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Diversity and genetic structure of natural populations of *Cedrela odorata* in Sierra del Lacandón, Guatemala

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Abstract

Cedrela odorata L., one of the most important Neotropical timber species, is threatened by deforestation and unsustainable logging in many parts of its natural range. Information on patterns of genetic variation helps plan reforestation and plant genetic resource conservation activities. However, to date, this information is not available in Guatemala. This study reports on genetic diversity between and within the four populations of *C. odorata* located in the Sierra del Lacandón in northern Guatemala, based on eight highly polymorphic microsatellite markers. There were a total of 93 alleles found throughout the eight loci, with an average of 6.38 alleles per locus. The level of genetic differentiation was low ($F_{st} = 0.022$), indicating high gene flow between populations ($N_m = 3.56$), while genetic diversity was high ($H_e = 0.721$, $H_o = 0.629$). However, the level of inbreeding was determined to be significant ($F_{is} = 0.127$), which is a strong indication of genetic erosion. One of the six $G'ST(Nei)$ pairwise comparisons indicated no genetic difference. We discovered a mixture of *C. odorata* trees from various populations using UPGMA hierarchical cluster analysis. Molecular analysis of variance revealed that only 3% of the variation is due to the effect between populations, while 97% of the variance is within populations. Compared to other studies, levels of connectivity between populations and the degree of genetic diversity are higher. The high genetic diversity found in the *C. odorata* germplasm suggests that it might be a valuable source of variable alleles that may be used for breeding programmes for this timber species. We suggest maintaining efforts to avoid population reduction through deforestation and illegal extraction, thus reducing the constant risk of erosion due to genetic drift.

Keywords: Gene flow, genetic erosion, genetic variability, inbreeding, Spanish cedar