

Genetic diversity and structure of the threatened Ecuadorian tree, *Ocotea rotundata* s.l. (Lauraceae)

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BACKGROUND

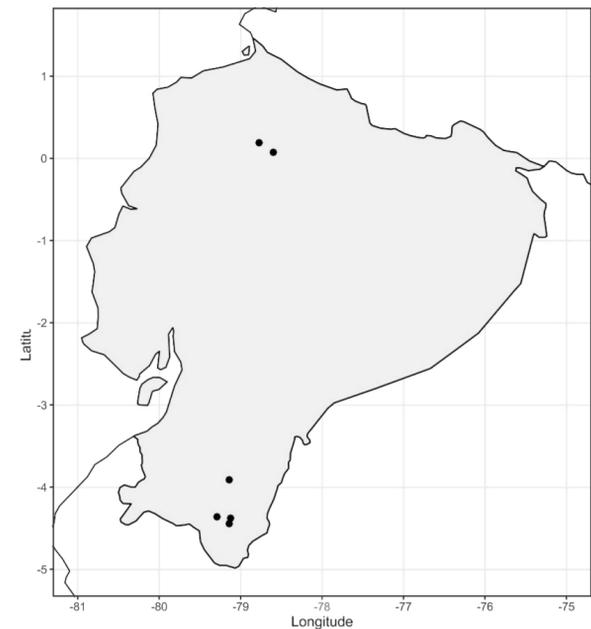
Forest fragmentation and deforestation often affect genetic diversity and the patterns of gene flow between species. However, long-lived outcrossing organisms such as trees might buffer these effects if gene flow occurs between forest patches.

In this study, we focused on *Ocotea rotundata* s.l. van der Werff, an endemic tree from South Ecuador with a very scarce number of known populations, occurring in fragmented patches of the Neotropical Forest. It is included in the IUCN Red List as Vulnerable due to a continuing decline in area, extent, and/or quality of habitat.

Genetic data that would help conservation efforts and future re-introductions are absent.

OUR GOALS

- (1) investigate if recent fragmentation and deforestation had a significant effect on the genetic resources of *O. rotundata*;
- (2) detect the patterns of species genetic diversity and differentiation between North (MAQ, PAQ) and South populations (ZAM, CER, CAT, YAN, LOJ);
- (3) identify the presence of gene flow within and between populations.



Population sampling of *Ocotea rotundata* in Ecuador.

Genetic diversity and population structure of *Ocotea rotundata*

- An average of 10.14 ± 2.12 total number of alleles was found among 160 *O. rotundata* samples although slightly higher in North than South populations.
- Moderate observed heterozygosity values were generally found across populations ($H_o = 0.67 \pm 0.11$) although much lower than the expected ones ($H_e = 0.80 \pm 0.59$) and overall higher in North and South populations.

Populations	N	Na	Ho	He	F
MAQ	20	12	0.72	0.85	0.10*
PAC	20	11	0.77	0.86	0.11*
North populations	40	11.5 ± 0.71	0.75 ± 0.04	0.86 ± 0.01	0.11 ± 0.01
LOJ	25	11	0.72	0.86	0.22*
CER	30	9	0.73	0.81	0.21*
YAN	30	10	0.69	0.73	0.19*
CAT	25	12	0.67	0.80	0.11*
ZAM	10	6	0.43	0.72	0.27*
South populations	120	9.60 ± 2.11	0.65 ± 0.11	0.78 ± 0.06	0.20 ± 0.07

N: sampling size; Na: average number of alleles; Ho: average observed heterozygosity; He: average expected heterozygosity; F: allelic fixation index. * indicates significant deviation from HWE.

- AMOVA showed that most of the genetic diversity found was explained by variance within populations (88%) being the remaining portioned among regions. Gene flow (N_m) was calculated to be 0.321, suggesting a strong restriction in gene flow between populations throughout the entire distribution area.
- The Bayesian clustering program STRUCTURE found the highest $\ln P(D)$ and ΔK values for $K = 2$ splitting North and South populations. Although admixture was found in some samples, results generally assigned individuals to their region of origin, e.g., North or South populations. Consistent with these results, the principal coordinate analysis (PCoA) also suggested the existence of two main groups.

MAIN CONCLUSIONS

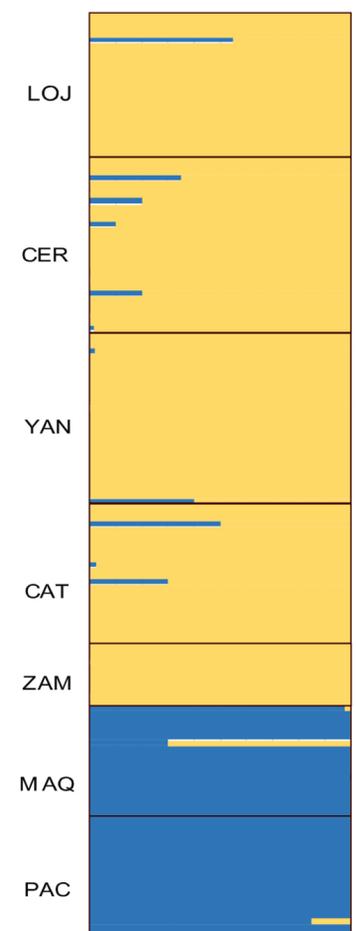
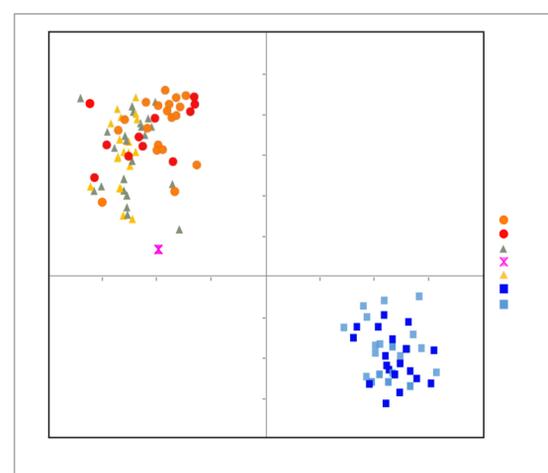
Our results show moderate to high levels of genetic diversity, except in one small population (ZAM) where low levels of heterozygosity and allele number were recorded. However, high genetic differentiation was found between North and South populations, with a clear division also reported in the patterns of genetic structure. These results, together with a general deficit in heterozygotes suggest the absence of gene flow between these populations.

Although long-lived organisms such as trees can often accumulate a surprising amount of genetic diversity, the results found here are an early sign of a decline in the diversity of *O. rotundata*.

Genetic structure of *Ocotea rotundata* samples collected in Ecuador.

A. Best assignment results retrieved by STRUCTURE ($K = 2$). Each sample is represented by a thin vertical line divided into K-colored segments that represent the individual's estimated membership fractions in K clusters.

B. Principal Coordinate analysis of the studied samples. Note that only a small number of individuals can be seen in ZAM since most samples have identical alleles.



Implications for conservation

Management plans should concentrate on *in-* and *ex-situ* conservation actions to promote effective gene flow and increase genetic variability. Specifically, we recommend the following actions:

- (1) seed collection for ex situ conservation and future tree planting in situ activities;
- (2) active planting or assisted regeneration in populations under high vulnerability such as ZAM;
- (3) creation of new populations to allow the future connectivity between patches. Seeds from several different populations should be collected, and the seedlings produced should be planted.