CHAPTER 2.

Large-Scale Patterns of Insect and Disease Activity in the Conterminous United States, Alaska, and Hawaii from the National Insect and Disease Survey, 2016

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INTRODUCTION

Insects and diseases cause changes in forest structure and function, species succession, and biodiversity, which may be considered negative or positive depending on management objectives (Edmonds and others 2011). An important task for forest managers, pathologists, and entomologists is recognizing and distinguishing between natural and excessive mortality, a task that relates to ecologically based or commodity-based management objectives (Teale and Castello 2011). The impacts of insects and diseases on forests vary from natural thinning to extraordinary levels of tree mortality, but insects and diseases are not necessarily enemies of the forest because they kill trees (Teale and Castello 2011). If disturbances, including insects and diseases, are viewed in their full ecological context, then some amount can be considered "healthy" to sustain the structure of the forest (Manion 2003, Zhang and others 2011) by causing tree mortality that culls weak competitors and releases resources that are needed to support the growth of surviving trees (Teale and Castello 2011).

Analyzing patterns of forest insect infestations, disease occurrences, forest declines, and related biotic stress factors is necessary to monitor the health of forested ecosystems and their potential impacts on forest structure, composition, biodiversity, and species distributions (Castello and others 1995). Introduced nonnative insects and diseases, in particular, can extensively damage the biodiversity, ecology, and economy of affected areas (Brockerhoff and others 2006, Mack and others 2000). Few forests remain unaffected by invasive species, and their devastating impacts in forests are undeniable, including, in some cases, wholesale changes to the structure and function of an ecosystem (Parry and Teale 2011).

Examining insect pest occurrences and related stress factors from a landscape-scale perspective is useful, given the regional extent of many infestations and the large-scale complexity of interactions between host distribution, stress factors, and the development of insect pest outbreaks (Holdenrieder and others 2004, Liebhold and others 2013). One such landscape-scale approach is detecting geographic patterns of disturbance, which allows for the identification of areas at greater risk of significant ecological and economic impacts and for the selection of locations for more intensive monitoring and analysis.

METHODS

Data

Forest Health Protection (FHP) national Insect and Disease Survey (IDS) data (FHP 2014) consist of information from low-altitude aerial survey and ground survey efforts by FHP and partners in State agencies. These data can be used to identify forest landscape-scale patterns associated with geographic hot spots of forest insect and disease activity in the conterminous United States and to summarize insect and disease activity by ecoregion in Alaska (Potter 2012, 2013; Potter and Koch 2012; Potter and Paschke 2013, 2014, 2015a, 2015b, 2016, 2017) and by island in Hawaii (Potter and Paschke 2015b, 2017). In 2016, IDS surveys of the conterminous United States covered about 216.75 million ha, of which approximately 144.99 million ha were forested (about 56.9 percent of the total forested area of the conterminous States); 107.74 million ha were surveyed using the new Digital Mobile Sketch Mapping (DMSM) approach (fig. 2.1). An additional 114.03 million ha were surveyed in 2016 using the legacy Digital Aerial Sketch Mapping (DASM) approach. (These numbers exceed the total area surveyed because of overlaps in locations covered by the two methodologies.) In Alaska, roughly 11.14 million ha were surveyed in 2016, using only the DMSM approach; of this, 7.37 million ha were forested, or about 14.3 percent of the total forested area of the State. While Hawaii was surveyed for mortality agents using DMSM, the surveyed locations (and the total area surveyed) were not recorded. Additionally, some of the mortality recorded in Hawaii occurred in years previous to 2016.

DMSM includes tablet hardware, software, and data support processes that allow trained aerial surveyors in light aircraft, as well as ground observers, to record forest disturbances and their causal agents. DMSM replaces the legacy DASM approach, and will greatly enhance the quality and quantity of forest health data while improving safety by integrating with programs such as operational remote sensing (ORS), which uses satellite imagery to monitor disturbances in areas of higher aviation risk (FHP 2016). Geospatial data collected with DMSM and DASM are stored in the national Insect and Disease Survey (IDS) database. DMSM includes both polygon geometry, used for damage areas where boundaries are discrete and obvious from the air, and point geometry, used for small clusters of damage where the size and shape of the damage is less important than recording the location, such as for sudden oak death, southern pine beetle (*Dendroctonus frontalis*), and some types of bark beetle damage in the West. Most of the points that did not overlap with a damage polygon of the same type were assigned an area of 0.809 ha (2 acres). Additionally, some damages that may be widespread and diffuse, such as those associated with gypsy moth (*Lymantria dispar*) and emerald ash borer (*Agrilus planipennis*), were recorded using grid cells (240, 480, 960, or 1920 m) in which the percent of trees affected was estimated. The entire areas of these grid cells were used in summing damage areas.

These surveys identify areas of mortality and defoliation caused by insect and disease activity, although some important forest insects [such as emerald ash borer and hemlock woolly adelgid (*Adelges tsugae*)], diseases (such as laurel wilt, Dutch elm disease, white pine blister rust, and thousand cankers disease), and mortality complexes (such as oak decline) are not easily detected or thoroughly quantified through aerial detection surveys. Such pests may attack hosts that are widely dispersed throughout forests with high tree species diversity or may cause mortality or defoliation that is otherwise

