Genetic Consequences of Tree Species Natural Regeneration in an Anthropogenic Area, Acre, Brazil

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Spanish cedar (*Cedrela odorat*a L., Meliaceae) and Yellow poui (*Tabebuia serratifolia* Nichols., Bignoniaceae) are economically valuable tropical tree species that have been threatened by predatory logging and forest fragmentation. Their seeds are wind-dispersed and both species colonize and grow in pastures. This study compared the genetic diversity of a 30 year pasture-established population to a forest population, located five km apart from each other in Rio Branco, Acre, Brazil. Thirty yellow poui trees were genotyped with five isozyme loci and fifty-four Spanish cedar trees were genotyped with four microsatellite loci. Genetic diversity was high in both the populations. In yellow poui, gene diversity was higher in the pasture population ($\hat{H}_e$ **=** 0,600) than in the forest population ($\hat{H}_e$ **=** 0,504). Differences exist with the loss of alleles in cedar pasture population ($\hat{A}$ = 11,75 alleles/locus) in relation to the forest population ($\hat{A}$ = 14,50 alleles/locus). Moreover, 31% of the cedar alleles were private to the forest population. Genetic divergence was null in yellow poui populations, but significant in cedar populations (2,2%). Pasture populations do not show evidence of severe genetic bottleneck for either species. Colonization of anthropogenic areas by these species was efficient, but it requires continuous gene flow, through successive generations, in order to restore (for Spanish cedar) and maintain (for yellow poui) the levels of genetic diversity observed in the forest population.

Keywords: *Cedrela odorata*; *Tabebuia serratifolia*; seed dispersion, connectivity, forest fragmentation

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