermountain West, at times reaching into forested portions of sections such as M313A—White Mountains-San Francisco Peaks, M331E—Uinta Mountains, and M341A—East Great Basin and Mountains. Notably, the *MID* grid for 2007 depicts normal to surplus conditions across much of the Central United States, particularly the southern Great Plains region; this was a major departure from the previous 2 years for this area, where drought conditions contributed to high wildfire incidence (O’Driscoll 2007).

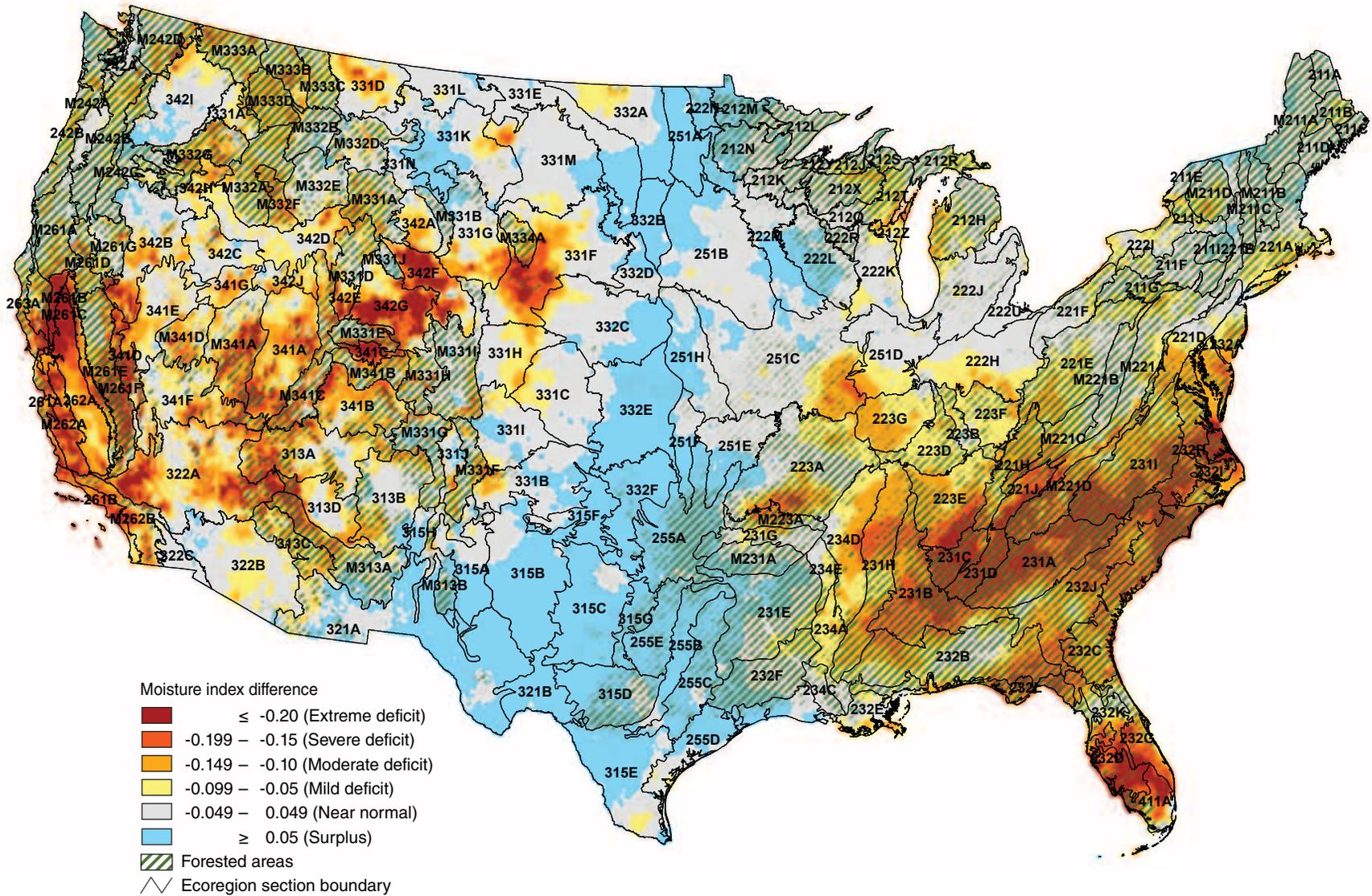


Figure 4.4—Map of the 2007 moisture index difference (MID) for the conterminous United States. Ecoregion section boundaries (Cleland and others 2007) and labels are included for reference. Forest cover data (overlaid green hatching) derived from MODIS imagery by the Forest Service, Remote Sensing Applications Center. (Data source: PRISM Group, Oregon State University)

Issues and Implications—In this chapter, we presented a methodology for characterizing drought on an annual time step and further applied the approach to estimate probabilities of different levels of drought severity for the conterminous United States. The *MID* approach is computationally simple and repeatable, requiring only climate variables and omitting soil or other environmental factors that are unavailable nationally at fine scales. Nevertheless, because the *MID* only accounts for part of the entire environmental moisture balance, it does not replace other drought indicators such as the PDSI or the many indices applied to hydrological or agricultural drought. Indeed, no drought monitoring tool is applicable for all analyses, especially since drought may be defined differently depending on whether the analyst is focused on moisture supply, moisture demand, or the socioeconomic consequences of a drought event (Brown and others 2008, Weber and Nkemdirim 1998). We must also acknowledge that our annual time window is arbitrary; drought events may last longer than a year, or even if < 12 months in duration, may start in the latter part of 1 year and continue into the next. The *MID* approach can be adapted for any period of consecutive months, although this complicates the calculation of a corresponding “normal” *MI* to subtract from the

MI for the time period of interest. Other high-resolution approaches to monitoring drought are currently in development. For example, the Vegetation Drought Response Index (VegDRI) combines traditional drought indices (PDSI and SPI) with remote-sensing-derived vegetation indices and other environmental data to map vegetative drought stress in close to real-time at a 1-km² spatial resolution; although it is currently at a regional pilot stage, there are plans to eventually expand the coverage of VegDRI to a national scale (Brown and others 2008). For monitoring of current drought conditions, this method or something similar may ultimately be a preferred alternative to our proposed *MID* approach. In the meantime, data generated using our approach may be useful as a high-resolution complement to other drought mapping products, e.g., Drought Monitor GIS data. Moreover, one noteworthy potential application of the *MID* approach is the generation of explanatory variables in predictive models pertaining to forest health issues, particularly if those models are intended to incorporate multiple decades of historical drought data. For instance, *MID* datasets could be employed in broad-scale risk analyses for forest pests that utilize drought-stressed trees or otherwise exhibit increased activity during drought conditions.

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Introduction

Analyzing patterns of forest pest infestation is necessary for monitoring the health of forested ecosystems because of the impact insects and diseases can have on forest structure and composition, biodiversity, and species distributions (Castello and others 1995). In particular, introduced nonnative insects and diseases can extensively damage the diversity, ecology, and economy of affected areas (Brockerhoff and others 2006, Mack and others 2000). Examining pest occurrences from a landscape-scale perspective is useful, given the regional extent of many infestations and the interaction between landscape patterns and the development of pest outbreaks (Holdenrieder and others 2004). The detection of geographic clusters of disturbance is one such landscape-scale approach, which allows for the identification of areas at greatest risk of significant impact and for the selection of locations for more intensive analysis.

Methods

We used nationally compiled low-altitude aerial survey and ground survey data, collected by the Forest Health Protection (FHP) of the Forest Service, U.S. Department of Agriculture, from 2006 to identify landscape-scale hotspots of forest insect and disease activity in the

conterminous 48 States, and to summarize insect and disease activity by ecoregion section in Alaska. Surveys in 2006 covered approximately 65 percent of the forested area in the conterminous United States and approximately 19 percent of Alaska's forested area (fig. 5.1). These surveys identify areas of mortality and defoliation caused by insect and pathogen activity. A pathogen or insect might be considered a mortality-causing agent in one location and a defoliation-causing agent in another, depending on the level of damage to the forest in a given area. Additionally, differences in data collection procedures among States and regions can complicate the analysis of the data and the interpretation of the results. Analysis of the survey data across multiple years is not appropriate in most situations because both the location and extent of the areas surveyed and the classification of forest tree mortality and defoliation agents varies across years.

We used a forest cover map (1-km² resolution) derived from Moderate Resolution Imaging Spectroradiometer imagery by the Forest Service, Remote Sensing Applications Center (U.S. Department of Agriculture Forest Service 2008) to determine the amount and location of forest within survey defoliation and mortality polygons. Areas reported here reflect polygons masked by forest cover.

CRITERION 3—

Chapter 5. Large-Scale Patterns of Insect and Disease Activity in the Conterminous United States and Alaska, 2006

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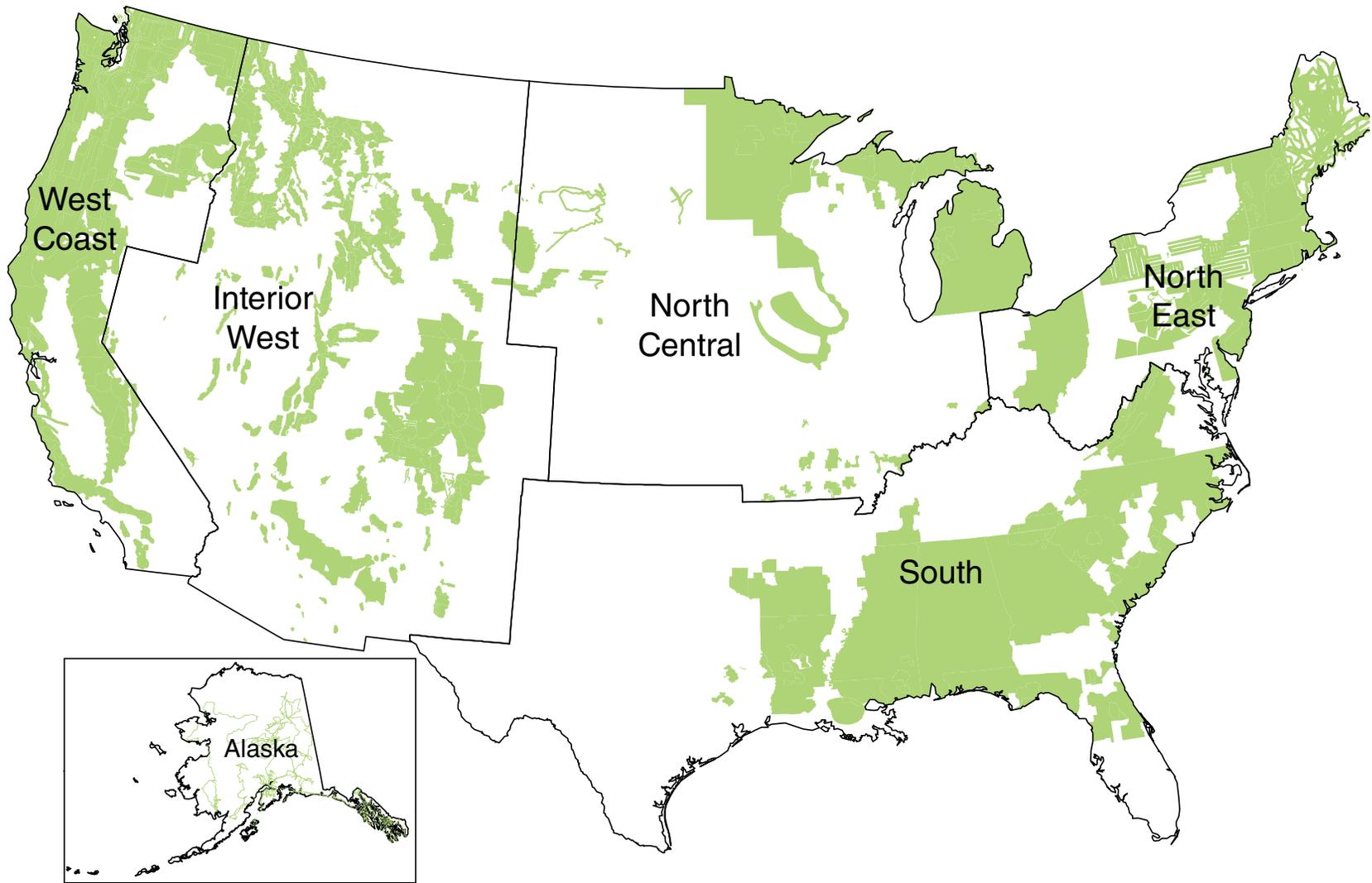


Figure 5.1—The extent of surveys for insect and disease activity conducted in the conterminous United States and Alaska in 2006 (shown in green). The lines delineate FHM regions. (Data source: Forest Service, Forest Health Protection)

We employed a Getis-Ord hotspot analysis (Getis and Ord 1992) to identify forested areas with the greatest exposure to mortality-causing and defoliation-causing agents. We intensified the Environmental Monitoring and Assessment Program North American hexagon coordinates (White and others 1992) to develop a lattice of hexagonal cells, of approximately 2500-km² extent, for the conterminous United States. This cell size allows for analysis at a medium-scale resolution of approximately the same area as a county. We then calculated the percent of forest area in each hexagon exposed to either mortality- or defoliation-causing agents. The Getis-Ord G_i^* statistic summed the differences between the mean values in a local sample, determined by a moving window consisting of each hexagon and its six adjacent hexagons, and the global mean of all the forested hexagonal cells in the conterminous 48 States. G_i^* is standardized as a z score with a mean of zero and a standard deviation of 1, with values greater than approximately 2 representing strong and significant local clustering ($p < 0.025$) of high values, and values less than approximately -2 representing significant local clustering of low values ($p < 0.025$).

Polygons associated with two specific mortality agents required additional processing because the data were reported at a coarser resolution than for the other agents. First, a single polygon classified approximately 4.25 million ha of land area (including 900 000 ha of

forest) in southeastern Michigan as experiencing emerald ash borer (*Agrilus planipennis*) mortality in 2006. We calculated overall ash mortality across the area as 13.3 percent, by multiplying the mortality rate (24.2 percent) by the percent of forest containing ash (*Fraxinus* spp.). We assumed that 55 percent of the forest in this area contained ash, because ash species occurred on 55 percent of the 1,120 Forest Inventory and Analysis plots within the area. We also assumed that ash experienced 24.2 percent mortality from emerald ash borer across the area, based on data collected in 2005 from 20 sites in southeastern Michigan (Witter and others 2006).

A second set of polygons, based on ground surveys by the Maine Forest Service, delineated an area of 2.9 million ha in eastern Maine experiencing fir mortality following balsam woolly adelgid (*Adelges piceae*) infestation. This area was divided into three tiers according to degree of fir mortality, with firs experiencing 24 percent mortality in the tier closest to the coast, 5 percent mortality in the next tier inland, and 1 percent mortality in the third inland tier (Laustsen 2006). We estimated the extent and location of mortality caused by the balsam woolly adelgid by multiplying mortality within each tier by the amount of forest in the spruce/fir forest-type group (U.S. Department of Agriculture Forest Service 2008). Spruce/ fir forest covered 45 percent of the overall delineated area.

Results and Discussion

The 2006 FHP aerial survey data identified 48 different biotic mortality-causing agents on 2 420 298 ha of forest across the conterminous United States, an area slightly smaller in extent than that of the commonwealth of Massachusetts. It is also slightly larger than the approximately 2.14 million ha of tree mortality estimated by the 2006 FHP report on forest insect and disease conditions in the United States (U.S. Department of Agriculture Forest Service 2007), which did not include the “sparse mortality” polygons for emerald ash borer in Michigan and balsam woolly adelgid in Maine. The mortality agents with the most widespread occurrence were mountain pine beetle (*Dendroctonus ponderosae*) (1 010 365 ha), emerald ash borer (504 964 ha), and balsam woolly adelgid (138 490 ha). Also in 2006, the survey identified 51 biotic defoliation agents affecting approximately 2 765 232 ha of forest across the conterminous United States, an area slightly larger than Massachusetts, with the largest areas exposed to defoliation by forest tent caterpillar (*Malacosoma disstria*) (960 986 ha), western spruce budworm (*Choristoneura occidentalis*) (787 282 ha), and gypsy moth (*Lymantria dispar*) (449 098 ha). The defoliation area estimates for these three pests are similar to those in the 2006 forest insect and disease conditions report (U.S. Department of Agriculture Forest Service 2007): 1 076 760 ha for forest tent caterpillar,

939 680 ha for western spruce budworm (an increase from 488 051 ha in 2005), and 522 044 ha for gypsy moth (an increase from 271 139 ha the previous year). For the mortality agents with the most widespread occurrence in the survey data, the forest insect disease conditions report estimated that approximately 1.17 million ha experienced mountain pine beetle mortality, but did not estimate the extent of mortality for emerald ash borer and balsam woolly adelgid.

Our national-scale hotspot analysis detected three hotspots of insect and disease mortality in the eastern two-thirds of the country, and approximately a dozen in the West (fig. 5.2A). Two of the largest eastern hotspots were associated with emerald ash borer and balsam woolly adelgid, despite our adjustments to the initial coarse-scale delineation of the extent of these mortality agents. The largest of the three eastern hotspots was located in the northern Midwest, where exposure to emerald ash borer created a mortality hotspot in the lower peninsula of Michigan. In the Northeast, balsam woolly adelgid mortality was reported across the forested areas of coastal Maine. A third, smaller mortality hotspot occurred in the Western Great Plains (ecoregion section 331F) in southwestern South Dakota and northwestern Nebraska, where pine engraver beetles (*Ips* spp.) represented an agent of mortality across the scattered ponderosa pine (*P. ponderosa*) forest.

Mountain pine beetle was the predominant agent associated with several mortality hotspots in the Interior West (fig. 5.2A). The most highly clustered of these hotspots occurred in northern Colorado and southern Wyoming. Here, spruce beetle (*Dendroctonus rufipennis*), subalpine fir (*Abies lasiocarpa*) mortality, pine engraver, Douglas-fir beetle (*Dendroctonus pseudotsugae*), and five-needle pine decline also contributed to mortality exposure. One hotspot in the Uinta Mountains (M331E) of northeastern Utah was caused mostly by mountain pine beetle, while another, smaller hotspot in the White Mountains-San Francisco Peaks area of southwestern New Mexico (M313A) was associated with western pine beetle (*Dendroctonus brevicomis*).

Further north, mountain pine beetle also accounted for most mortality-causing activity in a large complex of hotspots in Montana, Idaho, and Wyoming (fig. 5.2A). Western balsam bark beetle (*Dryocoetes confusus*) and Douglas-fir beetle also contributed significantly to mortality in this area. Subalpine fir decline and spruce beetle caused a separate and smaller hotspot in the nearby Bighorn Mountains of north central Wyoming.

Mountain pine beetle and western pine beetle were important factors in two mortality hotspots near the west coast (fig. 5.2A). One of these extended along the Cascade Mountains from northcentral Washington to southcentral Oregon. In nearby northeastern Washington,

another mountain pine beetle hotspot was located in the Okanogan Highland area (M333A). Fir engraver beetle (*Scolytus ventralis*), spruce beetle, and Douglas-fir beetle also contributed to mortality in the area.

A smaller hotspot along the southern coast of Oregon (fig. 5.2A) was caused primarily by Port-Orford-cedar root disease (caused by *Phytophthora lateralis*), along with the flatheaded borer (family *Buprestidae*), pine engraver, fir engraver, mountain pine beetle, and Douglas-fir beetle. Additionally, a single-hexagon hotspot in the Sierra Nevada of California (M261E) was associated with bark beetles and fir engraver.

Our analysis also detected six hotspots of 2006 defoliation activity (fig. 5.2B). The most extensive of these were in the Northeast, where the close proximity of two centers of high defoliation activity, associated mostly with forest tent caterpillar and gypsy moth, resulted in a single large hotspot. The eastern center of activity, in Lower New England (221A), included defoliation by forest tent caterpillar, gypsy moth, Nantucket pine tip moth (*Rhyacionia frustrana*), pine needleminer (*Exoteleia pinifoliella*), fall cankerworm (*Alsophila pomataria*), winter moth (*Operophtera brumata*), and orangestriped oakworm (*Anisota senatoria*). The western center of defoliation activity encompassed portions of southeastern New York and northeastern Pennsylvania. Defoliation here was caused by forest tent caterpillar, gypsy moth, and locust leafminer (*Odontota dorsalis*). The Northeast

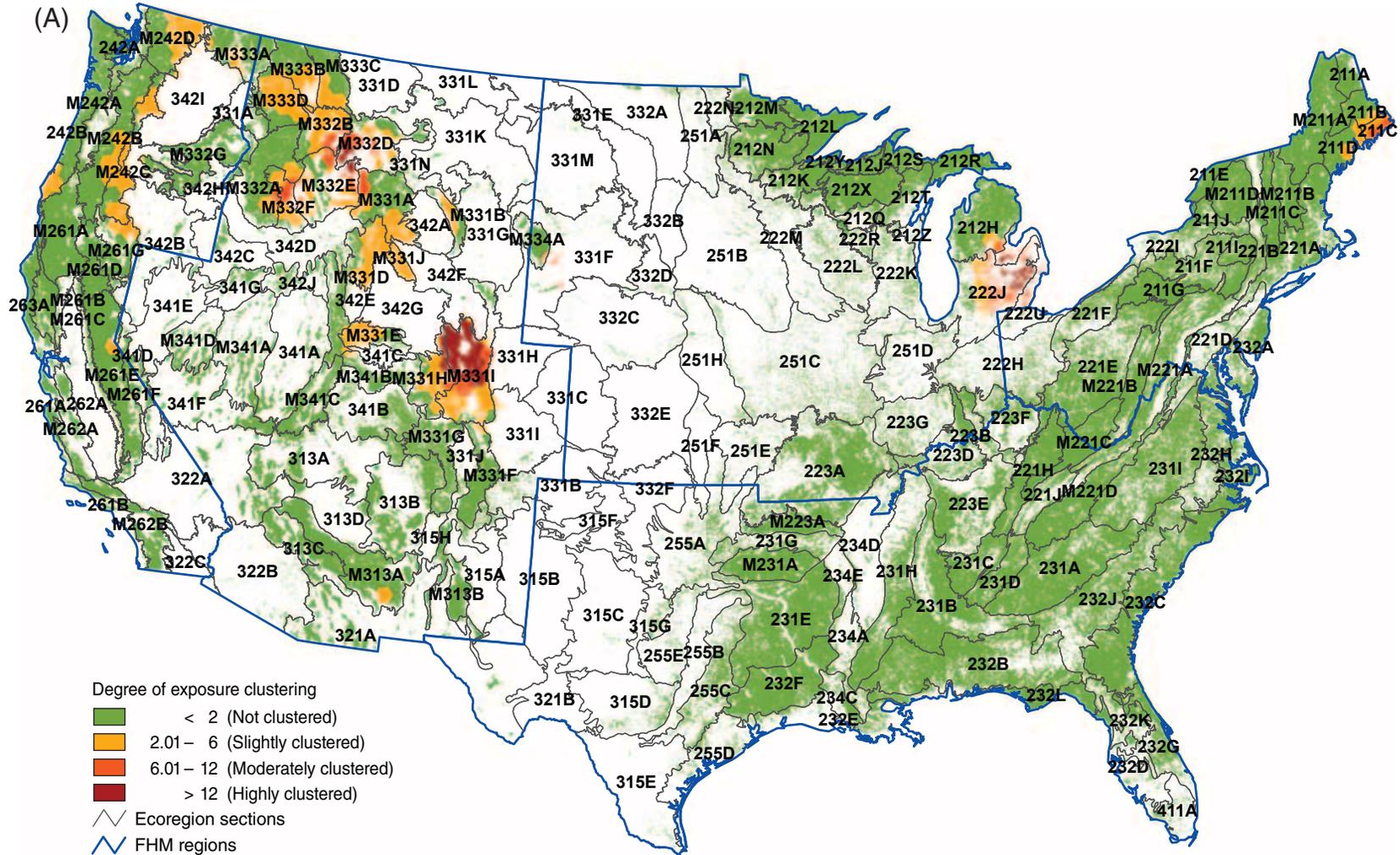


Figure 5.2—Hotspots of exposure to (A) mortality-causing insects and diseases and (B) defoliation-causing insects and diseases in 2006. Values are Getis-Ord G_1^* scores, with values > 2 representing strong and significant clustering of high percentages of forest exposed to damaging agents. The gray lines delineate ecoregion sections (Cleland and others 2007). Background forest cover is derived from MODIS imagery by the Forest Service, Remote Sensing Applications Center. (Data source: Forest Service, Forest Health Protection) (continued on next page)

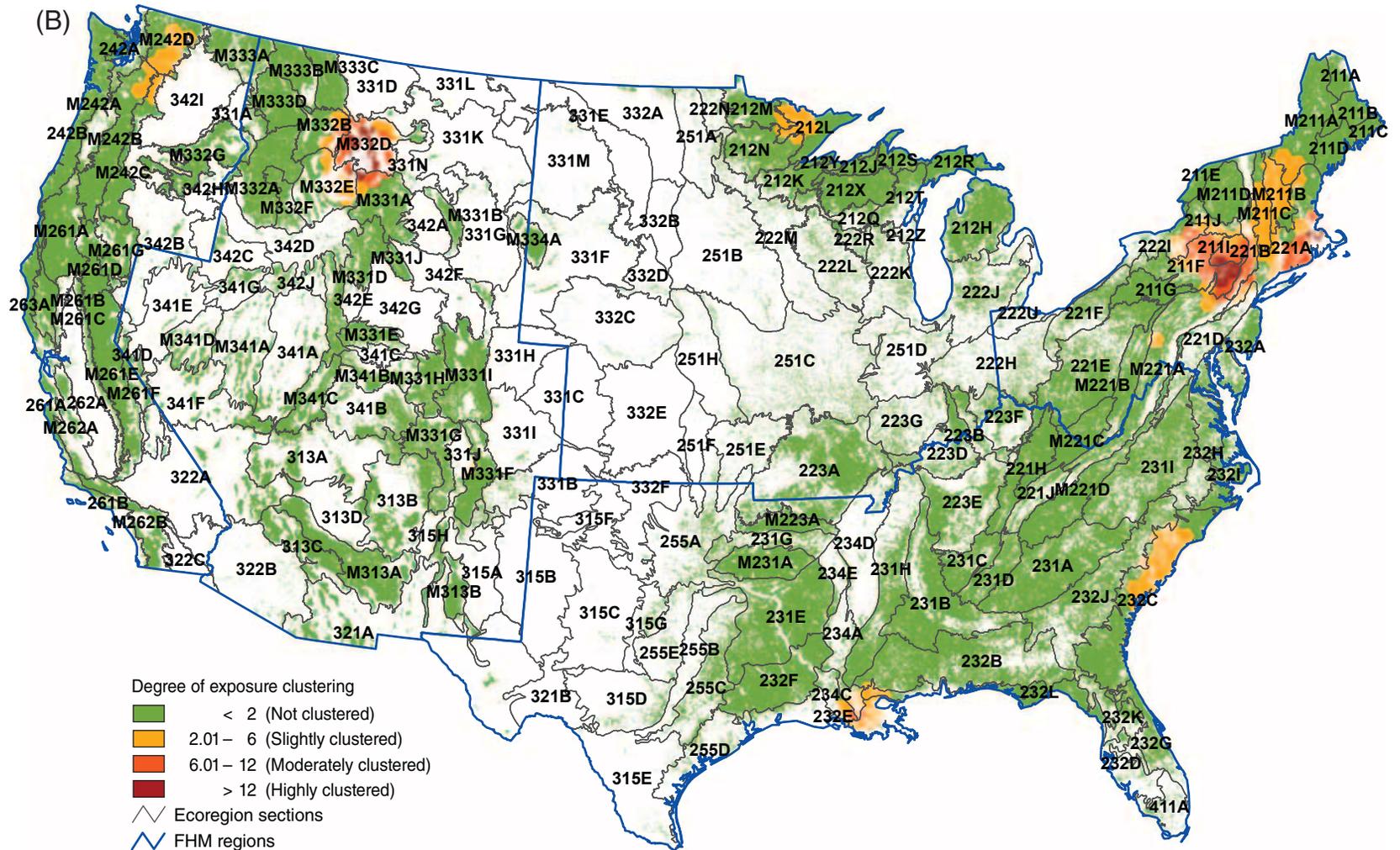


Figure 5.2 (continued)—Hotspots of exposure to (A) mortality-causing insects and diseases and (B) defoliation-causing insects and diseases in 2006. Values are Getis-Ord G_i^* scores, with values > 2 representing strong and significant clustering of high percentages of forest exposed to damaging agents. The gray lines delineate ecoregion sections (Cleland and others 2007). Background forest cover is derived from MODIS imagery by the Forest Service, Remote Sensing Applications Center. (Data source: Forest Service, Forest Health Protection)

hotspot extended north into Vermont, New Hampshire, and western Maine, where defoliation was caused by forest tent caterpillar, hardwood anthracnose (*Kabatiella apocrypta*), Septoria leaf spot (*Septoria alnifolia*), saddled prominent caterpillar (*Heterocampa guttivitta*), and birch leafminer (*Fenusa pusilla*).

Forest tent caterpillar also was associated with two defoliation hotspots in the South, one in coastal South Carolina and southeastern North Carolina, and the other encompassing southeastern Louisiana (fig. 5.2B). Baldcypress leafroller (*Archips goyerana*) was also an important defoliating insect in the latter hotspot.

Western spruce budworm was responsible for two hotspots of defoliation exposure in the West (fig. 5.2B). The more concentrated defoliation activity occurred in the Interior West, in southwestern Montana. A less concentrated hotspot on the west coast stretched across the Cascades. Black pineleaf scale (*Nuculaspis californica*) and needlecast also caused defoliation in this area.

A defoliation hotspot in northern Minnesota (fig. 5.2B), meanwhile, was associated primarily with spruce budworm and jack pine budworm (*Choristoneura pinus*), with smaller amounts of eastern larch beetle (*Dendroctonus simplex*) and larch casebearer (*Coleophora laricella*).

The low density of aerial survey data from Alaska in 2006 precluded the use of hotspot analyses for that State. Instead, mortality and defoliation data were summarized by ecoregion section. Four mortality-causing agents were

reported for Alaska, affecting 65 913 ha, which represented <1 percent of the forest surveyed (9.69 million ha). Spruce beetle had the largest extent, detected on 48 417 ha, mostly in the Northern Aleutian Range (M213A). This section also had the highest percent of exposure to forest mortality agents at 12.25 percent (fig. 5.3A), although forest in this section is fairly limited in extent. Two nearby ecoregion sections—the Bristol Bay Lowlands (213A) and the Ahklun Mountains (M129B)—also experienced a somewhat high amount of forest mortality (5.85 and 1.37 percent of total forest area exposed to mortality, respectively) as a result of the spruce beetle. Other more heavily forested ecoregion sections experienced <1 percent exposure to agents of forest mortality. Other causes of mortality were Alaska yellow-cedar (*Chamaecyparis nootkatensis*) decline, recorded on 12 849 ha, northern spruce engraver beetle (*Ips perturbatus*) (4433 ha), bark beetle (201 ha), and larch beetle (13 ha).

Alaska forests, meanwhile, were exposed to 13 defoliation agents recorded on 281 310 ha, or 2.9 percent of the surveyed forest area. Aspen leafminer (*Phyllocnistis populiella*) had by far the largest extent, observed on 185 306 ha across eastcentral Alaska. As a result of aspen leafminer, five ecoregion sections had relatively high percentages of exposure to forest defoliation agents (1 to 2 percent): the Yukon Bottomlands (131A), the Kuskokwin Colluvial Plain (131B), the Copper River Basin (135A), the Yukon Flats (139A), and the Dawson Range (M139C) (fig. 5.3B).