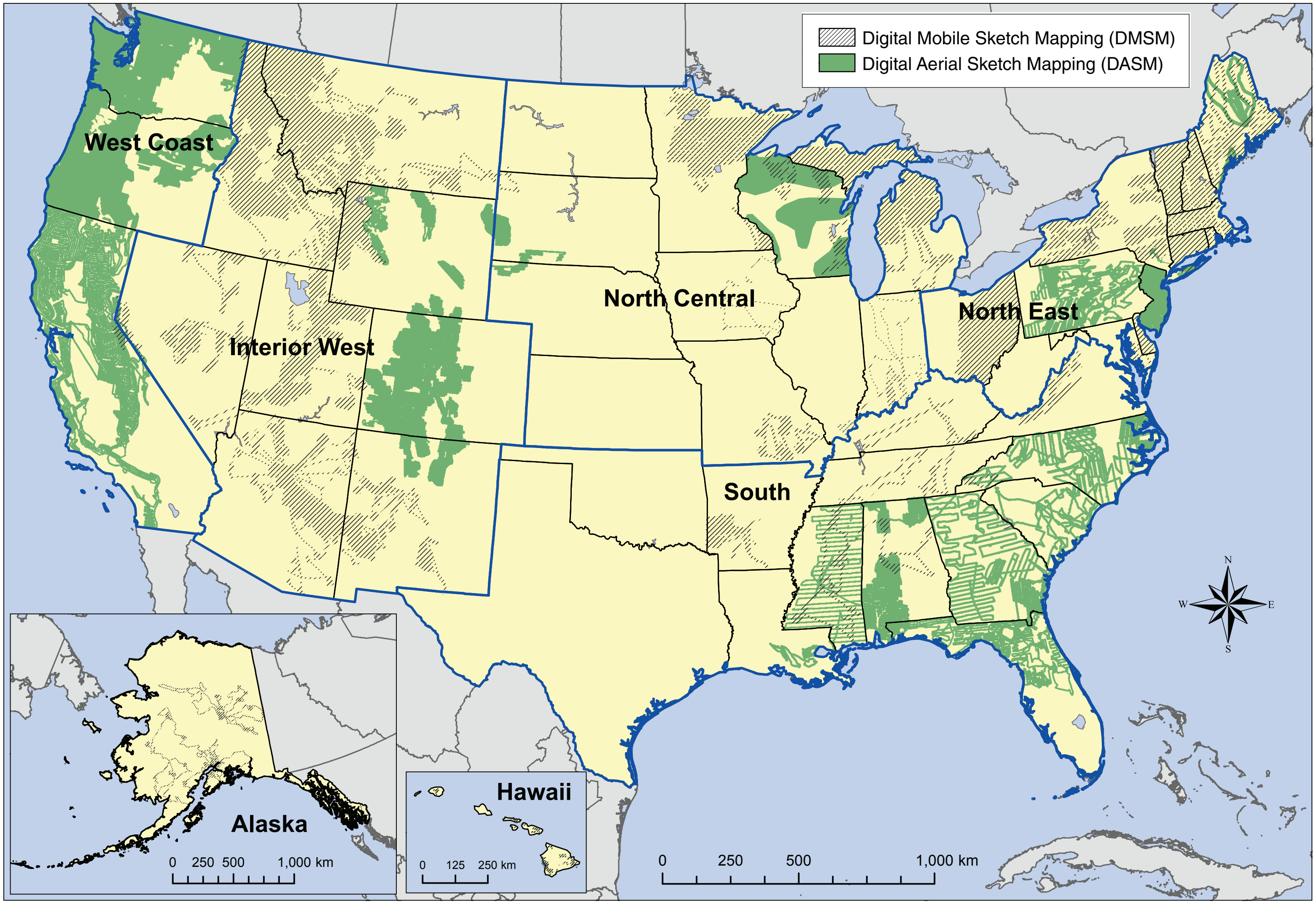

Figure 2.1—The extent of surveys for insect and disease activity conducted in the conterminous United States and Alaska in 2016. Cross-hatched areas were surveyed using the new Digital Mobile Sketch Mapping (DMSM) platform, rather than the older Digital Aerial Sketch Mapping (DASM) approach, which is portrayed in green. The blue lines delineate Forest Health Monitoring regions. Note: Alaska and Hawaii are not shown to scale with map of the conterminous United States. No flight lines were recorded for Hawaii in 2016. (Data source: U.S. Department of Agriculture, Forest Service, Forest Health Protection)

difficult to detect. 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 and the convergence of other stress factors such as drought. In some cases, the identified agents of mortality or defoliation are actually complexes of multiple agents summarized under an impact label related to a specific host tree species (e.g., "beech bark disease complex" or "yellow-cedar decline"). Additionally, differences in data collection, attribute recognition, and coding procedures among States and regions can complicate data analysis and interpretation of the results.

The 2016 mortality and defoliation polygons were used to identify the select mortality and defoliation agents and complexes causing damage on more than 5000 ha of forest in the conterminous United States in that year, and to identify and list the most widely detected mortality and defoliation agents for Alaska and mortality agents for Hawaii. Because of the insect and disease aerial sketch-mapping process (i.e., digitization of polygons by a human interpreter aboard the aircraft), all quantities are approximate "footprint" areas for each agent or complex, delineating areas of visible damage within which the agent or complex is present. Unaffected trees may exist within the footprint, and the amount of damage within the footprint is not reflected in the estimates of forest area affected. The sum of areas affected by all agents and complexes is not equal to the total affected area as a result of reporting multiple agents per polygon in some situations.

Analyses

We used the Spatial Association of Scalable Hexagons (SASH) analytical approach to identify surveyed forest areas with the greatest exposure to the detected mortality-causing and defoliation-causing agents and complexes (using data collected using both DMSM and DASM). This method identifies locations where ecological phenomena occur at greater or lower occurrences than expected by random chance and is based on a sampling frame optimized for spatial neighborhood analysis, adjustable to the appropriate spatial resolution, and applicable to multiple data types (Potter and others 2016). Specifically, it consists of dividing an analysis area into scalable equal-area hexagonal cells within which data are aggregated, followed by identifying statistically significant geographic clusters of hexagonal cells within which mean values are greater or less than those expected by chance. To identify these clusters, we employ a Getis-Ord *Gi** hot spot analysis (Getis and Ord 1992) in ArcMap® 10.1 (ESRI 2012).

The units of analysis were 9,810 hexagonal cells, each approximately 834 km^2 in area, generated in a lattice across the conterminous United States using intensification of the Environmental Monitoring and Assessment Program (EMAP) North American hexagon coordinates (White and others 1992). These coordinates are the foundation of a sampling frame in which a hexagonal lattice was projected onto the conterminous United States by centering a large base hexagon over the region (Reams and others 2005, White and others 1992). This base hexagon can be subdivided into many smaller hexagons, depending on sampling needs, and serves as the basis of the plot sampling frame for the Forest Inventory and Analysis (FIA) Program (Reams and others 2005). Importantly, the hexagons maintain equal areas across the study region regardless of the degree of intensification of the EMAP hexagon coordinates. In addition, the hexagons are compact and uniform in their distance to the centroids of neighboring hexagons, meaning that a hexagonal lattice has a higher degree of isotropy (uniformity in all directions) than does a square grid (Shima and others 2010). These are convenient and highly useful attributes for spatial neighborhood analyses. These scalable hexagons also are independent of geopolitical and ecological boundaries, avoiding the possibility of different sample units (such as counties, States, or watersheds) encompassing vastly different areas (Potter and others 2016). We selected hexagons 834 km^2 in area because this is a manageable size for making monitoring and management decisions in analyses that are national in extent (Potter and others 2016).

The variable used in the hot spot analysis was the percentage of surveyed forest area in each hexagon exposed to either mortality-causing or defoliation-causing agents. This required first separately dissolving the mortality and defoliation polygon boundaries to generate an overall footprint of each general type of disturbance, then masking the dissolved polygons using a forest cover map (1-km^2 resolution) derived from Moderate Resolution Imaging Spectroradiometer (MODIS) satellite imagery by the U.S. Department of Agriculture, Forest Service, Remote Sensing Applications Center (USDA Forest Service 2008). The same process was undertaken with the polygons of the surveyed area. Finally, the percentage of surveyed forest within each hexagon exposed to mortality or defoliation agents was calculated by dividing the total forest-masked damage area by the forest-masked surveyed area.

The Getis-Ord G_i* statistic was used to identify clusters of hexagonal cells in which the percentage of surveyed forest exposed to mortality or defoliation agents was higher than expected by chance. This statistic allows for the decomposition of a global measure of spatial association into its contributing factors, by location, and is therefore particularly suitable for detecting nonstationarities in a dataset, such as when spatial clustering is concentrated in one subregion of the data (Anselin 1992).

