

PREDICTING CLIMATE CHANGE EXTIRPATION RISK FOR CENTRAL AND SOUTHERN APPALACHIAN FOREST TREE SPECIES

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Abstract.—Climate change will likely pose a severe threat to the viability of certain forest tree species, which will be forced either to adapt to new conditions or to shift to more favorable environments if they are to survive. Several forest tree species of the central and southern Appalachians may be at particular risk, since they occur in limited high-elevation ranges and/or are currently threatened by nonnative insects and diseases. We are beginning an assessment of potential climate change impacts on more than 100 North American forest tree species, using the innovative Multivariate Spatio-Temporal Clustering (MSTC) technique. Combining aspects of traditional geographical information systems and statistical clustering techniques, MSTC statistically predicts environmental niche envelopes to forecast species' geographic ranges under altered environmental conditions such as those expected under climate change. We outline the objectives of this project, present some preliminary results for central and southern Appalachian tree species, and discuss the need for assistance from fellow scientists in the development of this work.

INTRODUCTION

Climate change is expected to result in extensive ecological, social, and economic effects for the forests of the United States (Malmsheimer et al. 2008). Climate change probably will threaten the viability of certain forest tree species, which will be forced either to adapt to new conditions or to shift their ranges to more favorable environments. Animal and plant species, including trees, are already exhibiting changes in phenology and distribution in response to climate change (Parmesan and Yohe 2003, Woodall et al. 2009), and many species are expected to go extinct as their access to suitable habitat becomes more limited (Thomas et al. 2004). Forest tree species with already limited ranges may be at particular risk (Schwartz et al. 2006).

High-elevation species, including those whose distributions include the central and southern Appalachian Mountains,

may be at elevated risk from climate change because of their tendency toward naturally small, isolated, and fragmented populations, which, in some cases, may result in lower genetic diversity and/or inter-population gene exchange (e.g., Potter et al. 2008b, Tang et al. 2008). Additionally, some high-elevation endemics may lack suitable habitat in which to move to match changes in climate, especially if changing climate conditions and inter-specific competition force these species to move their distributions toward higher elevations, which may not exist. Delcourt and Delcourt (1998), for example, predict that a 3 °C increase in the mean July temperature would raise climatically limited ecotones by ~480 m. This increase could result in the extinction of red spruce-Fraser fir forests in the southern Appalachians because these forests are already confined to the highest mountain elevations. The potential impacts of climate change on high-elevation species is of particular concern given the high biological diversity harbored by mountain systems, caused by the compression of climatic life zones and by small-scale habitat diversity (Koerner and Spehn 2002, Koerner and Ohsawa 2005).

Evolutionary biologists predict that plant species will respond in one of three ways to changes that push their current habitat out of their climatic tolerance limits: 1)

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adaptation, 2) migration (range shift), or 3) extirpation (Davis et al. 2005).

Although some evidence exists that trees have the capacity to evolve rapidly to new environmental conditions (Petit et al. 2004), adaptation via natural selection may be unlikely in many cases, given the long generation time for forest tree species (St. Clair and Howe 2007). Rehfeldt et al. (1999), for example, predict that tree adaptation to climate change would take 1 to 13 generations, or 100 to 1,000 years.

Tree species successfully migrated long distances during the climate changes of the Pleistocene, but may not be able to match climate shifts anticipated in the near future because they are expected to occur much more rapidly (Davis and Shaw 2001). Even when tree species possess propagule dispersal mechanisms that allow them to shift their ranges, their effective migration may be impeded by forest fragmentation (Opdam and Wascher 2004), they may experience inbreeding-reduced genetic diversity as a result of founder effects (Petit et al. 2004), and their genetically important “trailing edge” populations may be extirpated (Hampe and Petit 2005). It is worth noting that some of the most genetically distinct Appalachian populations of at least one forest tree species, eastern hemlock (*Tsuga canadensis* [L.] Carr.), are located near the very southern end of the range (Potter et al. 2008a).

Forest tree species or populations that are not able to shift their distribution or adapt in response to changing climatic conditions may instead face extinction or local extirpation. This possibility may be a concern particularly for species that have narrow habitat requirements, are located exclusively at high elevations, and/or are not able to disperse their propagules effectively across long distances. Even if not extirpated outright, populations of these and other species could experience significant inbreeding, genetic drift, and decreased genetic variation as a result of reduced population size. Such populations may then become more susceptible to mortality caused both by nonnative pests and pathogens and by the environmental pressures associated with climate change. This susceptibility could generate a cycle of mortality, loss of genetic variation, and inability to adapt to change that could ultimately result in population extirpation (Fig. 1).

