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

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Introduction

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 [1]. Information on patterns of genetic variation helps plan reforestation and plant genetic resource conservation activities [2]. The natural populations of *C. odorata* have been severely reduced to the point of being classified as vulnerable by the IUCN and it is listed in Appendix III of CITES [3]. This species has experienced a large reduction in its natural populations in recent years, which may have a direct consequence in the reduction of its genetic variation. The main objective of this study was to assess the genetic diversity and population structure of *C. odorata* in order to promote conservation activities and sustainable exploitation of the species in Guatemala.**

Methodology

From four natural populations (Figure 1), we obtained 53 *C. odorata* samples. DNA was extracted from the isolates and fingerprinted with 8 microsatellites [4] and the fragments were measured by capillary electrophoresis. Data analysis – genetic diversity indexes (poppr [5]), clustering analysis (Structure [6] DAPC [7] MSN [5]).

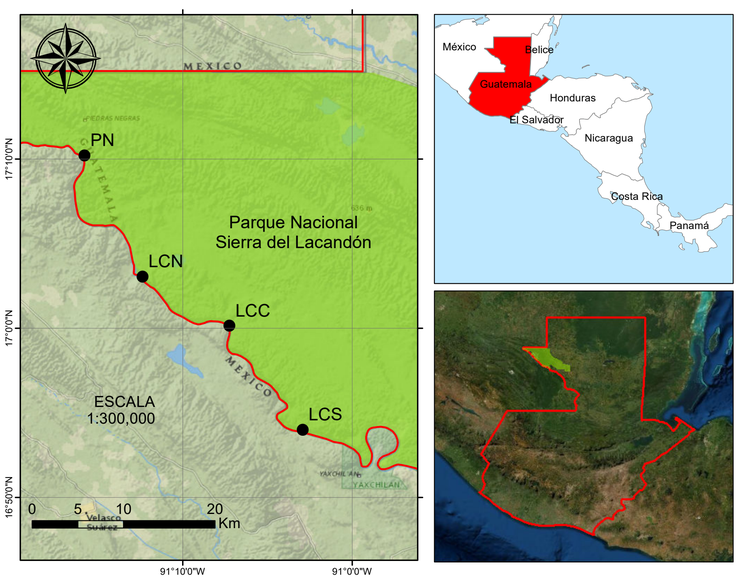

Figure 1. **Collecting sites**

Results

The genotype accumulation curve indicated that 100% of multilocus genotypes were detected with the SSRs employed (Fig 2).

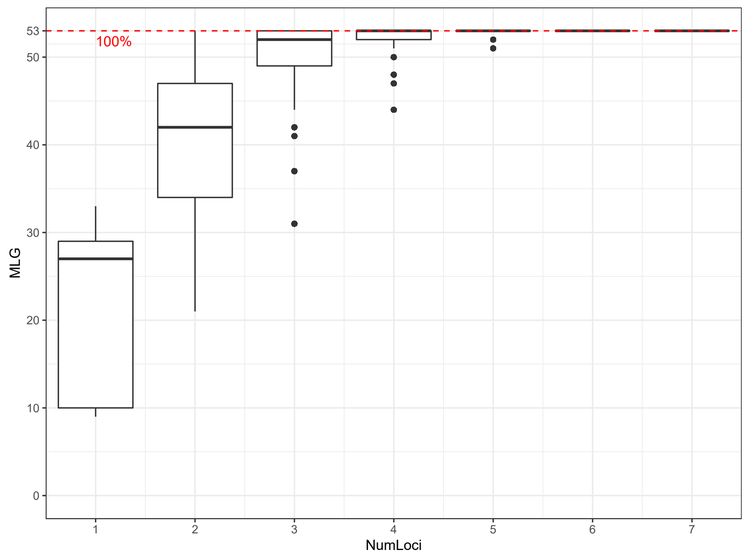

Figure 2. **Genotype accumulation curves for the *C. odorata* populations from Guatemala.**

The population structure could be composed of two genetic clusters. However, a weak structure was observed (Fig 3a, 3b, 3c).