The Getis-Ord G_i* statistic for each hexagon summed the differences between the mean values in a local sample, determined by a moving window consisting of the hexagon and its 18 first- and second-order neighbors (the six adjacent hexagons and the 12 additional hexagons contiguous to those six) and the global mean of all the forested hexagonal cells in the conterminous United States. It is then standardized as a *z*-score with a mean of 0 and a standard deviation of 1, with values > 1.96 representing significant ($p < 0.025$) local clustering of high values and values < -1.96 representing significant clustering of low values ($p < 0.025$), since 95 percent of the observations under a normal distribution should be within approximately two (exactly 1.96) standard deviations of the mean (Laffan 2006). In other words, a G_i^* value of 1.96 indicates that the local mean of the percentage of forest exposed to mortality-causing or defoliation-causing agents for a hexagon and its 18 neighbors is approximately two standard deviations greater than the mean expected in the absence of spatial clustering, while a G_i^* value of -1.96 indicates that the local mortality or defoliation mean for a hexagon and its 18 neighbors is approximately two standard deviations less than the mean expected in the absence of spatial clustering. Values between -1.96 and 1.96 have no statistically significant concentration of high or low values. In other words, when a hexagon has a G_i^* value between -1.96 and 1.96, mortality or defoliation damage within it and its 18 neighbors is not statistically different from a normal expectation. As described in Laffan (2006), it is calculated as

$$G_i^*(\boldsymbol{d}) = \frac{\sum_j w_{ij}(d)x_j - W_i^*\bar{x}^*}{s^*\sqrt{\frac{(ns^*_{1i}) - W_i^{*2}}{n-1}}}$$

where

G_i^* is the local clustering statistic (in this case, for the target hexagon),

$\boldsymbol{i}$ is the center of local neighborhood,

$\boldsymbol{d}$ is the width of local sample window,

w_{ij} is the weight of neighbor j from location i,

$\boldsymbol{n}$ is number of samples in the dataset,

W_i^* is the sum of the weights,

s^*_{1i} is the number of samples within d of the central location,

$\bar{x}^*$ is mean of whole dataset (in this case, for all 7,595 forested hexagons), and

s^* is the standard deviation of whole dataset.

It is worth noting that the -1.96 and 1.96 threshold values are not exact because the correlation of spatial data violates the assumption of independence required for statistical significance (Laffan 2006). The Getis-Ord approach does not require that the input data be normally distributed because the local G_i^* values are computed under a randomization assumption, with G_i^* equating to a standardized *z*-score that asymptotically tends to a normal distribution (Anselin 1992). The *z*-scores are reliable, even with skewed data, as long as the distance band used to define the local sample around the target observation is large enough to include several neighbors for each feature (ESRI 2012).

The low density of survey data in 2016 from Alaska and the absence of recorded survey locations in Hawaii (fig. 2.1) precluded the use of Getis-Ord G_i* hot spot analyses for these States. Instead, mortality and defoliation data were summarized by ecoregion section in Alaska (Nowacki and Brock 1995), calculated as the percent of the forest within the surveyed areas affected by agents of mortality or defoliation. (As with the mortality and defoliation data, the flown area polygons were first dissolved to create an overall footprint.) For reference purposes, ecoregion sections (Cleland and others 2007) were also displayed on the geographic hot spot maps of the conterminous United States.

RESULTS AND DISCUSSION

Conterminous United States Mortality

The national IDS survey data identified 62 different mortality-causing agents and complexes on approximately 2.99 million ha across the conterminous United States in 2016, slightly less than the combined land area of Maryland and Delaware. By way of comparison, forests are estimated to cover approximately 252 million ha of the conterminous United States (Smith and others 2009). Twenty-two of the agents were detected on more than 5000 ha.

Fir engraver (*Scolytus ventralis*) was the most widespread mortality agent in 2016, detected on 1.19 million ha (table 2.1). Six other mortality agents and complexes were detected on more than 100 000 ha in 2016: western pine beetle (*Dendroctonus brevicomis*) on 892 000 ha, mountain pine beetle (*Dendroctonus*

Table 2.1—Mortality agents and complexes affecting more than 5000 ha in the conterminous United States during 2016

Agents/complexes causing mortality, 2016	Area
	ha
Fir engraver	1 186 692
Western pine beetle	892 023
Mountain pine beetle	626 205
Jeffrey pine beetle	331 322
Emerald ash borer	303 332
Spruce beetle	237 173
Flatheaded fir borer	124 666
Western balsam bark beetle	71 208
Unknown bark beetle	70 326
Douglas-fir beetle	56 543
Unknown	37 621
Balsam woolly adelgid	33 571
Eastern larch beetle	28 350
Flatheaded borer	18 143
Pinyon ips	14 964
Southern pine beetle	12 848
Dutch elm disease	12 440
Ips engraver beetles	9151
Gypsy moth	7886
Pine engraver	7675
Root disease and beetle complex	7523
California flatheaded borer	6996
Other (40)	32 896
Total, all mortality agents	**2 990 684**

Note: All values are "footprint" areas for each agent or complex. The sum of the individual agents is not equal to the total for all agents due to the reporting of multiple agents per polygon.

ponderosae) on 626 000 ha, Jeffrey pine beetle (*Dendroctonus jeffreyi*) on 331 000 ha, emerald ash borer on 303 000 ha, spruce beetle (*Dendroctonus rufipennis*) on 237 000 ha, and flatheaded fir borer (*Phaenops drummondi*) on 125 000 ha. Mortality from the western bark beetle group, which encompasses 19 different agents in the IDS data (table 2.2), was detected on approximately 2.39 million ha in 2016, representing a large majority of the total area on which mortality was recorded across the conterminous States.

The Forest Health Monitoring (FHM) West Coast region had the largest area on which mortality agents and complexes were detected, about 1.95 million ha (table 2.3). Of the 26 agents and complexes detected, fir engraver was the leading cause of mortality and was identified on about 1.15 million ha, approximately 59 percent of the entire affected area. Other bark beetles, including western pine beetle, mountain pine beetle, Jeffrey pine beetle, and flatheaded fir borer, were the other widespread causes of mortality in the region.

For the third consecutive year, a very large hot spot of extremely high and very high mortality centered on the M261E–Sierra Nevada ecoregion section in east-central California and extended north into M261D–Southern Cascades, M261A–Klamath Mountains, M261G–Modoc Plateau, and M261B–Northern California Coast Ranges in 2016 (fig. 2.2). The primary causes of mortality in the area were fir engraver in white fir (*Abies concolor*) and California red fir (*Abies magnifica*); mountain pine beetle in lodgepole pine (*Pinus contorta*), western white pine (*Pinus monticola*), and sugar pine (*Pinus lambertiana*); Jeffrey pine beetle in Jeffrey pine (*Pinus jeffreyi*); flatheaded fir borer in Douglas-fir (*Pseudotsuga menziesii*); and western pine beetle in ponderosa pine (*Pinus ponderosa*).