Within the central and southern Appalachians, three forest tree taxa likely to be at greatest risk of extinction as a result of climate change are Fraser fir (*Abies fraseri* [Pursh] Poir.), intermediate balsam fir (*Abies balsamea* [L.] Mill. var. *phanerolepis* Fern.), and Carolina hemlock (*Tsuga caroliniana* Engelm.). All three are limited to small, high-elevation populations, and are under siege from exotic pests: the balsam woolly adelgid (*Adelges piceae* Ratz.) in the case of Fraser fir (Dull et al. 1988) and intermediate balsam fir (Bross-Fregonara 2002), and hemlock woolly adelgid (*Adelges tsugae* Annand) in the case of Carolina hemlock (Jetton et al. 2008). Other species, such as Table Mountain pine (*Pinus pungens* Lamb.), red spruce (*Picea rubens* Sarg.), and striped maple (*Acer pensylvanicum* L.) are less likely to experience range-wide extinction, but could have their southern and central Appalachian populations eliminated as a result of changing climate conditions. These populations may contain unique genotypes resulting from long-term biogeographical processes and from selection pressures that may be different from those experienced by these species in their more northerly populations.

We are in the early stages of a large-scale assessment of the risk posed by climate change to the genetic integrity of many North American species. Central to this project is the application of the innovative Multivariate Spatio-Temporal Clustering (MSTC) technique (Hargrove and Hoffman 2005). We are using MSTC to predict the future location and quality of habitat for tree species and, along with consideration of species' biological attributes, will assess whether range-shifting tree species might be able to track appropriate environmental conditions over time and avoid the loss of extensive genetic variation. We here present preliminary results for four southern and central Appalachian forest tree species.

METHODS

The U.S. Department of Agriculture Forest Service Forest Health Monitoring (FHM) program recently identified climate change as a priority area for funding projects through its Evaluation Monitoring grant program. Additionally, attendees at the annual FHM Working Group meeting in 2008 approved a resolution calling for a baseline

assessment of the climate change-associated risks of genetic degradation, local extirpation, or species-wide extinction of North American tree species.

That assessment will address three central questions: 1) Given the current distributions of forest tree species, where will the appropriate environmental conditions exist for each species in 2050 and 2100 under two climate change scenarios? 2) What portions of tree species' ranges are most at risk of extirpation because of their distance to expected future habitat, and how likely will they be to traverse that distance given existing forest fragmentation en route? 3) What is the risk of genetic degradation to populations of each tree species, given what we know about the biology of these species and the landscape of change they face?

Much innovative work has predicted the distribution of forest tree species under climate change (Iverson et al. 2004a, b; Rehfeldt et al. 2006; Schwartz et al. 2006). An assessment of the potential genetic impacts of climate change on forest tree species, however, requires a tool that:

- Can predict changes in appropriate habitat for a large number of species (in this case, approximately 200 across all regions of North America).
- Allows for flexible data inputs on the current locations for forest tree species occurrences, including for rare species that do not occur in the USDA Forest Service Forest Inventory and Analysis (FIA) database.
- Generates relatively high-resolution results applicable at the population level.
- Can predict acceptable habitat globally; this capability has the advantage of determining potential suitable habitat for U.S. species in Canada and Mexico, for example, and also allows for investigating any species worldwide for which we have good location information.
- Incorporates the pertinent environmental variables that determine plant distributions.

The MSTC approach developed by Hargrove and Hoffman (2005) meets these requirements. MSTC applies aspects of traditional geographic information systems (GIS) and statistical clustering techniques to statistically predict

