

Abstract

Genetic Diversity of the Endemic and Threatened Ecuadorian Tree, *Ocotea rotundata* s.l. (Lauraceae) [†]

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Abstract: Ecuador is considered one of the most biodiverse countries in the world but currently has one of the highest deforestation rates in South America. However, genetic knowledge needed to sustain conservation actions is generally absent in most species. In this study, we developed eight nuclear microsatellites (nSSR) to study the patterns of genetic diversity, population structure, and level of inbreeding of *Ocotea rotundata* van der Werff (Lauraceae), an endemic tree from South Ecuador occurring in five populations, and with a very low number of mature individuals. This study focused on these five populations where 140 adult trees were collected (populations: LOJ n = 25; CER n = 30; YAN n = 30; CAT n = 25; ZAM n = 30). We also included 40 individuals from two populations described in the North of Ecuador as *O. rotundata* (populations: MAQ n = 20, PAC n = 20). Our results show high levels of genetic diversity across populations (Ho: LOJ = 0.72; CER = 0.73; YAN: 0.69; CAT = 0.67; ZAM = 0.43; MAQ: 0.72; PAC: 0.77) although much lower than the expected ones (He = LOJ = 0.86; CER = 0.81; YAN: 0.73; CAT = 0.80; ZAM = 0.72; MAQ: 0.85; PAC: 0.86) and overall higher levels in the North and South populations. The number of alleles was also high (LOJ = 11; CER = 9; YAN: 10; CAT = 12; ZAM = 6; MAQ: 12; PAC: 11). The Bayesian clustering program STRUCTURE found the highest LnP(D) and ΔK values for K = 2, dividing North and South populations. A similar pattern was found in the principal coordinate analysis. Allelic fixation was always significantly greater than zero ($F = 0.17 \pm 0.06$) in all populations ($p < 0.05$) indicating a heterozygosity deficit across loci probably due to inbreeding. Conserving the genetic diversity of *O. rotundata* through future in and ex situ actions and the processes that determine it, would be crucial for increasing the resilience of Ecuador's forests. Altogether, these results indicate a low frequency of gene flow and connectivity between the North and South regions, being enough to promote differentiation. In fact, samples collected in the North had, generally, smaller leaves than the ones from South Ecuador, and some branches had pubescent flowers. The morphological differences in the Ecuadorian populations together with the genomic results found here could imply the existence of different species, a hypothesis that needs future taxonomic studies.

Keywords: Ecuador rainforest; Lauraceae; genetic diversity; deforestation; overexploitation



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