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POTENTIAL USE OF QUALITATIVE TRAITS FOR GENETIC DIVERSITY ANALYSIS IN *HEVEA* BREEDING

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The present study was undertaken to assess the utility of qualitative traits of *Hevea brasiliensis* in identification of diverse parents for hybridization programmes. Morhophological traits of 30 *H. brasiliensis* clones were scored based on their descriptors and analysed to group the clones based on their similarity. Ortet clones formed three clusters but did not reveal any relation with the geographical origin of the clones. UPGMA dendrogram constructed using similarity measure of 30 clones revealed four major clusters. Cluster I with 10 clones showed the lowest similarity with other clusters. The results of the present study indicate that there exists a genetic relationship among the clones clustered together based on discrete morphological traits. The possibility of using parents from distant clusters in future breeding programmes is discussed.

Keywords: Breeding, Divergence, *Hevea*, Parent selection, Qualitative traits

Increasing demand for natural rubber has necessitated the development of high yielding *Hevea brasiliensis* clones. Natural rubber productivity in India increased from 200 kg/ha/year with unselected seedlings during the 1920s to 2500 kg/ha/year during the 1990s with hybrid clones (Varghese *et al.*, 2006). The general pattern of rubber breeding is one of cyclical generation-wise assortative mating. Simmonds (1989) opined that so long as inbreeding is avoided, the results of crossing known parents are fairly predictable. The various approaches to genetic improvement in rubber demand judicious selection of genetically diverse parents to obtain substantial heterosis. However, information on genetic relationships among rubber clones is rather limited and most of the literature available on genetic diversity is based on wild germplasm and a limited number of cultivated accessions. Though molecular techniques like RAPD, SSCP and microsatellite markers (Varghese *et al*., 1997; Lekawipat *et al.*, 2003; Nakkanong *et al*., 2008) have been used for assessing genetic variability, wide utilization of these techniques is hindered as the procedures are cumbersome and involve high cost and skill. Several workers have described the clustering of varieties based on morphological descriptors in other crops (Sultana *et al.*, 2005; Chatan *et al*., 2009; Chipojola *et al.*, 2009; Al-Saghir, 2010). Minor morphological traits of clones of *H. brasiliensis* are considered to be stable

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and reliable indicators for clone identification (Mercykutty *et al*., 2002). This study is an attempt to assess the potential of using discrete morphological traits to estimate the genetic diversity among the popular clones.

Table 1. **Clones included in the analysis**

Clone	Parentage	Origin
RRII 105	Tjir 1 x Gl 1	India
RRII 5	Primary clone	India
RRII 203	PB 86 x Mil 3/2	India
RRII 118	Mil 3/2 x Hil 28	India
RRII 208	Mil 3/2 x AVROS 255	India
RRII 414	RRII 105 x RRIC 100	India
RRII 417	RRII 105 x RRIC 100	India
RRII 422	RRII 105 x RRIC 100	India
RRII 429	RRII 105 x RRIC 100	India
RRII 430	RRII 105 x RRIC 100	India
GT 1	Primary clone	Indonesia
PR 255	Tjir 1 x PR 107	Indonesia
PR 261	Tjir 1 x PR 107	Indonesia
Tjir 1	Primary clone	Indonesia
PB 260	PB 5/51 x PB 49	Malaysia
RRIM 600	Tjir 1 x PB 86	Malaysia
PB 28/59	Primary clone	Malaysia
PB 217	PB 5/51 x PB 6/9	Malaysia
RRIM 703	RRIM 600 x RRIM 500	Malaysia
PB 280	Primary clone	Malaysia
PB 311	RRIM 600 x PB 235	Malaysia
PB 235	PB 5/51 x PB S/78	Malaysia
RRIM 701	44/553 x RRIM 501	Malaysia
PB 86	Primary clone	Malaysia
Gl 1	Primary clone	Malaysia
RRIM 605	Tjir 1 x PB 49	Malaysia
RRIM 623	PB 49 x Pil B 84	Malaysia
PB 5/51	PB 56 x PB 24	Malaysia
PB 255	PB 5/51 x PB 32/36	Malaysia
RRIC 100	RRIC 52 x PB 86	Sri Lanka

Fifteen morphological traits were selected based on the descriptors of 30 popular clones (Table 1) during the early growth phase published by Mercykutty *et al.* (2002) and Thomas *et al*. (2006). Scores were assigned for the qualitative traits (Table 2) and analysis of the seven ortet clones was performed using Wagner Maximum Parsimony method (Phylip, version 3.68). Cluster analysis by UPGMA was performed on all the 30 clones based on Gower's General Similarity Coefficient (MVSP, version 3.13).