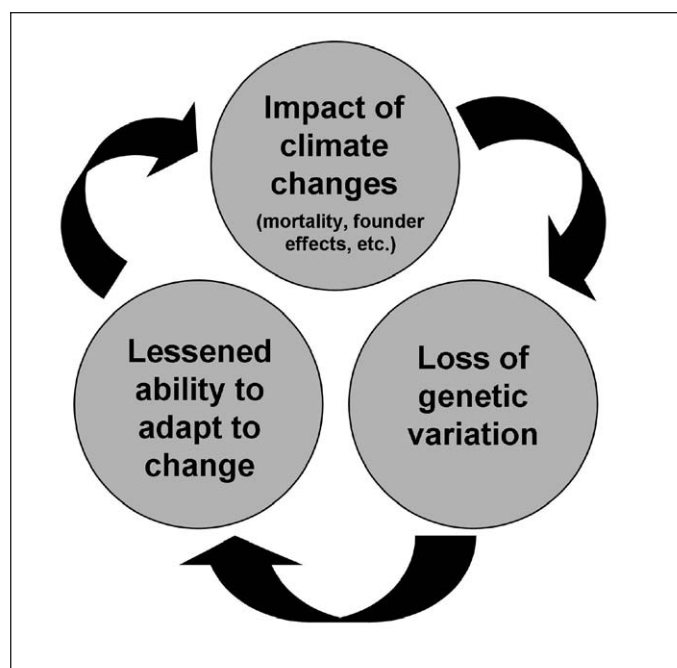


Figure 1.—The potential feedback cycle in which the impacts of climate change result in the loss of genetic variation within declining forest tree populations, which may in turn decrease the ability of those populations to adapt to change. A lessened ability to adapt to change may, finally, magnify additional future impacts of climate change. Note that this cycle would apply to declining species, but that some species may benefit genetically from the effects of climate change.

species' environmental niche envelopes. This approach can be used to forecast a species' geographic range under altered environmental conditions such as those expected with global climate change (Hargrove and Hoffman 2003). Global in scope, it incorporates 16 spatial environmental variables (Table 1) and generates maps at a resolution of 4 km².

MSTC employs nonhierarchical clustering on the individual pixels in a digital map from a GIS to classify the cells into types or categories. The technique uses the standardized values of each environmental condition for every raster cell in the map as a set of coordinates that together specify a position for that raster cell in a data space having a dimension for each of the included environmental characteristics. Two raster cells from anywhere in the map with similar combinations of environmental characteristics will be located near each other in this data space. Their proximity and relative positions in the data space will quantitatively reflect their environmental similarities,

allowing these cells to be classified into environmentally similar groups or “ecoregions” (Hargrove and Hoffman 2003, 2005). The MSTC process allows the user to determine the coarseness of the output maps, which display each 4 km² pixel within an “ecoregion” with other pixels possessing similar environmental conditions. The user can, in other words, choose whether the map contains many small ecoregions, each containing little environmental heterogeneity, or only a few ecoregions, each containing a relatively large amount of environmental heterogeneity. (Within a given map, each ecoregion contains roughly equal environmental heterogeneity; maps depicting coarser divisions contain greater heterogeneity within ecoregions than do maps depicting finer divisions.) The results presented here were generated using a fine division of the 4 km² pixels globally into 30,000 ecoregions.

For the first part of this assessment project, MSTC will predict the location and quality of habitat for at least 100 forest tree species under two climate change scenarios in 2050 and 2100 under the Hadley model and Parallel Climate Model, each under the A1 (higher-emissions) and B1 (lower-emissions) scenarios. Existing FIA data (USDA Forest Service 2009) will be used as training data for most species, providing the location of species and an “importance value” that represents the fitness of the species at each location. For rare tree species not well sampled by FIA, training data will come from other sources. These training data are used to determine the current environmental envelope or niche for each species by selecting the ecoregions containing two or more species occurrences using the FIA data. These current ecoregions are then compared to future ecoregions generated by MSTC under the various climate change scenarios; the future ecoregions most similar to current ecoregions in which the species of interest occurs therefore encompass the future areas with the closest fit to the current environmental niche for that species.

Table 1.—Spatial environmental variables included in the Multivariate Spatio-Temporal Clustering (MSTC) analysis.

Category	Spatial environmental variable
Soil	Plant-available water capacity
	Bulk density of soil
	Kjeldahl soil nitrogen
	Organic matter in soil
Temperature	In the coldest quarter
	In the warmest quarter
	Diurnal temperature difference
	Biotemperature
	Solar insolation
Precipitation	In the driest quarter
	In the wettest quarter
	In the warmest quarter
	In the coldest quarter
	Ratio of precipitation to evapotranspiration
Topography	Compound topographic index (convexness or concavity)
Growing season	Length in integer months

Although somewhat time-consuming in initial implementation, MSTC allows for the relatively rapid testing of many species, unlike the Regression Tree Analysis approaches often used to generate predictions of suitable habitat for tree species. Additionally, unlike Regression Tree Analyses, MSTC is a multivariate approach that includes all the variables simultaneously and that does not require imposing an importance order for the variables included. Finally, MSTC avoids the Regression Tree Analysis tendency to overfit models of suitable species habitat.