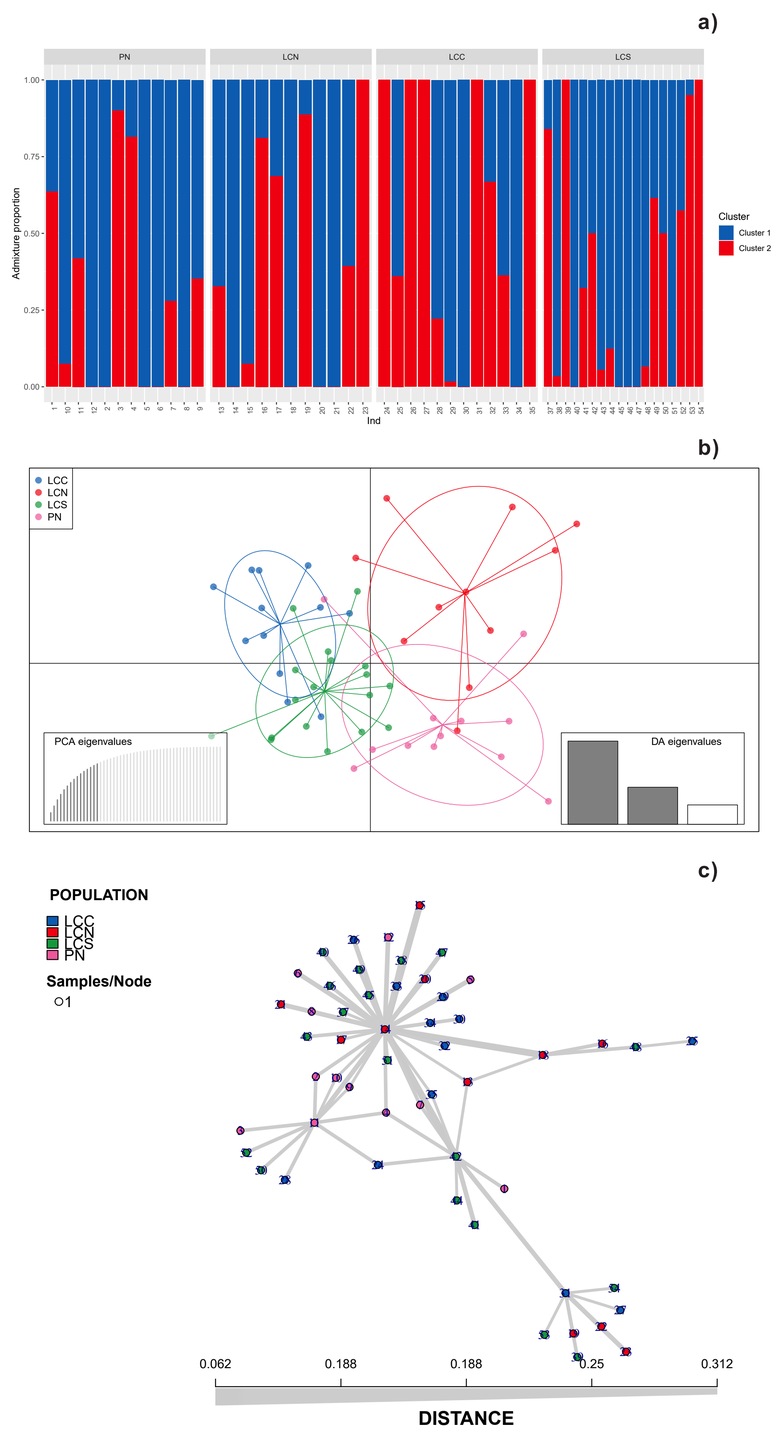

Figure 3. **a) Assignment of probabilities for the 53 individuals of *C. odorata* in each cluster inferred by STRUCTURE b) Population genetic structure based on a Discriminant Analysis of Principal Components (DAPC) and c) Minimum Spanning network**

The population LCN and LCS high diversity, whereas population PN and LCC presented lower levels of genetic diversity (Table 1). Molecular analysis of variance (AMOVA) showed a variance between and within populations of 3% and 97%, respectively. Nonetheless, Fst (0.22) statistics were not significant.

Table 1. Measures of genetic diversity of four populations of *C. odorata*.

Population	N	Na	I	Ho	He	Ar	F
PN	12	5.3	1.316	0.584	0.687	5.4	0.156*
LCN	11	5.5	1.285	0.641	0.679	6.3	0.046*
LCC	12	6.2	1.512	0.566	0.752	6.7	0.258**
LCS	18	8.3	1.699	0.727	0.764	8.2	0.049*
Mean	13.25	6.3	1.453	0.629	0.721	6.65	0.127*

N = population size, Na = number of alleles, I = Shannon's index, Ho = observed heterozygosity, He = expected heterozygosity, Ar = allelic richness, F = fixation index

Conclusions

The low genetic diversity is consistent with deforestation and unsustainable logging in the analyzed populations. The lack of population structure is attributed to the process of selection, the system of cross- pollination and the exchange of seedlings to which *C. odorata* is still subject. Protection of the genetic resource is suggested, as well as a complementary agromorphological characterization to establish an adequate strategy of exploitation through plant breeding programs.

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Acknowledgments

The study was supported by Dirección General de Investigación (Digi) through project no. B21-2020.