

ESTIMATING GENETIC EROSION USING THE EXAMPLE OF *PICEA CHIHUAHUANA* MARTINÉZ

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Resumen

Because it can be detrimental to the short-term viability of individuals and populations, the evolutionary potential of populations and species, and the direct use of genetic resources, various international and intergovernmental organizations and networks have recognized the need to assess and monitor plant genetic erosion in order to reverse this tendency. Genetic erosion can be viewed as the “*loss of genetic diversity, in a particular location and over a particular period of time, including the loss of individual genes, and the loss of particular combinations of genes such as those manifested in landraces or varieties. It is thus a function of change of genetic diversity over time*” (FAO/IPGRI, 2002).

In relation to estimating potential genetic erosion, the endemic and rare tree species *Picea chihuahuana* Martinéz, so known as Chihuahua spruce or prickly spruce, is an excellent research subject. It occurs in more than 39 often isolated relict populations between altitudes of 2,155 and 2,990 m in the Sierra Madre Occidental in the states of Durango and Chihuahua, Mexico. The population size varies from 21 to 5546 individuals including trees, saplings and seedlings. It is assumed that genetic erosion has proceeded in the species as a whole since the last glacial period. However, the question remains open whether genetic erosion was or is existent in single isolated populations recently or currently.

In this study we tested five populations of *Picea chihuahuana* M. in Durango State, Mexico, for genetic erosion in the last 200 years using *AFLP* fingerprints and Gregorius's total differentiation δ_T ($\delta_T = (N/(N-1)) * (1 - \sum p_i^2)$). The results show that if δ_T at 319 studied *AFLP* loci reflects δ_T in the genome as a whole, genetic erosion is not detectable currently because all age classes (natural regeneration to the class of oldest trees) possess similar total differentiations.