

Abstracts

Effects of forest deforestation in the genetic diversity of the endemic and threatened Ecuadorian tree, *Ocotea rotundata* (Lauraceae)[†]

Isabel Marques ^{1,*}, David Draper ^{2,3}, Lorena Riofrío ⁴ and Carlos Naranjo ⁴

¹ Forest Research Centre (CEF), Instituto Superior de Agronomia (ISA), Universidade de Lisboa, Lisbon, Portugal

² Center for Ecology, Evolution and Environmental Changes & CHANGE - Global Change and Sustainability Institute, Universidade de Lisboa, Lisbon, Portugal; ddmunt@gmail.com

³ Nova School of Business and Economics, Campus de Carcavelos, Carcavelos, Portugal

⁴ Universidad Técnica Particular de Loja (UTPL), Facultad de Ciencias Exactas y Naturales, Loja, Ecuador; mlriofrio@utpl.edu.ec (L.R.); cjnaranjo@utpl.edu.ec (C.N.)

* Correspondence: isabel.ic@gmail.com

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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. As a first step to overcome this gap, we used 8 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 with a very scarce population size occurring in fragmented patches of the Neotropical forest. Only 5 populations occur in the South of Ecuador and with a very low number of mature individuals. This study focused on these five populations where a total of 140 adult trees were collected (LOJ n=25; CER n=30; YAN n=30; CAT n=25; ZAM n=30). We further include 40 individuals from 2 populations recently described in the North of Ecuador as *O. rotundata* (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 in 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. FIS was always significantly greater than zero (F= 0.17 ± 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 forests. Altogether, these results indicate a low frequency of gene flow and connectivity between 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 lineages, a hypothesis that needs future taxonomic studies.

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