GENETIC PARAMETERS AND DIVERGENCE IN CERTAIN WILD GENOTYPES OF *HEVEA BRASILIENSIS* (Willd. ex Adr. de Juss.) Muell. Arg.

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BY

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Dedicated to

my parents and teachers

DECLARATION

I, **SAJI T. ABRAHAM** hereby declare that this thesis entitled **"GENETIC PARAM-ETERS AND DIVERGENCE IN CERTAIN WILD GENOTYPES OF *HEVEA BRASILIENSIS* (Willd. ex Adr. de Juss.) Muell. Arg.** is a bonafide record of the research work done by me at Rubber Research Institute of India, Kottayam-686009 and that no part thereof has been presented earlier for any degree or diploma of any other University.

Kottayam
06-12-2000

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CERTIFICATE

This is to certify that the thesis entitled **"GENETIC PARAMETERS AND DIVERGENCE IN CERTAIN WILD GENOTYPES OF *HEVEA BRASILIENSIS* (Willd. ex Adr. de Juss.) Muell. Arg.** is an authentic record of original research work carried out by SAJI T. ABRAHAM at the Rubber Research Institute of India, Kottayam-686009 under our joint supervision and guidance during the period September 1993 to November 2000 for the award of the degree of Doctor of Philosophy in the Faculty of Science, Mahatma Gandhi University.

The work presented in this thesis has not been submitted for the award of any other degree or diploma earlier. It is also certified that Saji. T. Abraham has fulfilled all the requirements and has passed the qualifying examination for Ph.D. of the Mahatma Gandhi University.

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CHAPTER 1

Introduction

Hevea brasiliensis (Willd. ex Adr.de Juss.) Muell.Arg., the Para rubber tree, meets almost exclusively the world's natural rubber requirement, which is an indispensable industrial raw material. In India, the rubber tree is grown in an area of 5,53000 ha and the country produces 6,05045 tonnes (1998-1999) of natural rubber (Anonymous, 1999). The rubber tree is native to the rain forests of the tropical region of the Great Amazonian basin in South America. Sir Henry Wickham introduced the original genetic material of *H. brasiliensis* to South East Asia in 1871, from a minuscule of the genetic range available near the Tapajoz river in Brazil (Wycherley, 1968; Schultes, 1977; Allan, 1984). This material with a narrow genetic base, referred to as the 'Wickham gene pool', had served as the base material for the subsequent spread of rubber cultivation and the crop has developed remarkably well from a wild jungle tree to a major domesticated crop.

From this original material with an average rubber yield of 200 – 300 kg/ha/year, rubber breeders could achieve substantial improvement in production, by means of selection and hybridisation, resulting in a ten fold increase to around 3000 kg/ha/year for the recently evolved clones, over a limited time span (Licy *et al.*, 1992; Varghese, 1992). However, the rigorous unidirectional selection practiced over the years, has further narrowed down the genetic base resulting in a slow down in genetic advance in recent years (Tan, 1987; Ong and Tan, 1987; Simmonds, 1989).

1.1 Origin and distribution

There are ten species reported in *Hevea.* They are *H.brasiliensis, H. benthamiana, H.guianensis,H .nitida, H. pauciflora, H. rigidifolia, H.camporum, H.camaragoana, H.spruceana and H.microphylla.* The genus has its origin in the whole of the Amazon river basin in Brazil, covering parts of Brazil, Bolivia, Peru, Columbia, Ecuador, Venezuela, French Guyana, Surinam and Guyana (Webster and Paardekooper, 1989). Absence of any biological barrier among these species has created natural hybrids and genetic variants in the population. The different species exhibit wide variation in growth habit and morphological traits.

