

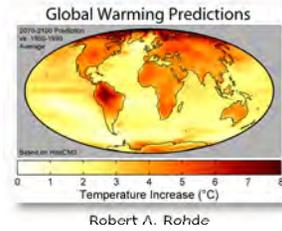


Population-Level Assessment of Climate Change Genetic Risk in North American Forest Trees

Kevin M. Potter¹, William W. Hargrove², Frank H. Koch¹

¹ Department of Forestry and Environmental Resources, North Carolina State University, Research Triangle Park, NC 27709

² Eastern Forest Environmental Threat Assessment Center (EFETAC), U.S. Forest Service Southern Research Station, Asheville, NC 28804



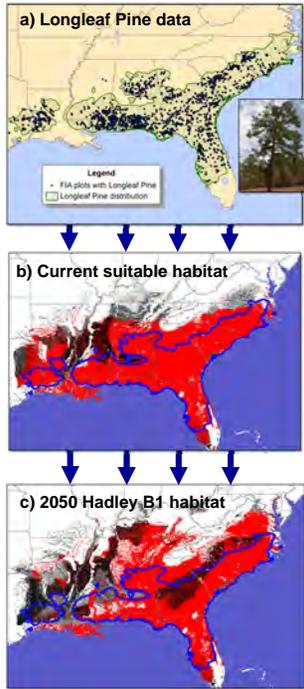
Introduction

Climate change is expected to result in extensive ecological, social and economic effects for U.S. forests (Malmshier *et al.* 2008). Many tree species will be forced to adapt to new conditions or shift their ranges to more favorable environments. Both could have negative genetic consequences (Inset 1).

Ecologists from N.C. State University and the U.S. Forest Service Eastern Forest Threat Center are cooperating to conduct a baseline assessment of the risk of climate change to the genetic integrity of North American tree species.

Objective 1

Forecast the location and quality of habitat for 300 North American forest tree species



❖ **Products needed:** Maps of future suitable habitat based on existing species occurrence data and pertinent environmental variables

- High-resolution and global
- Incorporate soils, temperature, precipitation, topography, growing season

❖ **Species data:** Forest Inventory and Analysis (Figure 1a) or Global Biodiversity Information Facility (rare spp.)

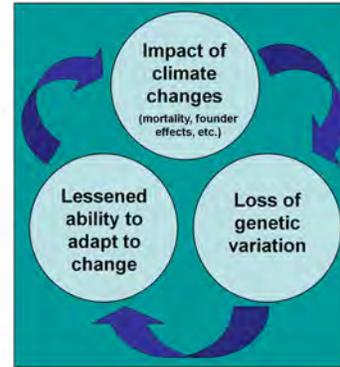
❖ **Map generation method:** Multivariate Spatio-Temporal Clustering (MSTC) (Hargrove and Hoffman 2005)

- Classifies each 4-km² pixel into one of 30,000 unique "ecoregions" using 16 environmental variables
- For each species, creates map of current potentially suitable habitat based on existing occurrence data (Figure 1b)
- Tracks current habitat regions into future regions in 2050 and 2100 (under Hadley and PCM models, high and low emissions) (Figure 1c)

Figure 2: MSTC results for Longleaf Pine: a) FIA data, b) current habitat prediction, c) 2050 Hadley A1 high emissions prediction

Inset 1: Genetics and climate change: Why should we care?

- ❖ Genetic variation = potential adaptability to changing environment
 - Degradation may increase susceptibility to stressors such as pests, pathogens, climate (Inset Figure 1)
- ❖ Potential genetic impacts of tree responses to climate change:
 - **Adaptation:** strong selection could reduce genetic variation
 - **Range shift:** founder effects, loss of trailing edge populations
 - **Population extirpation:** loss of unique genes or gene combinations



Inset Figure 1: Negative impacts of climate change may result in loss of genetic variation, decreasing the ability of populations to adapt to change.