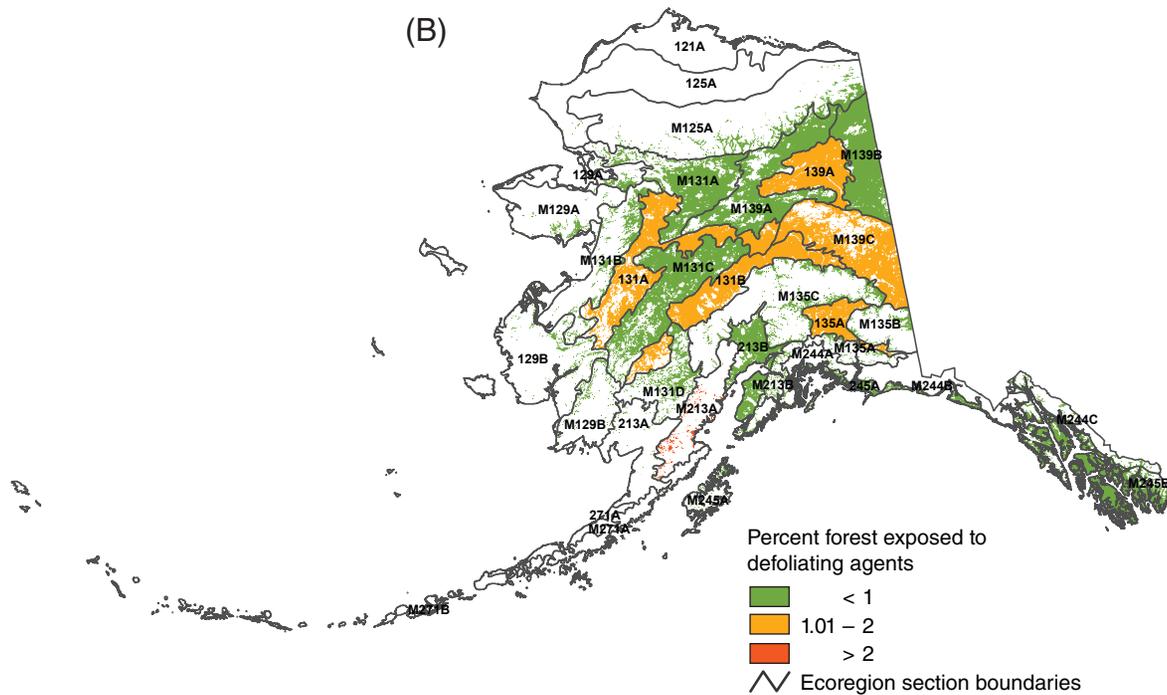
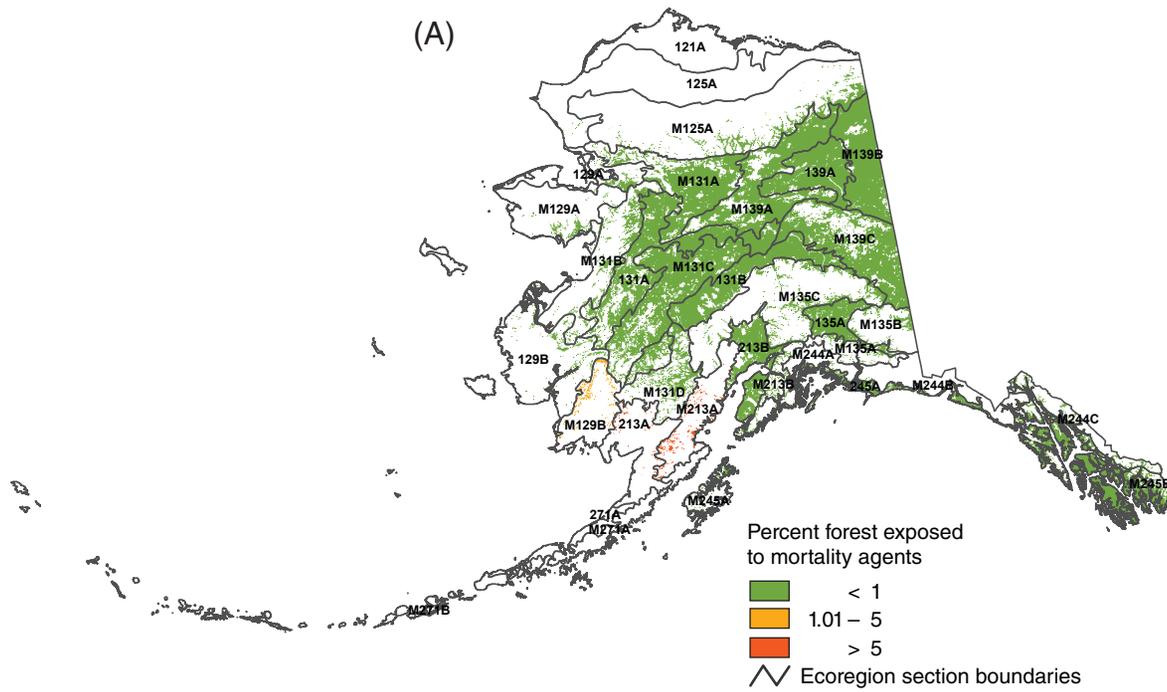


Figure 5.3—Percent of forest in Alaska ecoregion sections (Nowacki and Brock 1995) exposed to (A) mortality-causing insects and diseases and (B) defoliation-causing insects and diseases in 2006. Background forest cover is derived from MODIS imagery by the Forest Service, Remote Sensing Applications Center. (Data source: Forest Service, Forest Health Protection)

Other important defoliators in Alaska were spruce budworm (21 521 ha), willow leafblotch miner (*Micrurapteryx salicifoliella*) (20 471 ha), and large aspen tortrix (*Choristoneura conflictana*) (13 934 ha). The Northern Aleutian Range (M213A) had the greatest observed defoliation, with 2.4 percent of its forest exposed to defoliation by a hardwood skeletonizer, but only a small proportion (6.3 percent or 233 832 ha) of the section is forested.

Continued monitoring of these insect and disease outbreaks in the conterminous 48 States and Alaska will be necessary to determine appropriate followup investigation and management activities. As this analysis of mortality and defoliation exposure demonstrates, hotspot detection can help prioritize geographic areas where the concentration of these activities would be most useful.

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Introduction

Wildland fire represents an important ecological mechanism in many forest ecosystems. It shapes the distributions of species, maintains the structure and function of fire-prone communities, and is a significant evolutionary force (Bond and Keeley 2005). At the same time, fire outside the historic range of frequency and intensity can have extensive economic and ecological impacts. More than half the forested area in the conterminous United States is either moderately or significantly altered from historical fire regimes, potentially altering key ecosystem components such as species composition, structural stage, stand age, canopy closure, and fuel loadings (Schmidt and others 2002). Fire suppression and the introduction of nonnative plants, in particular, have dramatically altered natural fire regimes (Barbour and others 1999), while fire regimes altered by global climate change could cause large-scale shifts in spatial vegetation patterns (McKenzie and others 1996).

Methods

The Moderate Resolution Imaging Spectroradiometer (MODIS) active fire detections for the U.S. database

(U.S. Department of Agriculture Forest Service 2008a) allows analysts to spatially display and summarize fire occurrence on a yearly basis (Coulston and others 2005). The data are derived using the MODLand Rapid Response algorithm from the thermal infrared bands of imagery collected daily by two satellites at a resolution of 1 km², with the center of a pixel recorded as a point, i.e., a fire “occurrence,” when the satellites’ MODIS sensors identify the presence of a fire at the time of image collection (U.S. Department of Agriculture Forest Service 2008a). The data represent only whether a fire was active, because the MODIS sensors do not differentiate between a hot fire in a relatively small area (0.01 km², for example) or a cooler fire over a larger area (1 km², for example). The MODIS active fire database does well at capturing large fires but may underrepresent rapidly burning, small and low-intensity fires, as well as fires in areas with frequent cloud cover (Hawbaker and others 2008).

I determined the mean number of 1-km² pixels that experienced fire per 100 km² of forested area for each ecoregion section in the conterminous 48 States and Alaska over the years 2005 to 2007. This was done after screening out wildland fires on nonforested

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Chapter 6. Large-Scale Patterns of Forest Fire Occurrence in the Conterminous United States and Alaska, 2005-07

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pixels using a forest cover layer derived by the Forest Service, Remote Sensing Applications Center from MODIS imagery (U.S. Department of Agriculture Forest Service 2008b). I also compared the cumulative distribution functions of fire occurrence over each of the years.

Additionally, I employed a Getis-Ord hotspot analysis (Getis and Ord 1992) to identify forested areas in the conterminous 48 States with greater fire occurrence than expected by chance for each of the 3 years. I superimposed a hexagonal lattice, with cells of approximately 2500 km², over the conterminous United States, intensified from Environmental Monitoring and Assessment Program North America hexagon coordinates (White and others 1992). This cell size allows for analysis at a medium-scale resolution of approximately the same area as a county. I then calculated the number of 1-km² pixels that experienced fire in each hexagon per 100 km² of forested area. For each of the 3 years of data, I used the Getis-Ord G_i^* statistic to identify clusters of hexagonal cells with fire occurrence density values higher than expected by chance. Briefly, G_i^* sums the differences between the mean values in a local sample, determined in this case by a moving window of each hexagon and the six neighboring hexagons, and the global mean. It is then standardized as a z score with a mean of zero and a standard deviation of 1, with values greater than approximately 2 representing strong and significant local

clustering of high fire occurrence densities ($p < 0.025$) and < -2 representing local clustering of lower fire occurrence densities ($p < 0.025$) since 95 percent of the observations under a normal distribution should be within 2 standard deviations of the mean (Laffan 2006). Values between -2 and 2 , therefore, indicate no statistically significant concentration of high or low fire occurrence densities.

Results and Discussion

The MODIS active fire database captured 70,692 wildland forest fire occurrences in 2005; 45,924 in 2006; and 84,086 in 2007. These numbers are generally similar to the official wildland fire statistics, which report 66,753 fires in 2005; 96,385 fires in 2006; and 85,822 fires in 2007 (National Interagency Coordination Center 2008). The discrepancy between the figures for 2006 is attributable to the large number of nonforest wildland fires that year, mostly occurring in a belt stretching from North Dakota through Texas. The MODIS active fire database for 2006 reported 91,286 wildland fires before those on nonforest lands were screened out.

The official wildland fire statistics, which encompass all wildland fires regardless of land cover, show a dramatic increase in the area burned in recent years over the 10-year average, with 35 165 km² (8,689,389 acres) burned in 2005; 39 958 km² (9,873,745 acres) burned in

2006; and 37 749 km² (9,328,045 acres) burned in 2007 (National Interagency Coordination Center 2008). Of these, 2006 was an especially severe fire year, with approximately 52 percent more area burned than the 10-year average from 1998 to 2007 (26 227 km² or 6,480,833 acres). The largest number of fire occurrences for all 3 years was reported in the Southeastern United States, with the South experiencing half the national total number of fire occurrences in

2006 (National Interagency Coordination Center 2008). According to the MODIS data, despite its severity, the 2006 wildland forest fire season was the shortest of the 3 years, lasting approximately 98 days (from approximately July 9, 2006, to October 15, 2006), as determined by the visually identified sharp increase and decrease in the slope of the cumulative distribution function (fig. 6.1). Approximately 58 percent of wildland forest fires occurred during this

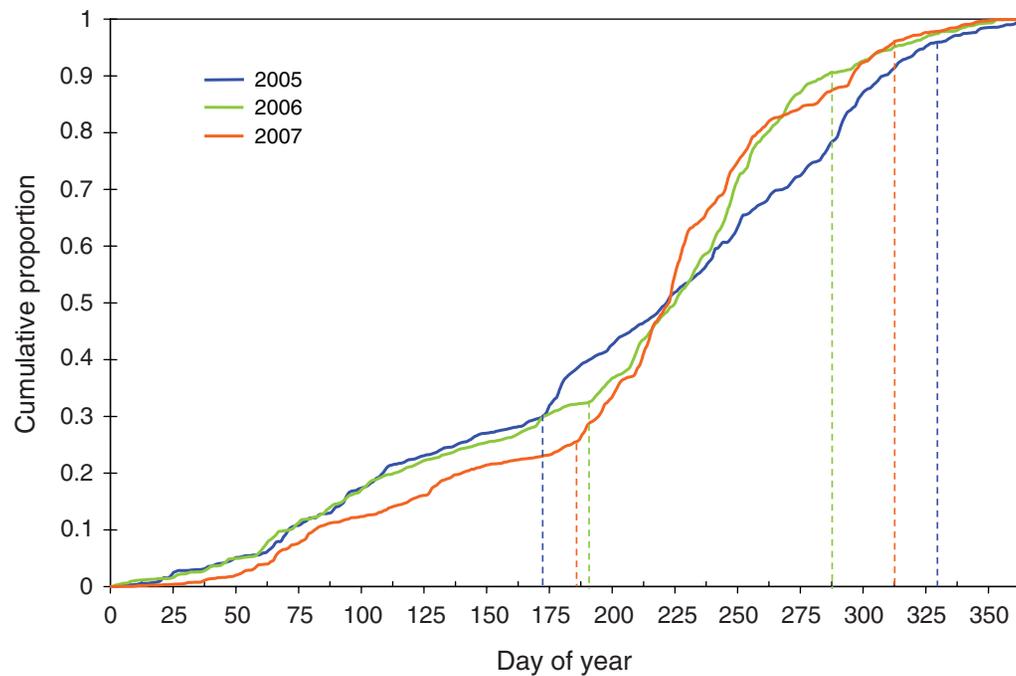


Figure 6.1—Cumulative distribution function of fire occurrence in 2005, 2006, and 2007 by day of the year. The vertical lines show the approximate start and end of the fire season for each year, as determined by visual inspection of sharp increases and decreases in the cumulative distribution function. (Data source: Forest Service, Remote Sensing Applications Center)

period. The 2005 fire season was the longest (approximately 158 days—June 21, 2005, to November 26, 2005), also accounting for 58 percent of fire occurrences. The 2007 fire season lasted from approximately July 5, 2007, to November 8, 2007 (126 days and 70 percent of fire occurrences).

The ecoregion sections with the greatest mean number of fire occurrences per year from 2005 to 2007 were all in the Western United States (fig. 6.2A). The Southern California Mountain and Valley section (M262B) had the most fire occurrences, averaging 18.6 per 100 km² of forested area; followed by the Challis Volcanics (M332F) (14.6 fire occurrences per 100 km² of forest); and Northern Rockies and Bitterroot Valley (M332B) (7.9 fire occurrences per 100 km² of forest). Other sections with more than six fire occurrences per 100 km² of forest were the Northern Rockies (M333C), the Flathead

Valley (M333B), Western Great Plains (331F), and the Northern Cascades (M242D). Few fire occurrences were reported in the Northeastern and Midwestern States, while several sections in the Southeast had an intermediate number of fire occurrences.

In Alaska (fig. 6.2B), the Olgivie Mountains (M139B) had the most fire occurrences between 2005 and 2007, averaging 8.6 per 100 km² of forested area. The Kuskokwim Mountains (M131C) averaged 4.7 fire occurrences, while three other sections [the Yukon Bottomlands (131A), the Upper Kobuk-Koyukuk (M131A), and the Yukon Flats (139A)] averaged approximately 3 fire occurrences per year for each 100 km² of forest.

Hotspots of fire occurrence generally differed by year, with the exception of a highly clustered and extensive hotspot that appeared each year in central Idaho and western Montana. The

two other highly clustered hotspots in 2005 (fig. 6.3A) include one in Arizona and one in east Texas, Louisiana, and Arkansas. Minor fire hotspots were located in southeastern Nevada/southwestern Utah, the Sierra Nevada of east central California, and southwestern Oregon. A large hotspot with low clustering also extended across several sections in the Southeast, east of the Mississippi River.

The most intense hotspot of 2006 (fig. 6.3B) was located in the Northern Cascades of northcentral Washington. California contained two highly clustered hotspots that year, one in the Klamath Mountains of the northwestern part of the State and one along the southern coast. This latter hotspot recurred in 2007 (fig. 6.3C). Other hotspots of 2007 included

one in southern Georgia and northern Florida, one in the northern Sierra Nevada of California, and two in the Coastal Plain of Mississippi and Alabama. Several slightly clustered but large hotspots had also occurred in the Deep South States during 2006.

The results of these hotspot analyses are not intended to quantify the severity of a given fire season but to offer insights into where fire occurrences were concentrated. When considered across multiple years, this information may be useful for the identification of areas for management activities and followup investigations of the ecological, economic, and sociological impact of fires that may be outside the range of historic frequency.

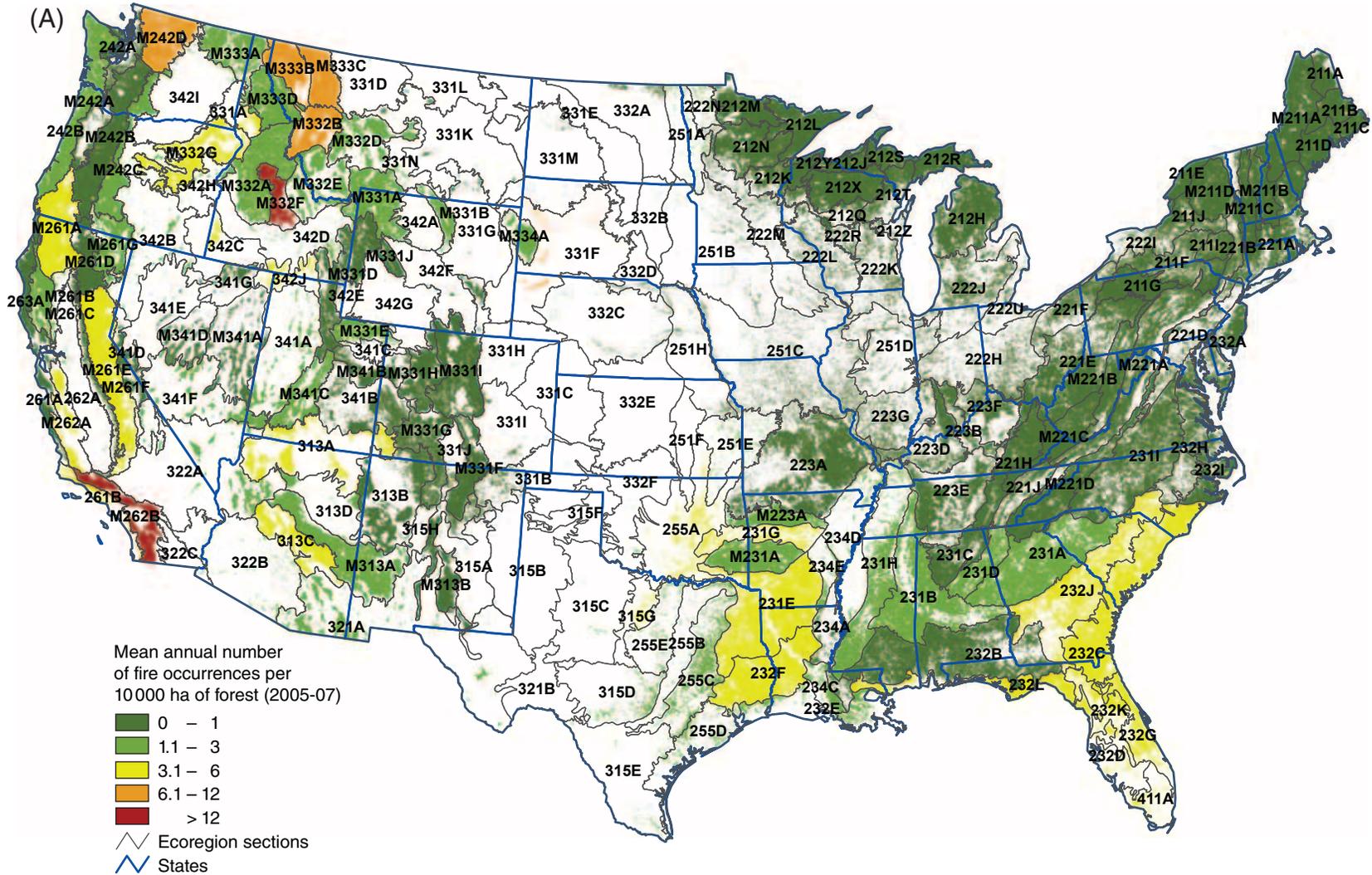


Figure 6.2—The mean annual number of daily forest fire occurrences per 100 km² (10 000 ha) of forested area for the years 2005-07 for ecoregion sections in (A) the conterminous 48 States and (B) Alaska. Forest cover is derived from MODIS imagery by the Forest Service, Remote Sensing Applications Center. (Data source: Forest Service, Remote Sensing Applications Center) (continued on next page)

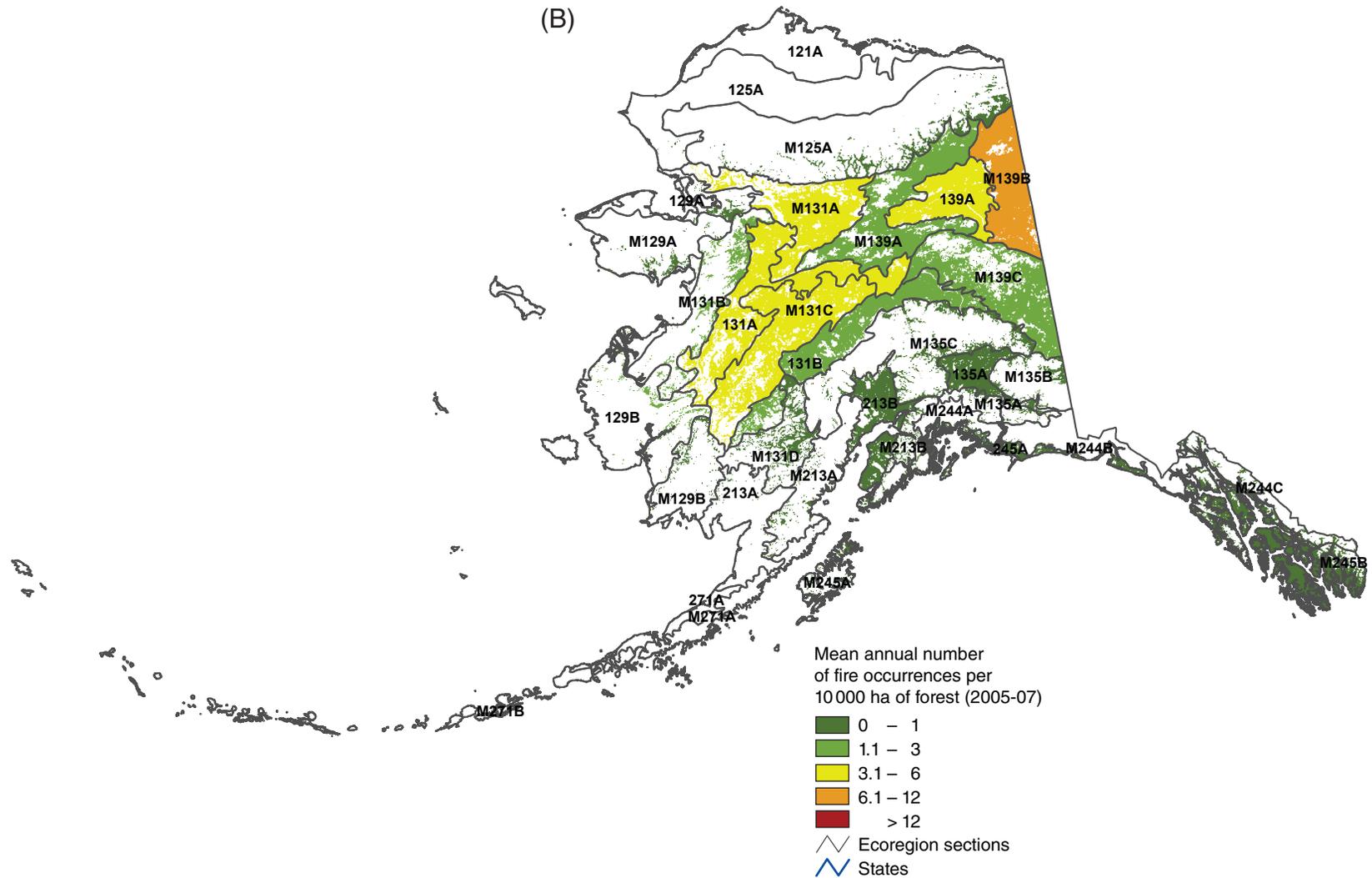


Figure 6.2 (continued)—The mean annual number of daily forest fire occurrences per 100 km² (10 000 ha) of forested area for the years 2005-07 for ecoregion sections (Nowacki and Brock 1995) in (B) Alaska. Forest cover is derived from MODIS imagery by the Forest Service, Remote Sensing Applications Center. (Data source: Forest Service, Remote Sensing Applications Center)

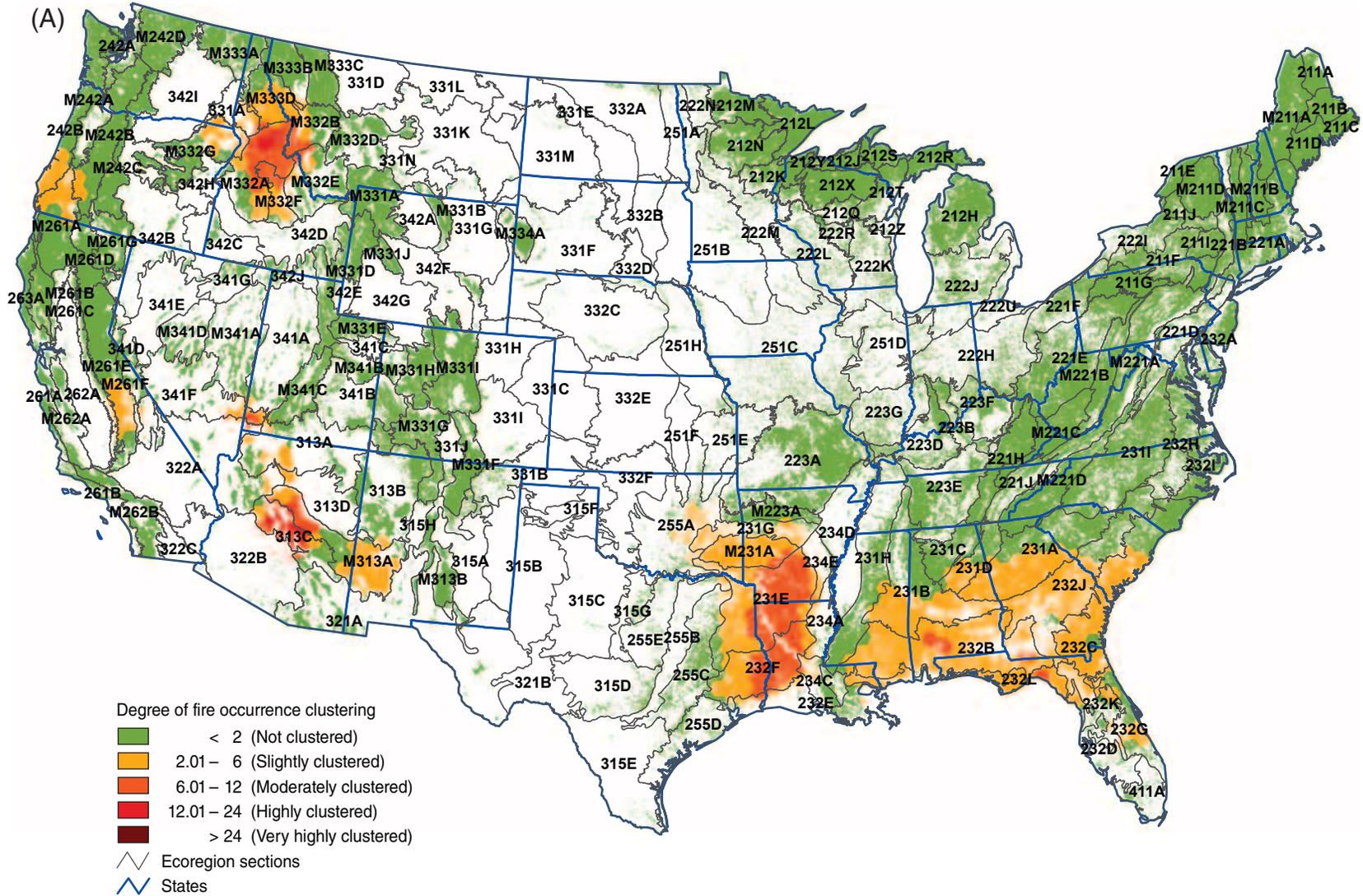


Figure 6.3—Hotspots of fire occurrence for (A) 2005, (B) 2006, and (C) 2007. Values are Getis-Ord G_i^* scores, with values > 2 representing strong and significant clustering of high fire occurrence densities. Background forest cover is derived from MODIS imagery by the Forest Service, Remote Sensing Applications Center. (Data source: Forest Service, Remote Sensing Applications Center) (continued on next page)

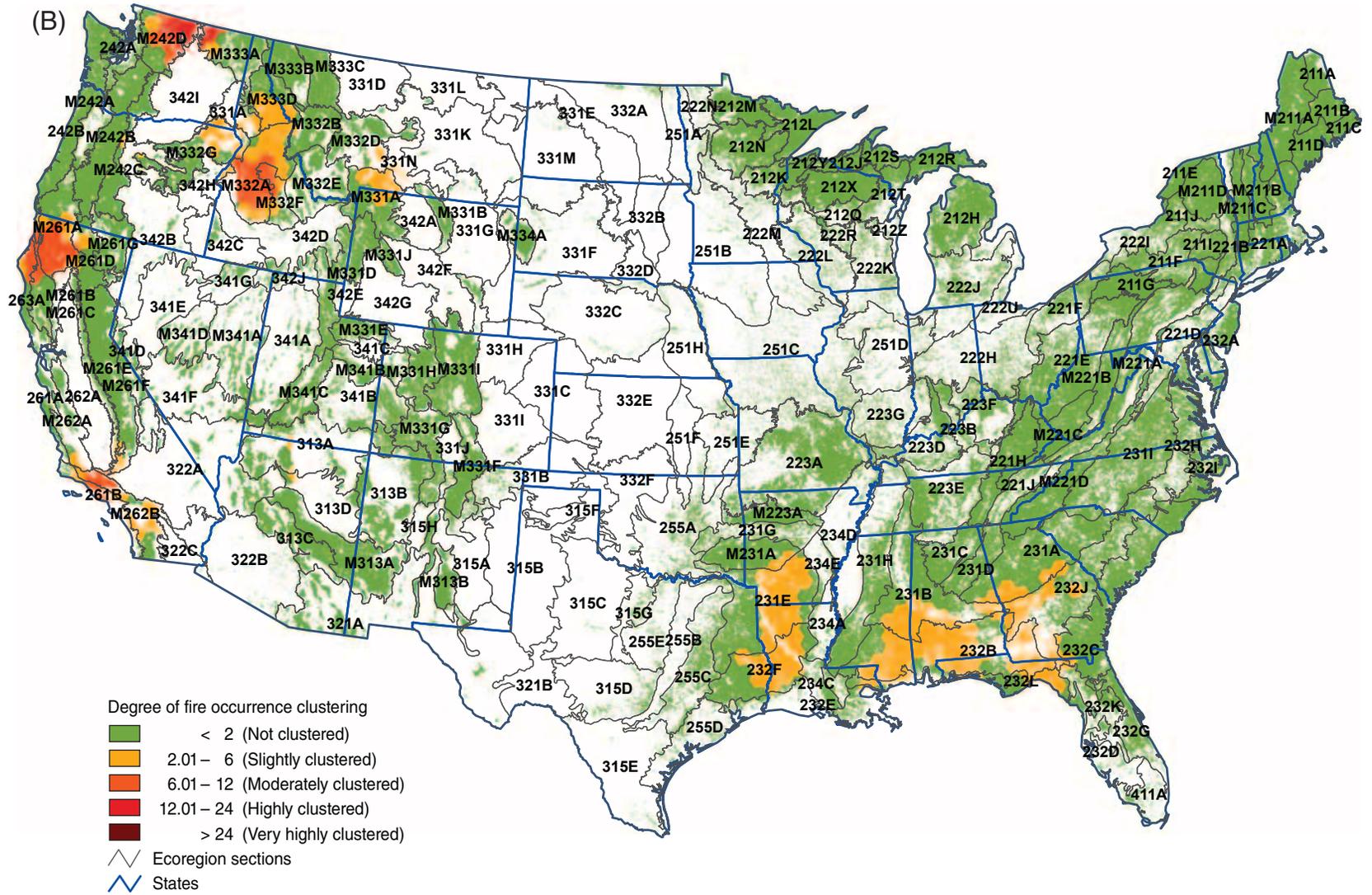


Figure 6.3 (continued)—Hotspots of fire occurrence for (B) 2006. Values are Getis-Ord G_i^* scores, with values > 2 representing strong and significant clustering of high fire occurrence densities. Background forest cover is derived from MODIS imagery by the Forest Service, Remote Sensing Applications Center. (Data source: Forest Service, Remote Sensing Applications Center) (continued on next page)

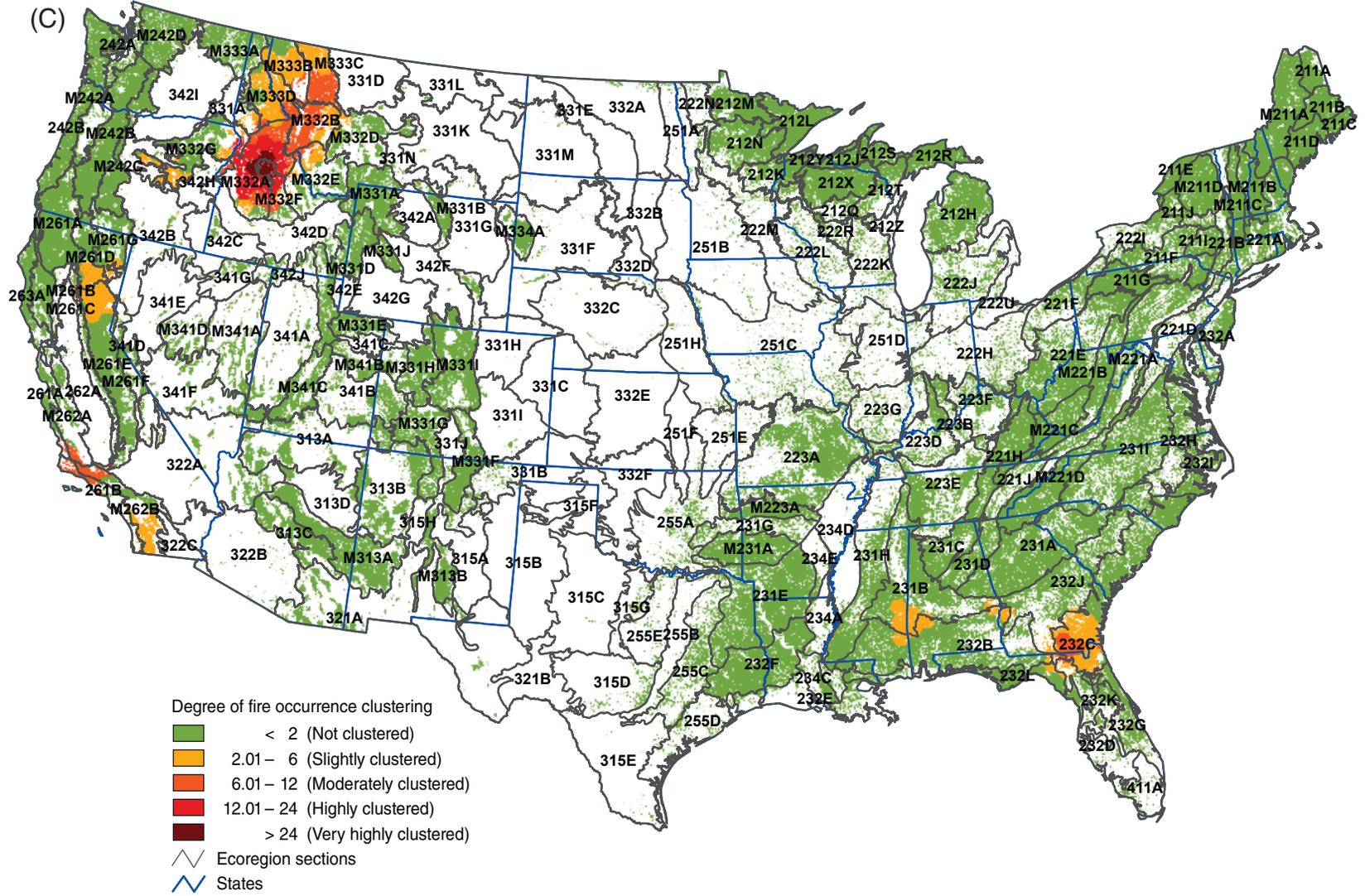


Figure 6.3 (continued)—Hotspots of fire occurrence for (C) 2007. Values are Getis-Ord G_i^* scores, with values > 2 representing strong and significant clustering of high fire occurrence densities. Background forest cover is derived from MODIS imagery by the Forest Service, Remote Sensing Applications Center. (Data source: Forest Service, Remote Sensing Applications Center)

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Introduction

Tree mortality is a natural process in all forest ecosystems. However, extremely high mortality can also be an indicator of forest health issues. On a regional scale, high mortality levels may indicate widespread insect or disease problems. High mortality may also occur if a large proportion of the forests in a region are made up of older, senescent stands.

