

GENETIC VARIATION BETWEEN PROGENIES of *Pinus caribaea* Morelet var. *caribaea*
BASED ON MICROSATELLITE MARKERS

Janete Motta da Silva¹, Ananda Virginia de Aguiar², Edson Seizo Mori³, Mario Luiz
Teixeira de Moraes⁴, Valderês Aparecida de Sousa⁵

^{1,4} Universidade Estadual de São Paulo (UNESP), Ilha Solteira, São Paulo, Brazil.

^{2,5} Embrapa Florestas - Estrada da Ribeira, Km 111 - 83411-000 - Colombo, PR (ananda.aguiar@embrapa.br)

³ Universidade Estadual de São Paulo (UNESP), Botucatu, São Paulo, Brazil

Background: Species of *Pinus* genus are widely used in homogeneous reforestation projects world wide, especially for their good adaptation to different climates and the wide use of their products (wood, resins, pulp, Sawn wood, paper, etc...) (1). Morphological and silvicultural traits of *Pinus* besides the introduction of *P. caribaea*, tropical species, contributed to geographical expansion of planted forests in Brazil. Reforested areas, previously restricted to the South, have been expanded, reaching the Southeast and Midwest beyond some areas of North and Northeast (2) regions. Currently microsatellite is the most polymorphic among the available markers. The first microsatellites were developed for *Pinus radiata* (3). Nearly 86 % of the genome of this species consisted of repetitive DNA elements (4). The aim of this study was to estimate genetic diversity within and among three progenies of *P. caribaea* var. *caribaea* classified according to their breeding values performed from diameter at breast height (d.b.h) based on SSR markers.

Material and methods: For the present study, 96 individuals of *P. caribaea* var. *caribaea* progenies were selected and tested in an experimental area located at the Farm Teaching and Research facility from – Universidade Estadual de São Paulo (UNESP), campus Ilha Solteira, in municipality of Selvíria, Mato Grosso do Sul State, Brazil. Values were predicted for total trees, based on the dbh at 14.3 years old. Individuals were classified into three groups (subpopulations) according to their breeding values: superior, intermediate, and inferior. Thirty inferior individuals were selected, 36 intermediate, and 30 superior. ADN of these groups was extracted following the protocol proposed by (5), and modified by (6). Genetic parameters were estimated using Tool for Population Genetic Analyses (TFPGA) software. Variation between and within subpopulations was performed through Wright's *F* statistics (8).

Results and discussion: For individuals from superior group variation in allele frequencies ranged from 0.5192 (allele 1 primer RPTest 09) to 0.9318 (allele 1 primer PtTX 2037). The highest and smaller allele frequencies were observed for allele 2. For intermediate group, allelic frequencies varied from 0.6667 (primer RPTest 09) to 0.9000 (primer APC13) for allele 1 and from 0.0571 (primer APC13) to 0.3333 (primer RPTest 09) allele 2. For inferior group alleles frequencies varied from 0.5352 (primer RPTest 09) to 0.9783 (RPTest 01) for allele 1; and from 0.0217 (01 RPTest) to 0.4348 (RPTest 09) allele 2. Average observed and expected heterozygosity values were very similar to three groups. The variability for superior group was slightly higher (0,3725 and 0,3363) than that for intermediate (0,3690 and 0,3207) and inferior (0,3430 and 0,2840) groups. According to the *F* statistics, there is fixation of alleles analyzing average of all loci, between groups (subpopulations) F_{ST} was near zero ($F_{ST} = 0.0075$), furthermore a heterozygotes

excess of ($FIS = -0.1489$). This means that the selection in the progeny test is favoring individuals heterozygous over homozygous.

Conclusion: Genetic variation within progenies was maintained, despite of intense selection either for subpopulations with inferior, intermediate and higher performance for dbh.

Acknowledgements: The Higher Education Personnel Training Coordination - CAPES for granting Ph.D. scholarship.

References:

- (1) SEBBENN, A.M.; PIRES, C.L.S.; STORCK, L.; CUSTÓDIO FILHO, A.; ROSA, P.R.F. Variação genética em progênies de meios-irmãos de *Pinus caribaea* Mor. var. *bahamensis* Bar.et Gol. na região de Bebedouro, SP. **Revista do Instituto Florestal**, São Paulo, v.6, p.63-73, 1994.
- (2) SILVA JÚNIOR, F.G. Utilização múltipla da madeira de *Pinus caribaea* var. *hondurensis* para produção de celulose kraft. In: ANAIS DO WORKSHOP “QUALIDADE DA MADEIRA EM *Pinus*”, Piracicaba, 1992. **Série Técnica do IPEF**, Piracicaba, v.9, n.27, p.56-62. 1993.
- (3) SMITH, D.N.; DEVEY, M.E. Occurrence and inheritance of microsattelites in *Pinus radiata*. **Genome**, Ottawa, v.37, p.977-983, 1994.
- (4) ELSIK, C.G.; WILLIAMS, C.G. Low-copy microsatellite recovery from a conifer genome. **Theoretical and Applied Genetics**, Berlin, v.103, p.1189-1195, 2001.
- (5) DOYLE, J. J., DOYLE, J. L. A rapid DNA isolation procedure for small quantities of fresh leaf tissue. **Phytochem Bull**, n.19, p.11-15, 1987.
- (6) GRATTAPAGLIA, D.; SEDEROFF, F.F. Genetic linkage maps of *Eucalyptus grandis* and *E. urophylla* using a pseudo-testcross mapping strategy and RAPD markers. **Genetics**, Austin, v.137, p.1121-1137, 1994.
- (7) WRIGHT, S. The interpretation of population structure by F-statistics with special regard to systems of mating. **Evolution**, Lancaster, v.19, p.395-420, 1965.