Analysis of genetic diversity by maximum parsimony as well as cluster analysis revealed similar divergence pattern among the seven ortet clones analysed. The seven primary clones clustered into three clades: clones Tjir 1 (Indonesia), Gl 1 (Malaysia) and PB 280 (Malaysia) in Cluster I, clones RRII 5 (India) and GT 1 (Indonesia) in Cluster II and PB 86 (Malaysia) and PB 28/59 (Malaysia) in Cluster III (Fig. 1). Clustering of ortets did not reveal any relation with the geographical origin of the clones and the lack of correlation between geographic origin and genetic diversity has

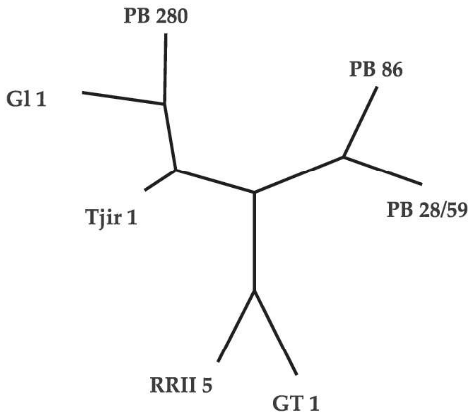

Fig. 1. Phylogenetic tree of ortet clones of *H. brasiliensis*

Table 2. **Description of qualitative traits used in the study**

Character		Description *
Nodes	Auxiliary bud	sunken (1),normal (2),protruded/prominent (3)
	Leaf scar	normal (1), prominent (2)
Leaf storey	Shape	bow (1), hemisphere/globe (2), conical (3), truncate (4)
	Separation	not well separated (1),well separated (2), diffuse (3)
	Density	closed (1), partially closed (2), open (3)
Leaves	Pulvinus	normal (1), swollen (2)
Petiole	Shape	arched (1), straight (2), concave (3), S shaped (4)
	Orientation	upward (1), horizontal (2), downward (3)
Leaf petiolule	Orientation	upward(1), horizontal (2), downward (3)
	Angle	narrow (1), average (2), wide (3)
Leaf blade	Texture	smooth (1), leathery (2)
	Shape	elliptical (1), obovate/pear (2), diamond elliptical (3)
	Margin	smooth (1), regular wavy (2), irregular wavy (3)
	Base	cuneate (1), attenuate (2), obtuse (3)
	Apex	aristate (1), acuminate (2), cuspidate (3), apiculate (4)

* Values in parentheses indicate the score assigned to the trait.

been reported earlier also based on molecular studies (Varghese *et al.*, 1997). Genetic diversity with respect to yield and related components in popular clones of rubber evolved from the Wickham base also did not show any relationship with geographical diversity (Mydin *et al.*, 1992). The improved rubber clones which are widely cultivated in the world have cytoplasm originating mainly from Tjir 1 or PB 56 (Priyadarshan and Goncalves, 2003). To introduce variability in cytoplasmic genes, ortet clones like GT 1 (Cluster III) showing less similarity with Tjir 1 (Cluster I) can be utilized as female parent in future breeding programmes. GT 1 is reported to be a prepotent clone (Mydin *et al.*, 2002).

UPGMA dendrogram constructed using the Gower Similarity Co-efficient measure, adopting the average genetic similarity (0.43) as the cut-off point, revealed four major clusters (Fig. 2) among the 30 clones. Cluster I had 10 clones dominated by clones involving Tjir 1 in their pedigree and included RRII 105, the popular clone in the traditional region of India. Cluster II consisted of nine clones and included the ortets RRII 5 and GT 1. Cluster III with four clones included ortets PB 86 and PB 28/59, as well as RRIM 600, the popular clone of the non-traditional rubber growing regions. Cluster IV included all the recently released RRII 400 series clones (except RRII 414) and their male parent RRIC 100. All clones included in Cluster IV had primary clones from Sri Lanka in their pedigree. The results indicate that there exists a genetic relationship among the clones clustered together based on discrete morphological traits. It was also interesting to note that RRII