In early national reports (2001–04) by the Forest Health Monitoring (FHM) program of the Forest Service, U.S. Department of Agriculture, tree mortality was analyzed using FHM and Forest Inventory and Analysis (FIA) phase 3 (P3) data. Those data spanned a relatively long time period, but the sample was not spatially intense (approximately one plot per 96,000 acres). In the 2007 FHM report (Ambrose 2012), a similar method was applied to FIA phase 2 (P2) data from a small number of Midwestern States, as a demonstration of how the more intensive P2 dataset might be used in forest health analyses. In this report, the method is applied over a much larger area of the Central and Eastern United States, using data from repeated measurements in a larger number of States.

Data

FIA P2 inventory data are collected using a rotating panel sample design (Bechtold and Patterson 2005). Field plots are divided into spatially balanced panels, with one panel being measured each year. A single cycle of measurements consists of measuring all panels. This “annualized” method was phased in, State by State, beginning in 1999. Mortality analysis was possible for areas where data from repeated plot measurements taken using consistent sampling protocols, i.e., measurements of one complete cycle plus at least one panel of the next cycle and no changes to the protocols related to measuring trees or saplings, were available.

Table 7.1 shows the 17 States from which consistent and repeated P2 measurements were available, the time period spanned by the data, and the number of panels of data available. The States included in this analysis, as well as the forest cover within those States, are shown in figure 7.1.

CRITERION 3—

Chapter 7. Tree Mortality

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Table 7.1—States from which repeated Forest Inventory and Analysis phase 2 measurements were available, the time period spanned by the data, and the number of panels of data available^a

Time period	States	P2 panels
		<i>number</i>
1999–2005	Maine	2
2000–05	Indiana, Kentucky, and Pennsylvania	1
2000–06	Iowa, Michigan, Minnesota, Missouri, and Wisconsin	2 ^{b c}
2001–06	Alabama, Illinois, Kansas, North Dakota, Nebraska, South Dakota, and Texas ^d	1
2002–06	Arkansas	1

P = phase.

^a Each panel represents approximately one-fifth of the plots in a State.

^b In Minnesota and Wisconsin the P2 inventory was done at twice the standard Forest Inventory and Analysis sample intensity, approximately one plot per 3,000 acres when the full five panels are measured.

^c In Missouri the P2 inventory was done at twice the standard Forest Inventory and Analysis sample intensity, approximately one plot per 3,000 acres when the full five panels are measured, on national forest lands and at the standard intensity on all other lands.

^d Annualized growth and mortality data were only available for eastern Texas.

Methods

FIA P2 tree and sapling data were used to estimate average annual tree mortality in tons of biomass per acre. The biomass represented by each tree (in tons) was calculated by FIA and provided in the FIA database (version 3.0) (U.S. Department of Agriculture Forest Service, Forest Inventory and Analysis Program 2008). To compare mortality rates across forest types and climate zones, the ratio of annual mortality to gross growth (MRATIO) is used as a standardized mortality indicator (Coulston and others 2005a). Trees removed (harvested) from sample plots were excluded from the analysis. Gross growth rate and mortality rate, in tons of biomass per acre per year, were independently calculated for each ecoregion section (Cleland and others 2005) using a mixed modeling procedure. The mixed model is efficient for estimation using data where not all plots have been measured over the same time interval (Gregoire and others 1995). MRATIOS were then calculated from the growth and mortality rates. For details on the mixed-modeling procedure and the method for calculating the MRATIO, see “Appendix A—Supplemental Methods” in “Forest Health Monitoring 2001 National Technical Report” (Coulston and others 2005b).

The MRATIO can be large if a forest is overmature and losing a cohort of older trees. When this is not the case, a high MRATIO (>0.6) may indicate high mortality due to some acute cause (insects or pathogens) or due to generally deteriorating forest health conditions. An MRATIO value >1 indicates that mortality exceeds growth and live standing biomass is actually decreasing.

In addition, the ratio of average dead tree diameter to average live tree diameter (DDL ratio) was calculated for each plot where mortality occurred. Low DDL ratios (much <1) usually indicate competition-induced mortality typical of young, vigorous stands, while high ratios (much >1) indicate mortality associated with senescence or some external factors such as insects or disease (Smith and Conkling 2004). Intermediate DDL ratios can be hard to interpret because a variety of stand conditions can produce them. The DDL ratio is most useful for analyzing mortality in regions that also have high MRATIOS. High DDL values in regions with very low MRATIOS may indicate small areas experiencing high mortality of large trees or locations where the death of a single large tree, such as a remnant pine in a young hardwood stand, has produced a deceptively high DDL.

To further analyze tree mortality, the number of stems and total biomass of trees that had died were calculated by species within each ecoregion. Identifying the tree species experiencing high mortality in an ecoregion is the first step in identifying what forest health issues may be affecting the forests. Although determining the particular causal agents associated with observed mortality with certainty is beyond the scope of this report; often there are well-known insects and pathogens that are “likely suspects” once the affected tree species are identified.

Results and Discussion

The MRATIO values are shown in figure 7.2. The highest MRATIOS occurred in ecoregion sections 332C—Nebraska Sand Hills (MRATIO = 2.78) and 332A—Northeastern Glaciated Plains (MRATIO = 2.26). While these ecoregions are rather large, they contain relatively small areas of forest (see figure 7.1), so only a small area of forest is experiencing these high mortality levels. Other areas where mortality exceeded growth occurred in northern Minnesota (ecoregion sections 212Y—Southwest Lake Superior Clay Plain, 212M—Northern Minnesota and Ontario, and 251A—Red River Valley); in South Dakota and Nebraska (ecoregion 331F—Western

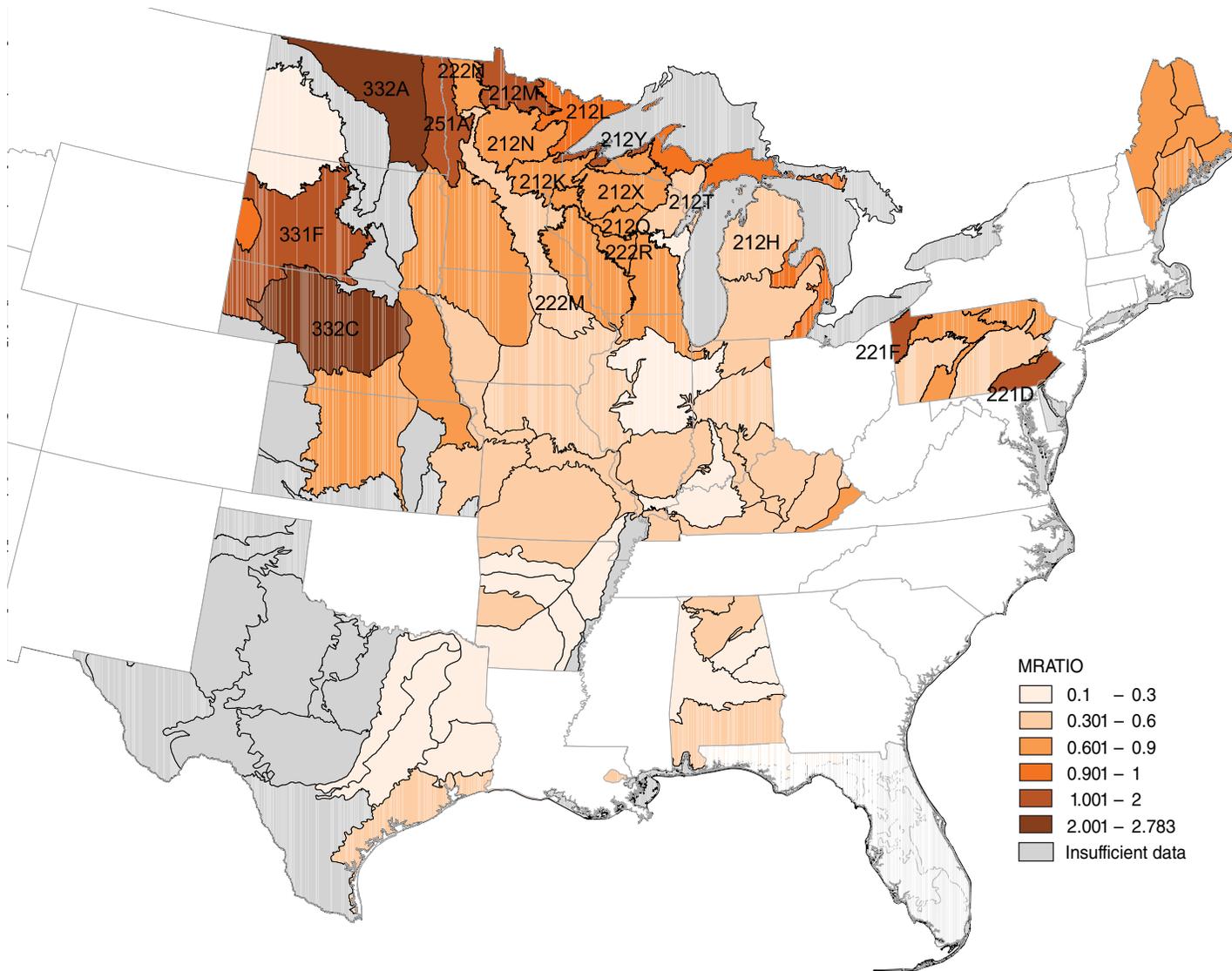


Figure 7.2—Tree mortality expressed as the ratio of annual mortality of woody biomass to gross annual growth in woody biomass (MRATIO) by ecoregion section (Cleland and others 2005). (Data source: Forest Service, Forest Inventory and Analysis Program)

Great Plains); and in Pennsylvania (ecoregions 221F—Western Glaciated Allegheny Plateau and 221D—Northern Appalachian Piedmont).

The DDL ratio on each plot is shown in figure 7.3 for the Eastern United States, the Lake States, and the Northeast. DDL ratio is a plot-level indicator and is so represented in the figure. However, the high density of FIA P2 plots causes an overlap of plot values markers when represented on a national scale map, so closeup views of the Lake States and the Northeast are also provided. In four of the ecoregions having high mortality (251A—Red River Valley, 331F—Western Great Plains, 332A—Northeastern Glaciated Plains, and 332C—Nebraska Sand Hills), the predominant vegetation is grassland, and there were very few forested plots measured. DDL values vary widely within each of these ecoregion sections. There are several plots with high DDLs, and they represent most of the biomass that died in these sections. However, on many of those plots the overall level of mortality is fairly low, as would be the case when remnant larger trees die, leaving young, vigorous stands behind. Tree growth is generally slow in these ecoregions because of naturally dry conditions. Where the number of sample plots is small and tree growth is slow, care must be taken in interpreting any mortality results over short time intervals.

In areas where the MRATIO was at least moderately high, i.e., Maine, northern and central Wisconsin, and Minnesota, many plots had high total mortality and DDL ratios of around 1 or higher. This suggests that the mortality observed in these areas was not all competition-induced but may instead be related to some forest health issue or stand senescence.

In ecoregion section 332C—Nebraska Sand Hills, where the MRATIO was highest, by far the largest amount of biomass that died was eastern cottonwood (*Populus deltoids*); more than twice as much cottonwood biomass died than had survived at the end of the analysis period. In contrast, the largest number of trees that died in the ecoregion were American elm (*Ulmus americana*), but the biomass associated with dead elms was only about one-seventh the biomass of the cottonwood that died.

In ecoregion section 332A—Northeastern Glaciated Plains in North Dakota, bur oak (*Quercus macrocarpa*), green ash (*Fraxinus pennsylvanica*), and quaking aspen (*P. tremuloides*) experienced the highest mortality in terms of both biomass and number of trees. For these species, about 5 percent of the trees, or 15 percent of the biomass, died over the analysis period. Aspens in North Dakota are known to be in poor health, in part because many stands

are overmature due to lack of fire disturbance or harvesting (North Dakota Forest Service; U.S. Department of Agriculture Forest Service 2007).

In ecoregions 212Y—Southwest Lake Superior Clay Plain, 212M—Northern Minnesota and Ontario, and 251A—Red River Valley (Minnesota and North Dakota), the tree species experiencing the most mortality was quaking aspen. Aspen was also the species exhibiting highest mortality (in terms of biomass) in other nearby ecoregion sections in Minnesota, Wisconsin, and northern Michigan: 212H—Northern Lower Peninsula (of Michigan), 212K—Western Superior Uplands, 212L—Northern Superior Uplands, 212N—Northern Minnesota Drift and Lake Plains, 212Q—North Central Wisconsin Uplands, 212T—Northern Green Bay Lobe, 212X—Northern Highlands, 212Y—Southwest Lake Superior Clay Plain, 222N—Lake Agassiz-Aspen Parklands, 222M—Minnesota and Northeast Iowa Morainal-Oak Savannah, and 222R—Wisconsin Central Sands.

A number of factors may be affecting the health of aspens stands in the region, including insect outbreaks, drought, and the advanced age of many of these stands. [For a more detailed discussion see Ambrose (2012).]

In future years, as more FIA P2 data are collected, these mortality analyses will be expanded to larger areas of the United States. The MRATIO and DDL, indicators that standardize mortality measurements across forest types and climate conditions, should prove to be of greater value as area of mortality analysis expands to a greater variety of ecological regions and forest types. At this point in time, mortality analysis using FIA data is limited to determining “baseline” mortality rates for each ecoregion and comparing regions of the United States with each other. Once a complete baseline is established and as additional cycles of FIA data are collected, it will be possible to start analyzing changes and long-term trends in forest mortality.

(A)

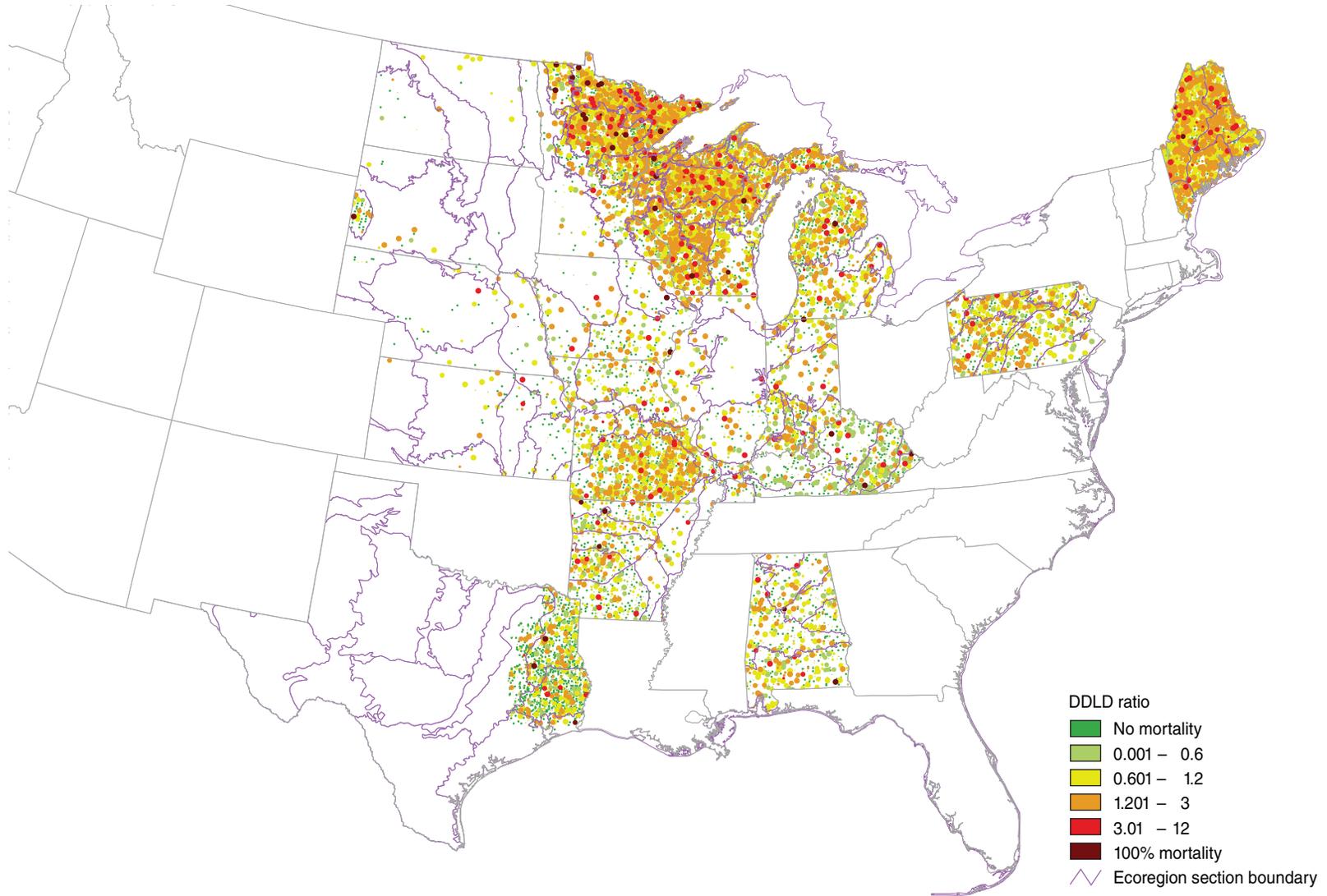


Figure 7.3 —The ratio of mean dead tree diameter to mean surviving tree diameter (DDLD) on each plot at the time of its last measurement: (A) Eastern United States, (B) Lake States, and (C) Northeast. Dot sizes are scaled relative to the biomass that died on each plot. Plot locations are approximate. (Data source: Forest Service, Forest Inventory and Analysis Program) (continued on next page)

(B)



DDL D ratio

■ No mortality

■ 0.001 – 0.6

■ 0.601 – 1.2

■ 1.201 – 3

■ 3.01 – 12

■ 100% mortality

∧ Ecoregion section boundary

Figure 7.3 (continued) —The ratio of mean dead tree diameter to mean surviving tree diameter (DDL D) on each plot at the time of its last measurement: (B) Lake States. Dot sizes are scaled relative to the biomass that died on each plot. Plot locations are approximate. (Data source: Forest Service, Forest Inventory and Analysis Program) (continued on next page)

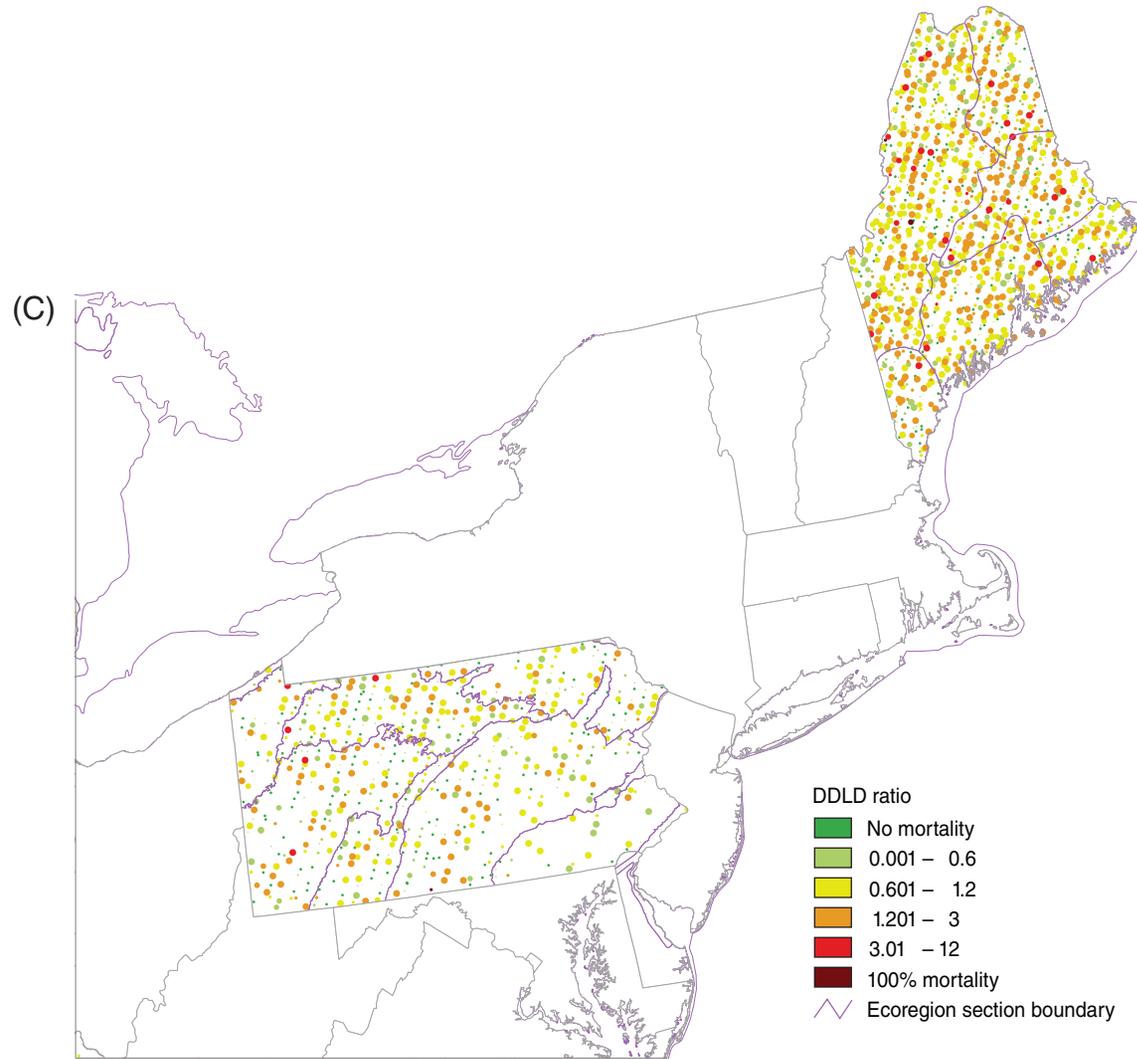


Figure 7.3 (continued) —The ratio of mean dead tree diameter to mean surviving tree diameter (DDL D) on each plot at the time of its last measurement: (C) Northeast. Dot sizes are scaled relative to the biomass that died on each plot. Plot locations are approximate. (Data source: Forest Service, Forest Inventory and Analysis Program)

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Introduction

Phytophthora kernoviae is a fungus-like pathogen of tree and shrub species recently described by researchers from the United Kingdom. It was first discovered in late 2003 in Cornwall (Southwestern England) during delimiting surveys of woodlands and gardens for *P. ramorum*, the pathogen that causes sudden oak death (Brasier and others 2005). *P. kernoviae* has not been found in the United States, but its similarity to *P. ramorum*, which has caused significant tree damage and mortality in California and Oregon, in terms of both epidemiology and affected hosts has raised concerns about its potential to become established in the United States were it to be introduced.

As with *P. ramorum*, the geographic origin of *P. kernoviae* is unknown. It has been speculated that it originated in temperate forests of Asia or South America (Brasier and others 2005). However, plant pathologists from New Zealand discovered through genetic testing that a previously unknown *Phytophthora* species found on custard apple (*Annona cherimola*, also called cherimoya) in 2002 was actually *P. kernoviae*; its genetic similarity to other *Phytophthora* species reported from Australia and New Zealand suggests that the pathogen may have originated in the region (Ramsfield and others 2007). Moreover, subsequent field studies revealed the pathogen to be present in soils of several

forested sites throughout New Zealand, while the examination of historical data showed the pathogen was actually present in the country at least as early as the 1950s (Ramsfield and others 2007). Its longevity in New Zealand without any noticeable outbreaks implies that it is not an aggressive pathogen there (Benson and others 2008). Yet, in the United Kingdom it has caused lethal infections in a number of tree and shrub species and has been detected in more than 40 sites, most in Cornwall, but also a few locations in South Wales and Northwest England (Beales and others 2006, Benson and others 2008, UK Forestry Commission 2010a).

Both *P. kernoviae* and *P. ramorum* cause distinct, host-dependent symptoms. When infected by either pathogen, certain tree species, e.g., *Quercus* spp., many of which are common in the forest overstory layer, develop bleeding cankers on their trunks. These cankers are situated in the tree's phloem, but the pathogen may also penetrate the cambium or xylem (Brown and Brasier 2007, Brown and others 2006). While trees that develop bleeding cankers may die, they represent an epidemiological endpoint, as the cankers do not yield spores. Nonetheless, both *P. kernoviae* and *P. ramorum* also cause leaf blight and/or stem dieback in certain other hosts, particularly ericaceous shrub species, e.g., *Rhododendron* spp. Sporangia form on necrotic portions of leaves, shoots, and fruits of these "foliar hosts" during wet time periods with

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Chapter 8. National-Scale Risk Mapping for *Phytophthora kernoviae*, a Potential New Forest Health Threat

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moderate temperatures (Benson and others 2008); the resulting spores may be dispersed aerially—usually by wind or wind-driven rain—allowing *P. kernoviae* and *P. ramorum* to disperse more rapidly than most other *Phytophthora* species, which generally spread through soil (Ristaino and Gumpertz 2000). Notably, with respect to both pathogens, few host species develop both trunk lesions and foliar symptoms (Denman and others 2006). Both pathogens also persist for several months in infected material of the forest litter layer (Webber and Jones 2007). Finally, there is high potential for long-distance dispersal of both *P. kernoviae* and *P. ramorum* via raw logs, wood products, or nursery stock, with serious implications for preventing the spread of the pathogens to previously uninfected areas through domestic and foreign trade (Benson and others 2008, Ivors and others 2006).

There are several key differences between *P. kernoviae* and *P. ramorum* that are pertinent when assessing the threat that the former species represents to U.S. forest health. First, much less is currently known about potential hosts for *P. kernoviae*, although there appear to be some important dissimilarities; for instance, *P. kernoviae* apparently infects yellow-poplar (*Liriodendron tulipifera*) while *P. ramorum* does not. Second, *P. kernoviae* may be more pathogenic and able

to spread more quickly than *P. ramorum*, as both lesion development and colonization of host tissue appear to be more rapid (Benson and others 2008, Brasier and others 2005, DEFRA-UK 2005a). Third, the phenomenon of apparently asymptomatic leaves producing spores appears to be much more common with *P. kernoviae* than *P. ramorum* (Denman and others 2008). This lack of visible symptoms represents a major obstacle to detecting and limiting pathogen spread. In addition, *P. kernoviae*, unlike *P. ramorum*, is homothallic, meaning the pathogen may produce oospores that enable better overwintering or long-term persistence after host plants die. Oospore production, however, has yet to be detected in field surveys (Benson and others 2008, Brasier and others 2005).

The primary objective of this chapter is to provide information to forest health managers regarding the potential threat of *P. kernoviae* to U.S. forests. In service of this objective, we develop a national-scale risk map for the pathogen, and then identify ecoregion sections facing the greatest risk of introduction and/or establishment. We also discuss some of our simplifying assumptions as well as current knowledge gaps regarding *P. kernoviae*.

Methods

We constructed the risk map through overlay of spatial data layers representing (1) climatic suitability; (2) host density, including separate layers for overstory and sporulating hosts; and (3) areas with a high likelihood of accidental introduction (i.e., areas with abundant pathways of introduction), into forested environments.

Climatic Suitability—We developed our climatic suitability layer for *P. kernoviae* using the NCSU-APHIS Plant Forecasting System (NAPPFASST). NAPPFASST is an Internet software application that employs a suite of climatic and additional environmental variables to model the potential geographic distributions of pathogens and other pest species (Magarey and others 2007). We used 10-year (1997–2006) daily climatic data and a previously developed infection model (Magarey and others 2005) to estimate the number of days in each year that are suitable for infection. The generic infection model utilizes a temperature response function scaled to a leaf wetness duration requirement; our number-of-day estimates were based on the combination of mean daily temperature and total leaf wetness hours.

We assumed that *P. kernoviae* would be constrained by temperature and minimum moisture requirements for growth and zoosporic infection. We adopted minimum, optimum, and maximum temperature thresholds for the pathogen of 3, 18, and 26 °C, respectively, based on previous laboratory research (Brasier and others 2005). Little is currently known about the moisture requirements of *P. kernoviae* for zoosporic infection (Benson and others 2008), but its overlap with the distribution of *P. ramorum* in the United Kingdom suggests the two species have similar needs. Therefore, we estimated a moisture requirement of at least 12 hours for *P. kernoviae* based on data describing the infection of tanoak (*Umbellularia californica*) leaves by *P. ramorum* (Hüberli and others 2003, Rizzo and Garbelotto 2003).

NAPPFASST generates gridded prediction maps with an approximately 10-km² spatial resolution, resampled to 1-km² resolution using a nearest-neighbor approach for this analysis. For each grid cell, each day was assigned a value between zero (unsuitable for infection) and 1 (suitable for infection), and then these values were accumulated for a 1-year period. We assumed a frequency of

≥60 accumulated suitable days in a year to be adequate for infection and long-term persistence of *P. kernoviae*. This 60-day threshold offers a moderate probability of consecutive wet days with moderate temperatures which greatly increases the likelihood of sporulation as well as the opportunity for inoculum buildup in forested locations (Davidson and others 2002, Rizzo and Garbelotto 2003). Hence, the suitability layer for the pathogen depicts, on a cell-by-cell basis, the proportion of years (out of 10) with ≥ 60 accumulated suitable days during the year (fig. 8.1).

Overstory Host Density—The category of “overstory hosts” for *P. kernoviae* includes all species that develop bleeding cankers on their trunks and potentially die from infection. In a few cases, e.g., yellow-poplar, host species may develop both cankers and foliar symptoms (Brasier and others 2005, DEFRA-UK 2005b, Rizzo and Garbelotto 2003); such species are included in both the overstory and sporulating host layers. We should reiterate that the host species list for *P. kernoviae* is speculative compared to that for *P. ramorum* since the former has only been observed at a limited number

of field locations in the United Kingdom, and relatively few laboratory susceptibility trials have been completed to date.

