Eastern hemlock is at risk from both pests and climate change

Spatial Assessments of Forest Tree Genetic Degradation Risk from Climate Change (SO-EM-09-01)

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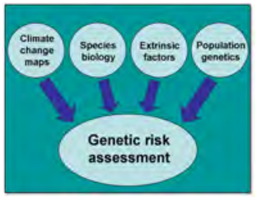


Genetic risk assessments incorporate threats and species attributes

Introduction

Climate change is expected to result in serious ecological, social and economic effects for U.S. forests. 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, particularly in tandem with other threats, such as insects and disease. Overlapping genetic risk assessments **(Inset 1)** can assist in prioritizing species and populations for monitoring, conservation, and restoration activities.

(A) Forecasts of Climate-Associated Shifts in Tree Species (ForeCASTS)

Objective 1: Forecast location and quality of habitat for more than 300 tree species

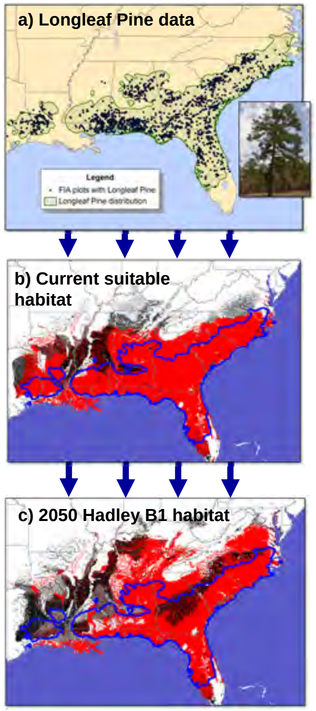


Figure 2: ***Results for Longleaf Pine: a) FIA data, b) current habitat prediction, c) 2050 Hadley B1 low emissions prediction***

❖ Maps of current and future suitable habitat

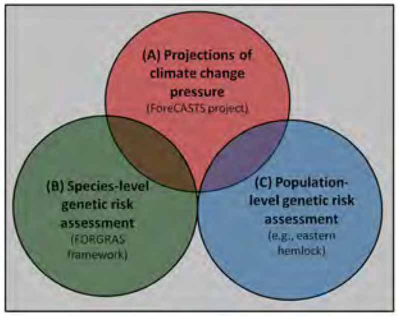
- High-resolution and global
- Incorporate soils, temperature, precipitation, topography, growing season
- Maps at:
  www.geobabble.org/~hnw/global/treeranges3/climate_change/

❖ *Species input data:* Forest Inventory and Analysis **(Figure 1a)**; Global Biodiversity Information Facility (for rare species, locations outside U.S.)

❖ *Multivariate Spatio-Temporal Clustering (MSTC):*

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

Inset 1: Spatially explicit genetic risk assessment tools



Inset Figure 1: ***Three overlapping genetic risk assessment tools; the ForeCASTS projections (A) are used in species-level and population-level risk assessments (B) and (C).***

❖ Genetic variation = potential adaptability to threats

- Degradation may increase susceptibility to stressors such as pests, pathogens, climate change

❖ Risk assessments can help prioritize species or populations for monitoring, conservation, etc.

- ForeCASTS **(A)** projects climate change pressure on species and populations, for use in **(B)** and **(C)**
- FORGRAS **(B)** prioritizes species most at risk from climate change and other threats
- Population-level risk assessments **(C)** integrate risk from multiple threats

Objective 2: Identify populations most at risk from climate change, given distance to future suitable habitat

❖ 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 2050 suitable habitat, based on Hadley B1 low emissions scenario

❖ Climate-pressure statistics (used in species, population assessments)

- Percent change over time in area of suitable habitat (area change)
- Percent of current habitat that remains suitable (habitat stability)
- Mean pixel distance from current to nearest future habitat (shift pressure)

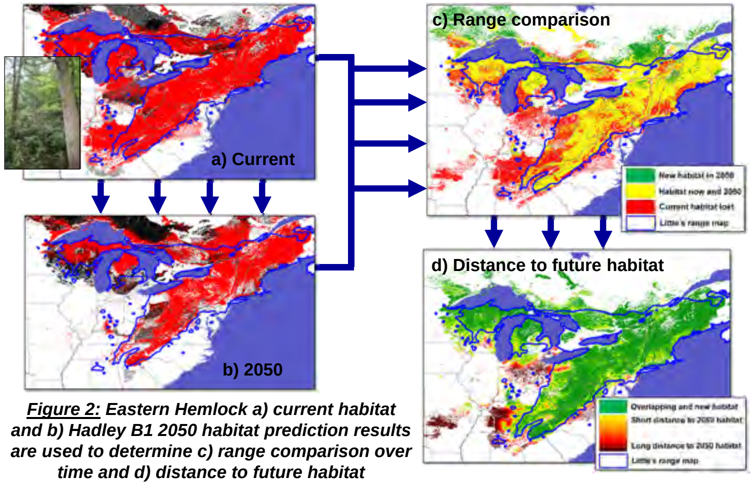


Figure 2: ***Eastern Hemlock a) current habitat and b) Hadley B1 2050 habitat prediction results are used to determine c) range comparison over time and d) distance to future habitat***

(B) Forest Tree Genetic Risk Assessment System (FORGRAS)

Ranks species based on characteristics and threats

❖ Framework accounts for threats and attributes predisposing species to genetic degradation

- Incorporates 8 factors and 25 sub-factors, based on review of ecological and life-history traits associated with genetic risk **(Table 1)**
- Information available from ForeCASTS and from public sources (e.g., Silvics Manual)
- Users assign weights to sub-factors; weighted scores summed to give risk ratings for each species

Table 1: ***Risk factors included in the FORGRAS framework (number of sub-factors in parentheses)***

Intrinsic Risk Factors
(A1) Population Structure (4)
(A2) Rarity/Density (2)
(A3) Regeneration Capacity (6)
(A4) Dispersal Ability (1)
(A5) Habitat Affinities (4)
(A6) Genetic Variation (3)
External Risk Factors
(B1) Insect and Disease Susceptibility (1)
(B2) Climate Change Pressure (4)

❖ Completed for 130 Southern Appalachian species; data now being collected for more than 300 North American tree species

(C) Population-level risk assessments

Rank populations based on multiple attributes

❖ Eastern hemlock vulnerability index for 60 populations **(Figure 3)**; combines:

- Genetic diversity index *(D)* from range-wide microsatellite marker study (includes four genetic diversity measures)
- Climate change vulnerability index *(C)* from ForeCASTS
- Hemlock woolly adelgid vulnerability index *(H)*, includes potential impact of climate change on HWA distribution

❖ Genetic vulnerability index = $(2D + C + H)/4$

- Higher values indicate higher relative genetic vulnerability

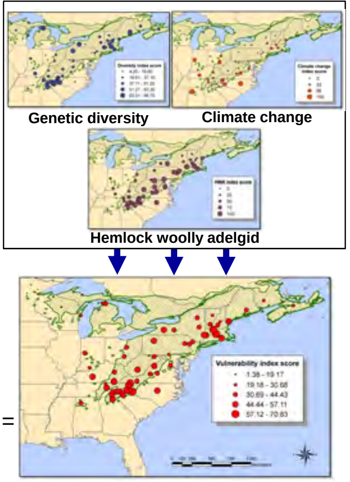


Figure 3: ***Eastern hemlock genetic vulnerability scores, by population***

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