Meanwhile, a hot spot of very high exposure to mortality was detected in eastern Oregon, in M332G–Blue Mountains, primarily associated with mountain pine beetle mortality

Table 2.2—Beetle taxa included in the "western bark beetle" group

Western bark beetle mortality agents	
Cedar and cypress bark beetles	*Phloeosinus* spp.
Douglas-fir beetle	*Dendroctonus pseudotsugae*
Douglas-fir engraver	*Scolytus unispinosus*
Fir engraver	*Scolytus ventralis*
Flatheaded borer	Family Buprestidae
Ips engraver beetles	*Ips* spp.
Jeffrey pine beetle	*Dendroctonus jeffreyi*
Mountain pine beetle	*Dendroctonus ponderosae*
Northern spruce engraver	*Ips perturbatus*
Pine engraver	*Ips pini*
Pinyon ips	*Ips confuses*
Root disease and beetle complex	–
Silver fir beetle	*Pseudohylesinus sericeus*
Spruce beetle	*Dendroctonus rufipennis*
Twig beetles	*Pityophthorus* spp.
Unknown bark beetle	–
Western balsam bark beetle	*Dryocoetes confuses*
Western cedar bark beetle	*Phloeosinus punctatus*
Western pine beetle	*Dendroctonus brevicomis*

– = not applicable.

Table 2.3—The top five mortality agents or complexes for each Forest Health Monitoring region, and for Alaska and Hawaii, in 2016

Mortality agents and complexes, 2016	Area
	ha
Interior West	
Spruce beetle	223 645
Western balsam bark beetle	67 490
Unknown bark beetle	56 231
Mountain pine beetle	48 189
Douglas-fir beetle	38 094
Other mortality agents (12)	75 149
Total, all mortality agents and complexes	**502 962**
North Central	
Emerald ash borer	288 020
Eastern larch beetle	28 350
Dutch elm disease	12 341
Unknown	6152
Beech bark disease complex	4835
Other mortality agents (12)	3390
Total, all mortality agents and complexes	**341 600**
North East	
Unknown	25 047
Southern pine beetle	12 147
Emerald ash borer	11 827
Gypsy moth	7886
Balsam woolly adelgid	6074
Other mortality agents (23)	8500
Total, all mortality agents and complexes	**71 217**
South	
Ips engraver beetles	5952
Emerald ash borer	3486
Unknown	1041
Southern pine beetle	701
Hemlock woolly adelgid	144
Other mortality agents (1)	3
Total, all mortality agents and complexes	**11 327**

Mortality agents and complexes, 2016	Area
	ha
West Coast	
Fir engraver	1 154 268
Western pine beetle	888 586
Mountain pine beetle	577 165
Jeffrey pine beetle	329 816
Flatheaded fir borer	124 666
Other mortality agents (21)	120 360
Total, all mortality agents and complexes	**1 948 078**
Alaska	
Spruce beetle	76 095
Yellow-cedar decline	15 931
Northern spruce engraver	5793
Spruce broom rust	109
Western balsam bark beetle	16
Total, all mortality agents and complexes	**97 944**
Hawaii	
Rapid ʻōhiʻa death	8808
Unknown	8748
Total, all mortality agents and complexes	**17 556**

Note: The total area affected by other agents is listed at the end of each section. All values are "footprint" areas for each agent or complex. The sum of the individual agents is not equal to the total for all agents due to the reporting of multiple agents per polygon.

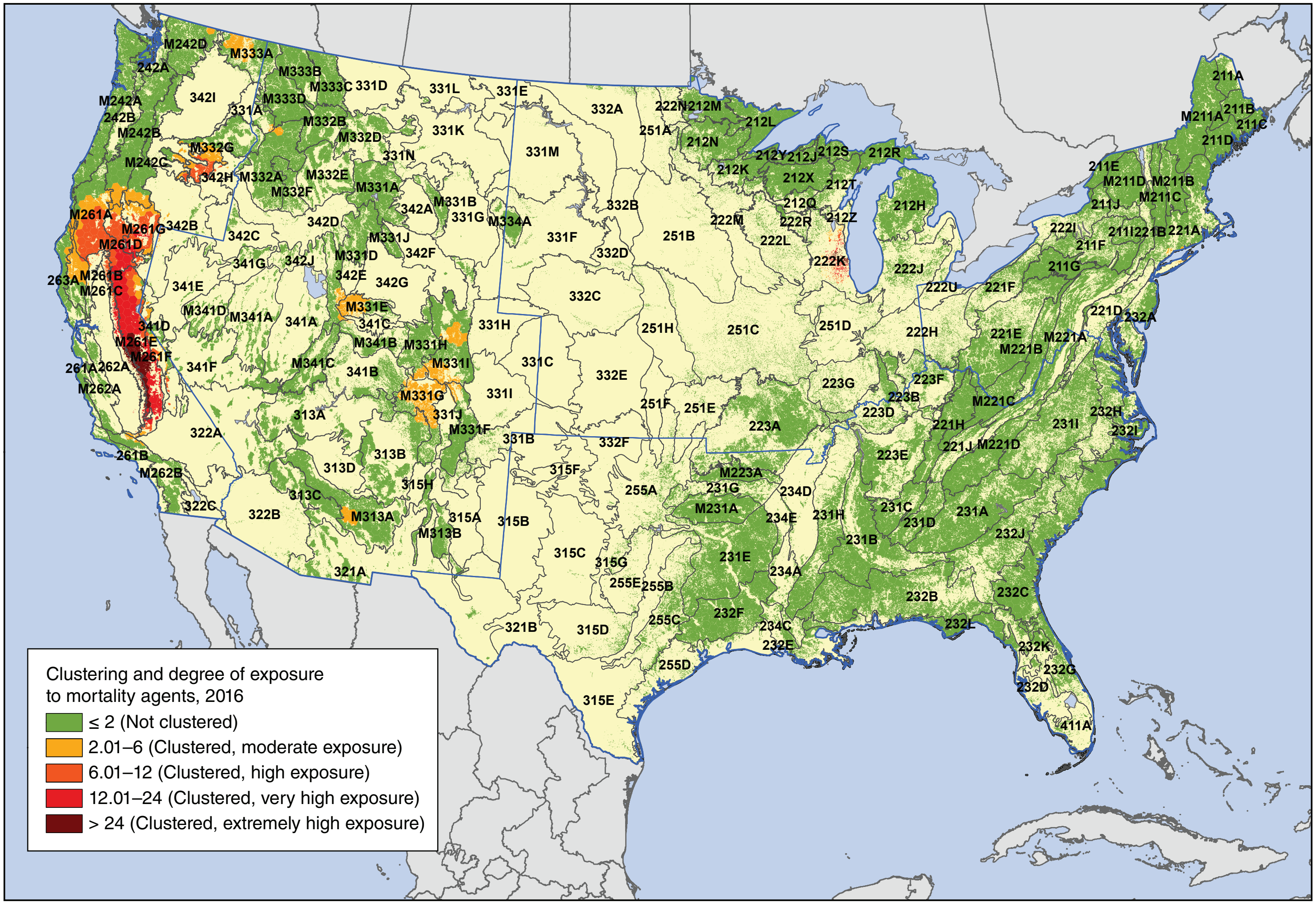

Figure 2.2—Hot spots of exposure to mortality-causing insects and diseases in 2016. Values are Getis-Ord G_i scores, with values > 2 representing significant clustering of high percentages of forest area exposed to mortality agents. (No areas of significant clustering of low percentages of exposure, < -2, were detected.) The gray lines delineate ecoregion sections (Cleland and others 2007), and blue lines delineate Forest Health Monitoring regions. Background forest cover is derived from MODIS imagery by the U.S. Forest Service Remote Sensing Applications Center. (Data source: U.S. Department of Agriculture, Forest Service, Forest Health Protection)*

in lodgepole pine and ponderosa pine and western pine beetle mortality in ponderosa pine (fig. 2.2). The same agents caused a hot spot of moderate mortality exposure in northeastern Washington State (M333A–Okanogan Highland).