So, for *P. kernoviae*, we chose a set of susceptible overstory species in which infection has been directly observed in the field or that are close relatives of these “natural” hosts (UK Forestry Commission 2010b). Yellow-poplar, which has been planted ornamentally in the United Kingdom, has exhibited both foliar symptoms and trunk cankers due to *P. kernoviae* infection, with at least one tree killed by a bleeding canker (DEFRA-UK 2005a). Lethal trunk cankers have also been observed on European beech (*Fagus sylvatica*) (Brasier and others 2005, DEFRA-UK 2005a); we subsequently included American beech (*Fagus grandifolia*), the only native North American beech species, in our host layer. Similarly, bleeding cankers have been observed on English oak (*Quercus robur*) (Brasier and others 2005, DEFRA-UK 2005b), a member of the white oak group (*Quercus* sect. *Quercus*), which includes many native North American species (Manos and others 1999). Therefore, we included all North American white oaks listed in the Forest

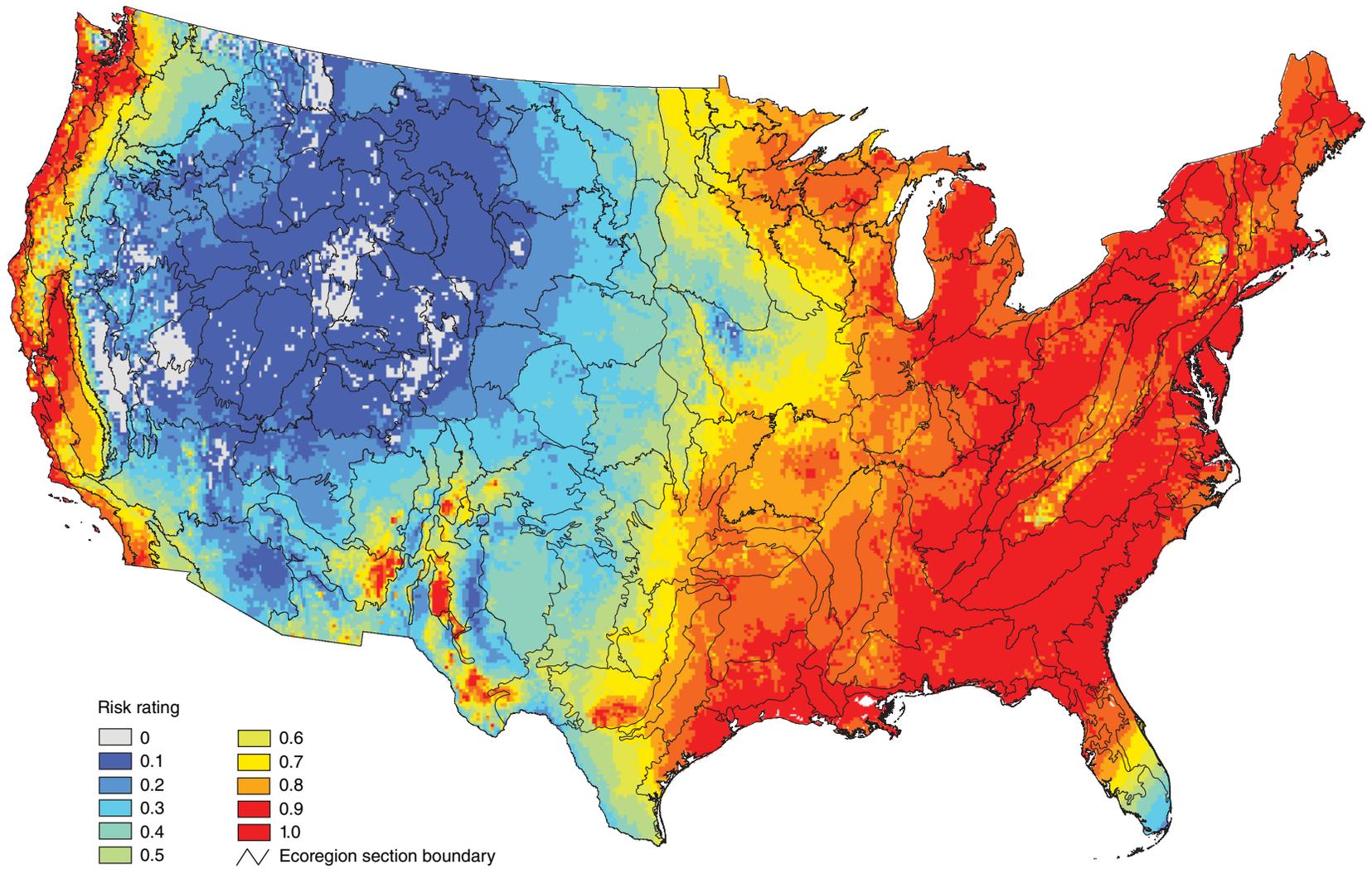


Figure 8.1—Climatic suitability layer for *Phytophthora kernoviae*. Risk rating is based on the number of years out of 10 where grid cell had at least 60 cumulative days suitable for infection. Ecoregion section boundaries (Cleland and others 2007) are included for reference. [Data source: NCSU-APHIS Plant Pest Forecasting System (NAPPFAST)]

Service, Forest Inventory and Analysis (FIA) database (U.S. Department of Agriculture Forest Service 2007) in our overstory host layer (table 8.1). Notably, neither American beech nor any North American white oak species have been tested for susceptibility to *P. kernoviae*.

For the conterminous United States, we constructed gridded surfaces of yellow-poplar, American beech, and white oak basal area (in square feet per acre) through ordinary kriging of FIA phase 2 (P2) plot data. We first identified all ecoregion sections (Cleland and others 2007) containing FIA plots where the species of interest were present. We then assembled all FIA plots that fell within these sections into geographically referenced samples of basal area values. We fitted spherical semivariogram models to each sample using weighted least squares (Cressie 1993). The semivariograms determined the kriging weights during the interpolation process. 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. To ensure that only ecologically similar plots were used in predicting values for unknown locations, we performed separate interpolations for each ecoregion section and then mosaicked

the results into a grid with a 1-km² spatial resolution. We used a forest cover map, developed from Moderate Resolution Imaging Spectroradiometer satellite data by the Forest Service, Remote Sensing Applications Center, to mask out nonforested areas from each of the three host grids. We created a single grid using map algebra, adding the yellow-poplar, American beech, and white oak basal area grids together and then dividing by the sum of the maximum basal area values observed in the three species grids (111.57 feet² per acre). This yielded an overstory host layer for *P. kernoviae* with values scaled between zero and 1 (fig. 8.2).

Sporulating Hosts—For aerially dispersed *Phytophthora* species such as *P. kernoviae*, sporulating hosts vary widely as inoculum sources. Most fundamentally, these hosts differ in raw sporulation potential (Brasier and others 2005, DEFRA-UK 2006, Tooley and Kyde 2007, Tooley and others 2004), but their height, number of leaves, leaf size, spatial distribution in forest stands, and other characteristics further shape their dispersal capabilities. For instance, tall hosts may disperse spores further than small shrubs, including to other sporulating hosts below them in the forest stand. Moreover, evergreen species represent potentially year-round inoculum sources. With these factors in

Table 8.1—White oak (*Quercus* sect. *Quercus*) species included in the overstory host layer for *Phytophthora kernoviae*^a

Species	Common name	Regional distribution
<i>Quercus alba</i>	White oak	Eastern United States
<i>Q. arizonica</i>	Arizona white oak	Southwestern United States
<i>Q. bicolor</i>	Swamp white oak	Eastern United States (especially Northeast)
<i>Q. douglasii</i>	Blue oak	California
<i>Q. engelmannii</i>	Engelmann oak	California
<i>Q. gambelii</i>	Gambel oak	Western United States
<i>Q. garryana</i>	Oregon white oak	West coast United States
<i>Q. lobata</i>	California white oak	California
<i>Q. lyrata</i>	Overcup oak	Eastern United States (especially Southeast)
<i>Q. macrocarpa</i>	Bur oak	Central and Eastern United States
<i>Q. margarettae</i>	Dwarf post oak	Southeastern United States
<i>Q. michauxii</i>	Swamp chestnut oak	Southeastern United States
<i>Q. minima</i>	Dwarf live oak	Southeastern United States
<i>Q. montana</i> (<i>Q. prinus</i>)	Chestnut oak	Eastern United States
<i>Q. muehlenbergii</i>	Chinkapin oak	Central and Eastern United States
<i>Q. oblongifolia</i>	Mexican blue oak	Southwestern United States
<i>Q. oglethorpensis</i>	Oglethorpe oak	Southeastern United States
<i>Q. prinoides</i>	Dwarf chinkapin oak	Eastern United States
<i>Q. rugosa</i>	Netleaf oak	Southwestern United States
<i>Q. similis</i>	Delta post oak	Southeastern United States
<i>Q. sinuata</i> var. <i>sinuata</i>	Durand oak	Southeastern United States
<i>Q. stellata</i>	Post oak	Eastern United States
<i>Q. virginiana</i>	Live oak	Southeastern United States

^a Data for all species listed were compiled from the Forest Inventory Analysis FIADB 3.0 database. Species distributions are based on Kartesz (2008) and Stein and others (2003).

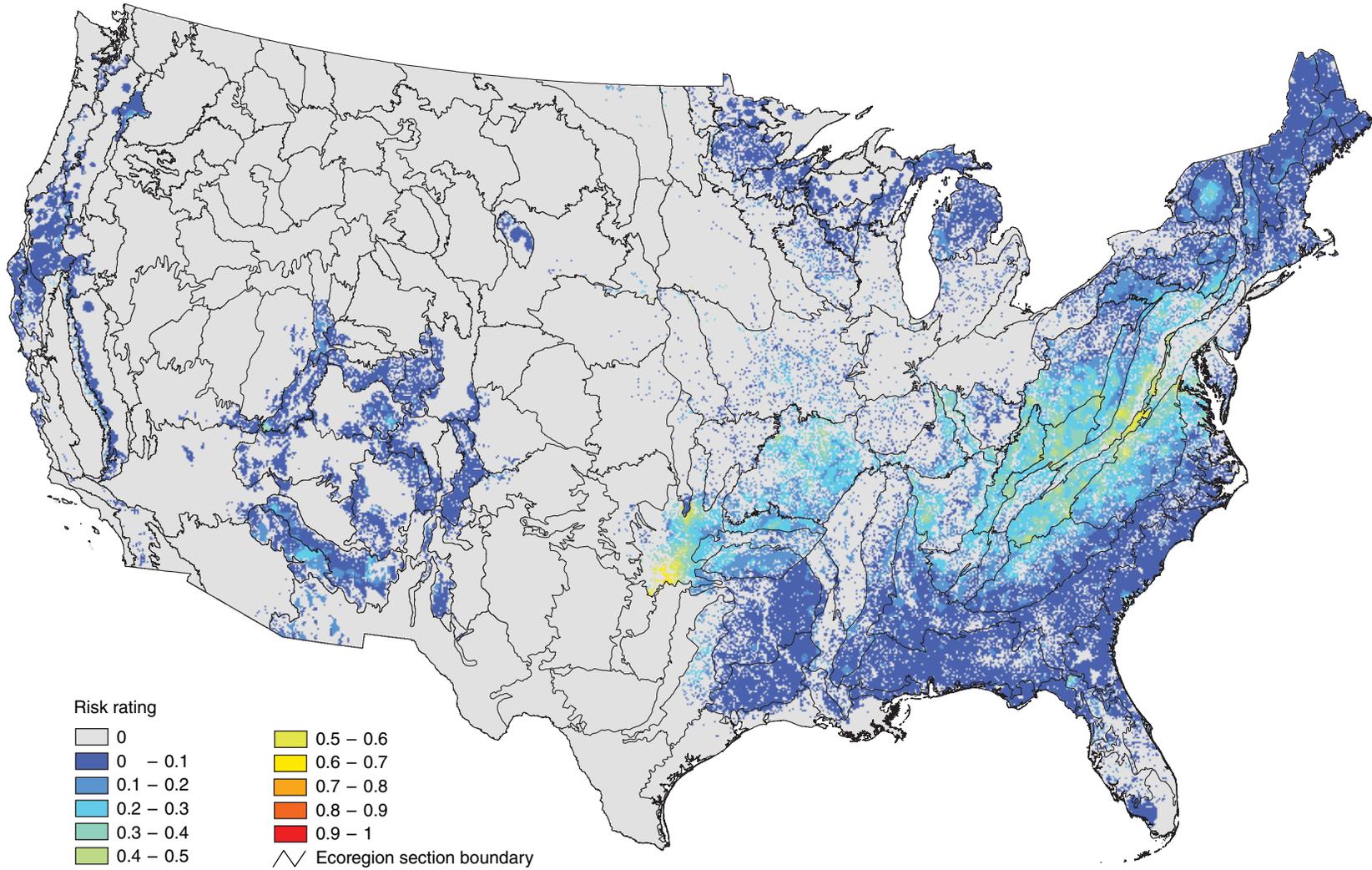


Figure 8.2—Overstory host density layer for *Phytophthora kernoviae*. For each grid cell, the risk rating is the proportion of the maximum overstory host basal area value observed in the layer (see text for details). Ecoregion section boundaries (Cleland and others 2007) are included for reference. (Data source: Forest Service, Forest Inventory and Analysis Program)

mind, we developed a list of sporulating host species for *P. kernoviae* (table 8.2) based on information from the United Kingdom (DEFRA-UK 2005b, 2006; Denman and others 2006; Milne 2004; UK Forestry Commission 2010b). A few of these species, e.g., yellow-poplar and California bay laurel, have been confirmed as sporulating hosts, but because the host list for *P. kernoviae* is currently underdeveloped, we also selected some North American species related to these known hosts. For example, *R. maximum* is closely phylogenetically related to *R. catawbiense* and *R. ponticum* (Kartesz 2008), both confirmed hosts in the United Kingdom, with the latter particularly associated with regional spread of the pathogen.

We assigned the sporulating hosts to one of four groups representing increasing levels of epidemiological importance, which we determined based on the aforementioned factors of height, leaf size, stand-level plant density, sporulation density, and whether the species was evergreen or deciduous (table 8.2). Group IV, the most epidemiologically important group, is composed of two evergreen species (*R. maximum*,

U. californica) that grow reasonably dense in forest understories and have high sporulation potential. Group III is largely composed of deciduous midstory sporulators, with some exceptions; for example, we assigned *Magnolia grandiflora* to group III because, although it is evergreen and can grow well into the understory, it tends to be sparsely distributed compared to the species in group IV.

For each of the four groups, we developed a gridded surface of values scaled between zero and 1. We developed the grids for groups I and II by rasterizing county-level presence-absence data (Frankel 2008). For each group, we counted the number of distinct genera represented in each grid cell (out of a maximum of three for group I and a maximum of four for group II) and then divided by the maximum value. We developed the surface for group III from density grids (in trees per acre) for each species interpolated from FIA P2 plot data in a manner similar to that for the species in the overstory host density layer. Using map algebra, we added the individual species density grids together and then divided the sum by the maximum

Table 8.2—Species groups used in the sporulating host layer for *Phytophthora kernoviae*

Group	Group definition and species	Risk value	Reference
I	Deciduous species with small leaves, sparse sporulation, and/or sparse distribution <i>Fagus sylvatica</i> ^a <i>Magnolia species</i> (<i>M. kobus</i> ^a , <i>M. stellata</i> ^a , <i>M. ×soulangiana</i> ^a) <i>Vaccinium species</i> (<i>V. alaskaense</i> , <i>V. angustifolium</i> , <i>V. arboreum</i> , <i>V. boreale</i> , <i>V. caesariense</i> , <i>V. caespitosum</i> , <i>V. corymbosum</i> , <i>V. delicosum</i> , <i>V. erythrocarpum</i> , <i>V. formosum</i> , <i>V. fuscatum</i> , <i>V. hirsutum</i> , <i>V. membranaceum</i> , <i>V. myrtilloides</i> , <i>V. myrtilus</i> , <i>V. ovalifolium</i> , <i>V. pallidum</i> , <i>V. parvifolium</i> , <i>V. scoparium</i> , <i>V. simulatum</i> , <i>V. stamineum</i> , <i>V. tenellum</i> , <i>V. uliginosum</i> , <i>V. virgatum</i> , <i>V. ×atlanticum</i> , <i>V. ×margarettae</i> , <i>V. ×marianum</i>)	0.1	BONAP
II	Evergreen species <i>Hedera helix</i> <i>Ilex aquifolium</i> ^a <i>Quercus ilex</i> ^a <i>Rhododendron species</i> (<i>R. carolinianum</i> , <i>R. catawbiense</i> , <i>R. chapmanii</i> , <i>R. lapponicum</i> , <i>R. macrophyllum</i> , <i>R. maximum</i> ^b , <i>R. minus</i> , <i>R. ×welleslyanum</i>) <i>Vaccinium species</i> (<i>V. crassifolium</i> , <i>V. darrowii</i> , <i>V. macrocarpon</i> , <i>V. myrsinites</i> , <i>V. ovatum</i> , <i>V. oxycoccos</i> , <i>V. vitis-idaea</i>)	0.3	BONAP
III	Midstory, deciduous, or sparsely distributed evergreen <i>Liriodendron tulipifera</i> <i>Magnolia species</i> (<i>M. acuminata</i> , <i>M. fraseri</i> , <i>M. grandiflora</i> , <i>M. virginiana</i> , <i>M. macrophylla</i> , <i>M. pyramidata</i> , <i>M. tripetala</i>)	0.6	FIA
IV	Midstory, dominant evergreen with generally dense sporulation <i>Rhododendron maximum</i> ^b <i>Umbellularia californica</i>	1.0	BONAP/FIA

BONAP = Biota of North America Program; FIA = Forest Inventory and Analysis.

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

^b *Rhododendron maximum* has a wide geographic distribution, but is a midstory dominant in only part of its range. Cells in the species' distribution map were assigned to group IV in 24 ecoregion subsections: 211Fa, 211Fb, 211Fc, 211Fd, 211Ff, 211Ga, 211Gb, 221Ae, 221Am, 221Ba, 221Bd, 221Dc, 221Ea, M221Aa, M221Ac, M221Ba, M221Bb, M221Bc, M221Bd, M221Bf, M221Da, M221Db, M221Dc, and M221Dd.

observed value (257.68). With respect to group IV, only county-level distribution data were available for *R. maximum*, although we did have an interpolated density grid for *U. californica*. To ensure equal weighting of these species, we also converted *U. californica* to presence-absence, such that cells in the grid for group IV had values of 1 (presence of either *R. maximum* or *U. californica*) or zero (absence of both species). We created a layer of combined sporulating host potential for *P. kernoviae* by multiplying each of the group surfaces by its corresponding risk rating value (table 8.2) and then added these four weighted surfaces together using map algebra. We then divided this sum surface by the maximum observed value (1.56) to scale the scores between zero and 1 for our final sporulating host layer, with 1-km² spatial resolution (fig. 8.3).

Introduction Pathways—We constructed a layer to represent areas with abundant pathways of potential introduction by analyzing spatial data depicting wildland-urban interface in the conterminous United States. Since 2004, there have been numerous detections of *P. ramorum* in nursery outlets in more than 20 States across the country; the pathogen was accidentally introduced when infected nursery stock was transported from large wholesale nurseries on the west coast (Radeloff and others 2005, Suslow

2008). However, ornamental plants typically remain in nurseries for only a short time before they are sold. For this reason, we believe that an appropriate classification of the wildland-urban interface, i.e., the interface between naturally vegetated landscapes and landscapes where potentially sporulating nursery stock may be planted, is a better representation of long-term epidemiological risk, and equally applicable for *P. kernoviae* as for *P. ramorum*.

We used wildland-urban interface data, developed by the University of Wisconsin-Madison and the Forest Service Northern Research Station, to represent areas with elevated risk of *P. kernoviae* establishment and spread were the pathogen to be introduced (Radeloff and others 2005). For our analysis, we started with polygon coverages of the wildland-urban interface for each State. The coverages are composed of U.S. Census blocks, with each block assigned a housing density value according to data from the 2000 census. In addition, 1992 National Land Cover Data were used to determine percentages of various land cover classes in each census block (Moralejo and others 2006). Based on its calculated housing density and land cover percentage values, each census block polygon was assigned to 1 of 14 wildland-urban interface categories (table 8.3).

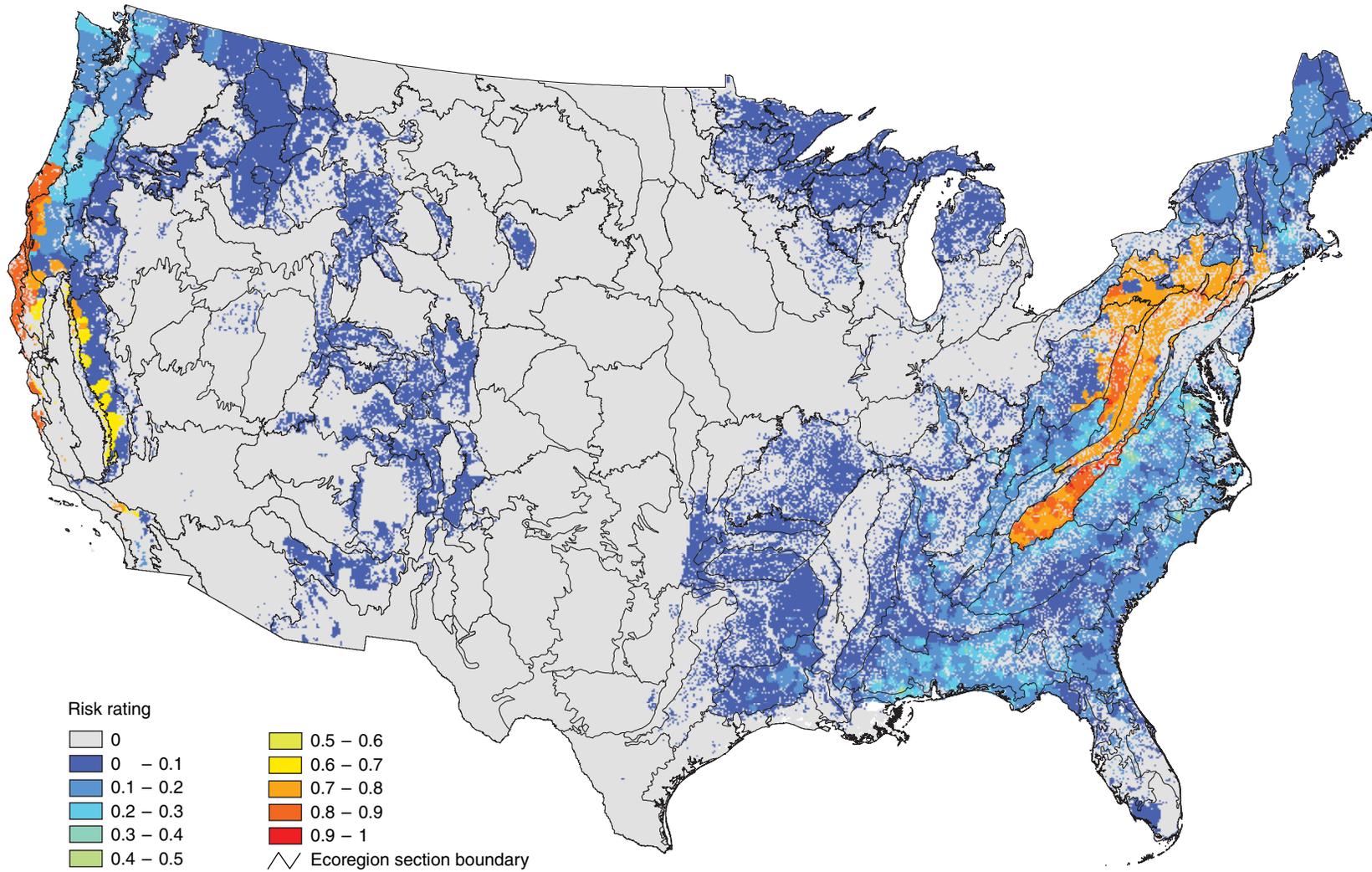


Figure 8.3—Sporulating host density layer for *Phytophthora kernoviae*. For each grid cell, the risk rating is derived from a combination of gridded surfaces for four different host groups, weighted according to their hypothesized epidemiological importance (see text for details). Ecoregion section boundaries (Cleland and others 2007) are included for reference. (Data sources: Forest Service, Forest Inventory and Analysis Program; Biota of North America Program)

Table 8.3—Original wildland-urban interface categories, with brief descriptions, and their new ranking values for the introduction pathways layer

Category	Description	New ranking
Low-density interface	Housing density $> = 6.177635$ and < 49.42108 units/km ² , vegetation ≤ 50 percent, within 2.414 km of area with ≥ 75 percent vegetation	2
Medium-density interface	Housing density $> = 49.42108$ and < 741.3162 units/km ² , vegetation ≤ 50 percent, within 2.414 km of area with ≥ 75 percent vegetation	2
High-density interface	Housing density $> = 741.3162$ units/km ² , vegetation ≤ 50 percent, within 2.414 km of area with ≥ 75 percent vegetation	1
Low-density intermix	Housing density $> = 6.177635$ and < 49.42108 units/km ² , vegetation > 50 percent	3
Medium-density intermix	Housing density $> = 49.42108$ and < 741.3162 units/km ² , vegetation > 50 percent	3
High-density intermix	Housing density $> = 741.3162$ units/km ² , vegetation > 50 percent	1
Uninhabited, low vegetation	Housing density = 0, vegetation ≤ 50 percent	-1 ^a
Very low density, low vegetation	Housing density > 0 and < 6.177635 units/km ² , vegetation ≤ 50 percent	-1 ^a
Low density, low vegetation	Housing density $> = 6.177635$ and < 49.42108 units/km ² , vegetation ≤ 50 percent	-1 ^a
Medium density, low vegetation	Housing density ≥ 49.42108 and < 741.3162 units/km ² , vegetation ≤ 50 percent	-1 ^a
High density, low vegetation	Housing density $> = 741.3162$ units/km ² , vegetation ≤ 50 percent	-1 ^a
Uninhabited, high vegetation	Housing density = 0, vegetation > 50 percent	0
Very low density, high vegetation	Housing density > 0 and < 6.177635 units/km ² , vegetation > 50 percent	0
Water	Water	-2 ^a

^a 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.

We reclassified the original wildland-urban interface categories to highlight those we believe present the greatest potential for spread of *P. kernoviae* into forested environments (table 8.3). In our new classification, we assigned the highest risk ranking of 3 to the low- and medium-density intermix categories because census blocks in these categories generally contain large inclusions of natural vegetation throughout. We assigned the 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 <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 homelots distributed throughout, likely resulting in smaller (although not necessarily fewer) inclusions of natural vegetation. Negative values for nonvegetated areas and water served as placeholders that were set to zero after we performed an additional “edge zone” analysis, described below.

We joined the reclassified State wildland-urban interface coverages into a single nationwide coverage, converted it to grid format at a 0.625 km² spatial resolution, and then resampled to a 1-km² grid using block majority

filtering. As a last step, we defined an edge zone composed of grid cells that were classified as either natural vegetation (risk ranking = 0) or high-risk intermix (risk ranking = 3) and that were adjacent to at least one grid cell in the other of these two categories based on an eight-neighbor rule, i.e., in addition to the four grid cells sharing an edge with the cell in question, the four cells that are immediately diagonal are also considered adjacent. We assigned grid cells in this edge zone a new risk ranking of 4. We added this edge zone category to our risk scale because, although a high-risk intermix label indicates that a grid cell contains sizeable patches of natural vegetation, the adjacency of cells where natural vegetation is predominant increases the chance that the pathogen will spread into large, vegetated tracts with substantially greater host presence where it would likely be more problematic to eradicate or contain an infection.

We multiplied the ranked grid by 0.05 to set values between 0 and 0.2 for the final introduction pathways layer (fig. 8.4). As documented in the next paragraph, this new “pathways” rating was intended to provide a proportional increase in total risk value when added to a “hazard” rating derived from host presence and climatic suitability.

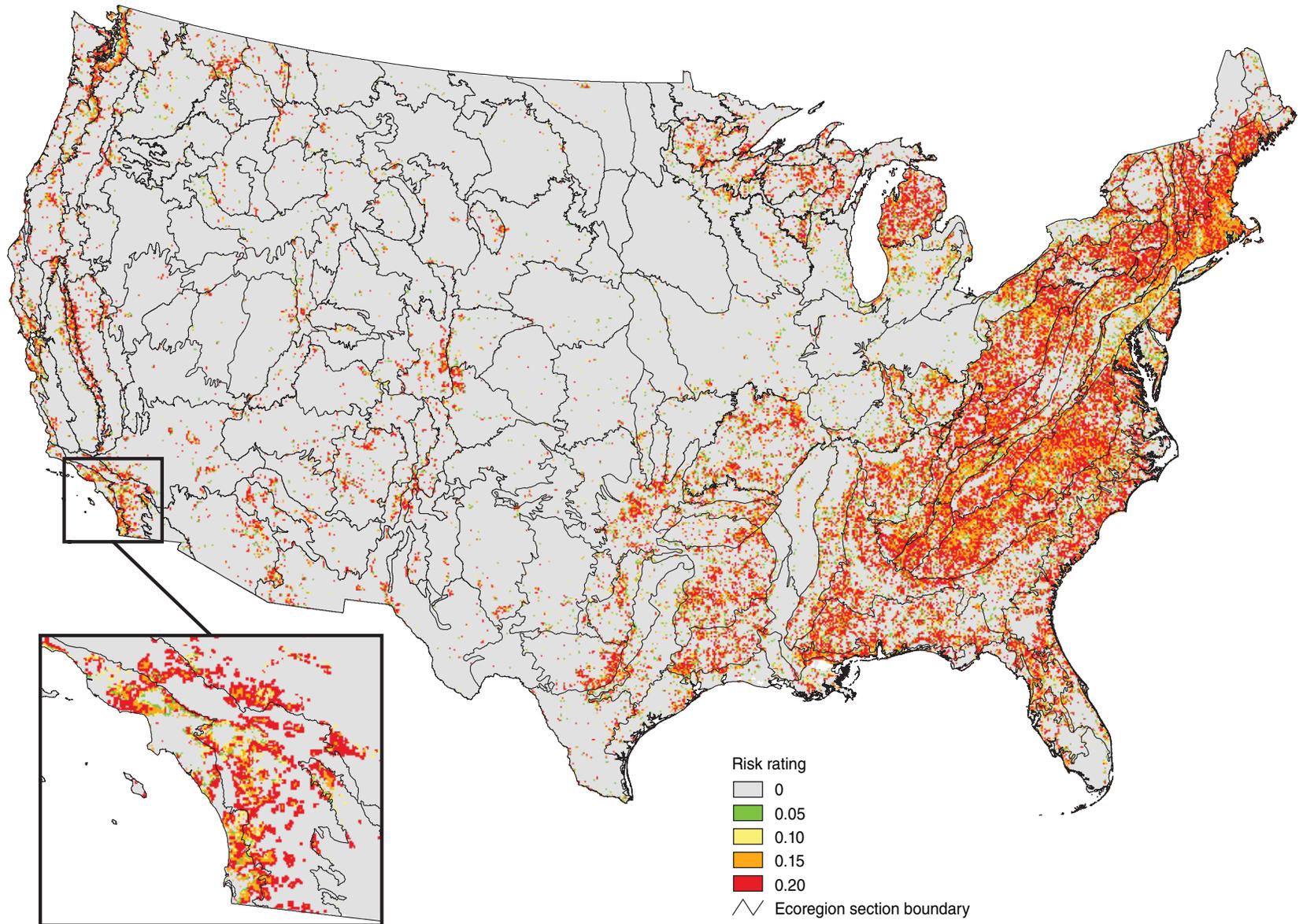


Figure 8.4—Introduction pathways layer for *Phytophthora kernoviae*. Risk rating is based on the amount and pattern of wildland-urban interface within each grid cell, and may also be influenced by the classification of neighboring cells (see text for details). Inset shows the spatial distribution of introduction pathways risk across the Los Angeles and San Diego metropolitan areas. Ecoregion section boundaries (Cleland and others 2007) are included for reference. (Data sources: University of Wisconsin-Madison; Forest Service, Northern Research Station)

Composite Risk Map—We created a composite risk map for *P. kernoviae* in two steps. First, we created a “hazard” layer for the pathogen by multiplying the climatic suitability, overstory host, and sporulating host layers using map algebra, then dividing the resulting grid by the maximum observed value (0.53) to scale values between 0 and 1. The hazard layer quantifies the level of susceptibility and the potential impact if *P. kernoviae* were to be successfully established at any given location, i.e., grid cell. The pathways layer, by contrast, depicts the relative likelihood that the pathogen will be introduced at a location. Risk may be subsequently defined as some combination of both factors. Therefore, we applied a simple set of decision rules to construct our final composite risk layer:

$$R = 0, \text{ when } H = 0$$

$$R = H, \text{ when } P = 0$$

$$R = (H + P)/1.2, \text{ when } H > 0 \text{ and } P > 0$$

where

R = the total risk rating

H = the hazard rating

P = the introduction pathways rating

Under the first rule, a location (grid cell) containing no hazard, i.e., no susceptible host to be impacted, exhibits no risk. Under the second rule, a location has some degree of risk if it contains susceptible host but no apparent pathway link. The logic behind this rule is that any location has some chance of receiving the pathogen, even if a pathway is not clearly distinguished. Our equal weighting of the hazard and pathways ratings in the third rule reflects our belief that the two factors, when co-occurring, contribute similarly to overall risk. The sum of the hazard and pathways ratings is divided by the maximum sum value (1.2) in this case so that all values in the composite risk map (fig. 8.5) are scaled between 0 and 1.

Results and Discussion

The composite risk map for *P. kernoviae* (fig. 8.5) shows few areas of elevated risk (risk rating >0.2) on the Pacific coast of the United States. Most notably, sections M261B—Northern California Coast Ranges and M261F—Sierra Nevada Foothills, each have a small percentage of grid cells with risk ratings between 0.3 and 0.4. These sections likely exhibit moderate risk because of the coincidence of limited overstory hosts (white oaks) and California bay laurel, a sporulating host with fairly wide distribution throughout the region (see figures 8.2 and 8.3).