Of the ten species, *H. brasiliensis* the commercially important species occupies about half of the range of the genus, mainly in the region south of Amazon, extending upto Acre, Mato Grosso and Parana areas of Brazil, parts of Bolivia, Peru, north of the Amazon to the West of Manaus as far as the extreme south of Columbia. The species is now grown mainly in the tropical regions of Asia, Africa and America, in countries like Malaysia, Indonesia, India, Sri Lanka, Thailand, China, Philippines, Vietnam, Kampuchea, Myanmar, Bangladesh, Singapore, Nigeria, Cameroon, Central Africa, Ivory Coast, Ghana, Zaire, Liberia and Brazil. However, major share of the total production in *H.brasiliensis* is from the tropical Asian countries.

1.2 Narrow genetic diversity

Unidirectional selection for yield, large scale adoption of cyclical generation-wise assortative breeding and wider adoption of the commercially accepted practice of clonal propagation by budding were the major factors which led to further limitation of the original narrow genetic base. In the crop improvement programmes, till recently the main objective of the selection was improvement in yield alone, ignoring the genetic variability with regard to secondary characters (Wycherley, 1969), which has reduced the genetic variability in the population. Breeding in *Hevea* involves generation wise assortative mating (GAM), where the best clones in one breeding cycle serve as parents for the next cycle and so on (Simmonds, 1989). Hence, the parentage of popular clones bred in various

rubber growing countries can be traced back to just a handful of parent clones (Tan 1987, Varghese, 1992). With the development of high yielding clones, extensive areas are being planted with a limited number of modern clones (Varghese and Abraham, 1999).

1.3 Broadening the genetic base for biotic and abiotic stresses.

South American Leaf Blight (SALB) caused by *Microcyclus ulei*, prevalent in the American hemisphere and specific to *Hevea* species (Chee and Holliday, 1986; Edathil, 1986), has been identified as a potential threat to the rubber tree in the east. None of the Wickham clones has been reported to have resistance to SALB (Baptiste, 1961; Wijewantha, 1965; Clement-Demange *et al* 1997). There are reports of lose of genes controlling resistance to *Oidium* sp. and *Gloeosporium* sp. in the original Wickham material (Wycherley, 1977). Besides these, there is the threat of several minor leaf diseases assuming epidemic proportions. The severe incidence of *Corynespora* leaf spot disease, observed in 1985 onwards affecting various clones in Sri Lanka, has become an important problem. Consequently a popular and high yielding clone, RRIC 103, had to be withdrawn from the planting recommendation necessitating replanting of vast areas under this clone (Liyanage *et al* 1991).

In India, two major leaf diseases –abnormal leaf fall and powdery mildew caused by *Phytophthora* spp. and by *Oidium* sp. respectively- result in considerable damage and crop loss in rubber. Recent reports on the incidence of *Corynespora* leaf diseases in plantations in North Kerala and some rubber growing tracts of Karnataka (Jacob, 1996) has caused great alarm about the possibility of this disease assuming endemic proportions. The emergence of a virulent strain of a pathogen, with favourable environmental conditions along with a susceptible host will create a 'disease triangle' and the probability of mono-cropped plantations of rubber facing a likely threat cannot be ruled out (George, 1989). Hence the breeder has to be active building up disease resistance in the commercial cultivars.

The scope for further expansion of rubber in traditional areas has become very limited due to non-availability of land. Thus, it has become necessary for the expansion of this crop into non-traditional rubber growing areas of the country, where the crop becomes

subjected to extremes of climate, and moisture stress, besides problems of high altitudes in many such areas. In the context of extending rubber cultivation to marginal and non-traditional areas, development of clones with resistance / tolerance to various abiotic stresses like drought, cold, high elevation etc assumes much significance. Hence, in order to develop / select such location specific clones; the base material on which the breeder has to work should contain ample genetic variability.

Considering all the above factors, the rubber breeders all over the world had realized the urgency of broadening of the genetic base of the crop by the introduction of fresh germplasm into the breeding cycles.