The FHM Interior West region had approximately 503 000 ha on which mortality-causing agents and complexes were detected in 2016 (table 2.3), second only to the West Coast region. About 44 percent of this was associated with spruce beetle; other agents recorded on large areas were western balsam bark beetle (*Dryocoetes confusus*) (13 percent), mountain pine beetle (10 percent), and Douglas-fir beetle (*Dendroctonus pseudotsugae*) (8 percent). A total of 17 mortality agents and complexes were detected in the region.

The Getis-Ord analysis detected four hot spots of moderate mortality exposure in the Interior West region in 2016 (fig. 2.2). A relatively extensive spruce beetle infestation in Engelmann spruce (*Picea engelmannii*) caused a mortality hot spot in south-central Colorado, centered on M331I–Northern Parks and Ranges, M331G–South-Central Highlands, and M331F–Southern Parks and Rocky Mountain Range. Similarly, a moderate-intensity hot spot in M331E–Uinta Mountains of northeastern Utah was mainly associated with spruce beetle-caused mortality in Engelmann spruce. Another hot spot in northern Colorado (M331I–Northern Parks and Ranges) was the result of both western balsam bark beetle mortality in subalpine fir and spruce beetle mortality in Engelmann spruce. Finally, a small hot spot in M313A–White Mountains-San Francisco Peaks-Mogollon Rim in east-central Arizona was associated with fir engraver mortality in white fir stands, Douglas-fir beetle mortality in Douglas-fir stands, and unknown bark beetle mortality in ponderosa pine stands.

In the North Central FHM region, the FHP surveys recorded 17 mortality-causing agents and complexes on approximately 342 000 ha (table 2.3). Almost all of this area (288 000 ha, or 84 percent of the total) was exposed to emerald ash borer mortality. Other widespread agents and complexes were eastern larch beetle (*Dendroctonus simplex*) (8 percent of the mortality area) and Dutch elm disease (4 percent). Emerald ash borer was the cause of a hot spot of extremely high mortality exposure in 222K–Southwestern Great Lakes Morainal (fig. 2.2) along the western shore of Lake Michigan in Wisconsin.

In the North East FHM region, mortality was recorded on approximately 71 000 ha. The cause of about 35 percent of this mortality was not classified, but southern pine beetle was the most widely identified causal agent, found on 12 000 ha, or 17 percent of the total mortality area (table 2.3). Of the 28 agents and complexes detected in the region, three others affected areas exceeding 5000 ha: emerald ash borer, gypsy moth, and balsam woolly adelgid (*Adelges piceae*). One small geographic hot spot of mortality was detected in the North East FHM region, caused by southern pine beetle in pitch pine (*Pinus rigida*) stands on Long Island (221A–Lower New England).

In the South, mortality was detected on about 11 000 ha, with Ips engraver beetles the leading causal agent, on 6000 ha (53 percent of the total) (table 2.3). Emerald ash borer was associated with 3500 ha of mortality. No geographic hot spots of mortality were detected in the South FHM region.

Conterminous United States Defoliation

In 2016, the national IDS survey identified 63 defoliation agents and complexes affecting approximately 1.99 million ha across the conterminous United States (table 2.4), an area slightly less than the land area of Massachusetts. The most widespread defoliation agent was western spruce budworm (*Choristoneura occidentalis*), detected on approximately 916 000 ha. Three other insects—gypsy moth, forest tent caterpillar (*Malacosoma disstria*), and spruce budworm (*Choristoneura fumiferana*)—also affected more than 100 000 ha each (table 2.4).

The Interior West FHM region had the largest area on which defoliating agents and complexes were detected in 2016, approximately 969 000 ha (table 2.5), of which the vast majority (93 percent, or 898 000 ha) was associated with western spruce budworm (table 2.5). Unknown defoliators, Marssonina blight, and spruce aphid (*Elatobium abietinum*) were the next most widely detected defoliation agents of the 20 that were identified.

The 2016 Getis-Ord analysis detected several defoliation hot spots in the Interior West region (fig. 2.3). Most of these were associated with western spruce budworm

Table 2.4—Defoliation agents and complexes affecting more than 5000 ha in the conterminous United States in 2016

Agents/complexes causing defoliation, 2016	Area
	ha
Western spruce budworm	916 207
Gypsy moth	420 661
Forest tent caterpillar	330 362
Spruce budworm	111 714
Baldcypress leafroller	64 106
White pine needle damage	62 040
Browntail moth	28 401
Unknown defoliator	26 185
Marssonina blight	16 472
Loopers	15 786
Spruce aphid	13 041
Tamarisk leaf beetles	9178
Larch casebearer	7691
Unknown	7501
Winter moth	6981
Emerald ash borer	5085
Other (47)	43 428
Total, all defoliation agents	**1 991 682**

Note: All values are "footprint" areas for each agent or complex. The sum of the individual agents is not equal to the total for all agents due to the reporting of multiple agents per polygon.

Table 2.5—The top five defoliation agents or complexes for each Forest Health Monitoring region and for Alaska in 2016

Defoliation agents and complexes, 2016	Area
	ha
Interior West	
Western spruce budworm	897 507
Unknown defoliator	21 477
Marssonina blight	14 483
Spruce aphid	13 041
Tamarisk leaf beetles	9178
Other defoliation agents (15)	14 636
Total, all defoliation agents and complexes	**969 108**
North Central	
Spruce budworm	111 714
Forest tent caterpillar	15 793
Larch casebearer	7392
Jumping oak gall wasp	4988
Oak skeletonizer	4575
Other defoliation agents (12)	11 057
Total, all defoliation agents and complexes	**155 520**
North East	
Gypsy moth	398 354
White pine needle damage	62 040
Forest tent caterpillar	46 767
Browntail moth	28 401
Loopers	15 786
Other defoliation agents (21)	23 575
Total, all defoliation agents and complexes	**536 962**

Defoliation agents and complexes, 2016	Area
	ha
South	
Forest tent caterpillar	266 219
Baldcypress leafroller	64 106
Gypsy moth	22 005
Unknown	732
Fall cankerworm	364
Other defoliation agents (3)	188
Total, all defoliation agents and complexes	**299 696**
West Coast	
Western spruce budworm	18 700
Lophodermium needle cast of pines	3371
Needlecast	2652
Marssonina blight	1989
Larch needle cast	1171
Other defoliation agents (11)	2575
Total, all defoliation agents and complexes	**30 396**
Alaska	
Aspen leafminer	82 581
Speckled green fruitworm	65 521
Willow leaf blotchminer	59 129
Unknown defoliator	37 934
Spruce aphid	13 971
Other defoliation agents (8)	13 310
Total, all defoliation agents and complexes	**272 301**

Note: The total area affected by other agents is listed at the end of each section. All values are "footprint" areas for each agent or complex. The sum of the individual agents is not equal to the total for all agents due to the reporting of multiple agents per polygon.