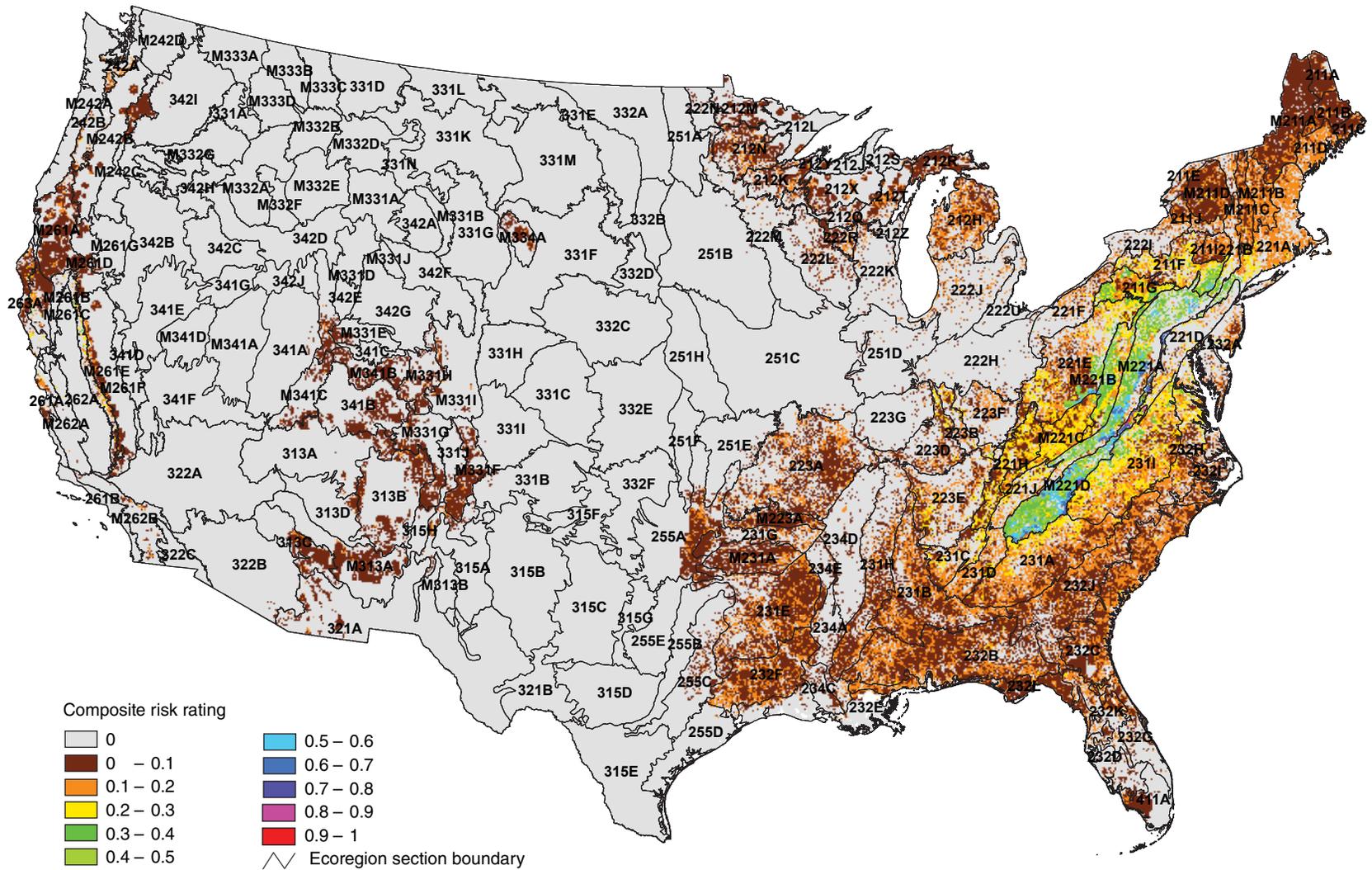


Figure 8.5—Final composite risk map for *Phytophthora kernoviae*. For each grid cell, the composite risk rating is derived from a rule-based combination of hazard and pathway ratings (see text for details). Ecoregion section boundaries and labels (Cleland and others 2007) are included for reference. [Data sources: NCSU-APHIS Plant Pest Forecasting System (NAPPPFAST); Forest Service, Forest Inventory and Analysis Program; Biota of North America Program; University of Wisconsin-Madison; Forest Service, Northern Research Station)

It is important to understand that the sporulating host layer for *P. kernoviae* (and indirectly, its overstory host layer) represents our best current hypothesis regarding the pathogen's epidemiology, which can be difficult to decipher completely (DEFRA-UK 2005a). It is possible that, as additional data are collected on the pathogen, more species endemic to the Pacific region will be added to its host list, shifting the overall balance of risk for *P. kernoviae* away from the Eastern United States and towards the West. Currently, the map depicts many very high risk (>0.5) areas distributed across ecoregion sections encompassing the Central Appalachian Mountains and adjacent plateaus: 211F—Northern Glaciated Allegheny Plateau, 221E—Southern Unglaciated Allegheny Plateau, M221A—Northern Ridge and Valley, M221B—Allegheny Mountains, and M221D—Blue Ridge Mountains. This is primarily due to the coincidence of high-overstory host density and high-sporulating host importance values throughout this geographic region. The sporulating host layer for *P. kernoviae* (fig. 8.3) emphasizes *R. maximum* as a critical and widespread sporulator. Given what we know about the role of the closely related *R. ponticum* in spreading *P. kernoviae* in the United Kingdom (Koch and Smith 2008), this emphasis seems reasonable. In truth, it is possible that we are underestimating the distribution of *R. maximum* as an important species in Eastern U.S. forests. This means that the total area we have labeled

as high risk may also be underestimated, but this would be difficult to rectify without better data describing the species' distribution. Better data would likewise be beneficial for characterizing the distributions of the pathogen's other understory hosts.

The climatic suitability map for *P. kernoviae* (fig. 8.1) resembles similar maps created previously for *P. ramorum* (Balci and others 2007, Magarey and others 2008) with the noteworthy exception that it does not include a cold-temperature mask. In these prior studies, a cold-temperature mask eliminated the risk of *P. ramorum* establishing in the extreme Northeastern United States, which is consistent with approximate geographic limits seen in field observations of other *Phytophthora* species (Davidson and others 2002). However, *P. kernoviae*, at least in theory, has oospores that should allow it to overwinter better than *P. ramorum*, essentially giving it greater cold tolerance. It should be noted again that this type of spore production has not been documented in the field, so risk values in the northern portions of the *P. kernoviae* risk map should be interpreted carefully with consideration of this uncertainty. The relatively coarse spatial resolution of the climate map should also be acknowledged, although we believe this is not problematic given the national scale of the assessment. Regardless, it is possible that certain variables that we did not include in our climatic suitability

analysis may actually prohibit the successful persistence and establishment of *P. kernoviae* in some regions, thus meaning we overestimated the risk in those areas. For example, previous research has suggested the importance of relative humidity in the distribution of aerially dispersed *Phytophthora* species (Tooley and others 2008, Venette and Cohen 2006). In our analysis, we could have explicitly eliminated portions of the United States that did not meet a specified threshold level of relative humidity. However, in prior work we discovered this would have likely removed only certain areas of the Intermountain West, all of which are low risk (<0.2) anyway. We also could have used a high-temperature mask, which would have eliminated risk across parts of the Southern United States. We did not include such a mask because recent research suggests that *P. ramorum* (and by extension, *P. kernoviae*) is relatively tolerant to high-temperature extremes (Davidson and Shaw 2003).

Our pathways layer (fig. 8.4) associates the inherent degree of establishment risk, i.e., the level of hazard, in forested landscapes, especially in the Eastern United States, with the potential avenues by which a pathogen may be introduced from developed landscapes into these forested landscapes. Hence, in the composite risk map (fig. 8.5) there are large areas of moderate risk (0.2 to 0.4) in many heavily forested ecoregion sections adjacent to

those named previously: 221A—Lower New England, 221H—Northern Cumberland Plateau, 231A—Southern Appalachian Piedmont, 231I—Central Appalachian Piedmont, and M221C—Northern Cumberland Mountains. Certainly, these sections contain some areas of high-overstory host density and sporulating host importance, but risk values in these sections also reflect a high level of intermix between forested and developed areas, as might be expected in the foothills of the Blue Ridge Mountains and other mountain chains. In general, forested areas with little intermix, i.e., connectivity, exhibited low-risk scores, but risk was elevated to a small degree whenever intermix was present. This explains why much of the Southeastern United States exhibits a risk pattern varying between the two lowest risk categories (0 to 0.1 versus 0.1 to 0.2), while forested areas in the Intermountain West and much of the southern Sierra Nevada Mountains are all solidly in the lowest risk category; the latter regions contain large tracts of wilderness with essentially no connectivity. In any case, the elevated, but still relatively low, risk values (0.1 to 0.2) in areas with limited hazard but high intermix reflects the current reality regarding *P. kernoviae*; although human-mediated pathways may be important for moving the pathogen (Coulston and others 2008, Kelly and Meentemeyer 2002), it is still uncertain how likely it would be that the pathogen could move across the forest-developed interface. Additional information

on infection likelihoods between forest and ornamentally planted host species, whether based on laboratory or field data, would be extremely helpful for minimizing uncertainty in the output risk map.

We must emphasize the transitory nature of the composite risk map. We often determined exact threshold values based on our own judgment, as informed by the current body of research literature. This map will almost certainly change if additional data become available. Acknowledging this limitation, the composite risk map depicts a spatial pattern that can be used to guide the implementation of detection surveys (e.g., Coulston and others 2008) or other Forest Health Monitoring protocols, as well as any additional countermeasures, for *P. kernoviae*. Notably, we generated a preliminary version of the *P. kernoviae* risk map for U.S. Department of Agriculture's National Plant Disease Recovery System, a program recently established by a Homeland Security Presidential Directive. A primary purpose of the compiled "*P. kernoviae* recovery plan" is to synthesize all information about the pathogen into a best-management strategy were the pathogen to be introduced to the United States. This further highlights the potential utility of risk maps in helping to identify broad-scale research and management priorities.

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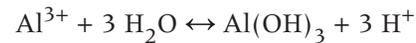
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Why Are Calcium and Aluminum Important?

The health and growth of forests depends upon soil nutrients. Calcium (Ca) is a cation—positive ion—used by plants to build cell walls (Marschner 1986). It is also involved in root and leaf development and the activation of plant enzymes (Potash and Phosphate Institute 1995). Soils that develop in areas with low rainfall tend to have greater Ca supplies than soils that form in humid regions of the country, and within any one soil profile, more Ca typically is found in lower parts of the soil profile than at the surface (Pritchett and Fisher 1987). Acidic deposition leads to soil Ca depletion (Lawrence and others 1999). Soil Ca depletion is the most important means by which acid deposition affects forest health (Fenn and others 2006).

Low concentrations of aluminum (Al) (<1 mg/l) can stimulate plant growth and may act as a fungicide, but Al is a cation generally considered to have negative effects on plants. The toxic effects of Al include the inhibition of root growth and reduced uptake of several key cations (phosphorus, magnesium, and Ca) (Marschner 1986). Al is closely linked with soil acidity. When soil pH is >5.0, Al tends to

precipitate as a solid called gibbsite, $\text{Al}(\text{OH})_3$. This reaction can be reversed to release Al at lower pH (<5.0) (McBride 1994):



At these lower pH ranges, it is not the soil pH that is toxic to plants but the increased amount of free and exchangeable Al (Marschner 1986, McBride 1994).

Exchangeable cations are bound in the soil because of their positive charge. The amount and types of cations held in the soil are indicative of a soil's fertility (Pritchett and Fisher 1987). The molar ratio of Ca:Al is particularly useful as an indicator of forest ecosystem stress since low values represent an increased likelihood of Al saturation (Cronan and Grigal 1995).

Methods

Soil samples for chemical analysis are collected as part of the soil quality indicator of the Forest Inventory and Analysis (FIA) Program of the Forest Service, U.S. Department of Agriculture. Between 2001 and 2005, samples were collected in most of the continental United States (fig. 9.1; sampling has not begun in Mississippi, New Mexico, and Oklahoma). The sample size will increase as work in these

CRITERION 4—

Chapter 9. Patterns of Soil Calcium and Aluminum Across the Conterminous United States

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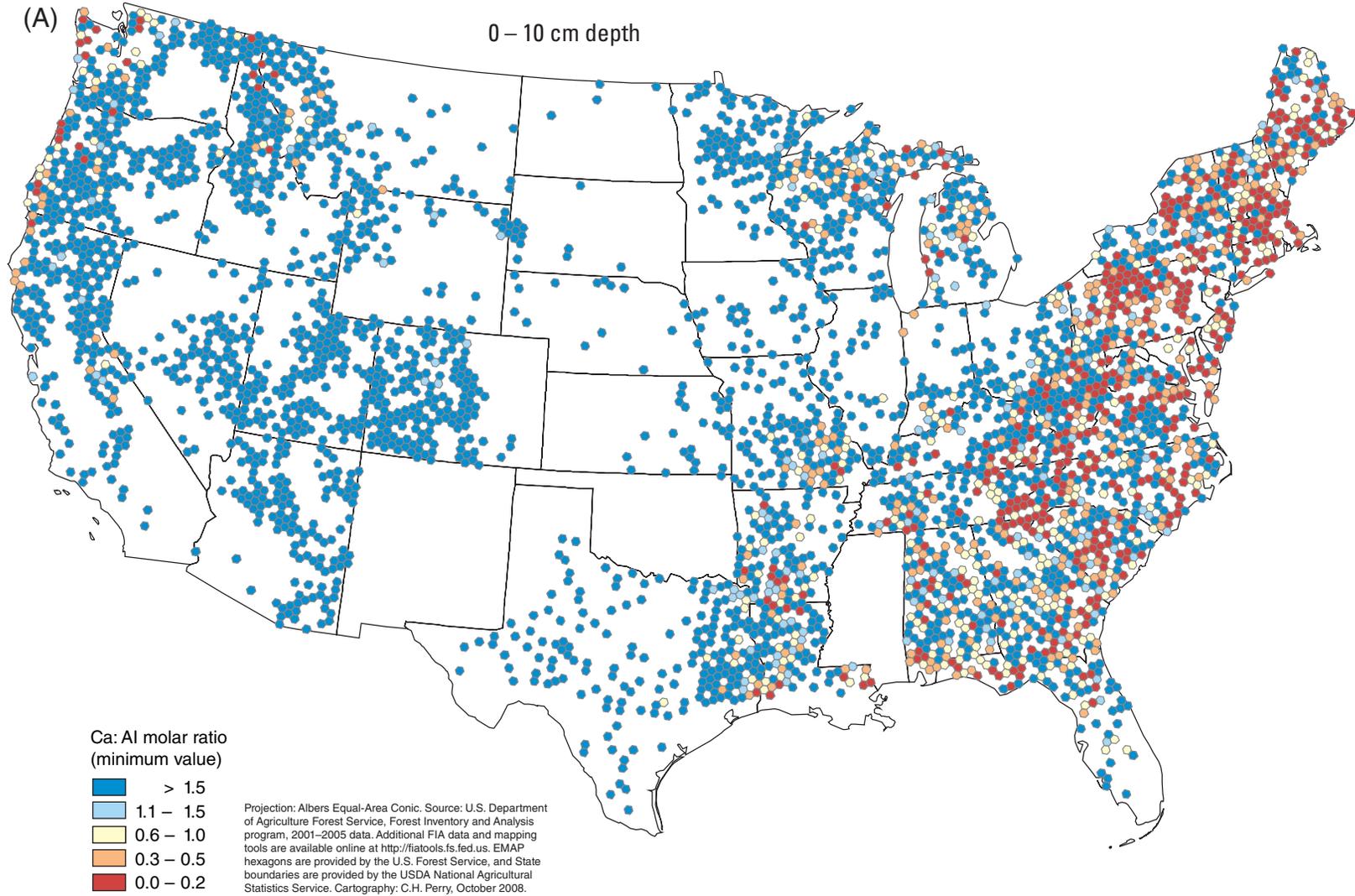


Figure 9.1—Spatial distribution of minimum Ca:Al molar ratios for two soil depths across the conterminous United States. Sampling has not begun in three States: Mississippi, New Mexico, and Oklahoma. (continued on next page)

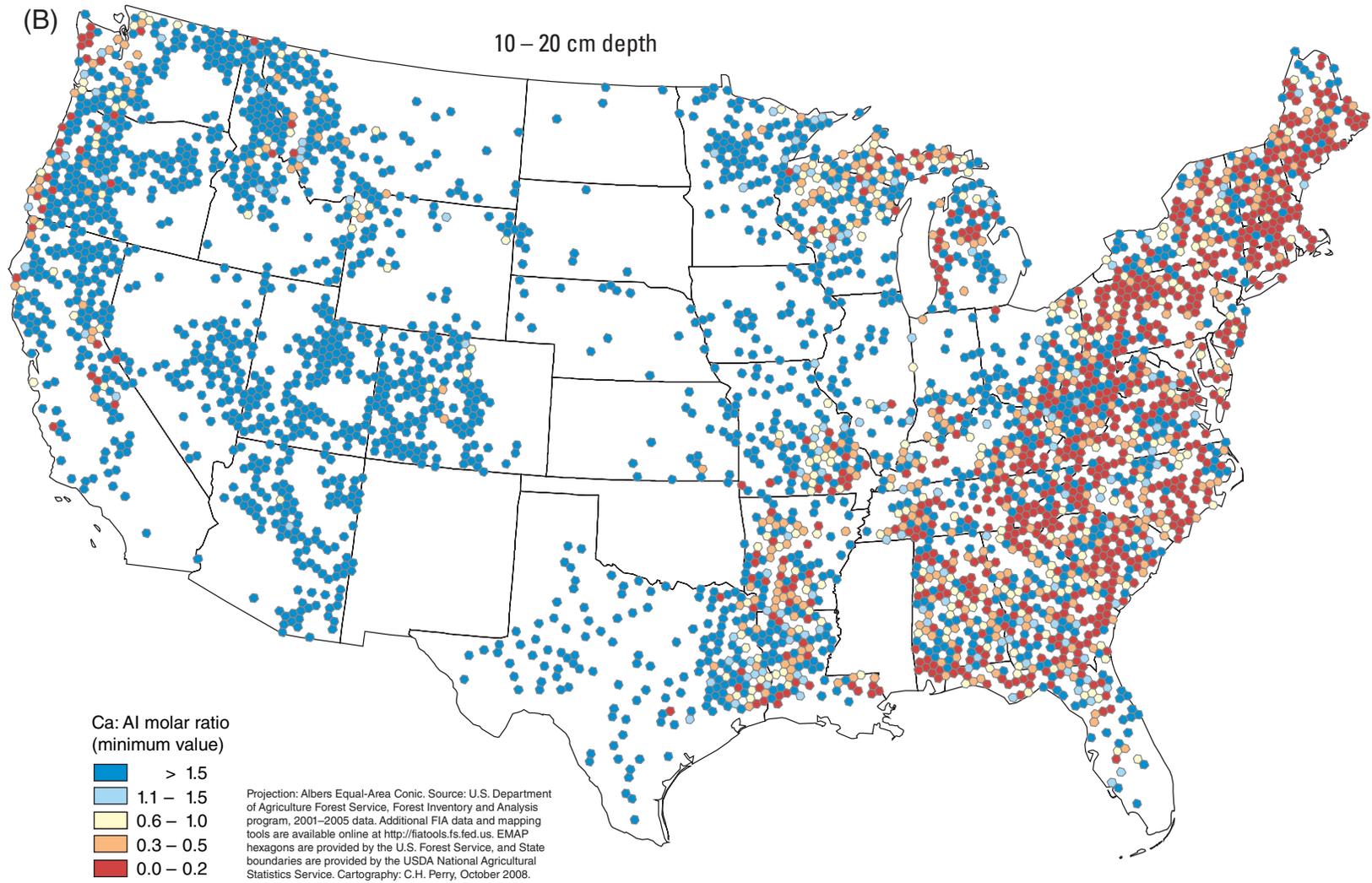


Figure 9.1 (continued)—Spatial distribution of minimum Ca:Al molar ratios for two soil depths across the conterminous United States. Sampling has not begun in three States: Mississippi, New Mexico, and Oklahoma.

States is completed and additional States are inventoried. The changing sample size and refinement of the database management and estimation algorithms together suggest that the results presented here should be considered preliminary.

One mineral soil sample is collected on each FIA phase 3 plot according to well-documented protocols^{2 3} and sent to regional laboratories for chemical analysis⁴. Additional details on field measurements, laboratory processing, and estimation procedures are available (O'Neill and others 2005).

Exchangeable Ca and Al values were obtained from the soils database. The exchangeable cation information was converted to a molar ratio of Ca:Al using the atomic weights of the two elements. Cronan and Grigal (1995) defined thresholds for Ca:Al ratios in soil solution, but our measurements are taken in the mineral

fraction. We have yet to establish firm thresholds for these data. Information on forest-type group was added to each plot record by linking the soils database with the condition-level information available from FIA (Alerich and others 2007). Two different soil layers were evaluated: 0 to 10 cm and 10 to 20 cm. For mapping purposes, soil chemical properties were assigned to hexagons developed by the Environmental Monitoring and Assessment Program of the U.S. Environmental Protection Agency (Spence and White 1992, White and others 1992). Each hexagon has an area of approximately 648 km², and their center points are roughly 27 km apart. Approximately 75 percent of the hexagons contained one measurement, 23 percent had two, and 2 percent had three or four observations. When multiple observations occurred in a hexagon, the results were summarized by finding the mean, minimum, and maximum values. Numeric data were imported into R for statistical analysis and

² U.S. Department of Agriculture Forest Service. 2007. Phase 3 field guide: soil measurements and sampling [Online]. Version 4.0. www.fia.fs.fed.us/library/field-guides-methods-proc/. [Date accessed: November 1, 2008].

³ U.S. Department of Agriculture Forest Service. 2007. Forest inventory and analysis national core field guide [Online]. Field data collection procedures for phase 2 plots. Version 4.0. Vol. 1. www.fia.fs.fed.us/library/field-guides-methods-proc/. [Date accessed: November 1, 2008].

⁴ Amacher, M.C.; O'Neill, K.P.; Dresbach, R.; Palmer, C. 2003. Forest inventory and analysis manual of soil analysis methods. 62 p. Unpublished report. On file with: U.S. Department of Agriculture Forest Service, Rocky Mountain Research Station, Forestry Sciences Laboratory, 860 North 12th East, Logan, UT 84321.

plotting (R Development Core Team 2008). Results for soil pH were aggregated into classes developed by Amacher and others (2007).

What Do the Data Show?

Figure 9.1 depicts the spatial distribution of Ca:Al molar ratios in the two sampled soil layers. There are several interacting factors that create this pattern. First, southeastern soils are more highly weathered than northern and western soils. Average annual precipitation is higher, and more water moves through the soil profile. This increases the opportunity for mobile cations, such as Ca, to be transported out of the soil. Second, western soils are often rich in Ca due to the presence of carbonates in the soil profile. Carbonate minerals such as calcite and dolomite can accumulate in the subsoils of arid region soils. In areas with less rainfall, chemical weathering tends to be slower because of less leaching. Thus, carbonate minerals will persist in soil profiles subjected to less chemical weathering and buffer soil pH to near neutral

to alkaline pH levels. Finally, soils in the mid-Western and Northeastern United States were subjected to significant acid deposition (National Atmospheric Deposition Program 2008). Acid deposition preferentially leaches Ca out of the soil profile while increasing Al concentrations (Bailey and others 2005).

A close examination of the distribution of the large number of plots with very low Ca:Al (<0.2) in the Eastern United States reveals at least two spatial features. Clusters of low Ca:Al areas in the top 10 cm of soil are found in the southern Blue Ridge Mountains, the Allegheny National Forest in northern Pennsylvania, and in portions of New England. High-elevation sites are receiving greater amounts of acid deposition (Southern Appalachian Man and the Biosphere 1996), and there are likely to be other influences related to the spatial distribution of certain soil types or forest types. These patterns suggest that an analysis combining the soil Ca:Al data with other predictors such as elevation and geology is worth pursuing.

Figures 9.2A and 9.2B depict the frequency distribution (density) of Ca:Al molar ratios in the two sampled soil layers for each conifer and deciduous forest-type group, respectively. The vertical lines are the 10 percent quantile values of Ca:Al for each soil depth; 90 percent of the sample population of Ca:Al values exists to the right of each vertical line for each soil depth. Median, 10 and 90 percent quantiles of Ca:Al for each soil layer, and forest-type group are summarized in table 9.1. For consistency, the forest-type groups are arranged by increasing Ca:Al in the 0- to 10-cm layer.

Perry and Amacher (2009) introduced the soil quality indicator dataset, which documented the interaction of Ca and Al with soil pH. There are strong regional interactions with generally higher pH for given Al concentrations in the West. Western soils, being more basic with naturally higher pH, are less likely to exhibit problems; recall the gibbsite reaction.

Forest-type groups commonly associated with the Western United States (e.g., lodgepole pine, Douglas-fir, ponderosa pine, pinyon-juniper, western aspen/birch, and western elm/ash/cottonwoods) are found on soils with higher Ca:Al ratios. This is to be expected given the amount of carbonates in western soils. Significant atmospheric deposition tends to occur in association with urban and agricultural areas, but some even originate in Asia (Fenn and others 2003b). The effects of nitrogen deposition in the West are a complicated mix of positive and negative outcomes that eventually alter the biotic community (Fenn and others 2003a). Studies of several of the major western tree species demonstrated reduced root growth with increased soil Al or soil acidification [see Pan and others (1991) for Douglas-fir, western larch, and Engelmann spruce; Keltjens (1990) for Douglas-fir; and Grulke and others (1998) for ponderosa pine].

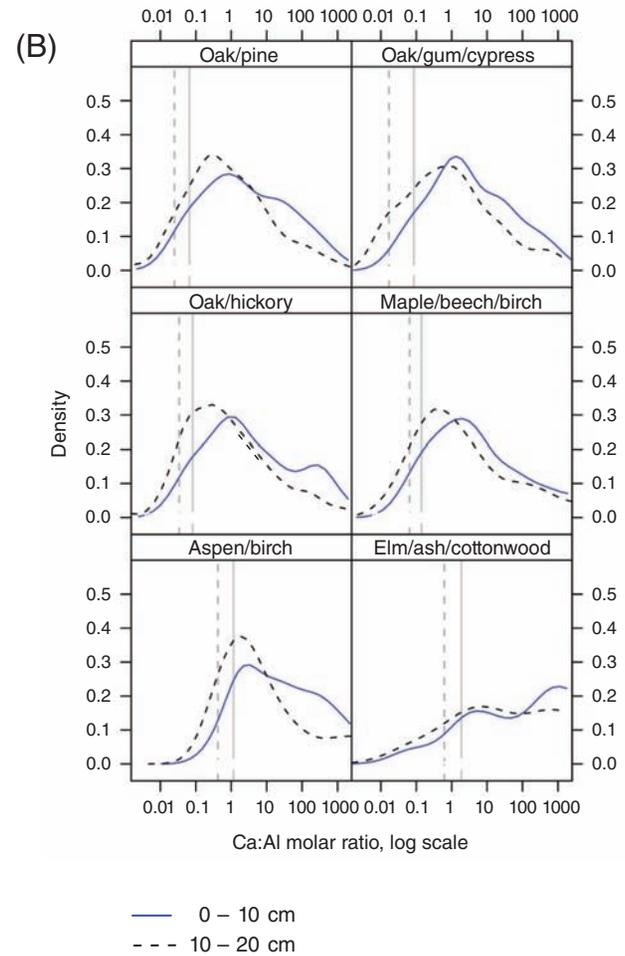
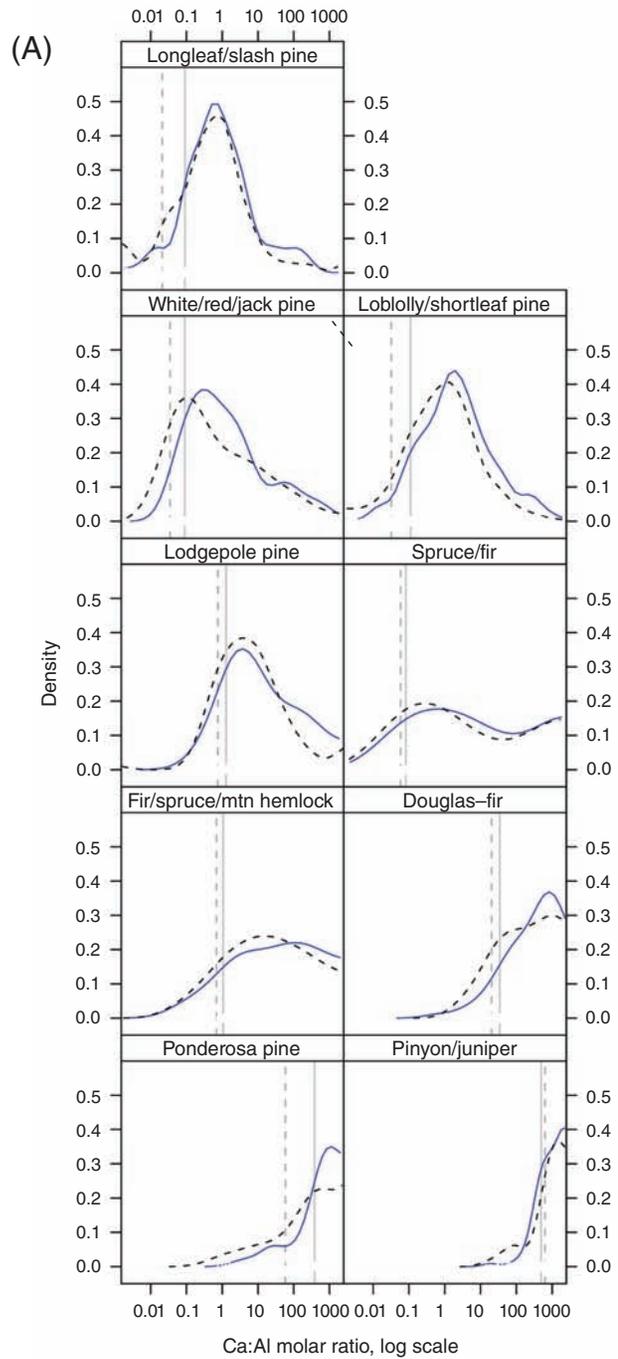


Figure 9.2 — Distribution of Ca:Al molar ratios for two soil depths by (A) coniferous and (B) deciduous forest-type groups.

Table 9.1—Molar ratios of exchangeable Ca:Al by forest-type group and soil depth

Forest-type group	N	Exchangeable Ca:Al mole ratio				
		Mean	Standard deviation	Median	Quantiles (percent)	
					10	90
0 to 10 cm						
Conifers						
Longleaf/slash pine	123	150.25	1,089.30	0.71	0.09	22.81
White/red/jack pine	91	724.74	3,841.84	0.79	0.09	95.46
Loblolly/shortleaf pine	528	52.55	471.07	1.81	0.11	46.92
Lodgepole pine	54	1,429.16	4,686.90	8.33	1.29	2,942.00
Spruce/fir	86	5,532.44	15,993.34	9.43	0.08	9,795.43
Fir/spruce/mountain hemlock	87	2,738.95	6,645.45	79.44	1.06	8,699.42
Douglas-fir	99	6,573.00	10,892.23	1,077.16	34.49	22,017.17
Ponderosa pine	63	9,666.50	11,242.04	5,789.74	381.99	26,188.48
Pinyon/juniper	220	13,254.30	14,013.84	8,852.92	495.36	33,645.13
Deciduous						
Oak/pine	247	685.92	4,094.63	1.98	0.07	240.93
Oak/gum/cypress	183	138.05	897.91	2.06	0.09	199.41
Oak/hickory	1,125	1,003.83	4,168.27	2.31	0.08	599.84
Maple/beech/birch	377	2,120.68	7,136.24	4.11	0.14	7,169.85
Aspen/birch	209	2,843.24	10,915.17	24.21	1.16	3,050.45
Elm/ash/cottonwood	128	7,278.46	14,002.26	480.64	1.88	25,994.59
Overall	3,620	2,411.18	7,902.92	5.2	0.12	5,983.63

continued

Table 9.1—Molar ratios of exchangeable Ca:Al by forest-type group and soil depth (continued)

Forest-type group	N	Exchangeable Ca:Al mole ratio				
		Mean	Standard deviation	Median	Quantiles (percent)	
					10	90
10 to 20 cm						
Conifers						
Loblolly/shortleaf pine	520	55.01	876.97	0.85	0.03	13.69
White/red/jack pine	84	529.44	2,859.72	0.26	0.04	58.91
Longleaf/slash pine	122	51.86	353.47	0.5	0.02	5.5
Lodgepole pine	51	3,508.64	15,152.89	6.97	0.76	3,924.91
Spruce/fir	82	5,385.19	15,524.27	2.68	0.06	8,673.84
Fir/spruce/mountain hemlock	79	3,366.50	12,792.04	32.81	0.69	4,802.79
Douglas-fir	85	4,786.37	9,013.69	558.51	20.41	16,495.38
Ponderosa pine	61	10,216.43	10,777.80	7,237.18	58.31	26,902.10
Pinyon/juniper	190	13,420.12	12,463.23	11,478.50	635.53	31,859.73
Deciduous						
Oak/pine	246	481.77	3,501.34	0.6	0.02	44.59
Oak/gum/cypress	180	222.01	1,731.18	0.82	0.02	45.35
Oak/hickory	1,100	596.19	3,326.15	0.59	0.03	117.65
Maple/beech/birch	369	1,536.70	6,053.03	1.39	0.07	1,075.81
Aspen/birch	205	2,639.13	8,724.88	4.12	0.42	9,032.00
Elm/ash/cottonwood	127	8,289.87	15,469.84	211.9	0.62	28,714.42
Overall	3,501	2,148.22	7,646.89	1.48	0.05	3,191.09

Ca= calcium, Al = aluminum.

