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ASSESSMENT OF YIELD ADAPTATION OF RUBBER TREE (*HEVEA BRASILIENSIS*) CLONES THROUGH PATTERN ANALYSIS

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ABSTRACT

Yield adaptation was assessed in twelve clones evolved in India (RRII 105, RRII 118, and RRII 208), Malaysia (RRIM 600, PB 5/51, PB 86, G l 1), Indonesia (PR 107, GT 1) and China (SCATC 88/13. SCATC 93/114, HAIKEN 1). The yield data of sub-optimal and optimal environments were separated into four environments of two successive years (1999-2001). GE biplot was made to assess adaptability of clones to the environments. The largest positive value is seen for RRII 208, indicating RRII 208 performs well across environments. At the other extreme is RRII 105 that extended to the negative side of vector A. When all clones are considered together, the ordering of interaction from most positive to most negative are RRII 208, SCATC 93/114, PB 86, RRIM 600, PR 107, RRII 118, GT 1, PB 5/51, HAIKEN 1, SCATC 88/13, G l 1 and RRII 105. The genotypes are well spread through the diagram and hence no obvious grouping of the clones is evident. To exercise selection based on both stability and yield, the PCA1 values were plotted against individual genotype means. PB 86 has a genotypic mean that is greater than general mean (31.49 g tree $^{-1}$ tap $^{-1}$) and the PCA value is almost zero, indicating thereby that PB 86 is stable over all environments. The clones exhibited differential trend of stability when PCA 1 values were depicted against environment means. RRII 208, RRIM 600 and Haiken 1 are seen to interact positively with varied environments, since their position is above zero value when depicted against both genotype and environment means.

INTRODUCTION

Rubber (*Hevea brasiliensis* Willd. ex Adr. de Juss. Muell.-Arg.) has become a prominent crop of marginal (non-traditional) areas of several tropical countries. Ideally grown under 15°N and S of the equator, the stress conditions experienced in the non-traditional areas falling under 16 – 23° N and S are low temperature, strong winds, higher altitude, water deficit and diseases (Pushparajah, 1983). Tripura state of northeast India (22° 56′ to 24° 32′ N and 91° 10′ to 92° 21′ E) offers a non-traditional environment for rubber. Rubber clones here exhibit two yielding regimes *viz.*, regime I (sub-optimal - May to September) and regime II (optimal - October to January) (Priyadarshan *et al.*, 2001). While the initial days of regime II that includes low temperature period tends to increase dry rubber yield, an atmosphere less than 15 °C ambient inculcates a recession. The sub-optimal period is the carried over effect of low temperature stress, defoliation, refoliation etc. (Priyadarshan *et al.*, 2000; 2001). Studies on interactions of plants with environment, especially in perennial species to judge their adaptability has been challenging since interactions under optimal and sub-optimal environments need to be viewed in different ways. GE interactions become vital when the rank of clones / varieties change under different environments. Under the alternation of environments, empirical breeding shall not be successful to gain early results. Assessment of stability / adaptability through GE interactions of clones with proven ability under other wise traditional areas is one way of gathering early data.

A wide variety of statistical approaches are available to assess stability / adaptability of genotypes over environments through GE interactions. Predominantly used methods are the joint linear regression analysis and its variants (Finlay and Wilkinson, 1963; Eberhart and Russell, 1966; Perkins and Jinks, 1968). However, these methods require an *a priorie* assumption of linearity and normality of yield response over environments. Most often, the data are rarely known to fulfill this assumption. Also, the recently developed Additive Main effects and Multiplication Interaction (AMMI) analysis (Gauch, 1992), basically an ordination technique, does not have a mechanism to classify environments. Pattern Analysis (PA) applied to many International Multi Environment Trials (IMETs) has been shown to be effective to classify environments and / or genotypes required to help identify the underlying patterns of GE structure in the environment and / or genetic population (Cooper *et al.*, 1996). Hence, PA is used here to assess yield adaptation of rubber tree clones.