The primary products of this work will be an extensive number of large-scale, ~4 km² resolution maps for more than 100 North American tree species. These will be packaged and available to the public as part of a new online assessment of North American forest trees’ genetic risk induced by climate change.

The current analysis reported here is limited to a handful of forest tree species present in the central and southern Appalachians. FIA occurrence data were used as the training data for three species: red spruce, mountain magnolia (*Magnolia fraseri* Walt.), and striped maple. For the larger

species, red spruce and mountain magnolia, these data encompassed plots containing at least one tree greater than 10 inches diameter at breast height (d.b.h.) or 30 feet in height. For striped maple, a smaller species, the plots included were those containing a tree greater than 5 inches d.b.h. or 20 feet tall. Other, more appropriate species location data were used for the rare species included in the study, Fraser fir and Carolina hemlock.

We note that the 4 km² resolution of the analysis could miss some important microhabitats for certain tree species. However, the use of coarser resolution data was the tradeoff for being able to use the MSTC approach at a global level, which we believe is an important advantage of MSTC. The goal of the analysis is to be able to predict general areas of current and future habitat suitability, some of which may be unexpected. Other approaches could then be employed to investigate habitat suitability at a finer resolution.

For the second part of the project, MSTC will measure the straight-line Minimum Required Migration (MRM) distance from each 4 km² grid cell in each species' existing distribution to the nearest favorable future habitat. The greater this distance, the less likely that the species will be able to reach the nearest future refuge, and the more likely that the species will become locally extinct. Information on the locations of future refuges will be integrated with existing forest fragmentation data to quantify the quality of those refuges and to determine the amount of biotic "resistance" species are likely to encounter as their ranges shift toward those refuges.

During the third part of the project, we will work with forest geneticists and ecologists to assess the risk of genetic degradation, including the susceptibility of extinction in all or part of the current range, for several forest tree species. Revolving around a set of factors that could increase the risk of genetic degradation for a tree species or population (Table 2), this analysis will synthesize results from the first two parts of the project with existing knowledge about the biology and genetic diversity of each species. It will incorporate the MSTC climate envelope maps, the MRM distance maps, information about the biology of individual tree species, knowledge about extrinsic factors impacting

those tree species (including forest fragmentation, pest or pathogen infestation, or over-exploitation), and our understanding of population genetic processes.

RESULTS AND DISCUSSION

To demonstrate the utility of this work to predicting the location of appropriate habitat for high-elevation species over time, we generated climate change prediction maps for four species based on the Hadley A1 (higher-emissions) scenario in 2050 and 2100: Carolina hemlock (Fig. 2), mountain magnolia (Fig. 3), red spruce (Fig. 4), and Fraser fir (Fig. 5). Within each figure, the green dots represent the species' occurrence locations used as training points in developing the maps. The red areas are regions environmentally identical to locations in which the species currently occurs, while darker gray shades indicate locations that are increasingly similar to the locations in which the species occurs. It is important to note that darker areas in the map do not necessarily represent suitable habitat, but rather are areas similar to habitat that we know to be suitable based on known existing species locations – the red areas that match current known occurrence locations of the species in question. This approach allows map users to determine the appropriate thresholds of similarity when assessing future suitable habitat for a given species.

The preliminary results presented here suggest that, at least under the Hadley A1 scenario, suitable habitat for several forest tree species of the central and southern Appalachian Mountains could expand somewhat by 2050, and then contract by 2100. For example, MSTC predicts that Carolina hemlock will see a dramatic expansion of matching (red) habitat to the east and west of the Appalachian core by 2050, followed by a contraction to fairly isolated higher-elevation patches by 2100 (Fig. 2). Mountain magnolia (Fig. 3), meanwhile, may have additional matching habitat to the southeast and northeast by 2050, but much of this habitat, as well as currently matching habitat to the west and north, may become less suitable by 2100. Red spruce (Fig. 4) may see a slight advance of matching habitat in the central and southern Appalachians by 2050, but some of this habitat disappears by 2100. It would be difficult to determine specifically which changing environmental conditions might

Table 2.—Factors, both intrinsic and extrinsic to a species or population of forest trees, that increase its risk of extinction, extirpation, or genetic degradation.