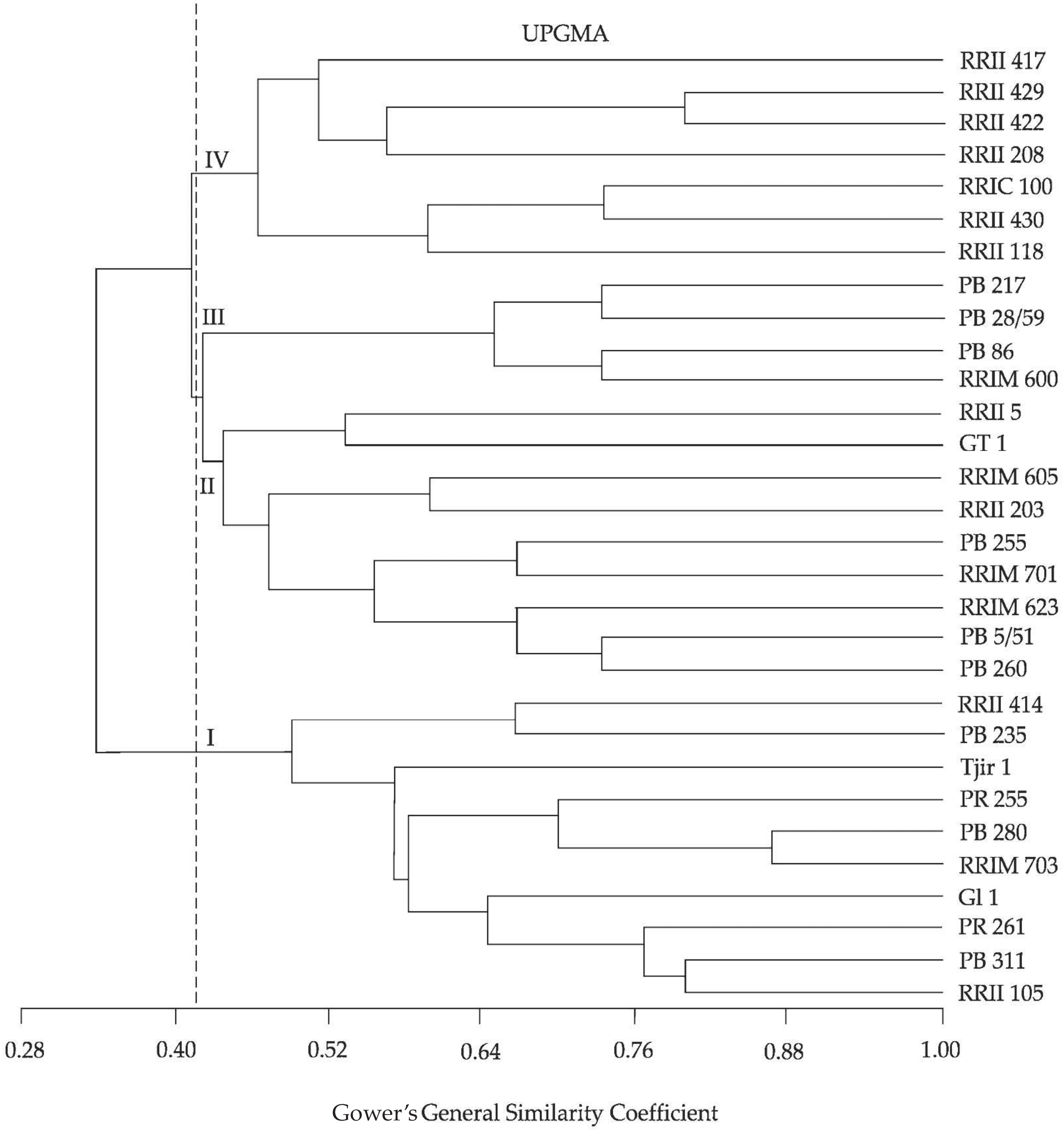

Fig. 2. Clustering of 30 popular *H.brasiliensis* clones based on 15 qualitative morphological traits

414, a Category 1 clone in the traditional region but a poor yielder in non-traditional regions, clustered with RRII 105 (Cluster I), while all other RRII 400 series clones clustered together in another group (Cluster IV). Clone PB 280 and RRIM 703 were most similar among the clones studied. The lowest similarity coefficient among the tested clones was observed between these two clones and RRII 417. Clone PB 260 (Cluster II), a high yielding prepotent clone (Sebastian and Saraswathyamma, 2005) with

PB 5/51 as its cytoplasmic donor, can be utilized as female parent in recombination breeding programme with suitable male parents from Cluster I or Cluster IV.

For the improvement of complex quantitative traits like yield, parents with desirable yield components are to be selected from clusters separated by medium to large genetic distances (Varghese *et al.*, 1997). The present analysis revealed that Cluster II and Cluster III were more closely related than the other two clusters. RRII 400 series clones with high yield potential are the progenies of RRII 105 (Cluster I) and RRIC 100 (Cluster IV). Clone RRIM 600 is the progeny of Tjir 1 (Cluster I) and PB 86 (Cluster III) indicating the heterotic effect of diverse parents.

The present study indicates the potential of utilizing qualitative traits for assessing the genetic diversity of *Hevea* clones. The results can be further validated using molecular techniques. Further investigations for selecting the morphological traits which will identify maximum diversity among clones as well as stability over environments will help in making reliable predictions on genetic divergence of *Hevea* clones for utilization in breeding programmes.

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