

POPULATION GENETIC STRUCTURE IN PROGENIES FROM TWO ORIGINS OF *COPAIFERA LANGSDORFFII* DESF. (LEGUMINOSAE - CAESALPINIOIDEAE).

Theme: Biodiversity Conservation Indicators

MANOEL, Ricardo de Oliveira¹; MORAES, Marcela Aparecida de¹; ALVES, Patrícia Ferreira¹; FREITAS, Miguel Luiz Menezes de²; MORAES, Mário Luiz Teixeira de¹; SEBBENN, Alexandre Magno².

¹ Faculdade de Engenharia de Ilha Solteira – UNESP

² Instituto Florestal de São Paulo

Keywords: Genetic diversity, gene flow, microsatellites, forest fragmentation

Copaifera langsdorffii is a tropical tree species, mostly found in broadleaf forest in the basin of Paraná. The study of this type of forest is important not only by potential ecological and economic of their species, but by the degree of devastation that has been featuring. The effects of forest fragmentation on genetic structure of progenies from two origins of *Copaifera langsdorffii* Desf. were evaluated by genotyping of eight microsatellite loci of 15 arrays trees of the grove (22 to 25 seeds per array) and 14 isolated trees in fields and pastures (20 seeds per array). The sampling understood progenies from two origins, of grove of São José do Rio Preto/SP and the edge of the state highways Feliciano Salles Cunha and Euclides da Cunha, both in the northwestern state of São Paulo. The loci used presented high levels of genetic diversity in the samples of adults and seeds from grove and of isolated trees. The higher number of alleles was observed in the progenies of single trees (212 alleles), followed by adults (186), and progenies of the grove (128) and the mean number of alleles per locus (\bar{A}) obviously followed same standard among the samples. The observed heterozygosity (H_o) was significantly higher in the adults ($H_o=0.757\pm0.013$ (mean \pm 95% IC) than in seeds from the grove (0.558 ± 0.006) and isolated seed-trees (0.557 ± 0.013). The estimated positive and significant fixation indexes in all samples suggest the occurrence of inbreeding. *C. Langsdorffii* is a predominantly species outcrossing, although certain rate selfing rate (8%) and mating among relatives (4%) have been detected. Selfing and mating among relatives generate inbreeding, so the average level of inbreeding in the grove ($F_o = 0.128$) and in isolated trees ($F_o = 0.154$) may have been generated by crossing between half-brothers ($\theta_{xy} = 0.125$). Another explanation for the high levels of inbreeding observed may be by the the presence of null alleles at the loci, by increasing the number of individuals supposedly homozygotes, whereas only one allele amplifies in the case of plants heterozygous for the null alleles. In general terms, the results showed that the spatial isolation of the population by forest fragmentation can increase inbreeding in future generations, there is gene flow via pollen, although the rate is low, making it necessary alternatives to promote gene flow between the forest remnants, favoring the dispersal of pollen and seeds between the fragments, action that would facilitate the maintenance of genetic diversity.

Apoio financeiro: FAPESP