1. Introduction

*Cedrela odorata* L. (Spanish Cedar) is a commercially valuable Neotropical timber species. It has been heavily impacted and is currently highly fragmented and reduced in numbers. To conserve genetic resources in this valuable species, it is necessary to quantify levels and distribution of natural genetic variation and identify units for management.

2. Methods

Samples were collected from 29 populations throughout Central America. Then, Chloroplast DNA was analysed using universal primers and restriction fragment digest (PCR-RFLP); 21 sets of primers were used to screen for polymorphisms in ten representative samples; the entire collection was screened with polymorphic primers. All samples were characterised for cpDNA haplotype. Dataset were analysed for within- and between-population diversity and population structuring, for both ordered and unordered data. Variation in environmental factors were also investigated, by grouping populations according to haplotype.

3. Results

- Nine insertion/deletion mutations were detected;
- Five haplotypes were characterised in three lineages;
- Total diversity was high ($H_T = 0.70$), but average population diversity was low ($H_S = 0.03$);
- Level of population structuring was very high ($G_{ST} = 0.96$);
- Geographic/genetic distance relationship deviates from a pattern of isolation by distance: unordered estimates of genetic distance and population structure increase with geographic distance.

4. Discussion

Divergence between Northern and Central haplotypes does not correspond with environmental differences because they are separated by greatest genetic distance. They are more likely to reflect an ancient fragmentation of the ancestral population, possibly following colonisation prior to the formation of the Isthmus of Panama.

Divergence between Southern and Central haplotypes corresponds to environmental differences; selection probably plays a role, but cannot be confirmed by neutral molecular data. A sharp distinction will probably reflect extinction and colonisation processes that accompanied the last glacial climatic cycle.

5. Conclusions

- Three cpDNA haplotype lineages indicate ancient vicariance origins of contemporary diversity.
- Conservation of populations in the three fragments should conserve sources of intraspecific historical variation.
- cpDNA loci form geographic markers for forensic identification of timber sources.