1.4 Germplasm resources

Hevea germplasm can be broadly classified into (a) those existing in the primary centre of diversity of Brazil and (b) those developed in the centres of secondary diversity. The primary centre of diversity includes the wild genotypes of the genus, along with naturally occuring hybrids and other variants. The commercial cultivars, obsolete clones and other genetic variants selected over the years are available in the secondary centres.

1.4.1 1981 International Rubber Research and Development Board (IRRDB) Collection.

Even though there were earlier collections of fresh germplasm of *Hevea*, the most important and largest of the collections was the expedition organised by IRRDB to the Amazon rain forests of Brazil in 1981. This effort could be considered as one of the most significant events in the history of rubber germplasm collection aiming very significant contributions to the genetic improvement of the crop. This expedition organised jointly with the Brazilian government, collected a total of 64736 seeds (Ong *et al* 1983; Mohd. Noor and Ibrahim, 1986) from the Brazilian states of Acre and Mato Grosso and the territory of Rondonia and budwood from 194 high yielding seedling trees (ortets) which were persumably free from *Microcyclus* and *Phytophthora* spp. (Ong *et al* 1983). Varying proportions of this fresh germplasm were distributed to the IRRDB member countries, including India.

India received her share of this new germplasm from the distribution centre in Malay-

sia, during the period 1984-1990, which was established in Central Experiment Station in South Kerala and in the Noth- East Research Complex, of Rubber Research Institute of India. A total number of 4967 accessions (George, 2000) have been established for conservation, evaluation and utilisation, in the traditional and non-traditional areas, in India

1.4.2 Characterisation, evaluation and utilisation of wild germplasm.

Evaluation of germplasm introduced and their incorporation in the breeding programmes are the two most important steps involved in broadening the genetic base (Chevallier 1988). Evaluation includes biometric study of the morphological traits (Lesprit and Nouy, 1984) and related characters of individual genotypes. One of the serious constraints in the successful and quick utilisation of the wild germplasm is the delay in characterisation, evaluation and cataloguing of the wild germplasm. Morphological characterisation is carried out using a set of chosen descriptors, which clearly describes each of the accessions for easily identifiable traits.

In the process of evaluation, plant breeders are concerned with a wide range of characters in the crop species. Most of such characters in rubber are complex, being under the control of a number of genes as well as being considerably influenced by the environment. Quantitative characters are mediated by joint action of a number of supplementary genes each having a small effect in relation to the total variation (genetic and environmental) and have been designated as polygenic systems and the genes as quantitative trait loci (QTLs) by Mather (1941). Since the effect of these individual genes cannot be identified except in special conditions, polygenic variation cannot be handled by classical Mendelian techniques and consequently biometrical methods involving statistical measures like means, variances, covariances etc have to be applied. The variability available in a population could therefore be partitioned into heritable and non-heritable components with the aid of genetic parameters like phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in the broad sense (H^2) and genetic advance (GA) which serve as the basis of any selection programme.

1.5 Genetic studies

1.5.1 Coefficients of variation

When variations have to be compared for different characters, each represented by different units, variance ratio alone is not adequate. This can be done by converting the different units of all the characters into a unitless measurement. Coefficient of variation thus provides such a measurement for comparing the extent of variation between different characters measured in different scales. Coefficients of variation are estimated at the phenotypic and genotypic level. Genotypic coefficient of variation defines the relative magnitude of the variability as contributed by the genotype and helps in the comparison of the genetic variability present in a population for different characters.

1.5.2 Heritability and genetic advance

The term heritability was first coined by Fisher (1918) as the ratio of the fixable genetic variance to the total genetic variance. For any selection to be carried out successfully, the breeder should know how much of the phenotypic variability estimated is heritable. Genetic advance is a measure of the change at the mean phenotypic level of the population consequent to selection and depends upon the heritability of the character and the selection differential. High heritability along with high genetic advance indicates the presence of additive gene action for the character and helps in an efficient selection.