MATERIAL AND METHODS

The experiment was conducted at the Regional Research Farm of the Rubber Research Institute of India at Taranagar (Tripura State, North East India - 23° 53′ N; 91° 15′ E; 30 m MSL). Yield data from a clonal trial involving 12 clones of Indian (RRII 105, RRII 118, RRII 208), Malaysian (RRIM 600, PB 5/51, PB 86, G l 1) Indonesian (PR 107, GT 1) and Chinese (SCATC 88/13. SCATC 93/114, HAIKEN 1) origin laid during 1987 in completely randomized design was utilized for the investigation. The planting materials were multiplied through bud grafting onto seedlings. Spacing was 5 x 5 m. Initially, there were 40 trees /clone. The latex coagulum (dry rubber yield - g tree $^{-1}$ tap^{-1}) was collected from every tree once a month, squeezed through rollers to drain water, dried in a smokehouse and weighed.

The yield data was from regimes that were separated into four environments of two years *viz.*, A: regime I of 1999-2000; B: regime II of 1999-2000; C: regime I of 2000-2001 and D: regime II of 2000-2001. ANOVA and other statistical calculations were undertaken as per standard procedures (Snedecor and Cochran, 1980; Girden, 1992). Pattern analysis was conducted following Cooper *et al.* (1996). A biplot is a graphical display of entries (e.g. clones) and testers (e.g. environments) of a two-way data. When the two-way data is subjected to singular value decomposition, it is decomposed in to three matrices: the singular value matrix, the entry eigen vector matrix and the tester eigen vector matrix. The singular value matrix is diagonal matrix, and can be somehow partitioned into the entry and tester eigen vector matrices. After singular values are partitioned, the positions of the entries and testers are defined by entry eigen vectors and tester eigen vectors respectively.

RESULTS AND DISCUSSION

All clones showed two yielding regimes: optimal and sub-optimal (Table 1; Fig. 1). ANOVA conducted also proved differences among clones and clones x months interactions were significant (Table 2). The genotypes are well spread through the diagram and hence no obvious grouping of the clones is evident. The biplot clearly shows that environments A and C coincide in the diagram (Fig.2). Likewise, B and D coincide. Hence, interaction of any clones under A is same as that of C. The largest positive value is that of RRII 208. This means that RRII 208 performs well across environments. At the other extreme is RRII 105 that extends in to the negative extension of vector A. When all the genotypes are considered together, the ordering of the interaction from most positive to most negative are RRII 208, SCATC 93/114, PB 86, RRIM 600, PR 107, RRII 118, GT 1, PB 5/51, HAIKEN 1, SCATC 88/13, G l 1 and RRII 105. Since the vectors B/D and A/C are in the opposite sides, their interactions are just the opposite. The genotypes are well spread out through the diagram and hence no obvious grouping of the genotypes is evident.

