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Studies On Genetic Divergence in *Hevea brasiliensis*

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Abstract

Knowledge about the genetic divergence existing in a population is highly beneficial in plant breeding programs exploiting gene recombination and heterosis. Multivariate analysis for genetic divergence was done by the D2 statistic in 35 exotic clones selected from a Wickham population of Rubber (*Hevea brasiliensis*). The variable studied were girth, rubber yield, total volume of latex, dry rubber content, latex flow rate, plugging index, bark thickness, TLVR, DLV and diameter of latex vessels. The clones were grouped into 9 clusters. The first cluster had 17 clones, the second had 5 clones, the third had 4 clones, the fourth, fifth and sixth clusters had 2 clones each and the seventh, eighth and ninth cluster had a single clone each. The inter and intra-cluster distance have been worked out along with the cluster means for the various characters.

Introduction

Hevea brasiliensis (Wild.ex Adr.de Juss.) Muell. Arg. being an out breeder showing both inbreeding depression and heterosis, is a crop where the breeder has to work mostly with polygenic systems biometrically. In search of highly heterozygous clonal segregates resulting from heterotic combinations, the breeder is always in need of 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). Any plant breeding programme desiring the exploitation of gene recombination and heterosis between populations can be successful with the assessment of genetic divergence existing between the selected populations. Measure of genetic distance based on a wide range of characteristics related to the breeding objectives can contribute greatly to the success of any breeding programme.

Divergence analysis is performed to identify the diverse clones in a selected population for hybridization purpose by clustering the population using Mahalanobis D^2 statistic. The use of multivariate analysis and the generalized distance (D^2) as a quantitative measure of genetic divergence are well illustrated in other crop plants (Vairavan *et al.*, 1973; Bavappa and Jacob Mathew, 1982) and Kavitha *et al.*, (1992) in Rubber.

Today efforts are undertaken to broaden the narrowing genetic base of the Wickham clones due to the unidirectional selection for yield over the years. But even the Wickham material is expected to possess sufficient genetic diversity (Markose, 1984; Chevallier, 1988; Kavitha *et al.*, 1992), which can be maintained by further crossing. The present experiment was conducted to estimate the genetic divergence among certain Wickham clones mainly of Malaysian origin along with a few clones from Brazil, India and Liberia. The information gathered from this study will enable the identification of divergent clones for use in breeding programs.

Materials and methods

The materials selected for the study comprised of 35 clones of *Hevea brasiliensis*. The clones were planted in a randomized block design in 1979, with three replications and five trees per plot, in normal spacing. The data on yield and its components along with various morphological and anatomical attributes were recorded at the sixth year after opening, from three trees per plot. The list of the clones included in the study are given in Table 1.

Data on the following characters were recorded:-

(i) girth of the trees in cm in the month of November.

(ii) dry rubber yield as the average weight of two recordings (g/t/t).

(iii) Total volume of latex (ml/t/t).

(iv) Dry rubber content as percentage on a weight by volume basis (drc).

(v) The initial rate of latex flow recorded as the quantity in ml per minute of flow.

(vi) Plugging index (PI) computed following Milford *et al.*, (1969).

(vii) Bark thickness of clones in mm.

(viii) Total number of latex vessel rows (TLVR).

(ix) Density of latex vessel rows (DLV).

(x) Diameter of latex vessels in um.

The data recorded in the peak production season of 1993 was subjected to analysis of variance to test the significance of the variance ratios and also to the estimation of genetic divergence employing the Mahalanobis D^2 statistics (Mahalanobis 1936). Clustering of the clones is based on the criterion that the intra-cluster distance between any two clones in a cluster will be smaller than the inter-cluster distance between them. The contribution of individual characters towards the genetic divergence was determined as per Singh and Chaudhary (1985).

Results and discussion

Analysis of variance of the data was carried out to assess the significance of the clonal variation for all the characters studied. An abstract of the ANOVA along with the range and population mean for each character is given in Table 2. It was found that there was significant clonal variation for all the characters studied. All the characters studied had significant variation at 1% level of significance except DLV and diameter of latex vessels, which were significance except DLV. and diameter of latex vessels, which were significant at 5 % level. The clone RRIM 612 was found to have the maximum value for girth, dry rubber yield, total volume of latex and the initial flow rage of latex. The popular clone RRII 105 ranked first in terms of its highest values for TLVR and dry rubber content.