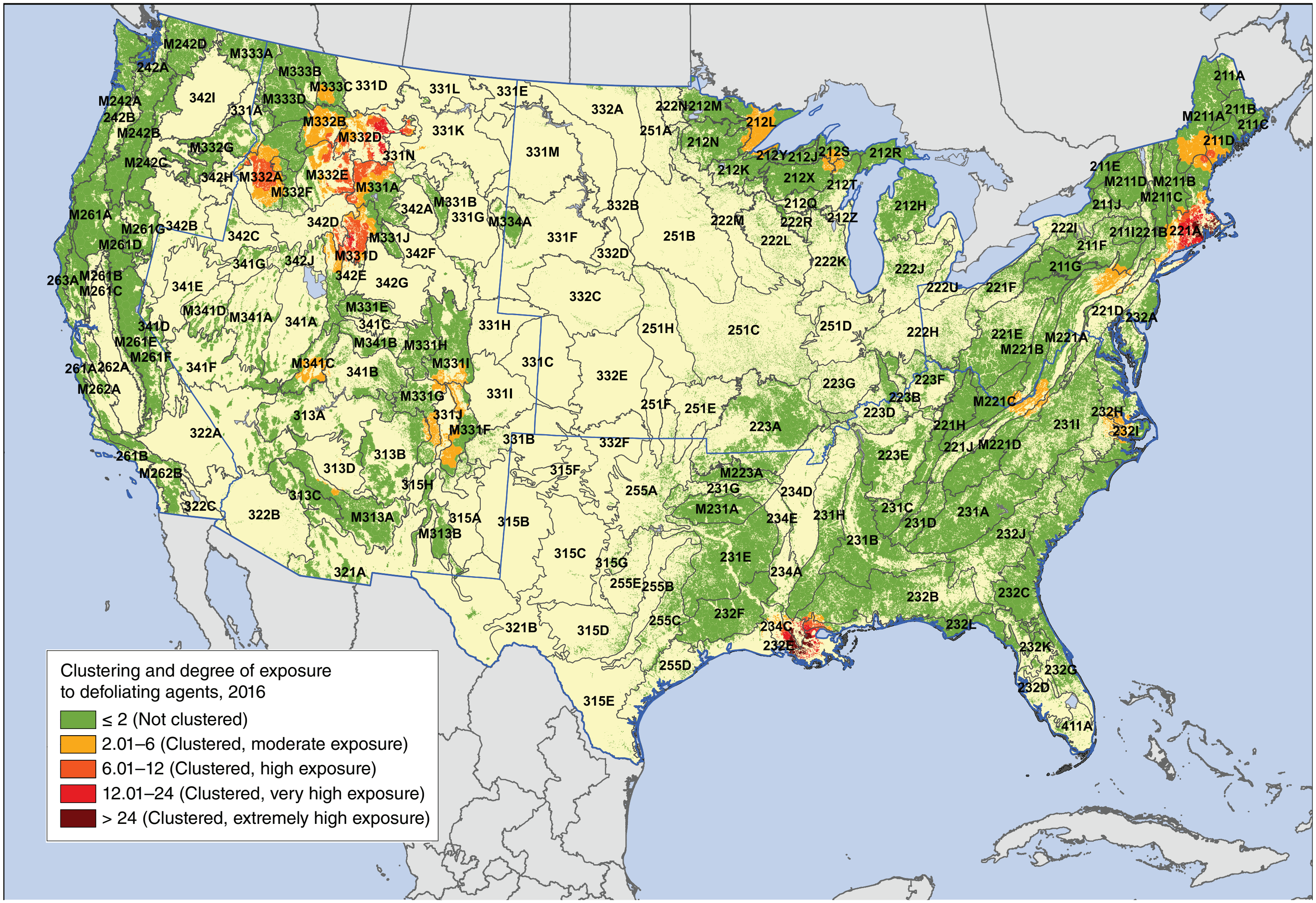

Figure 2.3—Hot spots of exposure to defoliation-causing insects and diseases in 2016. Values are Getis-Ord G_i scores, with values > 2 representing significant clustering of high percentages of forest area exposed to defoliation agents. (No areas of significant clustering of low percentages of exposure, < -2, were detected.) The gray lines delineate ecoregion sections (Cleland and others 2007), and blue lines delineate Forest Health Monitoring regions. Background forest cover is derived from MODIS imagery by the U.S. Forest Service Remote Sensing Applications Center. (Data source: U.S. Department of Agriculture, Forest Service, Forest Health Protection)*

(along with other agents) and overlapped a similar hot spot from 2014 (Potter and Paschke 2016) and 2015 (Potter and Paschke 2017). The largest of these, of very high defoliation exposure in western Montana, was centered on M332D–Belt Mountains, M332E–Beaverhead Mountains, M332B–Northern Rockies and Bitterroot Valley, and M331A–Yellowstone Highlands, roughly corresponding to hot spots the two previous years. It was associated with western spruce budworm in subalpine fir and Douglas-fir forests. Also as in 2014 and 2015, western spruce budworm activity in Douglas-fir forests and subalpine fir resulted in a hot spot of high defoliation exposure in central Idaho (M332A–Idaho Batholith) as well as one of very high and high exposure in western Wyoming and southeastern Idaho (M331D–Overthrust Mountains).

Again, as in recent years, western spruce budworm outbreaks also resulted in hot spots of defoliation in north-central New Mexico and south-central Colorado, in M331G–South-Central Highlands, M331F–Southern Parks and Rocky Mountain Range, and M331I–Northern Parks and Ranges (fig. 2.3). Another hot spot of moderate western spruce budworm defoliation exposure appeared in M341C–Utah High Plateau.

Twenty-six defoliation agents and complexes were identified on about 537 000 ha in the North East FHM region, with gypsy moth the most widely detected on more than 74 percent of this area (more than 398 000 ha). White pine needle damage was recorded on more than 62 000 ha, forest tent caterpillar on nearly 47 000 ha, and browntail moth (*Euproctis chrysorrhoea*) on 28 000 ha (table 2.5). One gypsy moth outbreak in Massachusetts, Rhode Island, and Connecticut resulted in a hot spot of extremely high defoliation exposure in 221A–Lower New England, while another in eastern Pennsylvania generated a hot spot of moderate defoliation exposure centered in M221A–Northern Ridge and Valley (fig. 2.3). Meanwhile, a third hot spot in the North East region was located in southern Maine and northern New Hampshire (211D–Central Maine Coastal and Embayment, 221A–Lower New England, and M211A–White Mountains), associated with white pine needle damage, browntail moth, winter moth (*Operophtera brumata*), and forest tent caterpillar.