Intrinsic factors	Extrinsic factors
Limited range	Extensive fragmentation
Small/disjunct populations	Pest/pathogen infestation
Limited to high elevations	Large shift of range with climate change
Long lifespan	Exploitation
Long time to reproduction	Exposure to atmospheric deposition
Low fecundity	Geographic dispersal barriers ^a
Physical habitat specialization	Anthropogenic dispersal barriers ^a
Limited seed/pollen dispersal	Exposure to sea-level rise ^{a,b}
Low species-wide genetic variation	
Late successional species	
Dependence on specific disturbance regime ^a	
Reliance on interspecific interactions ^a	
Sensitivity to temperature and precipitation change ^a	
Lack of phenological flexibility ^a	

^a From Young et al. (2009).

^b Not applicable to the Appalachian Mountains.

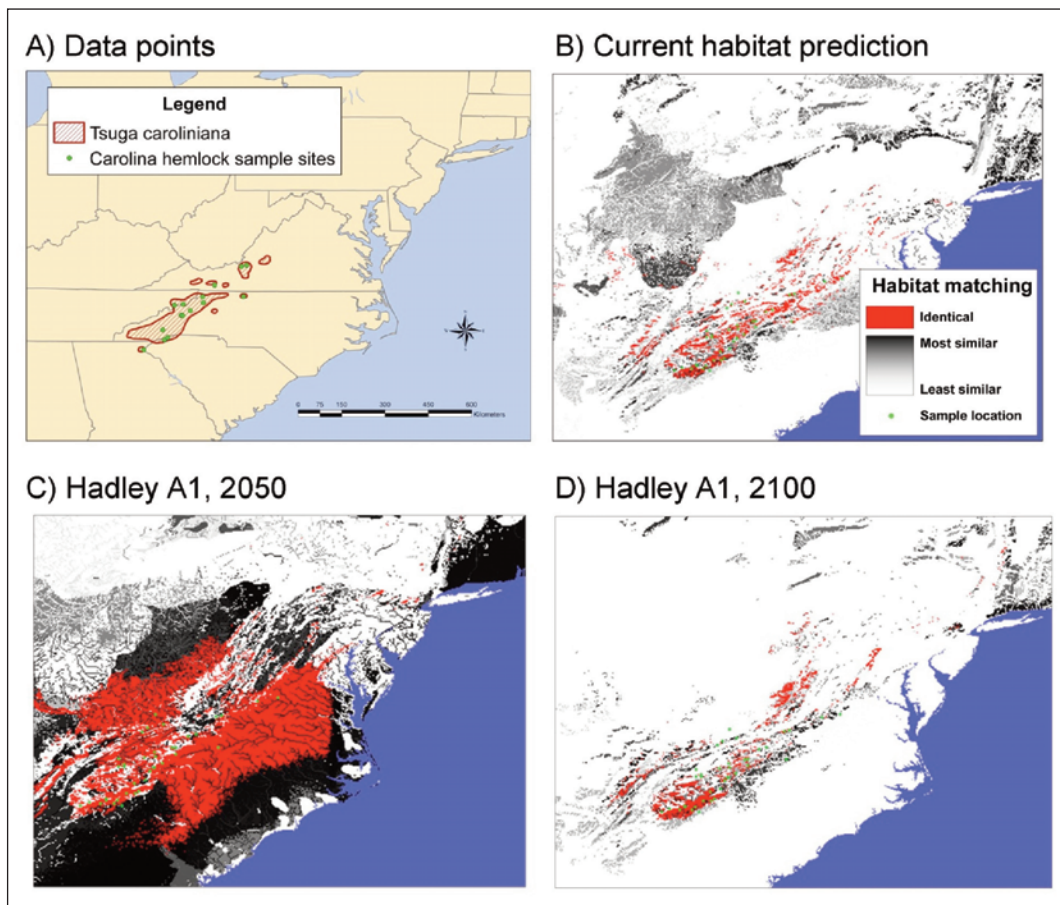


Figure 2.—Multivariate Spatio-Clustering predictions of current and future acceptable environmental conditions for Carolina hemlock. The coordinates of 15 known Carolina hemlock stands (the small green dots) were used along with FIA plot data as training data (A) to predict the location of currently acceptable habitat conditions (B), which was in turn used to predict the locations of acceptable environmental conditions in 2050 (C) and 2100 (D) using the Hadley A1 (higher-emissions) scenario.