The significant clonal variation for all the characters studied reveals the significant genetic differences among the clones and indicates the worthiness of the characters chosen to classify the clones accordingly. This result is in agreement with the similar study conducted in *Hevea brasiliensis* by Kavitha *et al.*, (1992).in a different set of clones.

On the basis of the relative magnitude of D^2 values, the 35 clones were grouped into nine clusters in which the D^2 values ranged from 1.55 to 43.19. The composition of these nine cluster is shown in Table 3. Among the nine clusters Cluster I was the largest with 17 clones. Out of the 17 clones, 15 were Malaysian clones including the popular clone RRIM 600, except for the two Brazilian clones IAN 717 and IAN 873. The second largest cluster grouped 5 Malaysian clones in Cluster II. Cluster III had 4 clones, which included Harbel 1. Cluster IV,V and VI had 2 clones each, with the cone IAN 713 in Cluster IV and the popular clone RRII 105 in Cluster V. Three Malaysian clones RRIM 612, RRIM 632 and RRIM 628 could not be grouped into any cluster and formed separate single clone clusters.

The inter and intra – cluster distances were worked out (Table 4). The intra – cluster distances ranged from 0.00 in the three single clone clusters VII, VIII and IX to a maximum of 10.21 in Cluster IV followed by the Clusters II,VI,V,III and Cluster I. The inter – cluster distances between the various combinations of clusters were worked out. It was found to range from a minimum of 12.06 between Cluster I and IX to a maximum distance of 39.15 between Cluster IV and VI.

Table 5 shows the mean values in each cluster for the ten characters studied. Cluster VII with the single clone RRIM 612 was found to be superior with respect to six characters – girth, dry rubber yield, diameter of latex vessels, total volume of latex, flow rate and dry rubber content. For the character bark thickness Cluster III was found to be superior while Cluster IV had the highest cluster mean for the character TLVR. Cluster VIII with a single clone RRIM 632 was found superior for DLV and Cluster IX with the clone RRIM 632 was superior for plugging index.

The majority of the 35 clones studied were Malaysian clones except for one Liberian, three Brazilian and one Indian clone. Inspite of this, the Malaysian cones could be grouped into genetically divergent clusters, which indicates the highly heterozygous nature of the crop. The popular Indian clone RRII 105 was grouped along with RRIM 602 both having the same parentage. RRIM 612 was grouped singly in Cluster VII and was found to be a superior cone with respect to yield and various yield attributes.

For the effective realization of heteroses in the F1 generation, it is ideal to select parents on the basis of their genetic distances. However, desirable and high magnitudes of heterosis need not always be directly related to the extreme parental divergence (Arunachalam *et al.*, 1984) and intermediate divergent classes would have high probability of producing heterotic hybrids (Thakur and Zarger, 1989). In the difficult process of genetically improving a complex quantitative trait like yield in *Hevea*, selection of parents based on a number of important components collectively will definitely be better than selection based on individual attributes (Kavitha *et al.*, 1992). Hence it is appropriate to select parents based on their superiority for the various yield-contributing characters from clusters separated by medium to high genetic distances. The inter – cluster distances among the nine clusters were found to be of the highest magnitude between the Cluster IV and VI followed by the Clusters IV and VII, VII and VIII, VI and VIII, II and VII, III and IV, II and V, VIII and IX, II and VI, III and IX, III and the clusters III and V which showed medium to high divergence between the Clusters and hence the clones.

Conclusion

The present study to identify genetically divergent clones in the selected population of 35 Wickham clones grouped them into nine genetically divergent clusters. Several combinations of clusters showed medium to high genetic divergence between them as indicated by their inter-cluster distances. These results thus bring out information on the genetically divergent clones, with their superiority for various yield-contributing characters. This shall serve as valuable supplementary information to breeders in their selection of parents for specific breeding programs.