In 2016, approximately 300 000 ha of defoliation was documented in the South FHM region. Almost 89 percent of this, or 266 000 ha, was associated with forest tent caterpillar (table 2.5). An additional seven agents and complexes were found, including baldcypress leafroller (*Archips goyerana*) on about 64 000 ha and gypsy moth on about 22 000 ha. A hot spot of extremely high exposure to defoliating agents, caused by both baldcypress leafroller and forest tent caterpillar, was located in three ecoregions of southern Louisiana, 234C–Atchafalaya and Red River Alluvial Plains, 234A–Southern Mississippi Alluvial Plain, and 232E–Louisiana Coastal Prairie and Marshes (fig. 2.3). Another hot spot of moderate defoliation exposure associated with forest tent caterpillar was detected in eastern North Carolina (in 232H–Middle Atlantic Coastal

Plains and Flatwoods and 232I–Northern Atlantic Coastal Flatwoods). Finally, a third hot spot, also of moderate exposure, was caused by gypsy moth and emerald ash borer in M221A–Northern Ridge and Valley, M221D–Blue Ridge Mountains, M221C–Northern Cumberland Mountains, and M221B–Allegheny Mountains.

Meanwhile, 17 agents and complexes were associated with about 156 000 ha of defoliation in the North Central FHM region (table 2.5). Spruce budworm was the most commonly detected defoliation agent in the region, found on a little less than 112 000 ha, or 72 percent of the defoliated area. Other widespread defoliators were forest tent caterpillar and larch casebearer (*Coleophora laricella*), affecting approximately 16 000 ha and 7000 ha, respectively (table 2.5). Our geographic hot spot analysis detected two clusters of moderate defoliation exposure in North Central FHM region (fig. 2.3). One in northeastern Minnesota (212L–Northern Superior Uplands) was associated with spruce budworm and forest tent caterpillar, and one in the Upper Peninsula of Michigan (at the intersection of 212S–Northern Upper Peninsula, 212X–Northern Highlands, and 212T–Northern Green Bay Lobe) was associated with spruce budworm and large aspen tortrix (*Choristoneura conflictana*).

Finally, western spruce budworm accounted for about 62 percent of the approximately 30 400 ha of defoliation recorded in the FHM West Coast region (table 2.5). Of the 16 defoliation agents and complexes detected in the region, the next most widely found was Lophodermium needle cast of pines (*Lophodermium* spp.) on 3400 ha. No geographic hot spots of defoliation were identified in the region.

Alaska and Hawaii

In Alaska, mortality was recorded on approximately 98 000 ha in 2016, attributed to five agents and complexes (table 2.3). This is a very small proportion (< 0.25 percent) of the forested area surveyed. Spruce beetle was the most widely detected mortality agent, recorded on about 76 000 ha, thereby encompassing about 78 percent of all mortality. Most of this mortality occurred in the south-central part of the State (especially in 213B–Cook Inlet Lowlands and M135C–Alaska Range). Yellow-cedar (*Chamaecyparis nootkatensis*) decline was the next most widely detected mortality agent, found on about 16 000 ha in the Alaska panhandle (M245B–Alexander Archipelago). Northern spruce engraver (*Ips perturbatus*) was detected on about 6000 ha, mostly in the east-central forested areas of Alaska.

The percentage of surveyed forest exposed to mortality agents in 2016 was highest in 213B–Cook Inlet Lowlands, where it was 5.9 percent (fig. 2.4) as a result of spruce beetle damage. Relatively high percentages of mortality were detected in the surveyed areas of M135C–Alaska Range (2.5 percent) and M245B–Alexander Archipelago (1.0 percent).

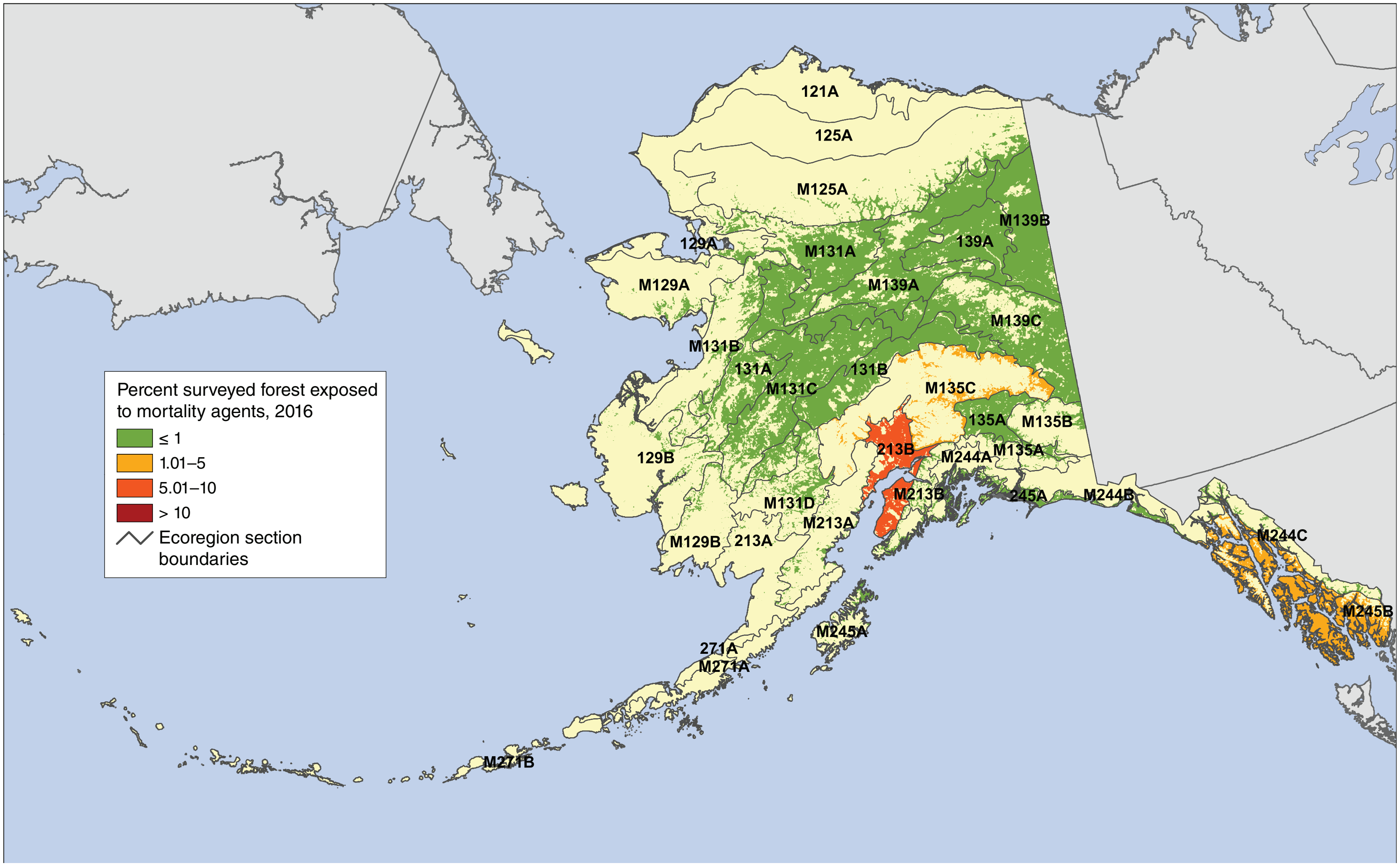

Figure 2.4—Percentage of surveyed forest in Alaska ecoregion sections exposed to mortality-causing insects and diseases in 2016. The gray lines delineate ecoregion sections (Nowacki and Brock 1995). Background forest cover is derived from MODIS imagery by the U.S. Forest Service Remote Sensing Applications Center. (Data source: U.S. Department of Agriculture, Forest Service, Forest Health Protection)