1.5.3 Correlation

Correlation was first defined by Galton (1889) and was later elaborated by Fisher (1918) and Wright (1921). Correlation studies meet one of the basic requirements in any genetic evaluation attempt. Correlation defines the degree of association between two characters and the intensity of this relation can be measured by correlation coefficient, which determines the degree to which the two related variants could vary together. Such information on the magnitude and direction of correlations existing between different characters the breeder is working, enables him to identify those characters on which he need to

apply selection pressure so that the associated characters will also be improved along with these selected characters. Burton (1952) had introduced the phenotypic and genotypic coefficients of correlation. Phenotypic, genotypic and environmental correlation coefficients were worked out among all the characters studied, using the variance and covariance components as suggested by Singh and Chaudhary (1985). Several attempts have earlier been reported correlating the morphological and bark anatomical traits with the yield in rubber (Gilbert, 1973; Narayanan *et al*, 1973; Lee and Tan, 1979; Hamzah and Gomez, 1982; Licy and Premakumari, 1988; Licy, 1997; Mydin. 1992a and Premakumari, 1992).

1.5.4 Genetic divergence

Genetic divergence defines the genetic distance between two populations because of their genetic make up. In any breeding programme inclusion of genetically divergent parents is essential in order to create new genetic variability, which could help in the recombination of valuable genes from different sources thus deriving maximum heterosis. Hybridizaton using highly divergent parents thus produces hybrids with high heterosis. Several workers have reported the importance of genetic divergence in plant breeding (Hayes and Johnson, 1939; Hayes *et al* 1955). Many statistical procedures have been developed to measure the divergence between two populations. The most commonly used technique is the D^2 analysis proposed by Mahalanobis (1928,1936). The method calculates the genetic distances between the individuals in a population and then they are clustered based on their inter and intra cluster distances.

Genetic divergence studies have revealed the existence of greater allelic wealth in the new germplasm than in the Wickham germplasm. It is normal to find atleast a few favourable allelic arrangements of the plant in the wild population of a crop species. They therefore need to be distinguished more precisely and introduced into a breeding scheme (Nicolas, 1992).

Factor analysis is a useful statistical tool to reduce the total number of characters to be studied by identifying marker characters, which will accommodate the inheritance of a set of associated characters. Identification of the best genotypes, based on an index from

the pooled performance of the set of the selected characters, is a pre requisite for the ultimate utilisation of the wild genotypes.

1.6 Objectives of the study

The present study was carried out with emphasis on morphological, leaf structural and bark structural characters. The main objectives were:

- characterisation of the wild genotypes for morphological characters at the juvenile phase,
- assessment of the nature and extent of variability present in the wild germplasm,
- estimation of genetic parameters like heritability and genetic advance,
- assessment of the productivity potential of the wild genotypes at the juvenile / early premature phase,
- study of the degree of associations between the different characters with the test tap yield and their inter-correlations,
- study of the extent of genetic divergence available in the wild population and identification of highly divergent wild clones and,
- selection of the best genotypes for incorporation into crop improvement programmes.

CHAPTER 2

Materials and methods

2.1 Location

The experiment was conducted in a newly planted field evaluation trial of wild *Hevea* germplasm, at the Central Experiment Station of the Rubber Research Institute of India, at Chethackal, Pathanamthitta District, Kerala State, India, located at 9^0 22' N latitude and 76^0 50' E longitude, at an altitude of 80 m above MSL. The site is located in the typical traditional rubber growing area of the country. The experimental area was previously planted with rubber and the land is gently sloppy.

2.2 Experimental materials

Eighty genotypes of the 1981 IRRDB collection of wild *Hevea* germplasm was selected randomly from the base population, maintained by the Germplasm Division of the Rubber Research Institute of India, for characterisation, evaluation and utilisation for crop improvement, and have been used for this study. The popular *Hevea brasiliensis* clone, RRII 105, was used as the control. The materials were planted as polybag raised plants, of appropriate vigour and growth and maintained well. The genotypes were selected in such a way so as to get more or less equal representation of the accessions from the three provenances of Brazil – Acre (AC), Rondonia (RO) and Mato Grosso (MT) (Table 1), from where the genotypes were collected by the joint exploration by the International Rubber Research and Development and Board (IRRDB) team.