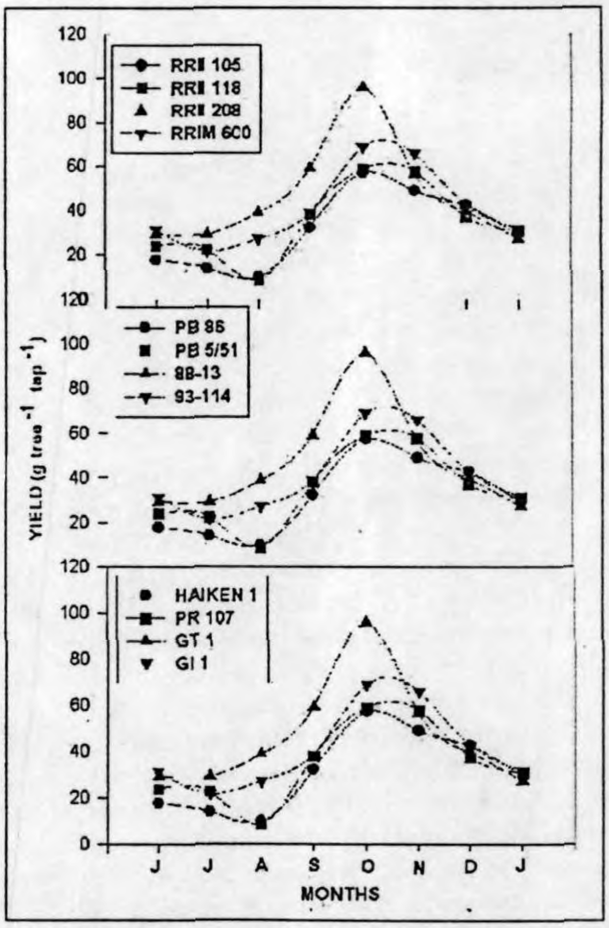

Fig. 1. Yielding trends of 12 clones over months

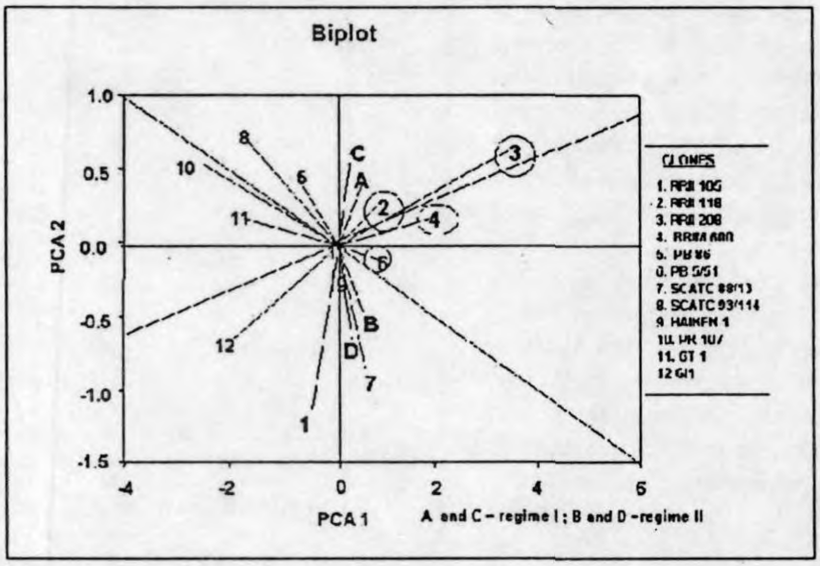

Fig. 2. Biplot for principal components 1 and 2 obtained from the ordination of environment standardized dry rubber yield data of 12 cones over four environments. The environments are indicated as vectors drawn from the origin (A, B, C, D).

Table 1. Yield (g tree $^{-1}$ tap $^{-1}$) of 12 clones under two yielding regimes

Clone	1999-2000		2000-2001	
	Regime I (env. A)	Regime II (env. B)	Regime I (env. C)	Regime II (env. D)
RRII 105	20.9	64.5	18.4	44.5
RRII 118	35.8	59.4	28.1	46.2
RRII 208	56.6	76.1	39.2	54.8
RRIM 600	45.2	62.2	29.6	52.3
PB 86	25.9	47.7	22.7	34.3
PB 5/51	34.8	60.4	25.8	46.3
SCATC 88-13	28.8	64.4	22.5	50.5
SCATC 93-114	25.0	40.4	18.8	30.3
HAIKEN 1	32.2	54.1	19.8	45.6
PR 107	15.0	35.4	13.6	23.9
GT 1	19.4	40.4	16.4	36.2
Gl 1	12.1	48.5	11.6	31.8

Sub-optimal environments: A and C ; Optimal environments: B and D
Regime I = May to September ; Regime II = October to January

Table 2. Analysis Variance for 12 clones over two years

Sum of Squares	d.f.	M.S.S.		F	Significance
Clones	1204444.5	11	109494.9	150.3	0. 00
Months x Clones	247461.0	165	1499.7	2.8	0. 00
Error (months)	2371661.7	4440			

To exercise selection based on both stability and yield, the PCA1 values were plotted against individual genotypic means (Fig. 3). PB 86 has a genotypic mean that is greater than general mean (31.49 g tree $^{-1}$ tap $^{-1}$) and the PCA value is almost zero, indicating thereby that PB 86 is stable over all environments. This conforms to the contention that PB 86 is a stable clone with lesser coefficient of variation and higher yield in a comparative analysis of 15 clones (Priyadarshan *et al.*, 2000). Since RRII 105 and HAIKEN 1 exhibited lower PCA values and higher yield (g tree $^{-1}$ tap $^{-1}$), these clones can also be considered stable. However, though RRII 208 exhibited higher genotype means, its shift from PCA value indicating that it has the tendency of performing better under favourable environments. The clones exhibited differential trends of stability when PCA 1 values were depicted against environment means (Figs. 4 & 5). RRII 118, RRII 208, RRIM 600, PB 5/51, SCATC 88/13 and Haiken 1 are seen to interact positively in the regime II (optimal environment), only RRII 208, RRIM 600 and Haiken 1 exhibited stability over both optimal and sub-optimal environments, since their depiction is above zero value when plotted against both genotype and environment means. In conclusion, the pattern analysis rationalized PB 86 as the most adapted over all environments followed by RRII 208, RRIM 600 and Haiken 1.