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Table: 1. List of clones

Country of origin	Clones
Malaysia	RRIM 604, RRIM 519, RRIM 621, RRIM 513, RRIM 701, RRIM 636, RRIM 707, RRIM 620, RRIM 605, RRIM 705, RRIM 501, RRIM 526, RRIM 704, RRIM 607, RRIM 600, RRIM 622, RRIM 617, RRIM 603, RRIM 611, RRIM 601, RRIM 610, RRIM 608, RRIM 703, RRIM 615, RRIM 706, RRIM 623, RRIM 602, RRIM 612, RRIM 632, RRIM 628.
India	RRII 105
Brazil	IAN 717, IAN 713, IAN 873.
Liberia	Harbel I.

Table: 2. Variability for the various characters studied.

Characters					Population mean	Variance ratio
	Minimum	Clone	Maximum	Clone		
Girth cm	63.07	RRIM 617	100.33	RRIM 612	78.90	3.78 **
Yield (g/t/t)	31.67	RRIM 632	117.67	RRIM 612	63.37	2.74 **
Bark thickness - mm	7.50	IAN 713	10.53	Harbel I	9.16	3.72 **
TLV	24.17	RRIM 615	39.23	RRII 105	32.29	1.99 **
DLV	30.67	RRIM 615	37.57	RRIM 602	33.68	1.29 *
Diameter um	21.47	IAN 717	30.53	RRIM 610	25.23	1.34 *
Total Vol. of latex (ml)	52.67	RRIM 617	214.93	RRIM 612	133.24	3.70 **
P.I.	2.07	RRIM 628	5.67	RRIM 706	3.67	4.98 **
Flow rate ml/mt.	2.60	RRIM 628	7.90	RRIM 612	4.53	4.68 **
D.R.C.(%)	26.83	RRIM 632	42.93	RRII 105	34.25	4.9 **

** = Significance at 1 % level * = Significance at 5 % level

Table: 3. Clustering of the clones.

Cluster No.	No. of clones	Clones
I	17	RRIM 604, IAN 717, RRIM 519, RRIM 621, RRIM 513, RRIM 701, RRIM 636, RRIM 707, RRIM 620, RRIM 605, RRIM 705, RRIM 501, RRIM 526, RRIM 704, RRIM 607, IAN 873, RRIM 600.
II	5	RRIM 622, RRIM 617, RRIM 603, RRIM 611, RRIM 601.
III	4	RRIM 610, RRIM 608, RRIM 703, Harbel I.
IV	2	RRIM 615, IAN 713.
V	2	RRIM 706, RRIM 623.
VI	2	RRIM 602, RRII 105.
VII	1	RRIM 612.
VIII	1	RRIM 632.
IX	1	RRIM 628.

Table : 4. Inter & Intra – cluster Distance.

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	8.64	13.53	13.22	16.41	13.51	15.27	16.12	17.67	12.06
II		9.28	19.12	15.93	24.96	22.96	31.74	17.28	15.67
III			8.79	30.13	20.24	14.50	17.51	21.48	22.19
IV				10.21	17.55	39.15	34.89	18.69	18.65
V					8.9	26.67	17.57	13.47	17.09
VI						9.18	12.54	32.59	12.46
VII							0.00	33.35	18.03
VIII								0.00	24.94
IX									0.00

Diagonal values represent Intra – cluster distance.

Table:5. Cluster means for the various characters studied.

Cluster	Girth cm	Yield (g/t/t)	Bark thickness (mm)	TLVR	DLV	Dia-meter (μm)	Total.vol. of latex (ml)	Plugg-ing Index	Flow rate (ml/m)	DRC. (%)
I	78	64.85	9.06	32.96	33.31	24.92	137.36	3.31	4.26	33.28
II	74.78	44.47	8.64	31.91	33.82	24.66	80.78	4.50	3.71	33.97
III	77.21	60.23	10.48	32.96	33.71	26.99	130.23	3.1	4.09	33.17
IV	76.22	48.22	7.66	25.17	31.17	25.53	111.83	4.42	4.65	38.75
V	92.80	75.00	9.25	25.00	34.05	27.55	180.12	4.03	6.35	35.23
VI	82.50	86.50	10.03	38.92	35.95	23.86	154.08	4.18	6.13	41.25
VII	100.33	111.7	9.87	35.73	34.27	27.67	214.93	4.5	7.9	41.97
VIII	92.27	31.66	9.2	30.67	37.00	26.40	132.33	4.31	4.93	26.83
IX	63.20	83.5	8.7	32.17	35.07	22.09	151.9	2.07	2.6	31.13