Among the eastern coniferous forest-type groups, the right-skewed distribution and low 10 percent quantiles of Ca:Al ratios suggest that the longleaf/slash pine, white/red/jack pine, and loblolly/shortleaf groups are the most tolerant of Ca depletion and high exchangeable Al (table 9.1 and figure 9.2A). Messenger and others (1978) found white, red, and jack pine to be tolerant of high levels of Al; these species accumulate large quantities of Al in their leaf tissues. Loblolly and slash pine tolerate acute exposures to Al (Nowak and Friend 2006). Our data suggest that spruce/fir forest-type groups are also fairly tolerant of low Ca:Al, but high-elevation red spruce declines are linked to an imbalance between soil Al and Ca that reduces Ca supply to the trees (Schortle and Smith 1988). Our spruce/fir data are primarily (more than 70 percent) collected in northern white-cedar and balsam fir stands. Only 14 percent of our spruce/fir observations were made in red spruce stands. A greenhouse study found balsam fir roots were more tolerant of Al than red spruce (Schier 1985). The median Ca:Al associated with the most acid tolerant of these forest groups is <1, indicating that exchangeable Al can be greater than exchangeable Ca in soils supporting these forest-type groups. A 10-percent quantile of Ca:Al <0.1

(severe Ca depletion and high exchangeable Al) is only found associated with the most acid-tolerant conifer groups. Among the deciduous forest-type groups, the mixed oak forests, e.g., oak/hickory, are more tolerant of low Ca:Al than the maple/beech/birch group (table 9.1 and figure 9.2B). Sugar maple currently stands alone as a hardwood species with documented adverse effects linked to cation depletion (Fenn and others 2006).

Table 9.1 and figures 9.2A and 9.2B only show the frequency distribution of Ca:Al for each forest-type group. They provide no information about the health of the forests associated with these Ca:Al values. Still, the data do show what kinds of Ca:Al conditions are associated with different forest types. Given the statistical approach to sampling and the number of observations, we infer from the forest type and soil property distributions that certain forest groups either will not tolerate or cannot compete in conditions of soil Ca depletion and associated high exchangeable Al. Continued Ca depletion in hardwood-dominated forests of the southeastern Piedmont will yield Ca stocks below those required for merchantable timber production in approximately 80 years (Huntington and others

2000). Species dominance in northern hardwood forests shifts in response to a Ca gradient. Higher Ca soils were occupied by sugar maple, red maple, and white ash, while Ca-poor soils were dominated by beech, red oak, and eastern hemlock (van Breemen and others 1997). Thus, continued stress may cause some tree species to disappear and be replaced by other more acid-tolerant species. Since certain conifer groups tend to be more tolerant of low Ca:Al than most deciduous species, we can expect conifer replacement of some deciduous forests with increasing forest acidification. The range of red maple may also expand given the apparent benefits of acid deposition to its regeneration (Bigelow and Canham 2002). These effects of soil chemistry may interact with anticipated climate changes in ways that complicate models of species migration.

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Introduction

Down woody materials (DWM) may be defined as detrital components of forest ecosystems comprising fine and coarse woody debris. For the purposes of this study, coarse woody debris (CWD) are pieces, or portion of pieces, of down dead wood with a minimum small-end diameter of at least 7.62 cm at the point of intersection with a sampling transect and a length of at least 0.91 m. CWD pieces must be detached from a bole and/or not be self-supported by a root system with a lean angle more than 45 degrees from vertical (Woodall and Monleon 2008). Fine woody debris (FWD) are pieces, or portion of pieces, of down dead wood with a diameter <7.62 cm at the point of intersection with a sampling transect, excluding dead branches attached to standing trees, dead foliage, bark fragments, or cubicle rot.

It has been estimated that 35 percent of the total forest carbon (C) pool in the United States is in live vegetation, 52 percent in the soil, and 14 percent in dead organic material, such as DWM (Heath and others 2003). Together, annual CWD and FWD C sequestration offset approximately 1 percent of all carbon dioxide (CO₂) emissions in the United States (U. S. Environmental Protection Agency 2008). Terrestrial forest C pools, including FWD and CWD, represent a balance between the influx

of CO₂ fixed in photosynthesis and the efflux of CO₂ through woody decay processes (Malhi and others 1999). The decay rate of any individual piece of forest dead wood is determined by substrate quality, microbial activity, air temperature, and available moisture (Yin 1999). Similarly, the productive capacity of any given forest is partially governed by climatic variables such as temperature (Berry and Bjorkman 1980). Some studies have suggested that forest detritus production and decay may be in balance (Raich and others 2006), whereas others have suggested increased detritus decomposition rates due to climate change may ultimately cause forest detritus C pools to become net CO₂ emitters (Hamilton and others 2002, Sun and others 2004). Recently, Woodall and Liknes (2008a) have linked FWD and CWD C to climate and indicated that DWM's status as a C sink in a world of warming temperatures could be at risk. Initial assessments of forest DWM C flux is critical to predicting the future inventory of U.S. C stocks and subsequent greenhouse offsets. Therefore, developing empirical assessments of DWM C flux is critical to estimating future U.S. C stock inventories, greenhouse gas offset accounting, and climate change mitigation efforts. The goal of this study is to assess the flux of C in DWM across the North Central United States with specific objectives to: (1) estimate mean C flux by small FWD, medium FWD,

CRITERION 5—

Chapter 10. Carbon Flux of Down Woody Materials of the North Central United States

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large FWD, and CWD for the entire study area, for forest types, and for classes of latitude; (2) estimate changes in plot-level CWD diameter and decay distributions as a means to interpret CWD C flux dynamics; (3) estimate differences in decay class, total volume, large-end diameter, and C content for individually remeasured CWD pieces; and (4) develop suggestions for additional DWM C flux studies and analytical refinements.

Inventory Methods

The Forest Inventory and Analysis (FIA) Program of the Forest Service, U.S. Department of Agriculture, conducts a three-phase inventory of forest attributes of the United States (Bechtold and Patterson 2005). The FIA sampling design is based on a tessellation of the United States into hexagons approximately 2 428 ha in size with at least one permanent plot established in each hexagon. In phase (P) 1, the population of interest is stratified and plots are assigned to strata to increase the precision of estimates. In P2, tree and site attributes are measured for plots established in the 2,428-ha hexagons. P2 plots consist of four 7.32-m fixed-radius subplots on which standing live and dead trees are inventoried [for more information, see Woodall and Monleon (2008)].

Down woody material is sampled during the third phase of FIA's multi-scale inventory sampling design at a national sample intensity of one plot per 38 850 ha (Bechtold and Patterson 2005, Woodall and Monleon 2008). CWD is sampled on transects radiating from each FIA subplot center (at angles 30, 150, and 270 degrees, respectively). Each subplot has three 7.32-m transects totaling 87.8 m for a fully forested inventory plot. Information collected for every CWD piece intersected by transects includes transect diameter, length, small-end diameter, large-end diameter, decay class, and species. Transect diameter is the diameter of a down woody piece at the point of intersection with a sampling transect. Decay class is a subjective determination of the amount of decay present in an individual log. Decay class 1 is the least decayed (freshly fallen log) while decay class 5 is an extremely decayed log (cubicle rot pile). The species of each fallen log is identified through determination of species-specific bark, branching, bud, and wood composition attributes (excluding decay class 5). FWD with transect diameters <0.61 cm (small FWD) and 0.62 cm to 2.54 cm (medium FWD) are tallied separately on a 1.83-m slope distance transect (4.27 m to 6.09 m on the 150-degree transect). FWD with

transect diameters of 2.55 cm to 7.59 cm (large FWD) are tallied on a 3.05-m slope-distance transect (4.27 m to 7.32 m on the 150-degree transect). Although estimates of CWD should not be biased as a result, in 2001 there were only two CWD transects sampled per subplot (Woodall and Monleon 2008). These reduce the number of CWD pieces that may be matched upon remeasurement.

Data and Analysis

DWM plots established in 2001 were remeasured (one-fifth of total panel of plots) in 2006 for a total of 185 plots in the following States: Iowa (7), Illinois (11), Indiana (9), Kansas (7), Michigan (37), Minnesota (30), Missouri (38), North Dakota (2), Nebraska (4), South Dakota (6), and Wisconsin (34). Only plots that were fully forested in 2001 and 2006 were included in this analysis to avoid the shifting of nonforest condition boundaries that might confound this study's objectives. Furthermore, in order to evaluate changes in individual CWD pieces over time, the majority of individual CWD pieces were matched based on location (± 0.6 m transect length) along the same sample transect in both years. A number of CWD pieces were unmatched due to the possible

decay/disturbance of time 1 pieces and the accretion of new time 2 pieces. The volume and C content of FWD and CWD were determined through application of estimators detailed in Woodall and Monleon (2008). Briefly, the volume of FWD is estimated per unit area and then converted to an estimate of biomass using a bulk density and decay reduction factor based on forest type. An estimate of FWD C is then derived by reducing the biomass estimate by 0.5. For CWD, the volume is determined for every piece and then used in an estimator to estimate per unit area volume. Volume is converted into biomass and C using decay reduction factors, bulk density, and C conversion based on a piece's unique species and decay class.

The means and associated standard errors of C flux by small FWD, medium FWD, large FWD, and CWD were estimated for the entire study area, forest types, and classes of latitude, assuming simple random sampling with each forested plot as an observation. The diameter and decay distributions in CWD in both years were estimated. These analyses were conducted at the plot level using all CWD pieces from time 1 and time 2. In contrast, through the CWD-piece-matching algorithm, differences over time

in decay class, total volume, large-end diameter, and C content estimates were ascertained for individual CWD pieces ($n = 380$ pieces). Once again, simple random sampling was assumed for standard error computation with each CWD piece as a sample unit.

Down Woody Material Carbon Flux for Entire Region, Forest Types, and Latitude Classes—FWD and CWD were net emitters of C during the 5-year period between measurements (fig. 10.1). The total DWM C stock decreased on average nearly 0.3 t/ha annually. Among separate DWM components, large FWD decreased the most at an average of 0.2 t/ha/year followed by CWD at over 0.06 t/ha/year. The remaining components of small FWD and medium FWD had little change in C stocks. The total DWM C stock flux was close to the value of 0.21 t/ha/year for DWM found by Gough and others (2007) in an upper Great Lakes' forest. When viewed across the North Central States, the preponderance of plots with net increases in DWM C stocks (sequestration) were located in Central States, e.g., Missouri, while the preponderance of plots with DWM C losses (emissions) were located in Lake States, e.g., Wisconsin and upper Michigan (fig. 10.2).

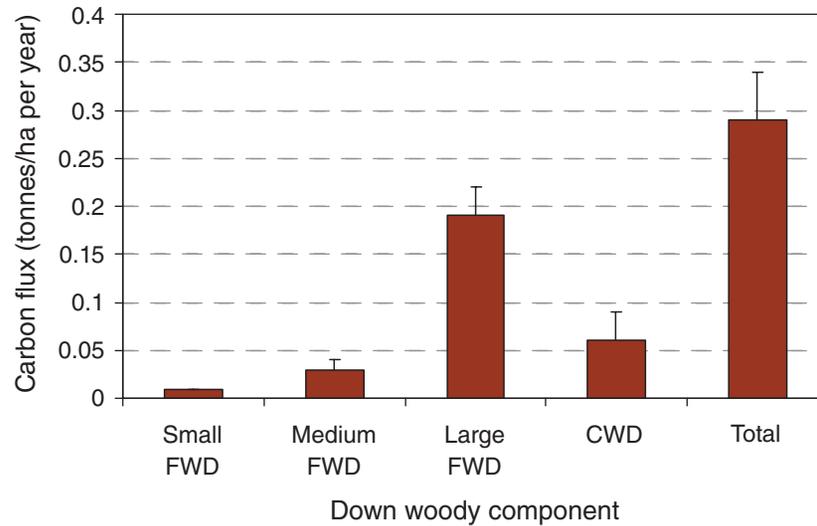


Figure 10.1—Average annual carbon flux (estimate time 2 – estimate time 1) for down woody material components (small fine woody debris, medium fine woody debris, large fine woody debris, coarse woody debris, and total) where a negative estimate indicates a net sequestration, Northcentral States, 2001 to 2006. (Data source: Forest Service, Forest Inventory and Analysis Program)

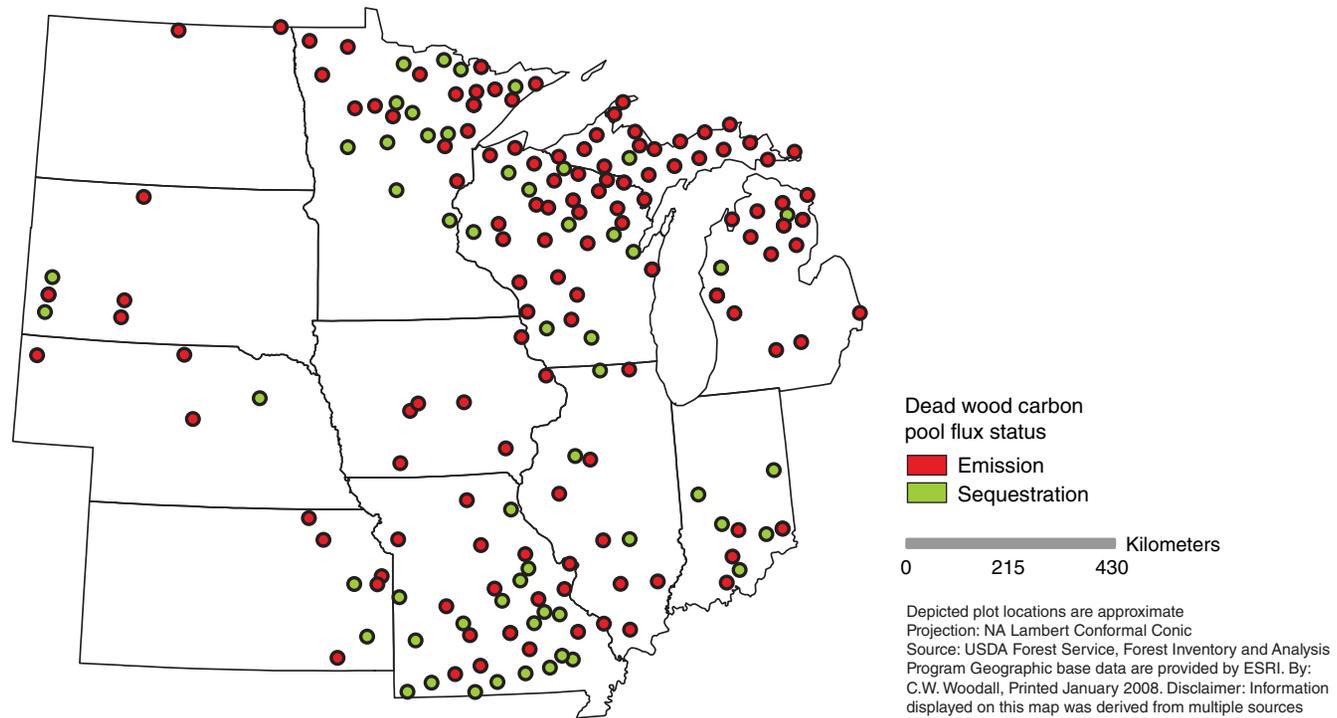


Figure 10.2—Total down woody material carbon flux status in forests of the Northcentral States, 2001 to 2006. (Data source: Forest Service, Forest Inventory and Analysis Program)

This is consistent with the view across latitudinal classes; only at the lowest latitudes were DWM C stocks found to be sequestering C annually, while higher latitudes demonstrated rates of C emission (except for the extremely high latitudes near the Canadian border) (table 10.1). When examining DWM C flux by forest type, it was evident that oak forest types were sequestering CWD C at fairly high annual rates (>0.24 t/ha/year) (table 10.2). In contrast, it was evident that ash/elm/maple and sugar maple/beech/yellow birch forest types were net emitters of C with annual rates of C flux exceeding 0.50 t/ha. Across most forest types, large FWD and CWD accounted for a majority of the total DWM C flux.

These initial results contrast with broad-scale DWM C trends reported annually in national greenhouse gas reports (U.S. Environmental Protection Agency 2008). DWM C stock fluxes have typically been reported as sinks (sequestration) due to dead wood C being modeled as dependent on stand age/stocking (Smith and others 2006). So, as forests in the United States generally age and increase in volume, it has been hypothesized that DWM C stocks have increased in tandem. Although this study only used 1 year's worth of remeasurement data in one region, it indicates that all DWM components were net emitters of C between 2001 and 2006. Most emissions came

Table 10.1—Average annual carbon flux by latitude class (3 degrees) for down woody material components (small fine woody debris, medium fine woody debris, large fine woody debris, coarse woody debris, and total) where a negative estimate indicates a net sequestration, North Central States, 2001 to 2006

Latitude class (degrees)	n	SFWD (t/ha)		MFWD (t/ha)		LFWD (t/ha)		CWD (t/ha)	
		Mean	Standard error	Mean	Standard error	Mean	Standard error	Mean	Standard error
< 37.99	24	0	0	0	0	-0.01	0.04	-0.03	0.03
38.00–40.99	37	0.21	0.1	0.01	0	0.15	0.09	-0.02	0.1
41.00–43.99	29	0.03	0.01	0.01	0.03	0.19	0.08	0.13	0.1
44.00–46.99	76	0.02	0	0.05	0.01	0.21	0.03	0.12	0.05
47.00+	27	-0.01	0.01	0.02	0.02	0.33	0.08	0.01	0.05

SFWD = small fine woody debris, MFWD = medium fine woody debris, LFWD = large fine woody debris, CWD = coarse woody debris.

Table 10.2—Average annual carbon flux by forest type for down woody material components (small fine woody debris, medium fine woody debris, large fine woody debris, coarse woody debris) where a negative estimate indicates a net sequestration, North Central States, 2001 to 2006

Forest type	n	SFWD (t/ha)		MFWD (t/ha)		LFWD (t/ha)		CWD (t/ha)	
		Mean	Standard error	Mean	Standard error	Mean	Standard error	Mean	Standard error
Black spruce	6	0	0	0.01	0.01	0.08	0.05	0.09	0.1
Northern white-cedar	8	0.04	0.01	0.18	0.05	0.4	0.12	0.06	0.02
Oak/hickories	35	0.01	< 0.01	0.02	0.02	0.1	0.04	0.08	0.09
White oak	5	0.02	0.1	0.01	0.03	-0.01	0.1	-0.36	0.24
Northern red oak	6	0.07	0.06	0.14	0.11	0.25	0.16	-0.24	0.19
Mixed upland hardwoods	7	0.02	0.02	0.04	0.07	0.01	0.12	0.08	0.15
Ash/elm/maple	5	0.33	0.12	0	0	0.29	0.14	0.89	0.49
Sugar maple/beech/yellow birch	22	0.02	0.01	0.04	0.02	0.28	0.09	0.21	0.11
Maple/basswood	7	0.03	0.2	-0.04	0.05	0.06	0.15	0.27	0.16
Aspen	28	0	0	0.04	0.01	0.3	0.07	-0.05	0.06
Paper birch	5	0.12	0.04	0	0	0.14	0.04	-0.03	0.08

SFWD = small fine woody debris, MFWD = medium fine woody debris, LFWD = large fine woody debris, CWD = coarse woody debris.

from larger sized dead wood pieces while most sequestration was in forest types that might be undergoing widespread mortality events, e.g., Missouri oak decline [see Woodall and others (2005)]. It may be concluded that the lack of any major disturbances (DWM recruitment events) in the North Central States between 2001 and 2006 provided little offset to the loss of C stocks through dead wood decay.

Changes in Individual Coarse Woody Decay Attributes—Because large pieces of DWM, e.g., CWD and large FWD, may be contributing the most to total DWM C flux, we examined changes in CWD piece attributes. Between 2001 and 2006, the distribution of CWD volume appeared to shift from large-sized CWD pieces (21 percent in 2001 to 9 percent in 2006) to a distribution favored by slightly smaller sized pieces (figs. 10.3A and 10.3B). In contrast, the decay class distribution remained rather static with decay classes 3, 4, and 5 accounting for 73 percent in 2001 and 65 percent in 2006 (figs. 10.3C and 10.3D). When examining individual CWD pieces by decay classes, it was evident that

decay increased over time while volume, large-end diameter, and C content all decreased (table 10.3).

The loss of C stocks in the larger sized dead wood pieces, such as CWD, was most likely through decay processes as opposed to large-scale fire events. At the plot level, the distribution of CWD-piece sizes shifted towards smaller sizes, while at the same time the decay distribution was rather static. These plot-level trends indicate that a possible influx of smaller sized, freshly fallen trees was not able to offset the decay of DWM C stocks since 2001. When excluding the CWD pieces recruited since 2001, individual CWD pieces all decreased in their carbon content. CWD pieces that had the largest C emission were CWD pieces that were decay class 1 or 2 in 2001. A CWD piece experiences its largest relative decrease in biomass/C as it decays from decay class 1 through 3 (Harmon and others 2008). Overall, CWD stock C emissions were most likely the result of decay with a lack of substantial DWM recruitment over a period of 5 years.

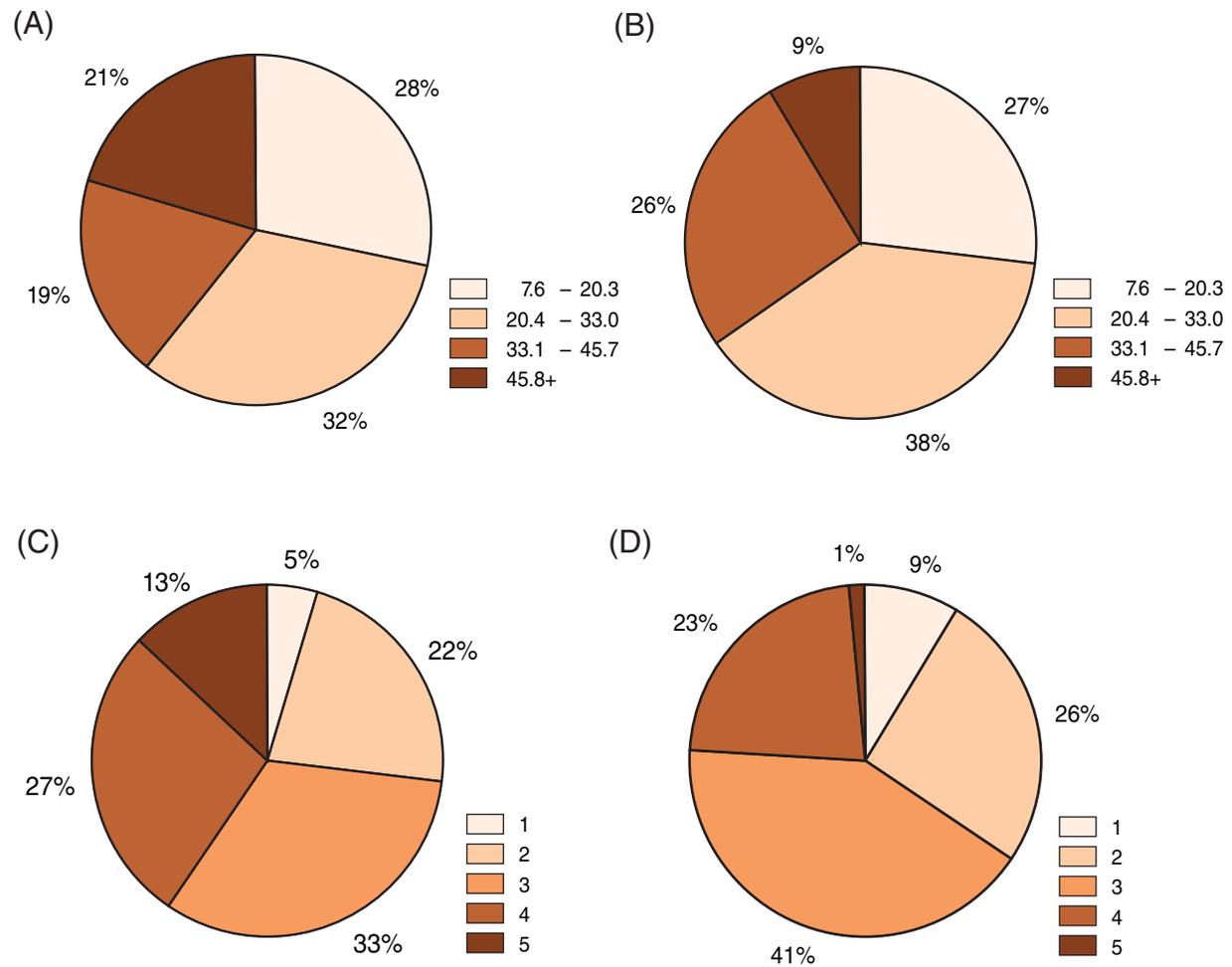


Figure 10.3—Volume (m^3/ha) of coarse woody debris by large-end diameter classes in years (A) 2001 and (B) 2006 and by decay classes in years (C) 2001 and (D) 2006 for Northcentral States. (Data source: Forest Service, Forest Inventory and Analysis Program)

Table 10.3—Average annual changes (time 1 – time 2) in individual coarse-woody-debris piece attributes in the North Central States, 2001 to 2006

Decay class	n	Decay difference ^a		Volume difference ^b (m ³)		Large diameter difference ^c (cm)		Carbon difference ^d (kg)	
		Mean	Standard error	Mean	Standard error	Mean	Standard error	Mean	Standard error
1	33	-0.27	0.03	0.01	0.01	0.06	0.23	3.89	1.83
2	107	-0.2	0.01	0.01	< 0.0001	0.16	0.11	2.15	0.83
3	145	-0.01	0.01	0.01	< 0.0001	0.18	0.07	0.93	0.4
4	82	0.1	0.02	0.01	< 0.0001	0.14	0.12	0.05	0.38
All ^e	380	-0.05	0.01	0.01	< 0.0001	0.13	0.05	1.35	0.35

^a Decay difference = decay class time 1 – decay class time 2.

^b Volume difference = volume time 1 – volume time 2.

^c Large diameter difference = large end diameter time 1 – large end diameter time 2.

^d Carbon difference = carbon content time 1 – carbon content time 2.

^e Includes decay class 5 logs.

Down Woody Material Carbon Flux Analytical Hurdles and Hypotheses—

This study is an initial assessment of DWM C flux using less than one-fifth of the eventual remeasurement dataset for only one region of the United States. As such, the most valuable conclusions may be made with respect to how to improve C flux estimation in future analyses. First, sampled forest conditions must be appropriately matched at two points in time. Land conversions, forest-type changes, and disturbance events may greatly alter forest conditions and thus complicate the task of change analysis. Second, possibly a far larger issue for DWM C flux estimation, are the differences in sample designs and impacts of not

tracking individual dead wood pieces through time. Although the 2001 DWM sample design employed fewer transects than 2006, estimators account for the transect length differences and should not bias population estimates. However, this study suggests that future change estimates try to focus efforts on utilizing identical sample designs for change estimation. Third, even though the C flux of some DWM components may be fairly substantial, they all need to be couched in the inherent measurement error in these field inventories. A 0.1-cm change in CWD large-end diameter may be negated by the measurement repeatability standard being ± 5.1 cm for field crews (Westfall and Woodall 2007). The further evaluation and resolution

of these issues should provide a foundation for future work with larger datasets eventually replacing simulations currently used in national greenhouse gas assessments (Woodall and others 2008).

Despite the use of an initial dataset, a few preliminary hypotheses may be forwarded regarding the dynamics of DWM C flux. Woodall and Liknes (2008a, 2008b) advanced a hypothesis that suggests that as the climate warms, increases in decay rates (emission) might more than offset dead wood C sequestration. This phenomenon would result in CWD and FWD C stocks being nearly equal, unless widespread mortality events occurred. This study found initial evidence that higher latitudes may be experiencing CWD C emission while FWD C stocks may remain relatively static. Building on this supposition, it may be suggested that DWM C stocks are at a greater threat to become net C emitters due to the possibility of increased decay rates. Standing live-tree C stocks can easily increase their respective C stocks without recruitment, i.e., regeneration, through stand growth, while a lack of DWM recruitment will always decrease DWM C stocks, resulting in an emission of C.

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Each year, the Forest Health Monitoring (FHM) Program of the Forest Service, U.S. Department of Agriculture, funds evaluation monitoring (EM) projects, which are “designed to determine the extent, severity, and causes of undesirable changes in forest health identified through Detection Monitoring and other means” (Forest Health Monitoring 2003). In addition, EM projects can produce information about forest health improvements. More detailed information about how EM projects are selected, the most recent call letter, lists of EM projects awarded by year, and EM project poster presentations can all be found on the FHM Web site <http://www.fs.fed.us/foresthealth/fhm/>.

Beginning in this report, each FHM national technical report will contain summaries of recently completed EM projects. Each summary provides an overview of the project and results, and provides a contact for more information. The EM project number and a Web address pointing to the project proposal, when available, are provided at the beginning of each summary. Seven project summaries, from projects completed in 2006 and 2007, are included in this report.

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SECTION 2. Evaluation Monitoring Project Summaries

Introduction

Forest vulnerability to invasion by exotic plants has been measured using a combination of biotic, abiotic, and disturbance variables. While disturbance may not be required for invasion, it has been characterized as one of the most reliable indicators of forest vulnerability to plant invasion (Lonsdale 1999). The association between invasion and disturbance has been attributed to changes in resource availability resulting from the disturbance (Davis and others 2000). Environmental conditions not associated with any particular disturbance also play an important role in determining site vulnerability to invasion. Sites with ample water and nutrients are often the first to be invaded (Huebner and Tobin 2006, Thompson and others 2001). Several studies also support a positive relationship between native plant richness and invasibility by exotic invasive species (Higgins and others 1999, Stohlgren and others 1999).

Currently, Forest Inventory and Analysis (FIA) plots are located approximately every 2 400 ha. The FIA plots within the Allegheny National Forest (ANF) are sampled under the same temporal scale but the plots are located approximately one per every 1 200 ha (Morin and others 2006). Additional measurements are also taken on the ANF FIA plots (also referred to

as phase 3 plots) and include understory vascular plants, soil variables, topography, and canopy conditions (Reams and others 2005).

The goal of this project was to evaluate the ability of coarse-scale FIA understory data to predict ANF vulnerability to invasion by exotic plant species. Based on the literature using fine-scale methods, we predicted that plant species richness, relatively mesic site conditions, disturbance, and anthropogenic landscape features were likely to be indicators of invasion.

Methods and Materials

The ANF is located in northwestern Pennsylvania within the unglaciated portion of the Allegheny Plateau. We used FIA data collected from 182 0.067-ha plots that were sampled between 1999 and 2006.

Analyses were organized around three variable types: (1) biotic, (2) abiotic, and (3) disturbance or landscape features related to disturbance. There were seven biotic variables: (1) invasive exotics, (2) all exotics, (3) noninvasive exotics, (4) native species presence and richness, (5) sapling density to tree density ratio, (6) sapling basal area to tree basal area ratio, and (7) forest type. The 10 abiotic (includes measures of biological resources but not biotic responders to these

Chapter 11. Patterns of Exotic Plant Invasions in the Allegheny National Forest, Pennsylvania

(NC-EM-05-01, <http://www.fhm.fs.fed.us/em/funded/05/ne-em-05-01.pdf>)

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resources) variables included: (1) crown density (percent), (2) foliar transparency (percent), (3) aspect, (4) slope (percent), (5) coarse woody debris (m^3), (6) soil pH, (7) total soil carbon (C) (percent), (8) total soil nitrogen (N)(percent), (9) aluminum (mg/kg), and (10) calcium (mg/kg). The nine disturbance variables were: (1) distance to the nearest paved road (m); (2) distance to the nearest dirt or gravel road (m); (3) stand age (years); (4) standing dead tree density; (5) presence of nonforest area; (6) fire; (7) defoliation by gypsy moth (*Lymantria dispar*), cherry scallop shell moth (*Hydria prunivorata*), and elm spanworm (*Ennomos subsignaria*); (8) mortality due to beech bark disease; and (9) distance to planting of exotic plant species.

The importance of all variable types as they relate to the presence or absence of invasive exotic species and all exotic species was evaluated using logistic regression analysis with backwards selection. Multicollinearity was reduced by not including variables in the same model that had a Pearson correlation coefficient of $r > 0.5$. Models in which variables that appeared to dominate a logistic regression model were also run without such dominant variables to better define the relative importance of the remaining variables.

