SILVICULTURE AND THE ASSESSMENT OF CLIMATE CHANGE GENETIC RISK FOR SOUTHERN APPALACHIAN FOREST TREE SPECIES

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Changing climate conditions and increasing insect and pathogen infestations will increase the likelihood that forest trees could experience population-level extirpation or species-level extinction during the next century. Gene conservation and silvicultural efforts to preserve forest tree genetic diversity present a particular challenge in species-rich regions such as the Southern Appalachian Mountains. Funds, however, will be limited for silvicultural management and gene conservation efforts to preserve forest tree genetic diversity. To facilitate the effective use of limited resources and to guide silvicultural activities, we developed the Forest Tree Genetic Risk Assessment System as a framework for users to rank the relative risk of genetic degradation for multiple forest tree species, and applied this framework for the Southern Appalachians.

Species differ in their silvicultural requirements, physiological tolerances, life-history strategies, and population dynamics (extinction, colonization, and dispersal abilities). These differences could drive variation among forest tree species in their potential responses to changing climate conditions and insect and pathogen infestations. Given these potential changes, diverse silvicultural and genetic strategies to support future desired conditions will be needed to ensure successful regeneration and restoration efforts. An important goal will be to safeguard existing adaptedness and create conducive conditions for future evolution, with a focus on the conservation of variability in adaptive traits (Myking 2002).

Following an extensive review of the ecological and life-history traits of tree species that predispose them to genetic degradation, we developed 10 indices to include in the risk assessment framework. These are divided into six intrinsic risk factors (describing characteristics of tree species and their distributions); two external risk factors (describing external threats to tree species) and two conservation modifiers (describing conservation value associated with species, Table 1). The risk factors further consist of several variables: 20 for the intrinsic and five for the external risk factors. Users can decide which of these risk factors and variables to include in their assessments, and how to assign the appropriate relative weights placed on each. The weighted factor scores are summed to give risk ratings for the species within a given region, which are then ranked.

We used this framework to conduct a risk assessment for 131 native forest tree species encompassed within the Southern Appalachian region, defined by seven high-elevation ecoregion sections south of the Mason-Dixon line (Figure 1). We completed this genetic risk assessment in four major steps: (1) determining the area of interest and the species encompassed by that region, (2) selecting risk factors and conservation modifiers to include in the assessment, (3) collecting relevant data for each species and calculating risk factor and conservation modifier index scores, and (4) weighting these index scores, calculating a final score for each species, and ranking the species based on their final scores. A detailed description of these steps is provided in Potter and Crane (2010). Most of the data used in the assessment are from publicly available sources. Several of the Southern Appalachian species at greatest risk of genetic degradation have small distributions, often at high elevations, and/or are currently threatened by insects and diseases.

The highest-ranking species, for example, is Carolina hemlock (*Tsuga caroliniana*), which occurs in a handful of scattered high-elevation populations. Carolina hemlock and eastern hemlock (*T. canadensis*), which also ranked among the top 25 species, are experiencing extensive mortality caused by the exotic hemlock woolly adelgid (*Adelges tsugae*). With funding from the USDA Forest Service, the Camcore gene conservation cooperative at North Carolina State University has collected seeds from both species since 2005 for gene conservation purposes. Fraser fir (*Abies fraseri*), the third most at-risk species, is limited to a few populations at the highest elevations in the Southern Appalachians, where the exotic balsam woolly adelgid (*Adelges piceae*) has killed many trees. Table Mountain pine (*Pinus pungens*), which ranked among the 10 most at-risk species, occurs in high-elevation stands where insufficient fire has proved a challenge for regeneration.

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In summary, we used ecological and life-history traits to rank the predisposition of Southern Appalachian tree species to genetic degradation from climate change and other threats. This approach can serve as a tool for planning silvicultural treatments, conservation efforts, evaluating species' genetic resources and detecting vulnerabilities. A key feature of the Forest Tree Genetic Risk Assessment System framework is its flexibility to suit the needs of users, allowing for its application across any area for which the relevant data exist for the species of interest. Only by considering extinction as a synergistic process of external threats and intrinsic biological traits will it be possible to make predictions of risk that approximate reality for most species, and therefore to increase the likelihood that conservation efforts will be effective (Brook and others 2008).

LITERATURE CITED

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Table 1—The intrinsic risk factors, external risk factors and conservation modifiers included in the Forest Tree Genetic Risk Assessment System for the assessment of the 131 tree species of the Southern Appalachians. We assigned a weight of 0.1 to each intrinsic risk factor, 0.15 to the external risk factors, and 0.05 to the conservation modifiers. (Weights sum to 1.)

Intrinsic Risk Factors	External Risk Factors	Conservation Modifiers
A1) Population Structure	B1) Pest and Pathogen Threats	C1) Endemism
A2) Rarity/Density	B2) Habitat Shift Pressure	C2) Conservation Status
A3) Regeneration Capacity		
A4) Dispersal Ability		
A5) Habitat Affinities		
A6) Genetic Variation		

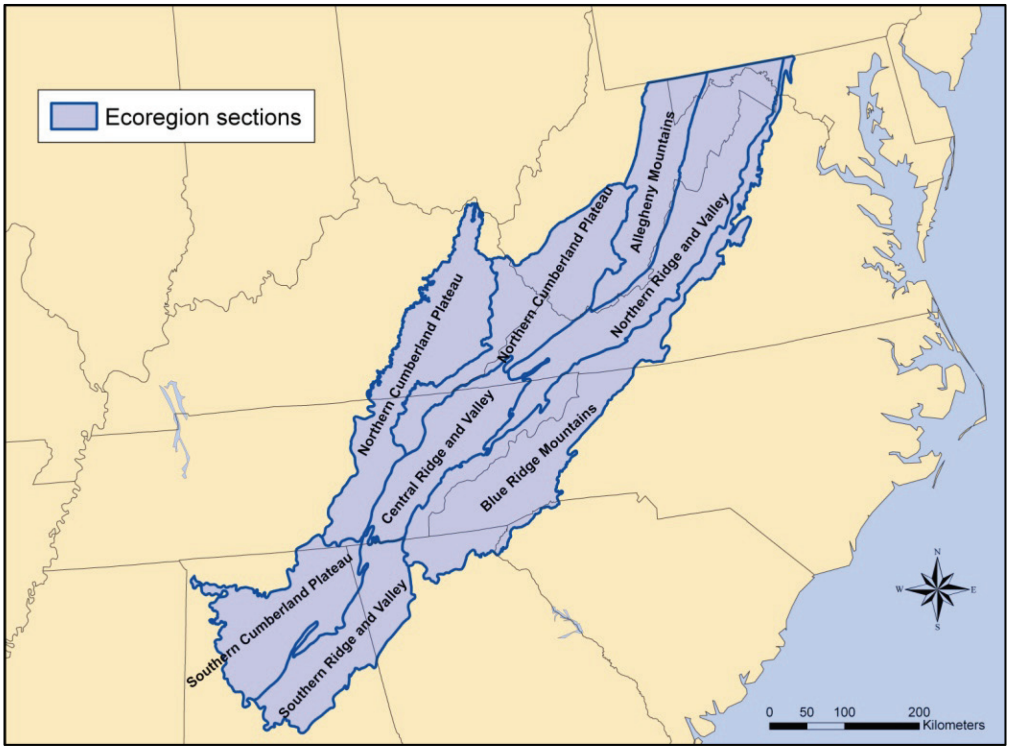

Figure 1—The Southern Appalachian region, as defined for this regional genetic risk assessment.