

TITLE: Assessing Forest Tree Risk of Extinction and Genetic Degradation from Climate Change

LOCATION: North America

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DURATION: Year 2 of 3 years **FUNDING SOURCE:** Base

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PROJECT OBJECTIVES: This project has three central objectives: **1)** Forecast the location and quality of habitat for at least 100 North American tree species under two climate change scenarios across federal, state and private lands. **2)** Predict the risk of extirpation under climate change for each location at which these tree species currently exist. **3)** Assess the susceptibility of populations of these species to genetic degradation and extirpation based on these results and on the biological characteristics of each species.

JUSTIFICATION: 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 is likely to pose a severe threat to the viability of forest tree species themselves, 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), and many species are expected to go extinct as their access to suitable habitat decreases (Thomas et al. 2004). Forest tree species with limited ranges may be at particular risk (Schwartz et al. 2006), as may those currently threatened by non-native insects and diseases.

Climate change is currently a priority area identified for Forest Health Monitoring Base Evaluation Monitoring projects, and in 2008 attendees at the annual FHM Working Group meeting approved a resolution calling for a baseline assessment of the risk of climate change causing or increasing the susceptibility of genetic degradation, local extirpation or species-wide extinction in North American tree species. Such a study, across all forest types and ownerships, is possible for a large number of North American species through the application of the innovative Multivariate Spatio-Temporal Clustering (MSTC) technique (Hargrove and Hoffman 2005). MSTC predicts the future location and quality of habitat for tree species and, along with consideration of species' biological attributes, allows for an assessment of whether migrating species might be able to track the appropriate environmental conditions over time and avoid the loss of extensive genetic variation. Such an analysis can and should be conducted at a continental scale and at high resolution, to encompass current and potential future habitat of tree species while adequately assessing the risk of genetic degradation at relatively small scales to approximate intra-species population processes.

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 FHM Detection Monitoring and Evaluation Monitoring activities, **2)** for *in situ* and *ex situ* 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.

DESCRIPTION:

a. Background: 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)** adaptation, **2)** range shift (migration), or **3)** extirpation (Davis et al. 2005). Adaptation via natural selection may be unlikely in many cases, given the long generation time for forest tree species (St. Clair and Howe 2007). 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).

This project addresses 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?

b. Methods: This project consists of three parts, each associated with one of the questions outlined above. The MSTC approach developed by Hargrove and Hoffman (2005) is central to the first two parts. Combining aspects of traditional geographical information systems and statistical clustering techniques, MSTC can be used to statistically model environmental niche envelopes to forecast a species’ geographic range under altered environmental conditions such as expected under global climate change (Hargrove and Hoffman 2000). Global in scope, it incorporates more than a dozen spatial environmental variables and generates maps at a resolution of 4 km².

For the first part of the project, MSTC predicts the future 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 (PCM), each under the A1 and B1 scenarios. Existing Forest Inventory and Analysis data is being used as training data for most species, providing the location of species occurrences and an “importance value” that represents the fitness of the species at each location. Potential plot-level importance values include basal area, overall abundance, and sapling abundance (as a measure of regeneration capacity). For rare tree species not well sampled by FIA, training data are coming from other sources, including range boundaries and information available the Global Biodiversity Information Facility (www.gbif.org).

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 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 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, the investigators will work with forest geneticists and ecologists inside and outside the Forest Service to assess the risk of genetic degradation, including the susceptibility of extinction in all or part of its current range, for each of the selected species. This analysis will synthesize existing knowledge about the biology and genetic diversity of each species with results from the first two parts of the project.

c. Products: The primary products of this work are an extensive number of large-scale, ~4 km² resolution maps for each of the tree species included in the study. These will be packaged and available to the public through a new online atlas of climate change genetic risk for North American forest trees. Additional products will include peer-reviewed journal manuscripts, posters at FHM Working Group meetings, and presentations at other professional conferences.

d. Schedule of Activities:

Year 1: Produce maps of the location and quality of current and future habitat of North American tree species using the Multivariate Spatio-Temporal Clustering (MSTC) technique.

Year 2: Generate maps predicting the risk of extirpation at each existing location of North American tree species, and create maps of the location and quality of potential future refuges for these species.

Year 3: Assess the risk of genetic degradation for each species, based on the maps generated, the biological characteristics of each species, and the input of forest ecologists and geneticists.

e. Progress Report: Although funding was not received by the North Carolina State University collaborators until the late summer of 2009, considerable progress has been made on the first objective of this project, the production of maps predicting the location and quality of current and future habitat of North American tree species using the MSTC technique. The Forest Inventory and Analysis input data have been processed, and additional sources of data for rare species, which are not typically sampled by FIA, have been identified. Maps have been generated for a set of eight Central and Southern Appalachian species, both to test the process and to generate maps for two conference presentations about the project.

The first of these presentations, titled “Predicting Climate Change Extirpation Risk for Central and Southern Appalachian Forest Tree Species,” was at the Conference on Ecology and Management of High-Elevation Forests of the Central and Southern Appalachian Mountains at Snowshoe, West Virginia. A conference proceedings paper was generated from this presentation, and is now in press. The second presentation, titled “Assessing the Potential Genetic Impacts of Climate Change to North American Forest Tree Species,” was given at the 30th Southern Tree Improvement Conference, in Blacksburg, Virginia.

COSTS:

	Item	Requested FHM EM Funding	Other-Source Funding	Source
YEAR 1				
Administration	Salary	\$24,500	\$30,000	EFETAC
	Domestic travel	\$3,500		
Procurements	Supplies	\$2,000		
	Total	\$30,000	\$30,000	

YEAR 2				
Administration	Salary	\$26,000	\$31,500	EFETAC
	Domestic travel	\$3,500		
Procurements	Supplies	\$2,000		
Total		\$31,500	\$31,500	

YEAR 3				
Administration	Salary	\$27,500	\$33,000	EFETAC
	Domestic travel	\$3,500		
Procurements	Supplies	\$2,000		
Total		\$33,000	\$33,000	

BUDGET JUSTIFICATION: Travel is for two trips to present research at scientific meetings per year, at a cost of \$1,500 each, and one trip for research collaboration in Asheville, North Carolina, at a cost of \$500. Supply costs are for journal article printing charges (color figures and/or page charges).

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