Results and Discussion

A total of 449 vascular, understory species were found over the 1999–2006 time period. Of the 449 total species, 11 percent were exotic, with 1 percent of the flora being classified as invasive. European buckthorn alder (*Frangula alnus*) was found in 13 of the 182 plots, followed by multiflora rose (*Rosa multiflora*) in 14 plots, Japanese barberry (*Berberis thunbergii*) in 8 plots, Asian smartweed (*Polygonum caespitosum*) in 4 plots, and crown vetch (*Coronilla varia*) in 3 plots. Sheep sorrel (*Rumex acetosella*), which occurred in 11 of the plots, is considered invasive in more open habitats, and thus, has been subjectively classified as just an exotic species here (fig. 11.1). (Some overlapping plots may not show in the figure.)

Approximately 0.8 percent of the vascular plants in the conterminous United States are exotic (Vitousek and others 1997). The ANF exotic plant percentage was higher than the approximate 7 and 3 percent found in the mid-Atlantic and northeastern regional Forest Health Monitoring plots, respectively (Stapanian and others 1998).

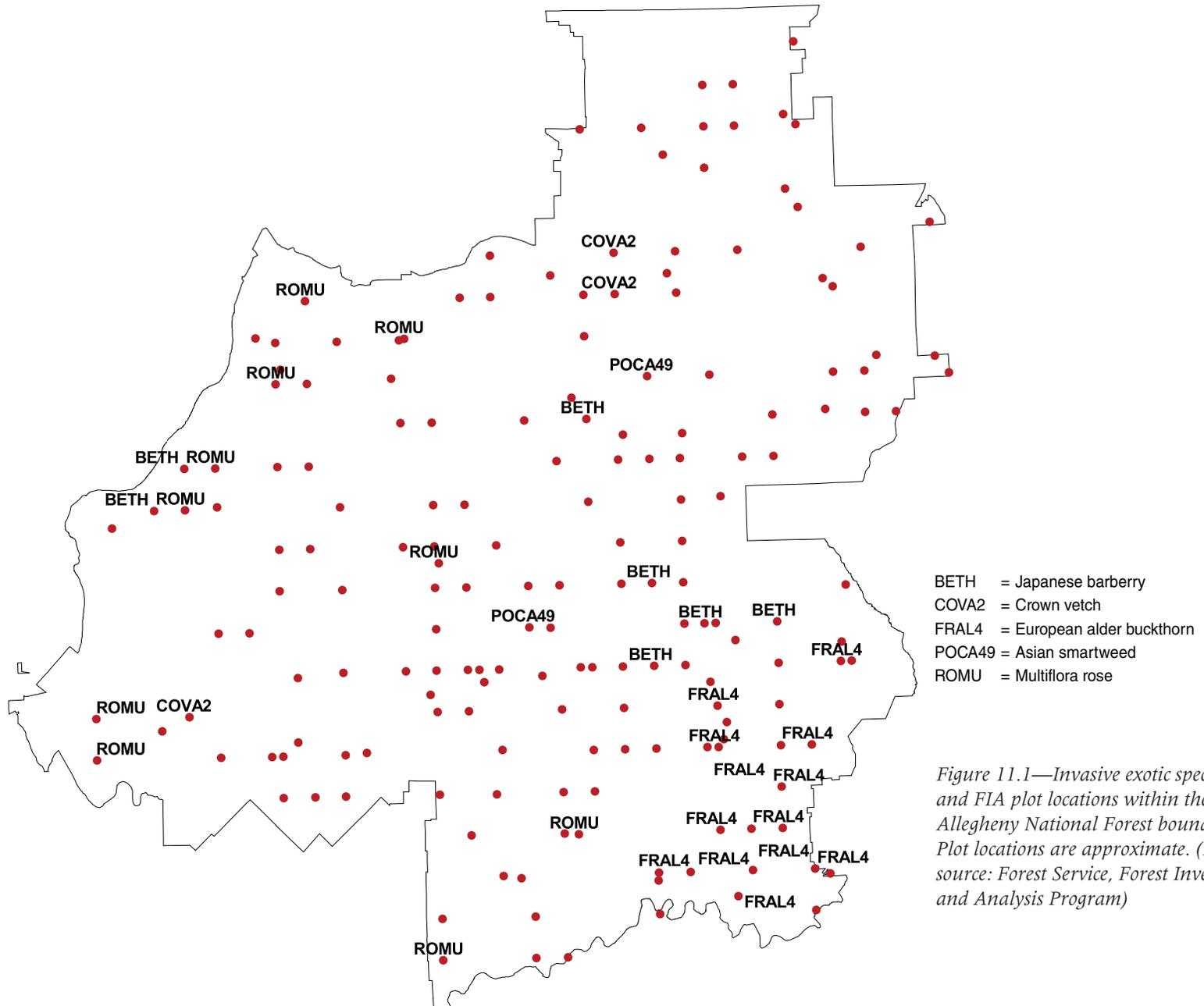


Figure 11.1—Invasive exotic species and FIA plot locations within the Allegheny National Forest boundary. Plot locations are approximate. (Data source: Forest Service, Forest Inventory and Analysis Program)

The logistic regression analyses showed that native species richness ($p = 0.0004$) was the only important biotic variable related to presence of invasive exotic plant species as a response variable. Presence of invasive exotic plants was more likely with high native species richness. Exotic species richness ($p = 0.023$) was significant, after removing native species richness from the model, showing that sites with high exotic species richness were more likely to be invaded. Soil pH ($p = 0.114$) was the only marginally important abiotic variable associated with the presence of invasive exotic plant species, with alkaline sites being more susceptible to invasion. In terms of the disturbance variables, stand age ($p = 0.07$) was marginally associated with the presence of invasive exotic plant species. Younger sites were more likely to be invaded.

Combining the three variable types that met a p -value ≤ 0.1 criterion with exotic invasive species as the response variable into a final logistic regression model showed that native species richness ($p < 0.0001$) was significant. Using exotic species richness instead of native species richness, both exotic species richness ($p = 0.031$) and pH ($p = 0.026$) were significant.

Invasion is more likely if there are many native and noninvasive exotic species and the soil is alkaline (table 11.1).

Our strongest variables, native and exotic species richness, soil pH, and stand age were measured at the same scale as the response variable. Plant and soil composition data are often spatially heterogeneous at fine scales. While our results predict that invasive exotic species are more likely to occur in alkaline soils within ANF's more species-rich areas, collecting soil pH and species richness data in order to spatially delineate these locations is labor intensive. We encourage FIA planners to utilize intensive plot sampling nationwide, but also to consider adding plots such that key variables like disturbance type (defoliation, burned, or harvested) and forest type have an adequate sample size for a given forest or region. This stratified approach will give variables measured at a coarser scale a more equal standing with variables that are measured at the same scale as the response variable. The latter may improve our ability to predict future invasions. A comprehensive paper on this project is currently being submitted to a journal for review.

Table 11.1—Logistic regression combined biotic, abiotic, and disturbance model using invasive exotic and all exotic species as the response variable and independent variables with $p < 0.1$ in the separate models

Model	Variable ^a		Unit	Odds ratio ^b		Confidence interval	
	IE	AE		IE	AE	IE	AE
Adj. R ² = 0.24							
N+pH+Stage+Dplant	N	NA	0.1	1.8	NA	1.30–2.50	NA
	Dplant		1	6.8		1.85–25.01	
Adj. R ² = 0.10							
E+pH+Stage+Dplant	E	NA	0.1	1	NA	1.01–1.04	NA
	Dplant		1	6.2		1.75–22.25	
Adj. R ² = 0.15							
N+pH+Stage	N	NA	0.1	1.8	NA	1.33–2.49	NA
Adj. R ² = 0.10							
E+pH+Stage	E	NA	0.1	1.2	NA	1.01–1.31	NA
	pH		0.1	3.7		1.18–11.87	
Adj. R ² = 0.40							
N+Stage+Bbdm	NA	N	0.1	NA	2.8	NA	2.01–4.05
		Stage	1		0.8		0.66–0.95
Adj. R ² = 0.41							
N+Stage	NA	N Stage	0.1 1	NA	2.8 0.8	NA	2.01–4.05 0.66–0.95

IE = invasive exotic species, AE = all exotic species, N = native species richness, Stage = stand age, Dplant = distance to exotic planting, NA = not applicable, E = exotic species richness (excluding invasive exotic species), Bbdm = beech bark disease mortality.

^a Variables in the variable list were significant at a $p \leq 0.05$.

^b The odds ratio can be defined as the chance of the response variable increasing or decreasing by each unit.

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Introduction

Black ash (*Fraxinus nigra*) is present throughout the upper Midwest and Northeastern United States and is often found in lowland hardwood forests. Black ash seed is an important food for birds and small mammals, and its twigs and foliage are used by ungulates. Black ash wood is valued for paneling and furniture as well as for Native American basketry. In recent years, the availability of quality trees used to make baskets has diminished because of black ash decline.

Black ash decline has been observed throughout the range of its host (Croxtton 1966, Livingston and others 1995, U.S. Department of Agriculture Forest Service 2004). In Minnesota, 2004 surveys showed over 27,000 acres of dieback occurring on black ash (U.S. Department of Agriculture Forest Service, Northeastern Area State and Private Forestry 2005). The cause of ash decline is unknown, but has been related to drought (Livingston and others 1995), subfreezing temperatures with little snow cover, or late spring frosts (U.S. Department of Agriculture Forest Service 2004). Black ash is a shallow-rooted species susceptible to varying water levels and winter freeze-thaw injury.

Our objectives in this study were to use Forest Inventory and Analysis (FIA) and Forest Health Monitoring (FHM) data to assess the pattern and extent of black ash decline in Minnesota and to relate this to mapped climatic, physiographic, and edaphic data (see Ward and others 2009).

Methods

Aerial survey data collected in Minnesota during 2004 were obtained from the FHM aerial survey results viewer (U.S. Department of Agriculture Forest Service, Northeastern Area State and Private Forestry 2005). Dieback and decline polygons in the black ash cover type were joined to three Minnesota Department of Transportation roads layers—major interstates and trunk highways, county and State roads, and city streets—to examine relationships between distance to road and decline symptoms. In addition, data collected in Minnesota from 1,605 black ash trees measured in the 1990-era inventory and remeasured in the 2003 inventory, were accessed from the FIA Spatial Data Services Center. The data included true plot coordinates which were spatially joined with several ancillary datasets: county boundaries, ecological subsections, temperature and precipitation, State Soil Geographic (STATSGO)

Chapter 12. Assessment of Black Ash (*Fraxinus nigra*) Decline in Minnesota

(NC-EM-05-02, <http://www.fhm.fs.fed.us/em/funded/05/nc-em-05-02.pdf>)

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soils data (U.S. Department of Agriculture Natural Resources Conservation Service, Soil Survey Staff 2007), the National Wetlands Inventory (<http://www.fws.gov/nwi/index.html>), and the National Hydrography Dataset (<http://nhd.usgs.gov/index.html>). Spatial relationships of black ash growth and mortality among State climate divisions, ecological subsections, and counties were analyzed using contingency tables. Linear regression was used to determine relationships between growth and mortality and the dependent variables mean temperature, mean precipitation, and STATSGO soil characteristics.

Results and Discussion

Black ash dieback/decline polygons were significantly closer to city streets ($P = 0.030$) and to county and State roads ($P < 0.001$) than were random black ash points. Distance to highways was not significantly different between dieback/decline polygons and random points ($P = 0.341$). Several factors could contribute to the relationship between dieback/decline and distance to city, county, and State roads. Construction of city, county, and State roads can alter the natural hydrologic flow through black ash stands and result in stagnant, standing water, which can adversely impact tree growth and survival. Other factors can include high

levels of road deicing salt spray and runoff on land adjacent to roads in the winter. Road salt spray causes bud death and twig dieback in deciduous trees, and high levels of soil salt can damage leaves and reduce tree growth and vigor. In addition, road salt can decrease the cold hardiness of plants. However, direct salt spray related decline should be restricted to near roadside distances. Vegetation near roadways can also be exposed to damaging pollutants from car and truck emissions.

Recorded black ash mortality at the time of sampling increased by 18 percent between the 1990 and 2003 inventories, and levels of mortality were spatially concentrated. The increase in mortality between the two time periods differed among 16 counties ($P < 0.001$) (fig. 12.1), being greatest in Mahnomen County (56 percent) and least in Crow Wing and Mille Lacs Counties (6 and 7 percent, respectively). Mortality also differed among five Minnesota climate divisions in 1990 ($P \leq 0.001$), but was not significantly different among divisions in 2003 ($P = 0.176$). Mortality between 1990 and 2003 was highest in the central (24 percent higher), northwest (23 percent), and north central (15 percent) divisions. In 1990, significant differences in black ash mortality ($P = 0.02$) existed among 20 ecological

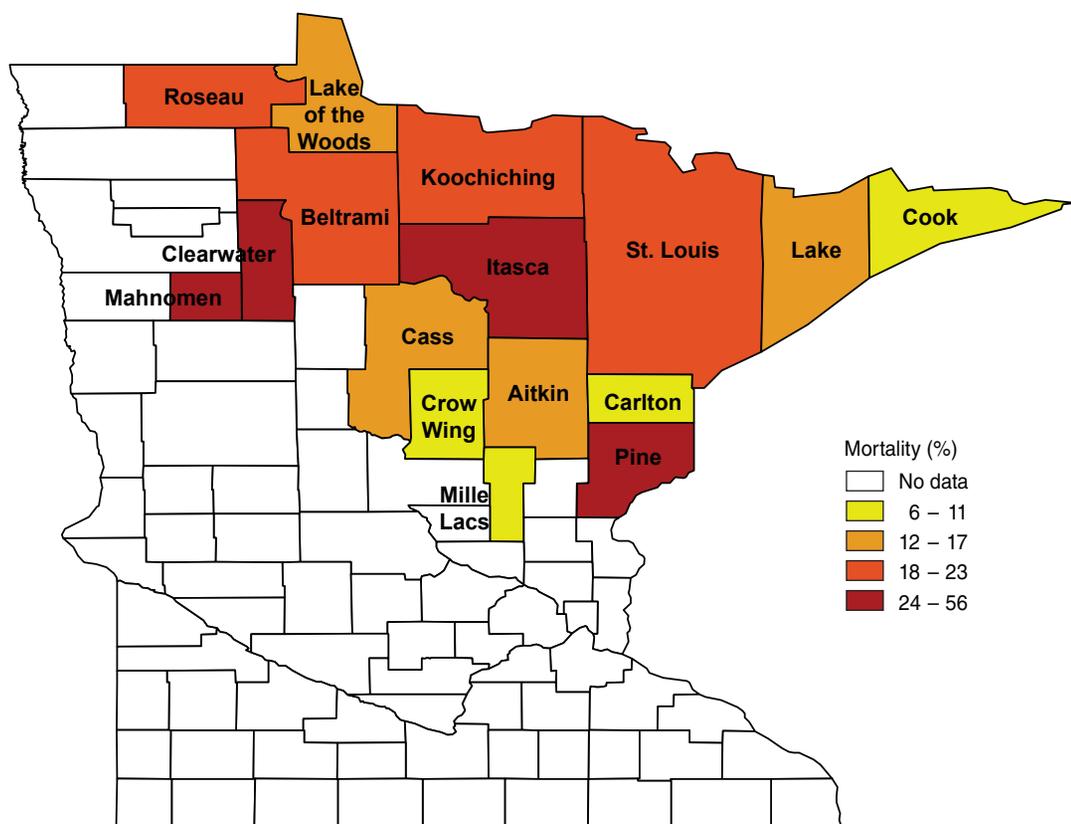


Figure 12.1—Changes in recorded levels of black ash tree mortality among Minnesota counties between the 1990 and 2003 inventories. (Data source: Forest Service, Forest Inventory and Analysis Program)

subsections (*sensu* Cleland and others 1997), with the greatest mortality occurring in the Mille Lacs Uplands subsection (212kb) (note: the Mille Lacs subsection encompasses but is much larger than Mille Lacs County). Mortality was not significantly different among ecological subsections ($P = 0.540$) in 2003. Little variation in tree mortality was explained by STATSGO soil variables in the 1990 cycle ($R^2 = 0.10$) or the 2003 cycle ($R^2 = 0.02$).

In summary, FIA growth and mortality data proved valuable for determining spatial variation in black ash decline across the study region, and for relating decline to broad regional ecological factors. No FIA variables were found to separate declining trees from nondeclining trees. The results suggest that incidence of mortality is increasing in the region, but that it is spatially variable as to occurrence. Continued mortality could severely impact the sustainability of the black ash resource in the region.

Based on this study we are now examining field plots across northern Minnesota to investigate the influence of finer scale site (soil moisture drainage), tree age, and road influences on incidence and severity of decline.

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Western white pine (*Pinus monticola*) (WWP) was once a significant component of the forest ecosystems of Washington State. Around 1910, *Cronartium ribicola* J.C. Fisch, the causal organism of white pine blister rust (WPBR), was introduced into Western North America from Europe, causing widespread mortality throughout the range of five-needle pines. In the last two decades the Forest Service and the University of Idaho have established breeding programs to genetically enhance WWP for resistance to WPBR. During this time, the Washington Department of Natural Resources has been steadily increasing the outplanting of WWP seedlings. Those outplantings occurred on State lands and included genetically enhanced (F2 progeny).

There are no current surveys that assess the incidence and severity of WPBR on genetically enhanced WWP in Washington. This study is helping us to quantitatively describe the relative success over time of genetically enhanced WWP in resisting infection and mortality caused by WPBR.

During the summers of 2002, 2003, and 2005, 22 permanent plots were established on State land across Washington (fig. 13.1) to assess the development of WPBR in young plantations of F2 WWP progeny. On each plot, the first 100 living and/or dead WWP trees were tagged and visually assessed for blister rust cankers. The number of cankers and the class to which they belonged were recorded for each tree (classes are listed in table 13.1). Preexisting WWP mortality was recorded at the time of plot establishment.

The number of trees infected with WPBR increased each year on those plots where the disease was present. Plot data on the incidence and severity of the WPBR showed that even though the infection rates on several plots were relatively high (54 to 93 percent, fig. 13.2), mortality rates remained low (<0.01 percent). All plots will continue to be monitored over time for the presence and severity of WPBR in order to better evaluate the field performance and resistance mechanisms of F2 genetically resistant WWP.

Chapter 13. White Pine Blister Rust in Juvenile Western White Pine on State Lands in Washington

(WC-EM-04-04, <http://www.fhm.fs.fed.us/em/funded/05/wc-em-04-04.pdf>)

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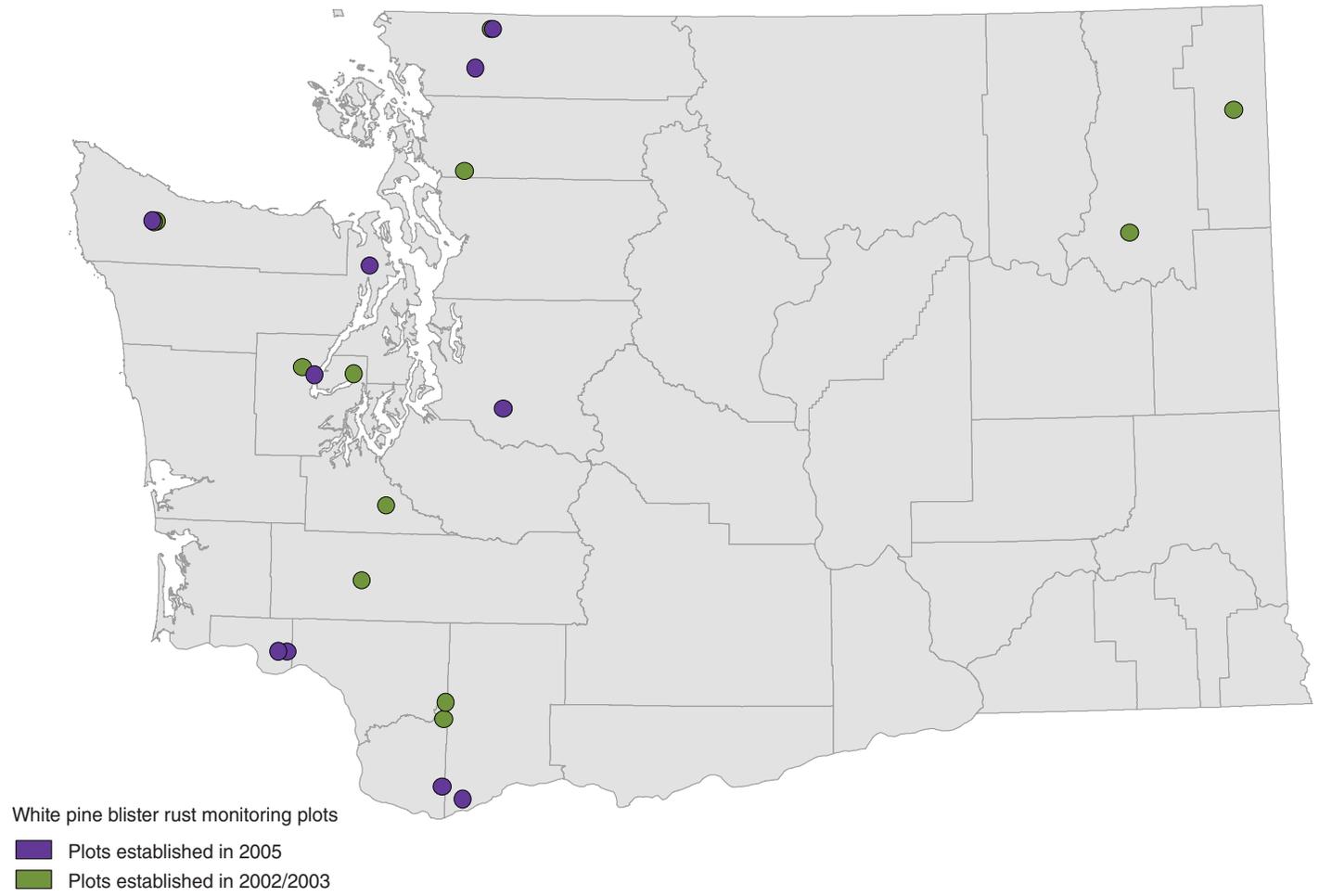


Figure 13.1—Location of white pine blister rust permanent monitoring plots.

Table 13.1—Canker classes

Class code	Class name	Description
A	Absent	No cankers present
B	Minor	Most severe canker > 24 inches from main stem
C	Moderate	Most severe canker is between 24 and 6 inches of main stem
D	Severe	Most severe canker present on main stem
E	Stem canker	Canker present on main stem
F	Top kill	Canker girdling main stem with dead top and live foliage below canker
G	Dead	Main stem girdled, no live foliage

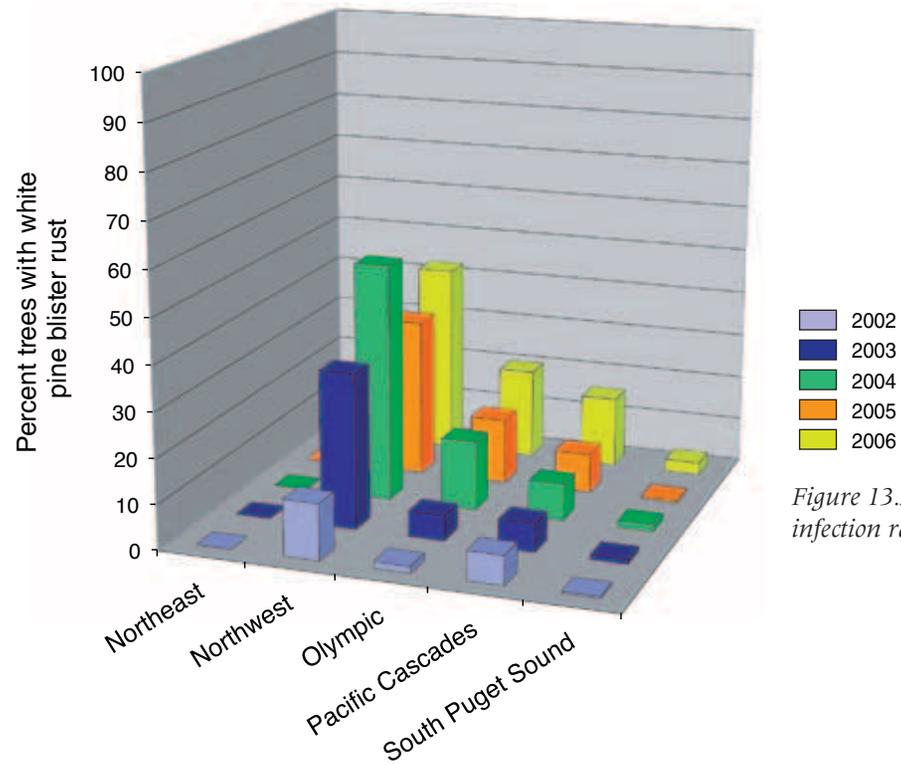


Figure 13.2—Regional blister rust infection rates from 2002 through 2006.

This evaluation monitoring project had two components: (1) installation of transects to monitor alder dieback and mortality, conducted by Forest Health Protection staff; and (2) assessment of the impact of alder dieback on ecosystem nitrogen (N) balance, conducted by University of Alaska Fairbanks staff.

Project 1: Installation of Monitoring Transects

Notable dieback and mortality of thinleaf alder (*Alnus tenuifolia*) within riparian communities is occurring in south-central and interior Alaska. This is causing concern because alder is an important floodplain colonizer and keystone N-fixing species. Monitoring transects were first installed in affected riparian communities in the Matanuska-Susitna Valley (M-S Valley) in 2004, Kenai Peninsula (KP) in 2005, and in the interior in 2006. Monitoring will continue in subsequent years. With these transects we are able to: (1) monitor the spread and intensification of dieback and mortality; and (2) assess site conditions, associated canker fungi, and insect defoliation as potential factors influencing dieback and mortality.

Twenty-one 30-m transects were installed representing 1,394 ramets (stems) within 301 genets (clumps of stems) across south-central

and interior Alaska. For each *A. tenuifolia* genet within a transect, stem condition, sprout abundance and condition, defoliation severity, presence of stem canker, distance to stream, and distance to road measurements were collected. For three genets per transect, every stem was marked and additional data were collected on dieback severity and canker location. At each site, the dominant overstory and understory vegetation were recorded.

Remeasurement of the south-central transects (M-S Valley and KP) and installation of interior transects occurred in 2006. Monitoring of transects in 2007 was only partially successful due to unexpected flooding, thus 2007 results are not included. Monitoring has indicated:

- *Valsa melanodiscus* (anamorph *Cytospora umbrina*) and 11 other similar stem canker pathogens that typically attack hosts under stress were consistently associated with stem mortality (100 percent of dead stems in the interior, 83 percent in the M-S Valley, and 76 percent on the KP). These pathogens typically cause long narrow girdling cankers on the main stem and lateral branches. Cankers were found in the aboveground plant parts, not in the root crown or roots.

Chapter 14. Assessment of the Extent, Severity, and Impact of Alder Dieback and Mortality in Alaska

(WC-EM-05-04, <http://www.fhm.fs.fed.us/em/funded/05/wc-em-05-04.pdf>)

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- Despite the cooler and wetter-than-normal summer statewide in 2006, alder dieback and mortality intensified to some degree at all sites. Across six sites in the M-S Valley, thinleaf alder have undergone a dramatic twofold increase in stem mortality in 2 years with an average of 25 percent dead in 2004, 41 percent in 2005, and 56 percent in 2006. The trend at 10 sites on the KP is less striking with a 7-percent increase in dead stems from 2005 to 2006. In newly installed transects in the interior in 2006, 26 percent of the stems were dead.
- The proportion of transects with at least one dead genet is 100 percent in the M-S Valley, 70 percent on the KP, and 20 percent in the interior.
- Live sprouts were absent from at least half of the dead genets in 50 percent of the M-S Valley, 60 percent of the KP, and 20 percent of the interior transects. We originally thought that death of the aboveground stems would not impact root sprouting and genet recovery. However, we are now less certain whether genet recovery will occur. This suggests potential long-term ecological consequences from the loss of alder.
- Alder dieback and mortality appear unrelated to distance to stream, distance to road, defoliation severity, or soil drainage in

any of the geographic areas. Although insect defoliation did not seem to directly affect dieback or mortality, this factor may contribute indirectly to host stress, and thus, increased canker infection.

- We have only begun to consider climate as part of this story. Climate records indicate that summer temperatures in Alaska since 1976 are the highest sustained levels since 1800. Long-term climatic shifts may contribute to host stress and/or favor the infection process for *V. melanodiscus* and other similar stem canker pathogens of alder.

Project 2: Impact of Alder Dieback on Ecosystem Nitrogen Balance

This study (1) established replicated long-term plots (N = 3, 20- by 20-m plots/region) along riparian forests within three Alaskan regions: interior (Tanana River), M-S Valley (Eagle River), and KP (Quartz Creek); (2) tagged ramets and assessed stem canker infection and related mortality and the degree of basal area and canopy losses from stem canker within these plots; and (3) measured rates of N fixation and associated characteristics of both soils (climate and chemistry) and plants (nodule biomass, leaf morphology and leaf chemistry, and *Frankia* genetic structure) across a range of infected alder within each plot. A complete characterization of the vegetation within each of these regions; our

experimental design; and field, laboratory, and analytical methods are provided in Ruess and others (2009).

The percentage of ramets either colonized or dead with canker ranged from 54 ± 7 percent at Quartz Creek to 76 ± 2 percent at the Tanana River plots ($P = 0.07$). The incidence of canker disease on live ramets was also significantly higher along the Tanana River (66 ± 3 percent) compared with plots at either Eagle River (29 ± 5 percent) or Quartz Creek (34 ± 6 percent). However, these differences were strongly influenced by the disease status of the large proportion of smaller diameter ramets, for which the typical diffuse canker disease symptoms were more difficult to characterize than for larger ramets. The percentage of live ramets >4 -cm diameter with main ramet canker averaged 17 ± 3 , 18 ± 5 , and 7 ± 2 percent at Quartz Creek, Eagle River, and Tanana River, respectively ($P = 0.12$). Other suggestions of a more advanced stage of canker infection at Quartz Creek and Eagle River relative to the Tanana River were the percentages of basal area dead with canker (28 ± 11 , 30 ± 8 , and 11 ± 4 percent; ns), and the percentage of canopy loss associated with canker (20 ± 8 , 15 ± 8 , and 2 ± 1 percent; ns) at the three sites, respectively. The relationship between these two metrics provides a simple means for predicting disease-related percent basal area loss (percent DEADBA) from percent canopy loss

(percent CANLOSS), a parameter that can be rapidly assessed in the field ($\%DEADBA = 1.07 * \%CANLOSS + 3.03$; $r^2 = 0.84$, $P < 0.0001$). Several pieces of evidence suggest that although the disease is severe along the Tanana River, thinleaf alder canker infection has developed much more rapidly along the Tanana River relative to the other two regions.

N fixation rates at Quartz Creek (5.52 ± 1.23 $\mu\text{mol N/g/hour}$) were significantly less than those at Eagle River (8.57 ± 0.78 $\mu\text{mol N/g/hour}$) and Tanana River (9.75 ± 1.05 $\mu\text{mol N/g/hour}$), which did not differ ($P < 0.05$). Canker damage varied substantially among the 90 plants measured for N fixation rate across sites; however, we found no evidence that N fixation rate at the nodule level was influenced by the incidence of disease or related mortality of individual plants.

Live nodule biomass beneath *A. tenuifolia* canopies averaged 28.01 ± 5.9 , 22.0 ± 4.4 , and 36.4 ± 2.0 g/m^2 at Quartz Creek, Eagle River, and Tanana River sites, respectively. The proportion of nodule biomass dead at Tanana River (37.7 ± 3.5 percent) and Eagle River (42.9 ± 6.4 percent) was significantly greater than that at Quartz Creek (25.6 ± 3.4 percent) ($P < 0.05$). Tanana River sites had significantly higher ratios of nodule biomass to basal area relative to either of the other sites, for ratios expressed as either

total ($P < 0.05$) or live components ($P < 0.05$). There were also notable differences in the size distributions of live nodules among regions, with Tanana River sites having a significantly higher proportion of nodules in smaller size classes relative to the other two regions, suggesting high nodule turnover at these sites. Across all sites, live and dead nodule biomass were correlated with a number of measures of canker disease incidence and related mortality, suggesting that higher incidences of the disease led to declines in live nodule biomass at all sites. The most useful relationship for estimating the negative effects of canker disease on nodule biomass was the inverse correlation between live nodule biomass (LIVENOD, g/m^2) and the percentage of ramets dead or with main ramet canker (percent CANK) ($\text{LIVENOD} = 36.35 \times e^{(-0.0147 \times \% \text{CANK})}$, $r^2 = 0.21$, $P < 0.01$).

We developed region-specific relationships between basal area and canopy area of individual shrubs to scale our canopy-based measures of nodule biomass to the stand level. We then predicted stand-level N inputs for each of the three replicate stands within each region as the product of nodule biomass and N fixation rates, assuming a step function of plant growth between May 20 and September

15. This generated N fixation input estimates of 22.3 ± 9.3 , 42.3 ± 10.2 , and 106.9 ± 17.4 kg N/ha/year for Quartz Creek, Eagle River, and Tanana River sites, respectively. To determine the extent to which canker disease incidence and related mortality has impacted N fixation inputs, we estimated what live nodule biomass would have been in the absence of canker by developing regional-specific negative exponential relationships between LIVENOD and percent CANK (see above). Estimates suggest that live nodule biomass has been reduced 24.4, 25.3, and 22.5 percent by the canker infection and related mortality at Quartz Creek, Eagle River, and Tanana River stands, respectively. We view the translation of these values to declines in N fixation inputs on these stands as conservative, because the percentages of dead nodule biomass that we found far exceed values we saw a decade ago when we conducted similar N input estimations along the Tanana River.