Meanwhile, defoliators in Alaska were detected on nearly three times as much surveyed area than mortality during 2016, with 13 defoliating agents recorded on approximately 272 000 ha (table 2.5). Of this area, about 30 percent (83 000 ha) was attributed to aspen leafminer (*Phyllocnistis populiella*). Meanwhile, speckled green fruitworm (*Orthosia hibisci*) was detected on about 65 500 ha, and willow leaf blotchminer (*Micrurapteryx salicifoliella*) was recorded on 59 000 ha.

The Alaska ecoregion section with the highest proportion of surveyed forest area affected by defoliators in 2016 was 139A–Yukon Flats (9.4 percent of surveyed forest) (fig. 2.5), where willow leaf blotchminer and aspen leafminer were commonly reported in willow (*Salix* spp.) and quaking aspen (*Populus tremuloides*) stands. Several ecoregion sections in the central and southwestern parts of Alaska had moderate levels of detected defoliation, including M213A–Northern Aleutian Range (6.3 percent, speckled green fruitworm in hardwood stands), M135C–Alaska Range (4.4 percent, also speckled green fruitworm), and M129B–Ahklun Mountains (4.0 percent, speckled green fruitworm and willow leaf blotchminer).

In 2016, approximately 18 000 ha of mortality was recorded in Hawaii (table 2.3), with about half of unknown cause and half attributed to rapid ʻōhiʻa death, a wilt disease caused by the fungal pathogen *Ceratocystis fimbriata* that affects ʻōhiʻa lehua *(Metrosideros polymorpha)*, a highly ecologically and culturally important tree species in Hawaiian native forests (University of Hawaiʻi 2017).

CONCLUSION

Continued monitoring of insect and disease outbreaks across the United States will be necessary for determining appropriate followup investigation and management activities. Due to the limitations of survey efforts to detect certain important forest insects and diseases, the pests and pathogens discussed in this chapter do not include all the biotic forest health threats that should be considered when making management decisions and budget allocations. However, large-scale assessments of mortality and defoliation exposure, including geographical hot spot detection analyses, offer a useful approach for identifying geographic areas where the concentration of monitoring and management activities might be most effective.

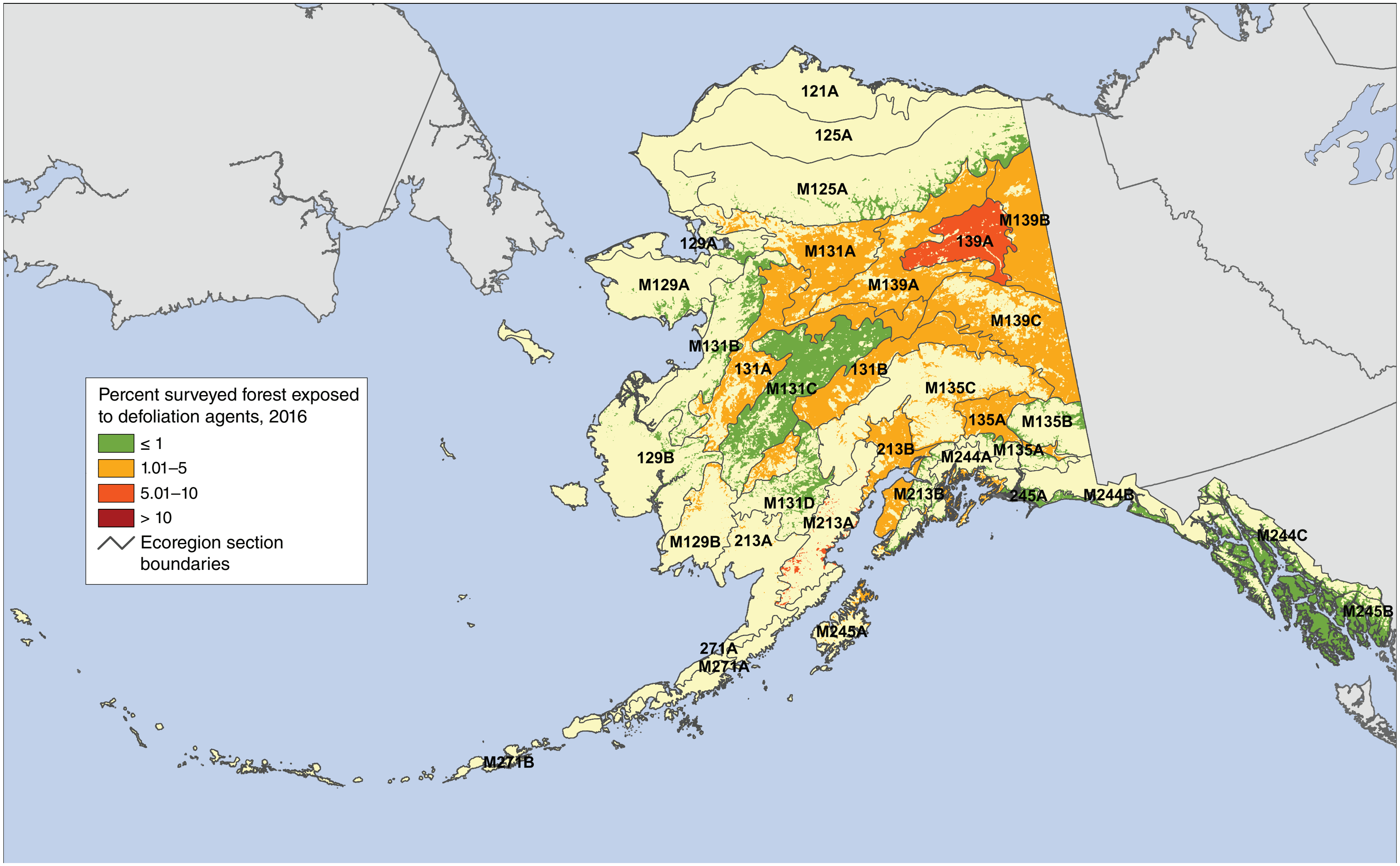

Figure 2.5—Percentage of surveyed forest in Alaska ecoregion sections exposed to defoliation-causing insects and diseases in 2016. The gray lines delineate ecoregion sections (Nowacki and Brock 1995). Background forest cover is derived from MODIS imagery by the U.S. Forest Service Remote Sensing Applications Center. (Data source: U.S. Department of Agriculture, Forest Service, Forest Health Protection)

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