Objective 2

Identify existing populations most at risk from climate change, based on distance to future suitable habitat

- ❖ **Products needed:** Maps of areas potentially at risk from changes in suitable habitat (Figure 2)
 - Areas of overlapping habitat
 - Minimum Required Movement (MRM) distance between current and future suitable habitat
- ❖ Incorporate movement barriers
- ❖ Identify possible corridors between current and future habitat
- ❖ Find potential "lifeboat" areas preserving multiple species from broad regions

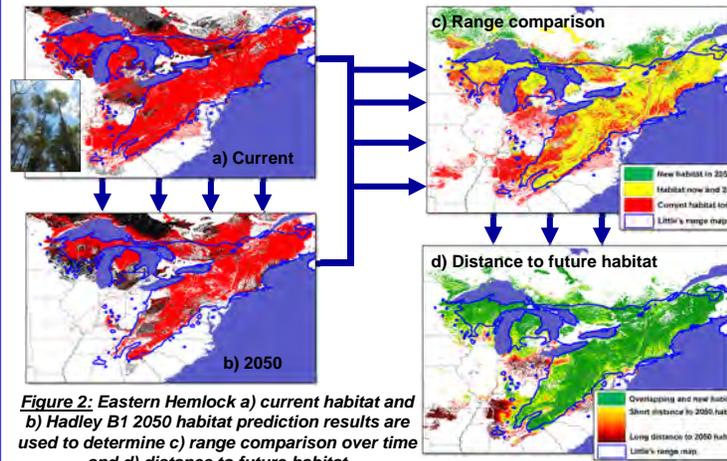


Figure 2: Eastern Hemlock a) current habitat and b) Hadley B1 2050 habitat prediction results are used to determine c) range comparison over time and d) distance to future habitat

Objective 3

Assess overall susceptibility of species and their populations to genetic degradation and extirpation

- ❖ **Products needed:** Spatially explicit assessments of which populations are most at risk
- ❖ Synthesize map results with existing knowledge about species biology, population genetics and extrinsic factors (Figure 4)
- ❖ Incorporate expert opinion from geneticists, ecologists and other species specialists within a Bayesian Belief Network framework

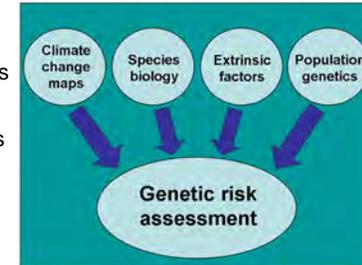


Figure 4: The spatially explicit assessment of genetic susceptibility will incorporate the result maps and knowledge about species biology (fecundity, seed dispersal, etc.), extrinsic factors (fragmentation, exploitation, etc.), and population genetics.

Availability of Results

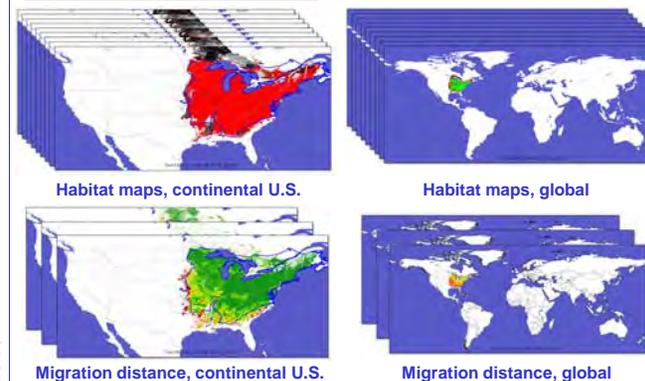


Figure 4: This project will generate at least 24 predictive maps for each of the ~300 species included in the analyses. These will be made available online.

References

- Hargrove, W.W.; Hoffman, F.M. 2005. Potential of multivariate quantitative methods for delineation and visualization of ecoregions. *Environmental Management*. 34(Suppl. 1):S39-S50.
Malmshier, R.W., *et al.* 2008. Forest Management solutions for mitigating climate change in the United States. *Journal of Forestry*. 106(3):115-173.



This research was supported in part through Cooperative Agreement 09-CA-11330146-078 between the USDA Forest Service and North Carolina State University (SO-EM-09-01).