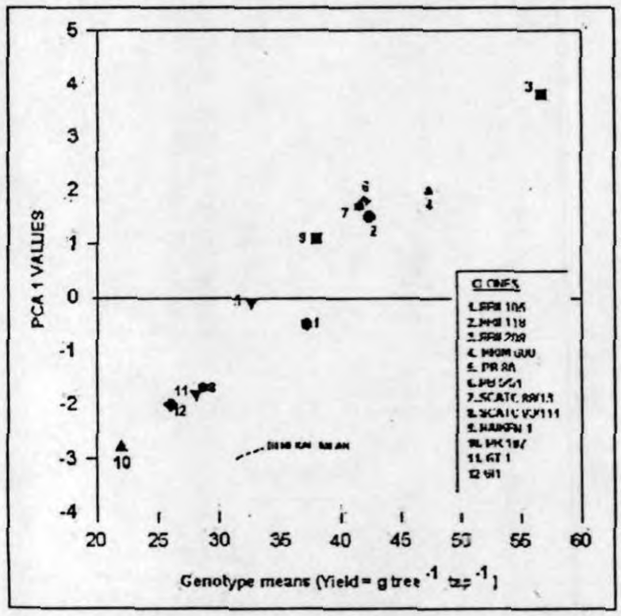

Fig. 3. Depiction of genotype means against PCA values

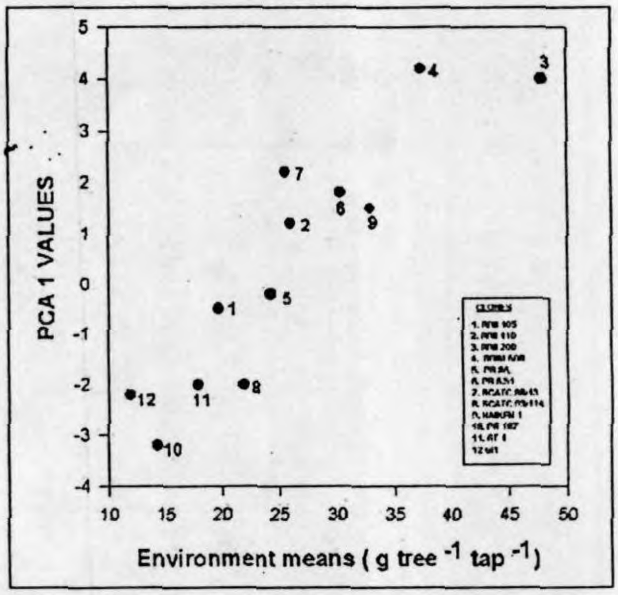

Fig. 4. PCA values plotted gainst environment means (regime I)

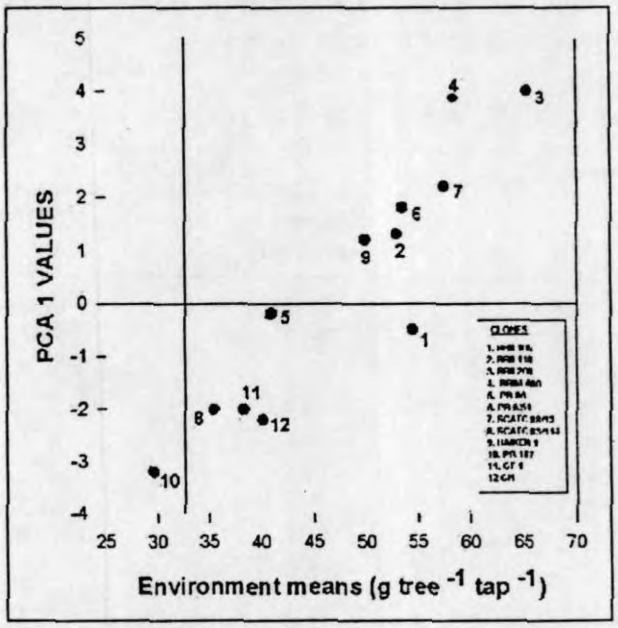

Fig. 5. PCA values plotted gainst environment means (regime II)

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