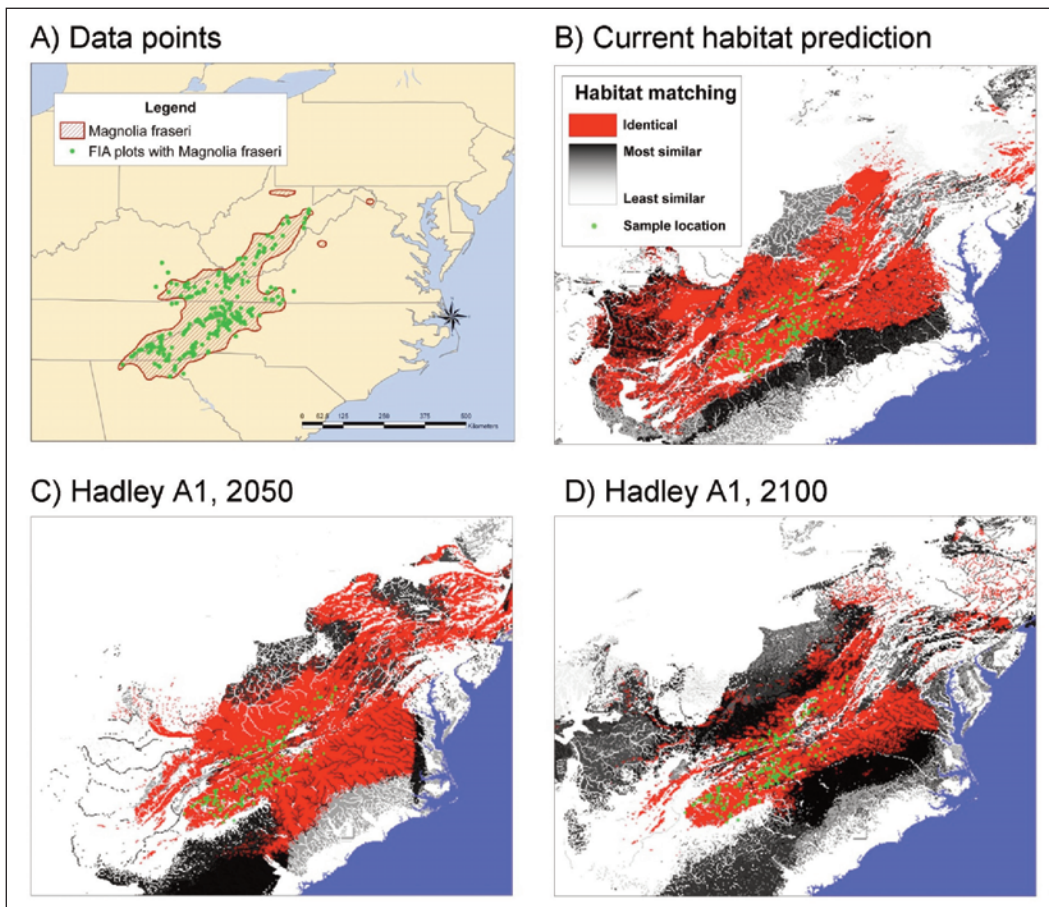


Figure 3.—Multivariate Spatio-Clustering predictions of current and future acceptable conditions for mountain magnolia. The small green dots in all four subfigures depict the 562 Forest Inventory and Analysis plot locations that were used as training data (A) to predict the location of currently acceptable habitat conditions (B), which was in turn used to predict the locations of acceptable environmental conditions in 2050 (C) and 2100 (D) using the Hadley A1 (higher-emissions) scenario.

cause this pattern, but these results suggest that, in general, the climatic and edaphic factors expected to occur under this climate change scenario might result in larger areas of acceptable habitat for red spruce than currently exist.

Somewhat surprisingly, Fraser fir (Fig. 5) showed a pattern of suitable habitat contraction in 2050 and slight expansion into 2100, with the matching habitat at the later date similar in extent to the current predicted matching habitat.

It is important to reiterate here that we are not, in fact, modeling habitat, but rather using an empirical clustering approach to predict habitat suitability in the present and the future based on the environmental characteristics existing at known locations of individual tree species. We are confident that the results are accurately predicting suitable habitat given the environmental variables we are using and the resolution at which these data are available. We acknowledge that in some cases the resolution of the data (4 km²) may result in missing some microhabitat niches that may be

important for certain Appalachian species. In such cases, we believe the results are still useful because they allow for the identification of places where other, finer-resolution analyses could help identify locations for habitat protection, gene conservation efforts, translocations of trees from other locations, and other measures.

