

ADAPT, MOVE, OR DIE: FIA DATA IN ASSESSMENTS OF FOREST TREE GENETIC DEGRADATION RISK FROM CLIMATE CHANGE AND OTHER THREATS

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Abstract.—Changing climatic conditions may pose a severe threat to forest tree species, forcing three potential population-level responses: 1) toleration/adaptation, 2) movement to suitable environmental conditions, or 3) extirpation. All could have negative genetic consequences. It will be important, therefore, to safeguard existing adaptedness and to create conditions conducive for future productivity and evolution. To efficiently conserve the genetic variation of species, it is necessary to understand where climate change pressure will be greatest, and what species and populations are more highly predisposed to genetic degradation from climate change and other threats. Forest Inventory and Analysis (FIA) data represent an unmatched resource for conducting broad-scale, spatially explicit assessments of the risk posed by climate change and other threats to the genetic integrity of forest tree populations and species. We used FIA data to 1) generate 4 km² resolution maps predicting the genetic pressure that could be imposed by climate change on forest tree species; and 2) compile information about the biological attributes and genetic diversity of individual species. The first assessment tool, Forecasts of Climate-Associated Shifts in Tree Species (ForeCASTS), has generated climate change pressure maps for more than 300 North American tree species and quantifies potential climate change genetic pressure, as defined by the straight-line Minimum Required Movement (MRM) distance from the existing locations of each species to the nearest favorable future habitat. The second assessment tool, the Forest Tree Genetic Risk Assessment System (FORGRAS) framework, ranks the predisposition of forest tree species to genetic degradation, based on demographic and occurrence information, ecological and life-history traits, species-specific projections of climate change pressure, and predictions of pest and pathogen susceptibility. Both assessment tools should be valuable for scientists and managers attempting to determine which species and populations to target for monitoring efforts and for proactive gene conservation and management activities.

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