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## Evaluation of *Hevea* Germplasm: III. Genetic Divergence in certain genotypes of *Hevea*

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### Abstract

Genetic divergence analysis was done by  $D^2$  statistics in 102 genotypes from the wild Brazilian germplasm of *Hevea brasiliensis* for girth, height, bark thickness, yield and single leaf area. The genotypes were grouped into five clusters. The first cluster had 76 genotypes, the II<sup>nd</sup> cluster had 9, the III<sup>rd</sup> and V<sup>th</sup> cluster had 3 each and IV<sup>th</sup> cluster had 4 genotypes. 7 genotypes could not be grouped. Maximum inter cluster distance of 970.1 was between I and V. The genetic diversity was found to be independent of geographic origin and genotypes from Acre provenance exhibited wide genetic diversity.

Key words: *Hevea brasiliensis*, Germplasm, Provenance, Genetic Divergence, Cluster.

### Introduction

Rubber (*Hevea brasiliensis*) being an out breeder showing both inbreeding depression and heterosis, is a crop where the breeder had to work mostly with polygenic systems biometrically. In search of highly heterozygous clonal segregates resulting from heterotic combinations, the breeder is always in need for very distantly related parents, with the maximum genetic diversity between them. Strong positive relationships have been found between genetic distance and heterosis in a wide range of crop species (Balasch *et al.*, 1984; Shamsuddin, 1985). Wide crosses between well established parental clones and exotic materials of effectively unknown worth can be expected occasionally to give large specific Combining ability effects apparent as heterosis. Divergence analysis is performed to identify the diverse genotypes in a population for hybridization purpose by clustering the population using Mahalanobis  $D^2$  statistics. The application of multivariate analysis and the use of generalized distance ( $D^2$ ) as a quantitative measure of genetic divergence has been reported in other crop plants also (Viravan *et al.*, 1973; Bavappa and Jacob Mathew, 1982) and in Rubber (Kavitha *et al.*, 1992). Clusters separated by the largest statistical distance (D) shows the maximum genetic divergence showing their suitability as parents in wide crosses. This study was undertaken with the objective of getting some preliminary information about the extent of genetic divergence existing in the Brazilian germplasm of *Hevea*, as no such study had been reported in this material so far.

## Materials and methods

The material for the present study was a random sample of 100 genotypes from a population of *Hevea brasiliensis* Wild. (ex A. de JUSS.) Muell Arg. Belonging to the 1981 IRRDB Germplasm collection from Brazil. The materials received in India are being conserved by the Rubber Research Institute of India for characterization, cataloguing and evaluation. The material represents three different agro climatic zones in Brazil, namely Acre, Rondonia and Matto Grosso. The plants have been selected from the base nursery at 24 months age, planted in 1 X 1 m spacing, linearly, and six plants were selected randomly from each genotype for recording the observations. The characters recorded were girth of the plant at 40 cm height from the bud union (cm), total height of the scion (cm), bark thickness at 40 cm height from bud union (mm), Single Leaf Area (cm<sup>2</sup>) and Total Yield of five test tappings (g/t/t). The two popular clones GTI and RRH 105 were taken as the control.

The data was then subjected to multivariate analysis using Mahalanobis D<sup>2</sup> statistics described by Mahalanobis (1936). The clustering of the genotypes for their genetic diversity was done by Tocher's method as per Single and Choudhary (1979). The criterion used for clustering was that any two genotypes belonging to the same cluster, on an average show a smaller intra cluster distance than the inter cluster distances.

## Results and discussion

By D<sup>2</sup> analysis 100 genotypes were grouped into five cluster. Among the five cluster, cluster I was the largest with 76 genotypes. There were 9 genotypes in cluster II, 3 genotypes in cluster III, 4 in cluster IV and 3 genotypes in cluster V. 7 genotypes could not be grouped (Table. 1).

Cluster I had 28 Rondonia genotypes, 25 Matto Grosso genotypes and 21 Acre genotypes. It was noted that 28 out of the 30 genotypes from Rondonia and 25 out of the 29 genotypes from Matto Grosso, had been grouped in this cluster, while only 21 out of the 41 genotypes from the provenance of Acre was grouped in cluster I. The two control clones GTI and RRH 105 were also included in cluster I. The minimum D<sup>2</sup> value of 0.03 and the maximum D<sup>2</sup> value of 3685 X 10<sup>-4</sup> in the population was also found in cluster I.

Another feature that could be noted was that the 20 genotypes in cluster I was distributed in 3 genetically divergent clusters II, IV and V the remaining genotypes were not

grouped in a cluster. This shows the wide genetic diversity in the genotypes from the provenance of Acre, compared to that of Rondonia and MattoGrosso genotypes. But in the sample studies, few divergent genotypes from Rondonia and Matto Grosso could be observed. One Rondonia genotype (RO 309) was found to cluster in cluster III and another Rondonian genotype (RO 306) remained independent. Similarly 4 genotypes from Matto Grosso showed genetic divergence from the rest of the Matto Gross genotypes grouped in cluster I. MT 1022 and MT 1016 were grouped together in cluster III while MT 930 and MT 1008 remained independent and hence divergent, not being grouped in any cluster. In general it can be seen that among the three provenances, the clustering pattern does not indicate any strong relation between genetic divergence and geographical distribution which is in agreement with the earlier findings of Markose (1982) and Kavitha *et al.*, (1992) in Rubber. But within the genotypes from a common provenance genotypes from Acre exhibited the maximum genetic divergence compared to Rondonia and Matto Grosso.

Table 2 show the mean values in each cluster for the five characters studied. It can be observed that the traits height of the plant, single leaf area and total yield contribute much to the genetic divergence in the population.

The average Intra and Inter cluster distances (D) are depicted in Table 3. The maximum genetic distance was observed between cluster I and cluster V (970.1), followed by cluster II (928.7). The maximum genetic distance was between cluster II and IV (241.1) followed by II and V (242.0). The intra cluster distance ranged from 153.2 to 696.3, in clusters III and I respectively.

### Conclusion

1. The genotypes from the provenance of Acre exhibited wide genetic diversity compared to Rondonia and Matto Grosso.
2. Selection of parents form different cluster can be expected to produce variability by crossing among themselves or with known clones.

Table. I. Distribution of genotypes in 5 clusters

Cluster	No. of genotypes	Distribution
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I	76	Acre - 21 Rondonia - 28 Matto Grosso - 25 GT I and RRH 105
II	9	Acre - 9
III	3	Matto Grosso - 2
IV	4	Acre - 4
V	3	Acre - 3

Table 2. Cluster mean values for 5 characters

Cluster	Girth (cm)	Height (cm)	Bark thickness (cm)	Single Leaf area (cm <sup>2</sup> )	Total yield (g)
I	15.25	570.2	0.24	121.5	0.76
II	15.65	618.2	0.23	123.8	0.52
III	15.89	513.7	0.24	91.3	1.03
IV	15.61	530.7	0.23	114.4	0.20
V	15.45	590.7	0.24	138.7	0.33

Table 3. Average Intra and Inter Cluster distance

Cluster	I	II	III	IV	V
I	696.3	928.7	299.9	788.0	970.1
II		358.6	719.1	241.1	242.0
III			153.2	715.0	682.6
IV				182.6	250.7
V					170.0

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