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Ruess R.W.; McFarland, J.; Trummer, L.M.; Rohrs-Richey, J.K. 2009. Disease-mediated declines in N-fixation inputs by *Alnus tenuifolia* to early-successional floodplains in interior and south-central Alaska. DOI: 10.1007/s10021-009-9237-5. New York: Springer New York. Ecosystems; 12(3): 489-502.

Introduction

Swiss needle cast (SNC), caused by the fungus *Phaeocryptopus gaeumannii*, is one of the most damaging diseases affecting Douglas-fir (*Pseudotsuga menziesii*) in the Pacific Northwest region of the United States (Hansen and others 2000). Annual Douglas-fir volume-growth losses from SNC are estimated to average about 23 percent over 187,000 acres in the northern Oregon Coast Range with some losses as high as 52 percent (Maguire and others 2002). Although impact from SNC occurs in the northern Cascade Mountains of Oregon, it is assumed to be less than the impact in the Coast Range. The objectives of our project were to determine changes after 5 years (2001 to 2006) in (1) tree diameter and total-height growth and (2) SNC severity as estimated by needle retention, stomata occlusion by fruiting bodies of the fungus (*pseudothecia*), and crown length/sapwood area ratio in 59 stands in the northern Oregon Cascade Mountains.

Methods

From April to June, 2001 and 2006, prior to Douglas-fir budbreak, 59 stands were examined. Sampled stands were 10 to 23 years old and contained >50 percent Douglas-fir. Stands were located on lands administered by the Forest Service, U.S. Department of the Interior Bureau of Land Management, Weyerhaeuser

Corporation, Port Blakely Tree Farms, and Longview Fibre Company in the northern Oregon Cascade Mountains. One transect was installed in each stand with a random starting point at the stand edge. Five sample points were located at 50-foot intervals along the transect. Data collected in 2001 at the center of the stand included (1) elevation, (2) slope aspect, (3) percent slope, and (4) Global Positioning System coordinates. At each sample point, the nearest codominant or dominant Douglas-fir on each side of the transect was selected, for a total of 10 trees per stand. Data collected for each tree included (1) stand, point, and tree number; (2) diameter at breast height (d.b.h.); (3) total height; (4) height to lowest live branch; (5) ocular estimate of foliage retention in the midcrown (0 to 6 years); (6) foliage retention index of a sampled branch; and (7) percentage of the stomata occluded by *pseudothecia* (only sampled in 2002). In 2006, crown length to sapwood area ratio was estimated for one tree in each plot pair (five trees per stand) (Maguire and Kanaskie 2002). Because some stands were thinned and stand density can influence tree growth, total basal area per acre and basal area per acre of Douglas-fir were calculated around one tree at each of the five sample points. All data were entered into an Excel® spreadsheet where R² values were calculated from selected graphed data.

Chapter 15. Impacts of Swiss Needle Cast on Douglas-fir in the Cascade Foothills of Northern Oregon: 5-Year Results

(WC-FHM-06-01)

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Results

In 2001 and 2006, we examined 590 Douglas-firs in 59 stands in the northern Oregon Cascade foothills. Stands ranged in elevation from 500 to 4,200 feet, slope from 0 to 60 percent, and total basal area per acre from 20 to 158 square feet. Mean 5-year-d.b.h. growth was 2.4 inches (range = 1.2 to 3.4) and total-height growth was 11.9 feet (range = 7.7 to 15.5). Mean needle-retention index increased by 3.4 (range = -3.4 to 11.8) over 5 years, and midcrown retention increased by 1.2 years (range 0.2 to 2.3). Mean percentages of stomata occluded by *pseudothecia* were 13.6 percent for 2000 needles (2-year-old) and 1.7 percent for 2001 needles (1-year-old) sampled only in 2002, and 13.3 percent for 2004 needles (2-year-old) sampled in 2006. Mean

crown length to sapwood area ratio was 13.2 inches per square inch and ranged from 5.8 to 22.9 in 2006.

There were poor correlations ($R^2 < 0.3$) among all variables except for stand elevation. There was a moderate relationship between stand elevation and percent stomata occluded in 2000 ($R^2 = 0.43$, fig. 15.1) and 2004 ($R^2 = 0.50$); briefly, there were fewer *pseudothecia* at higher elevations. There were poor correlations between 2001 foliage retention and 5-year d.b.h. growth ($R^2 = 0.02$, fig. 15.2). Our interpretation of these results is that 5 years between measurements is not enough time to yield detectable effects of SNC on Douglas-fir growth in the Oregon Cascades or, alternatively, there was no actual significant effect of the latest outbreak of SNC on Douglas-fir growth.

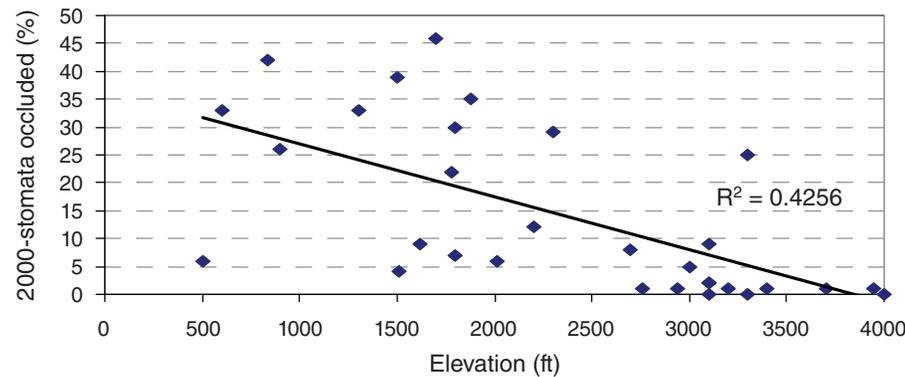


Figure 15.1—The correlation between the percentage of 2000 (2-year-old) needles occluded by *pseudothecia* of *Phaeocryptopus gaeumannii* and mean stand elevation. *Pseudothecia* decreased with increasing elevation.

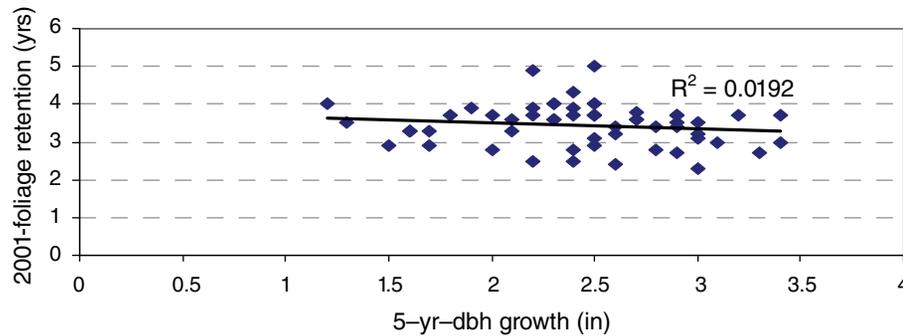


Figure 15.2—The correlation between the number of years of 2001 foliage retention at midcrown and 5-year d.b.h. growth of Douglas-fir from 2001 to 2006.

Discussion and Conclusions

There are at least two possible reasons why there may be no appreciable effect of SNC on Douglas-fir 5-year diameter and height growth during the latest SNC outbreak in the Cascade Range:

1. Oregon Cascade Range site characteristics, including plant associations, soil chemistry and parent material, air temperatures, and monthly precipitation and leaf wetness may not be as conducive to elevated populations

of the causal fungus, *Phaeocryptopus gaeumannii*, and subsequent severe defoliation, as in the Oregon Coast Range.

2. The genetics (lineage 1) of isolates of the causal fungus in the Oregon Cascades more closely resemble isolates from Idaho, Europe, and New Zealand than isolates from the Oregon Coast Range (Winton and Stone 2004). Also, lineage 2, which is abundant in the Oregon Coast Range, has not been reported in the Cascade Mountains.

Based on our results and their interpretation, forest managers need not alter their current practices in the northern Oregon Cascades, and managing a mix of Douglas-fir and western hemlock (*Tsuga heterophylla*) at lower elevations and noble fir (*Abies procera*) at higher elevations will help offset any future stand-growth declines due to SNC or other pest outbreaks (Filip and others 2000). Mixtures of tree species are known to mitigate pest damage through growth loss in infected trees being compensated for by additional growth in adjacent nonhost trees. There are plans to resample the Cascade stands in 5 years (2011).

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Michigan, Wisconsin, Maine, and Minnesota have experienced extensive mortality of tamarack (eastern larch) (*Larix laricina*). The Minnesota Department of Natural Resources reported tamarack mortality on 54,000 acres of Minnesota forests between 2001 and 2006 (Minnesota Department of Natural Resources 2006). Although the exact cause of tree mortality has been difficult to determine, eastern larch beetle (*Dendroctonus simplex*) may be playing a key role (Minnesota Department of Natural Resources, Division of Forestry; U.S. Department of Agriculture Forest Service 2006). Although eastern larch beetles often attack stressed tamarack, recent attacks in Minnesota have occurred on healthy trees. Similar observations were made in New York and Vermont during the 1970s (Drooz 1985).

Recent warm winters in Minnesota may have allowed a greater fraction of the eastern larch beetle population to survive the winter, which could put greater pressure on tamarack during subsequent spring and summer months. The insect overwinters as adults, pupae (rarely), or late instars. Eastern larch beetle is a freeze-intolerant species (A. Walter, unpublished data)²; individuals will die if they freeze. To survive winters, eastern larch beetles lower the temperature at which they freeze. The supercooling point is the lowest temperature

an insect's body will reach before it freezes. A fraction of the population may also die from chill injury prior to freezing. The objectives of this study were to measure seasonal changes in the supercooling point and lower lethal temperature of eastern larch beetle and to relate these measures to historical winter temperature records in Minnesota.

Methods

Naturally infested tamarack was cut in July and September 2007 from a field site near Swan Lake, MN. Bolts from the September collection were stored outside at St. Paul, MN. At monthly intervals, bark was peeled from at least one randomly selected bolt. All available eastern larch beetle life stages were collected, and sex of adults was determined. The supercooling point and lower lethal temperature were measured following established protocols (Carrillo and others 2004, 2005). Temperature treatments for the lower lethal temperature assay were 0, -5, -10, -15, -20, and -25 °C for insects collected in July and 0, -15, -30, -40, -50, and -55 °C for insects collected in December and April. Results were compared with the supercooling point of the insects at the time the studies were conducted. Because of the difficulty in determining whether diapausing larvae were alive or dead, lower lethal temperatures were

Chapter 16. Connecting Overwintering Success of Eastern Larch Beetle to Health of Tamarack

(NC-B-07)

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measured for adults. In this report, we only present results for July 2007 (summer baseline), December 2007 (lowest mean supercooling point), and April 2008 (spring reference). Pairwise nonparametric statistics (Kruskal-Wallis) were used to compare supercooling points among months and life stages, i.e., month x life stage was coded as the treatment. A Bonferroni adjustment was applied to account for the number of comparisons and to maintain an overall alpha of 0.05. Kruskal-Wallis tests were used to compare potential differences in supercooling points among males and females within each month, respectively. Nonparametric tests were used due to heterogeneity of variance and nonnormality of data in some seasons.

Results and Discussion

The overwintering population of eastern larch beetle was comprised entirely of adults and larvae. The mean supercooling points of adults and larvae changed seasonally (fig. 16.1). In July, supercooling points for larvae and adults did not differ and were approximately $-16\text{ }^{\circ}\text{C}$ ($-3.2\text{ }^{\circ}\text{F}$). In December, larvae typically supercooled at a lower temperature [$-49\text{ }^{\circ}\text{C}$ ($-56\text{ }^{\circ}\text{F}$)] than adults [$-42\text{ }^{\circ}\text{C}$ ($-43\text{ }^{\circ}\text{F}$)]. In April, supercooling points for larvae were no different from the summer baseline, but adults supercooled about $3\text{ }^{\circ}\text{C}$ colder. These results

should be interpreted with some caution. The design of the experiment did not allow us to separate the effects of season from the potential effects of a single log on supercooling point, and greater variation may exist among individuals than we observed due to host effects. Sex of the beetle did not affect the supercooling point on any observation date.

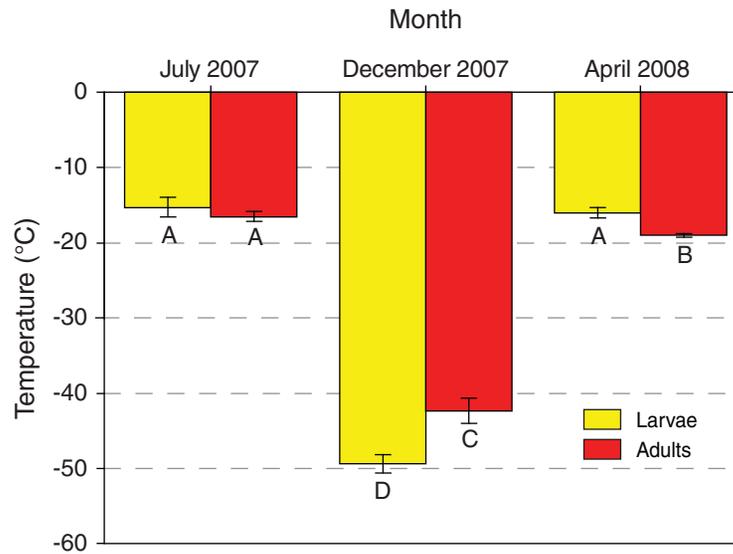


Figure 16.1—Seasonal changes in the mean supercooling point (\pm SEM) of larval and adult *Dendroctonus simplex*. Mean separation tests are based on pairwise Kruskal-Wallis tests with a Bonferroni adjustment (overall $\alpha = 0.05$)

Lower lethal temperatures were determined in December on cold-acclimated adults and in April on adults that had survived the winter but were less cold acclimated than in December. At both time periods, mortality was not significantly different from the control (0 °C treatment) until temperatures were very near to the adult supercooling point (data not shown). These results suggest that adults do not experience much mortality from chill injury.

Over the past 40 years, winters have become less severe in Minnesota (fig. 16.2). Low winter

temperatures in Isle, MN, for example, have increased approximately 0.25 °C per year from 1964–2004. Larvae are extremely cold tolerant and were consistently predicted to have a high degree of winter survivorship (fig. 16.2). Survivorship of adults, however, seems more sensitive to winter temperatures. On average, adult survivorship has increased 0.7 percent per year from 1964–2004. Greater overwintering success by *D. simplex* places greater pressure on tamarack, which may lead to tree mortality.

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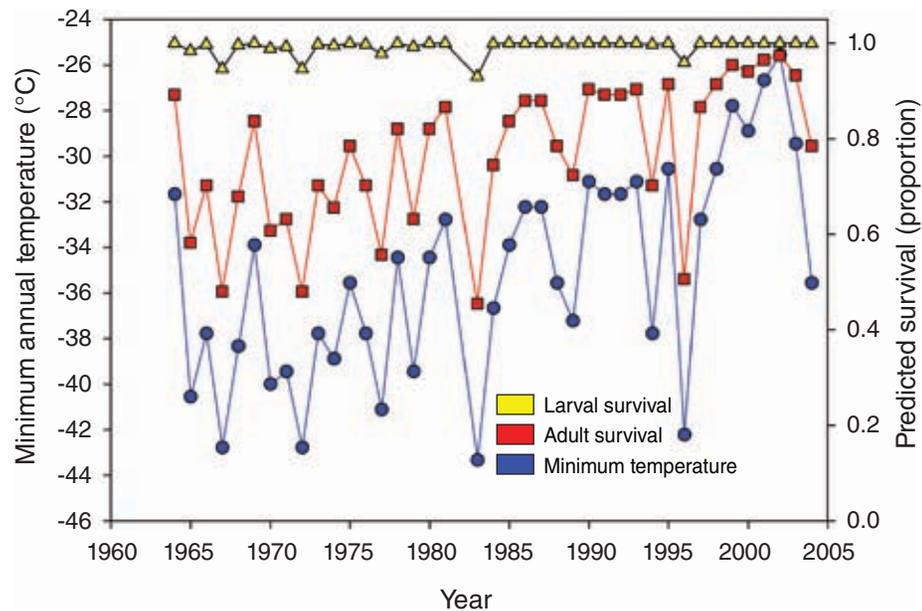


Figure 16.2—A comparison of annual lowest temperature recorded and predicted larval and adult survivorship of *Dendroctonus simplex* in Isle, MN.

Introduction

This project was established to analyze the changes in cover of indicator species and ground and aerial cover in burned areas. It was located in Hells Canyon National Recreation Area (HCNRA), which contains one of the largest contiguous areas on native bunchgrass grasslands in the Western United States and experiences an occurrence of high fire frequency. The project was set up to monitor how plant communities, specifically, bluebunch wheatgrass (*Agropyron spicatum*) and Idaho fescue (*Festuca idahoensis*), change after fire especially in relationship to invasive plants. Our overall objective was to analyze postfire changes in aerial and ground cover values for bunchgrass and various indicator species. We also utilized various treatment options on the invasive plants to expedite the recovery of the native bunchgrasses. These treatment options included herbicide, biological, competitive seeding, and manual. More specifically, we wanted to:

- Determine the extent and direction of spread of known noxious weed sites.
- Survey for new noxious weed sites within the fire perimeter.
- Evaluate the relationship between weed response and fire intensity/severity.

- Monitor current vegetation survey (CVS) plots within the fire perimeter for noxious weeds and native plants.
- Evaluate the survival of biological agents that were released within the fire area but prior to the fire for treatment efficiency.

Study Area

The project area was located in HCNRA on the Wallowa-Whitman National Forest in Oregon and Idaho. The HCNRA contains one of the largest contiguous areas of native bunchgrass communities in the Western United States. The area is subject to frequent low-to-medium severity fire and has a high occurrence and a large diversity of invasive plant species. These factors made it an ideal location to evaluate the relationship between fire and invasive plants (weeds) in bunchgrass communities.

Methods

Since year 2000, over 180,000 acres have burned in HCNRA as a result of low-burn intensity wildfires. Land managers began documenting a change in vegetative types resulting in a concern for the health of native bunchgrass plant communities. A study was proposed to evaluate the impacts of low-intensity fires to bunchgrass grasslands.

Chapter 17. Impacts to Bunchgrass Plant Communities from Fires of Low-Burn Intensity

(WC-F-06-06, <http://www.fhm.fs.fed.us/em/funded/06/wc-f-06-06.pdf>)

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Generally speaking, we used baseline data from existing CVS plots and supplemented them with additional invasive plant monitoring plots located within known weed infestations. Together, these plots provided information on density of weed infestation, rate of spread, and change within the native plant communities.

Initially we used baseline data from existing CVS plots that were located in previously burned areas. However, the initial readings did not include invasive plants. When the CVS plots were remeasured, invasive plant data were collected. We supplemented these plots with additional plant monitoring plots located within known weed infestations. The supplemented weed plots were located in burned areas where various treatment options were possible. On all of the plots we collected data on a 37-foot circular plot, measuring percent cover using the Daubenmire classification of selected plant categories. A full species list was generated from each and we determined the apparent trend of invasive plants by comparing current data with past monitoring. Site condition was determined using vegetation types.

The supplemented weed plots also recorded treatment types and treatment efficiency in relationship to native bunchgrass recovery. To monitor for herbicide treatment we recorded type, time of application, and amount of herbicide and monitored for treatment efficiency. To monitor for competitive seeding we recorded

amount of seed, type, timing, and regeneration results. To monitor for the survival of biological agents postfire, we recorded agents present. This was accomplished by visual observations of buds, stems, and/or roots.

Results and Discussion

Our analysis of CVS plot data indicated that there was an overall increase in weed densities during the initial greenup stage following the fire (fig. 17.1). Herbicide treatments were applied to these invasive plant infestations. We found that herbicide treatments applied during the first growing season after the fire (2006) resulted in increased treatment efficiency (fig. 17.2). By the second plot reading in 2007,

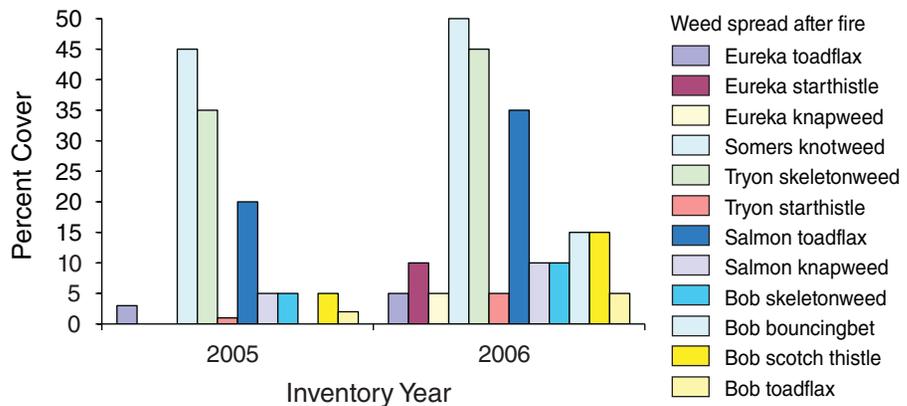


Figure 17.1—The major invasive plants (weeds) found within the project area and their rate of spread 1 year after 2005 fire.

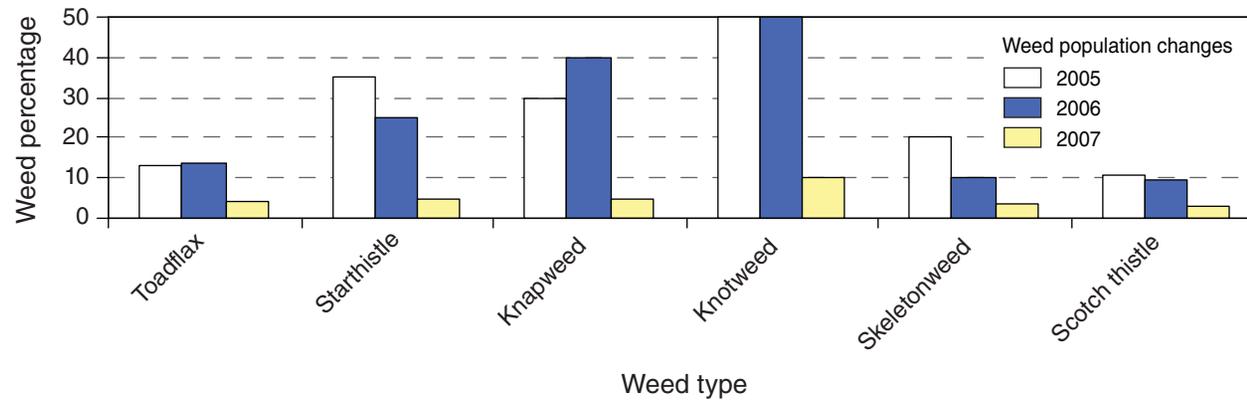


Figure 17.2—The spread of major weeds and treatment response: 2005 plot reading—ground still black from fire, rosettes present; 2006—stunted grasses, consistent weed populations, weeds treated; 2007—posttreatment, reduced weeds, increased grasses.

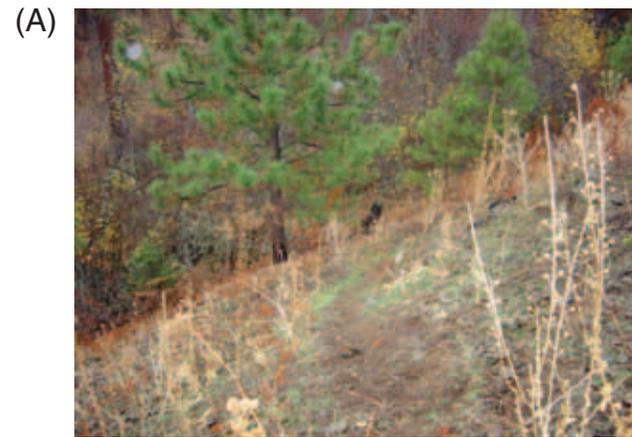
invasive plants were greatly reduced and native grasses were on the increase. Other observations we made that pertain to our study area are:

- Grassland fire of low-to-medium severity can result in removal of nearly all aboveground vegetation, but do no damage to underground roots or seed banks from previous vegetation.
- Invasive plants were the first to take advantage of the exposed surface, enhanced nutrients, and increased light that resulted from fire; these factors can increase seed germination.
- Herbicide treatments of invasive plants in the first year after fire are effective and enhance native plant reestablishment by removing competing invasives.
- Idaho fescue appears to be more resilient to low-medium severity fire, but bluebunch and fescue will reestablish naturally if prefire bunchgrass populations are significant (30 percent of plant community).
- Invasive plants were found to have an accelerated rate of spread after fire, which is likely due to removal of competing vegetation. The accelerated spread rate could also be attributed to internal winds created by the fire and fire suppression activities. Internal fire winds have the potential to transport seed heads over long distances. For instance, during the initial inventory immediately following fire (still black), two rush skeletonweed (*Chondrilla juncea*) rosettes were found three-fourths of a mile upslope from the closest known site.

- Removal of weed species as competing vegetation improved visibility during inventory, which then contributed to an increase in weed census numbers.

Finally, we found that to effectively control invasive species, it is essential to work in burned areas during the initial greenup stage (fig. 17.3). This timing provides excellent visibility for ground surveys and also seems to be the most effective treatment window for herbicide treatments. This factor alone greatly enhances the ability of native grasses to reestablish and reduces the need for reseeded.

Several guidelines for fire management and Burned Area Emergency Rehabilitation (BAER) on the Wallowa-Whitman National Forest were developed as a result of this project. They were developed specifically for Wallowa-Whitman National Forest vegetation types. The guidelines include:



*Figure 17.3—This photo series displays postfire effects on vegetation: (A) 2005—nearly complete removal of aboveground vegetation, (B) 2006—almost solid yellow starthistle (*Centaurea solstitialis*) rosettes, and (C) 2007—previous year herbicide treatment has reduced yellow starthistle and promoted native bunchgrass. (photo courtesy of Leigh Dawson and Beckijo Smergut-Wall, U.S. Forest Service)*

- An abstract for information pertaining to “The Relationship Between Fire and Invasion of Exotic Species”
- A table on “Invasive Plants Displaying Habitat Preference and Response to Fire”
- A chart displaying “Perennial Forbs Used for Post-Fire Rehabilitation”
- Guidelines on “Native Vegetation Species Recommended for Restoration Seeding To Reduce Noxious Weed Infestation”
- A matrix for “Resource Advisor Guidelines and Fire Restoration Alternatives”

Other accomplishments included:

- Monitoring of biological agents concluded that stem weevils on dalmation toadflax (*Linaria dalmatica*) and seed feeders on yellow starthistle (*Centaurea solstitialis*) can survive late summer, low-severity burns that move quickly through grasslands; however,

numbers may be significantly reduced. Therefore, biological treatment effectiveness is initially reduced as a result of fire.

- Cooperative monitoring efforts were accomplished by Forest Service fire and weed crews; the Oregon Department of Agriculture, Cooperative Weed Management Areas; The Nature Conservancy; Wallowa Resources; and volunteers.
- The creation of an educational presentation was targeted for fire crews showing fire effects on invasive plants and prevention guidelines.
- CVS data collection requirements were updated to include invasive plants.

In conclusion, we will continue to use these monitoring techniques and incorporate findings from this project in our education and prevention program as well as in the development of BAER plans.

Acknowledgments

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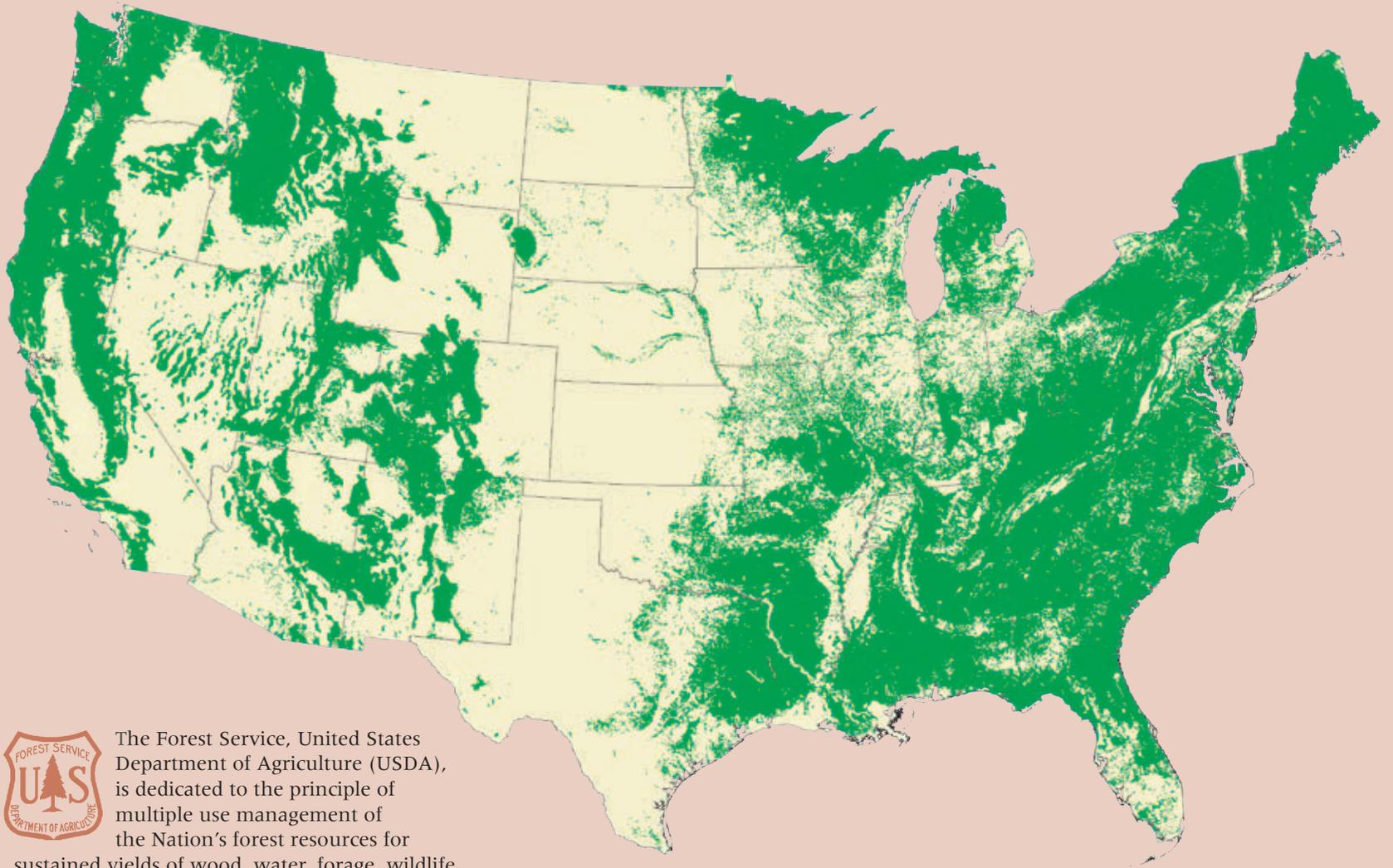
The Forest Health Monitoring (FHM) Program's annual national technical report has three objectives: (1) to present forest health status and trends from a national or a multi-State regional perspective using a variety of sources, (2) to introduce new techniques for analyzing forest health data, and (3) to report results of recently completed evaluation monitoring projects funded through the FHM national program. The first section of the report, which addresses the first two objectives, is organized according to the Criteria and Indicators for the Conservation and Sustainable Management of Temperate and Boreal Forests. A new phylogenetic approach is described for assessing the health of forest communities from an evolutionary perspective. Also depicted are new tools that allow the public to retrieve high-resolution maps of land cover patterns for specific locations. A methodology is described for the comparison of moisture conditions between different geographical areas and time periods. Aerial survey data are used to identify hotspots of insect and disease activity based on the relative exposure to defoliation- and mortality-causing agents. Satellite data are employed to detect geographic clusters of forest fire occurrence. Forest Inventory and Analysis data from 17 States are employed to detect regional differences in tree mortality. *Phytophthora kernoviae* is described as a developing threat to forest health, and a national map of *P. kernoviae* establishment risk is presented. Soil quality indicator data are analyzed to determine regional trends in soil chemistry characteristics that play an important role in the growth of forest trees. Finally, annual change in woody carbon stocks is presented in an initial assessment of down woody material carbon flux in the North Central United States. In the second section of the report, seven recently completed evaluation monitoring projects are summarized, addressing a variety of forest health concerns at smaller scales. These projects include an evaluation of exotic plant invasion vulnerability in Pennsylvania, a description of black ash decline in Minnesota, an assessment of white pine blister rust in Washington State, an evaluation of alder dieback impact on ecosystem nitrogen balance in Alaska, an assessment of the impact of Swiss needle cast on Douglas-fir in Oregon, an examination of the effect of Minnesota winter temperatures on eastern larch beetle, and an evaluation of native bunchgrass communities in Oregon and Idaho following fire.

Keywords—Drought, evaluation monitoring, fire, forest health, forest insects and disease, soil, tree mortality.



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