Table 1. List of the 80 wild genotypes selected for the study

Sl. No	National Accession number	International genotype code	Sl. No	National Accession number	International genotype code
1	AC 426	AC/F/5/117	41	RO 369	RO/C/8/130
2	AC 453	AC/F/5/220	42	RO 380	RO/C/8/177
3	AC 604	AC/S/11/1	43	RO 381	RO/C/8/179
4	AC 624	AC/S/11/107	44	RO 395	RO/C/8/302
5	AC 626	AC/S/11/111	45	RO 399	RO/C/8/327
6	AC 627	AC/S/11/113	46	RO 859	RO/CM/12/26
7	AC 629	AC/S/11/155	47	RO 868	RO/CM/12/44
8	AC 632	AC/S/11/198	48	RO 876	RO/CM/12/91
9	AC 644	AC/S/11/282	49	RO 879	RO/CM/12/10
10	AC 647	AC/S/11/327	50	RO 883	RO/CM/12/110
11	AC 650	AC/S/11/348	51	RO 886	RO/CM/12/115
12	AC 654	AC/S/9/5	52	RO 894	RO/CM/12/136
13	AC 657	AC/S/10/15	53	MT 899	MT/IT/16/2
14	AC 706	AC/S/12/18	54	MT 901	MT/IT/16/6
15	AC 733	AC/S/10/21	55	MT 906	MT/IT/16/12
16	AC 754	AC/S/10/79	56	MT 920	MT/IT/16/81
17	AC 953	AC/F/6B/11	57	MT 922	MT/IT/16/94
18	AC 959	AC/F/6B/21	58	MT 929	MT/IT/16/135
19	AC 963	AC/F/6B/27	59	MT 931	MT/IT/16/138
20	AC 966	AC/F/6B/35	60	MT 935	MT/IT/16/174
21	AC 979	AC/F/6B/79	61	MT 944	MT/IT/16/208
22	AC 986	AC/F/6B/104	62	MT 945	MT/IT/16/210
23	AC 995	AC/F/6B/169	63	MT 947	MT/IT/16/212
24	AC 1043	AC/S/12/365	64	MT 948	MT/IT/16/213
25	AC 1090	AC/F/6A/121	65	MT 1005	MT/C/1/60
26	RO 254	RO/OP/4/12	66	MT 1007	MT/C/1/68
27	RO 255	RO/OP/4/15	67	MT 1008	MT/C/1/69
28	RO 256	RO/OP/4/27	68	MT 1011	MT/C/1/75
29	RO 257	RO/OP/4/49	69	MT 1021	MT/C/1/91
30	RO 287	RO/OP/4/139	70	MT 1024	MT/C/1/99
31	RO 311	RO/C/9/127	71	MT 1025	MT/C/1/102
32	RO 316	RO/C/9/141	72	MT 1028	MT/C/1/108
33	RO 317	RO/C/9/142	73	MT 1029	MT/C/1/109
34	RO 319	RO/C/9/152	74	MT 1030	MT/C/1/113
35	RO 322	RO/C/9/157	75	MT 1031	MT/C/1/116
36	RO 328	RO/C/9/174	76	MT 1055	MT/C/10/20
37	RO 330	RO/C/9/179	77	MT 1057	MT/C/10/24
38	RO 338	RO/C/9/203	78	MT 1063	MT/C/10/94
39	RO 352	RO/C/9/308	79	MT 1064	MT/C/10/102
40	RO 364	RO/C/8/98	80	MT 1077	MT/C/7/37

2.3 Experimental methods

The field evaluation trial for this study was laid out in August 1992. The experiment was laid out in simple lattice design, with four replications and four plants per plot. A close spacing of 2.5 x 2.5 m was adopted. All cultural operations were carried out uniformly as per the package of practices recommended by the Rubber Board. The wild genotypes were characterised during the fourth quarter in the first year of observations, for their morphological characteristics using a descriptor designed for *Hevea*. Various quarterly and annual observations on morphological and anatomical characters including test tap yield, were recorded for the first three years, starting from six months after planting, Details of the descriptors used for the juvenile characterisation and the other morphological and anatomical characters for which data were collected are explained below.