Additionally, we plan to use one or more measurements of how well a species is adapted at each location in which it occurs, such as basal area or importance value derived from the FIA data, to further identify not only those areas that match any current habitat, but also those that match the best current habitat. We can then be more confident (given data limitations) that our maps will identify locations with the best current and future habitat suitability.

The results of this work will be valuable for scientists and policymakers attempting to determine which forest tree species and populations, in the face of climate change, should be targeted 1) for monitoring efforts, including

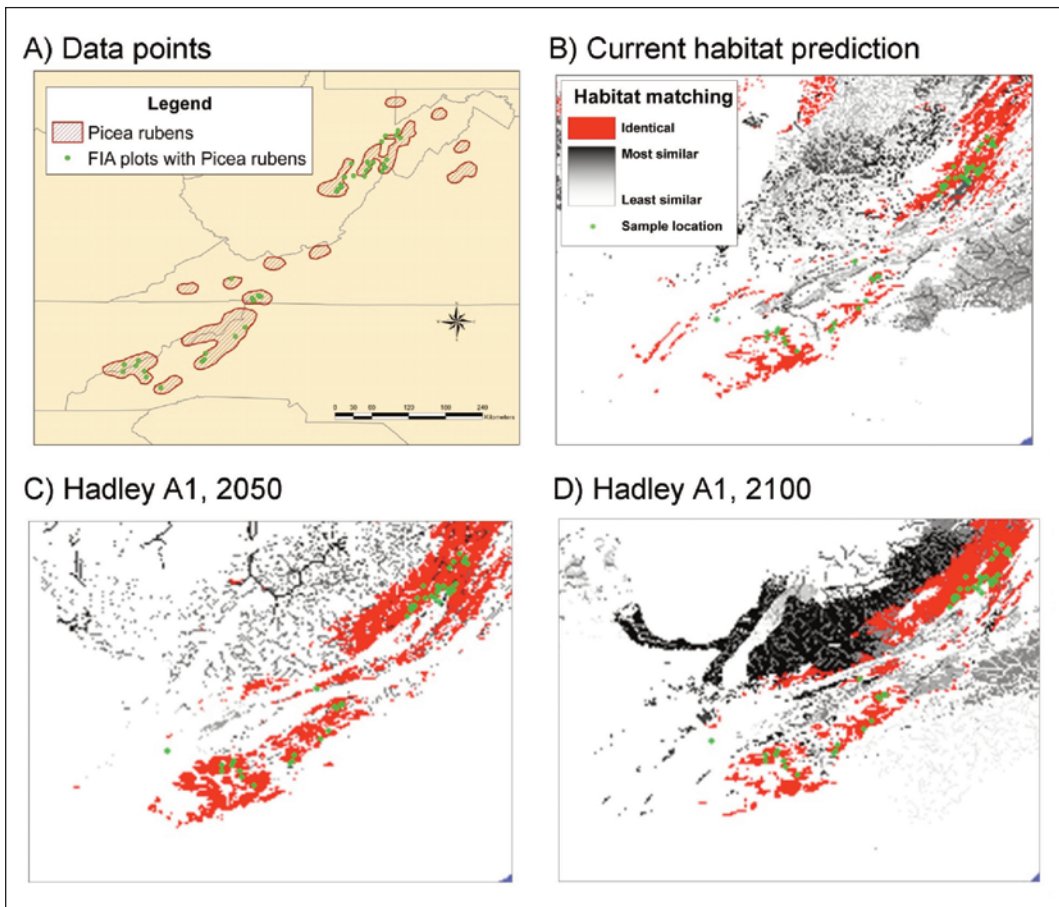


Figure 4.—Multivariate Spatio-Clustering predictions of current and future acceptable environmental conditions for red spruce in the central and southern Appalachian Mountains. The small green dots in all four subfigures depict the Forest Inventory and Analysis plot locations (2,274 plots across eastern United States) that were used as training data (A) to predict the location of currently acceptable habitat conditions (B), which was in turn used to predict the locations of acceptable environmental conditions in 2050 (C) and 2100 (D) using the Hadley A1 (higher-emissions) scenario.

