

Determining Genetic Erosion in Fourteen *Picea chihuahuana* Martínez Populations¹

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Picea chihuahuana is an endemic species in Mexico and is considered endangered, according to the Mexican Official Norm (NOM-ECOL-059-2010). This species covers a total area of no more than 300 ha located in at least 40 sites along the Sierra Madre Occidental in Durango and Chihuahua states. A minimum of 42,600 individuals has been estimated, although the number of mature individuals is uncertain and could be less than 2,500. The size of the populations varies from 21 to 5,546 individuals, including trees, saplings, and seedlings. Theory suggests that small populations can be more susceptible to loss of genetic variability due to genetic drift, inbreeding depression and strong unidirectional selection. The predicted result is the total loss of genetically distinct populations, the loss of alleles or change in frequency of specific alleles within populations or over the species as a whole, or the loss of allelic combinations. Therefore, the principal aim of the present study was to determine genetic erosion in 14 populations of *P. chihuahuana* by comparing the genetic diversity among trees sorted into diameter classes (as a substitute variable for age classes). Needles were sampled from about 700 randomly chosen individuals of *P. chihuahuana* from these 14 populations, and genetic data were obtained through AFLP technology. In order to determine genetic erosion, the genetic diversity was quantified by measuring mean total differentiation (δ_T), the proportion of polymorphic fragments (pr_{poly}), DW (a parameter to quantify rare markers within cohorts), and genetic distance using GenAlEx 6.5. Finally, a two-sided permutation test was performed for the observed degrees of covariation (C). If the value of C is positive and $P(Z \geq C)$ is statistically significant (i.e., $P < 0.025$; two-sided permutation test), we can assume that genetic erosion has occurred in a defined area.

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