2.3.1 Descriptors for the juvenile characterisation

The genotypes were characterised when the plants were 18 months old. The descriptors included plant height, girth at 15 cm height above bud union, branching habit, nodal morphology, nature of leaf storeys and characters of leaf and leaflet.

1. Plant height

The height of the plants from the bud union to the terminal bud was measured for all the plants in all the replications. Accordingly the genotypes were grouped into three categories – dwarf, medium tall and tall. For assigning the genotypes into the different categories, the range of the character was divided into three equal classes. The ranges in respect of each category were: -

1.1 Dwarf (between 100.89 cm and 174.92 cm).

1.2 Medium tall (between 174.92 cm and 248.95 cm).

1.3 Tall (between 248.95 cm and 322.99 cm).

2. Girth of the plants

Diameter of all the plants in all the replications was measured at 15 cm height above the bud union, using vernier calipers and converted into girth of the plant. The genotypes were grouped into three categories, with - below average girth, average girth and above

average girth. For assigning the genotypes into the different categories, the range of the character was divided into three equal classes. The ranges in respect of each category were:-

2.1 Below average girth (between 4.72 cm and 6.61 cm).

2.2 Average girth (between 6.61 cm to 8.50 cm).

2.3 Above average girth (between 8.50 cm to 10.41 cm).

3. Branching habit

All plants in all the replications were observed for early branching, if any. Accordingly the genotypes were grouped under the two classes:

3.1 Branching.

3.2 No branching.

4 Nodes

Morphology of the nodes was observed visually, in two plants from each replication. The characters included nature of axillary buds and appearance and prominence of leaf scars.

4.1 Axillary buds

4.1.1 Protruding (axillary buds raised on the stem).

4.1.2 Sunken (axillary buds sunken on the stem).

4.1.3 Normal (axillary buds neither raised nor sunken).

4.2 Leaf scars

Leaf scars were observed after senescence and leaf fall and morphology of the margin of the scars examined.

4.2.1 Pronounced margin (margin of the leaf scar on the stem very pronounced).

4.2.2 Normal margin (margin of the leaf scar on the stem not pronounced).

4.3 Nature of leaf scars

4.3.1 Sunken (centre of the scar sunken from the surface)

4.3.2 Normal (leaf scar plain surfaced)

5 Leaf storeys

Leaves on stem are produced in flushes and appearance of the individual leaf storeys, arrangement of the storeys on the axils and the compactness of the storeys were observed visually on two plants from each replication.

5.1 Shape

The genotypes were grouped under four classes based on the external appearance of the leaf storeys.

5.1.1 Conical (top of the storey tapering from the lower side).

5.1.2 Truncate (leaf storey having a trapezium shape with a short flat top).

5.1.3 Bow shaped (leaf storey having the shape of a bow, with a small dip on the top outline).

5.1.4 Hemispherical (dome shaped leaf storey).

5.2 Separation

The genotypes were grouped for the arrangement of leaf flushes based on their inter flush distance into three categories- closely placed flushes, intermediately separated and well separated flushes. For assigning the genotypes into the different categories, the range of the character was divided into three equal classes. The ranges in respect of each category based on the inter flush distances were: -

5.2.1 Closely placed flushes (between 13.86 and 18.73 cm).

5.2.2 Intermediately separated flushes (between 18.73 and 23.60 cm).

5.2.3 Well separated flushes (between 23.60 and 28.46 cm).

5.3 External appearance

Placement of leaves in each storey.