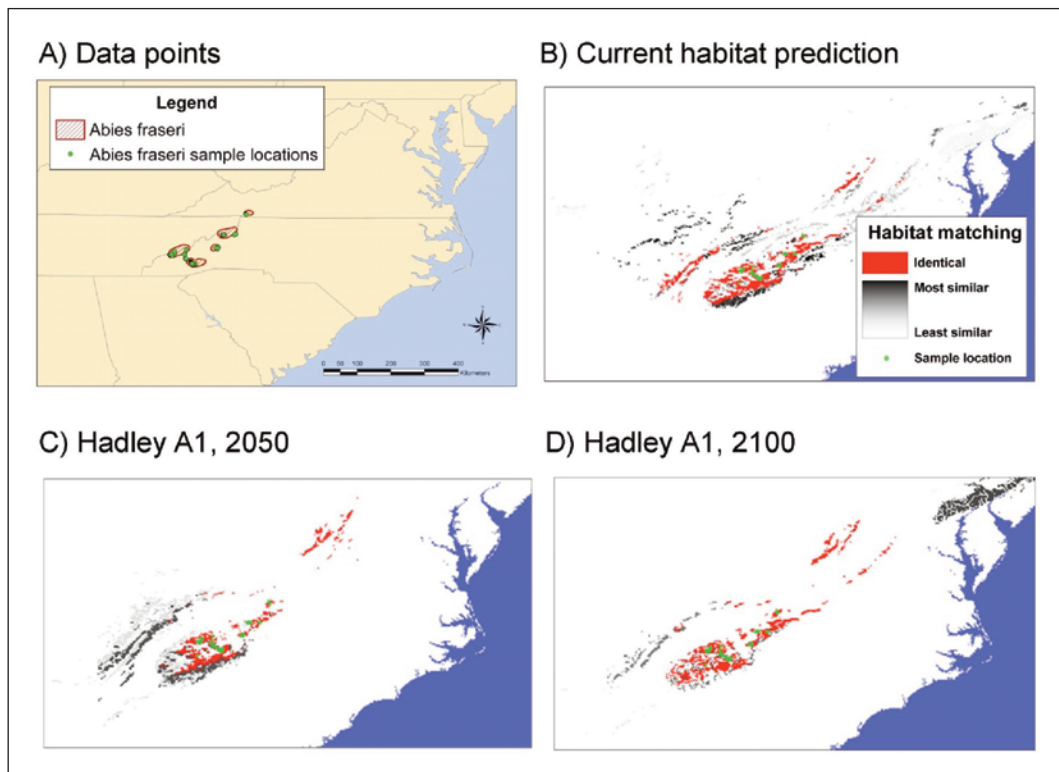


Figure 5.—Multivariate Spatio-Clustering predictions of current and future acceptable environmental conditions for Fraser fir. The coordinates of 302 known Fraser fir locations (the small green dots) were used as training data (A) to predict the location of currently acceptable habitat conditions (B), which was in turn used to predict the locations of acceptable environmental conditions in 2050 (C) and 2100 (D) using the Hadley A1 (higher-emissions) scenario.

FHM Detection Monitoring and Evaluation Monitoring activities; 2) for on-site and off-site conservation actions; and 3) for molecular marker studies that quantify the genetic architecture and diversity of at-risk species. The results also should be useful for land-use planners and conservation organizations interested in identifying geographic locations that could be preserved as important future habitat for at-risk tree species.

FUTURE WORK

This work is merely the beginning of a project that aims to predict suitable environmental conditions for more than 100 North American forest tree species, to quantify the distance between the current locations of these species and their future locations, and to assess whether these changes will negatively affect the genetic integrity of these species and their populations.

As we proceed, we will need assistance from forest ecologists, geneticists, and species specialists. Our most immediate need is to identify coordinate data of rare species and species with ranges that extend into Canada, since the FIA plot grid does not sample rare species well and is limited to the conterminous United States and southern Alaska.

In the longer term, we will need assistance from other scientists to assess the potential genetic impacts of climate change on North American forest tree species. These species-level assessments may be accomplished in the context of a Bayesian Belief Network approach, which is a tool that incorporates expert opinion into models of biological systems useful for making ecological predictions and aiding in resource-management decision-making (Marcot et al. 2006, McCann et al. 2006). Anyone interested in assisting should contact the lead author at the email address listed at the beginning of this paper.

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