5.3.1 Open (leaves in a storey placed in such a way that they are not crowded and not overlapping each other).

5.3.2 Close (very closely placed leaves in a storey giving a densely packed view).

6 Leaves

Various single leaf characters were recorded from two leaves each in two whorls from two plants in each replication.

6.1 Pulvinus

6.1.1 Large (excessively swollen).

6.1.2 Normal (pulvinus of normal size).

6.2 Petiole

6.2.1 Shape

Shape of the petiole when it is observed at eye level.

6.2.1.1 Arched (arch-shaped; with a convex shaped middle portion).

6.2.1.2 Concave (inverted arch shaped).

6.2.1.3 Straight (more or less straight).

6.2.1.4 'S' shaped

6.2.2 Size

Depending on their actual length, the petioles were grouped into three categories- short, medium and long petioles. For assigning the genotypes into the different categories, the range of the character was divided into three equal classes. The ranges in respect of each category were: -

6.2.2.1. Short petiole (between 13.03 and 19.51 cm).

6.2.2.2. Medium petiole length (between 19.51 and 25.99 cm).

6.2.2.3. Long petiole (between 25.99 and 32.47 cm).

6.2.3. Angle

Angle of insertion of the petiole to the axis was measured and the genotypes were grouped into three classes.

6.2.3.1. Acute (less than 90^0).

6.2.3.2. Horizontal (petioles placed more or less at right angles on the stem).

6.2.3.3. Optuse (greater than 90^0).

6.3. Petiolule

6.3.1. Orientation

Angle of placement of the petiolules with reference to the petiole.

6.3.1.1. Upward (upwardly oriented petiolules when the leaflet with petiole is held at eye level and viewed laterally).

6.3.1.2. Horizontal (petiolules placed horizontal with the petiole).

6.3.1.3. Downward (downwardly oriented petiolules)

6.3.2. Size

Length of the petiolules was assessed visually and the genotypes grouped into three classes.

6.3.2.1. Long (petiolules extra long)

6.3.2.2. Medium (petiolules of normal length)

6.3.2.3. Short (very short petiolules).

6.3.3. Extra floral nectary

Extra floral nectary present at the region of insertion of the petiolules on the petiole was observed and genotypes classified into two groups.

6.3.3.1. Prominent (very prominent visually)

6.3.3.2. Less prominent (not prominent / rudimentary).

6.4. Leaflets

Leaflets were observed for colour, lustre, shape, size, margin, cross sectional appearance, tip, lateral appearance, orientation, prominence and colour of veins and lamina texture. Observations were recorded from three leaflets of two leaves each, from each of the two whorls from two plants each in each replicate.

6.4.1. Colour

Genotypes were grouped into two classes based on the colour of the leaflets.

6.4.1.1. Green (dull or light green).

6.4.1.2. Dark green (dark or dense green).

6.4.2. Lustre

Two groups were identified based on the lustre of leaflets.

6.4.2.1. Glossy (shiny lamina surface).

6.4.2.2. Dull (dull surface, not shiny).

6.4.3 Shape

Based on the shape of the leaflets genotypes were grouped into three classes.

6.4.3.1 Elliptic (oval outline, being narrowed to rounded ends, widest at or about the middle).

6.4.3.2 Lanceolate (broader at the base, tapering towards the apex).

6.4.3.3 Obovate (terminal half broader, narrowing towards the base).

Genotypes were classified into three classes based on single leaflet area- small, medium and large sized leaflets. For assigning the genotypes into the different categories, the range of the character was divided into three equal classes. The ranges in respect of each category were: -.

6.4.4.1 Small (between 99.71 cm^2 and 151.26 cm^2).

6.4.4.2 Medium (between 151.26 cm^2 and 202.81 cm^2).

6.4.4.3 Large (between 202.81 cm^2 and 254.37 cm^2)

6.4.5 . Margin

6.4.5.1 Entire (smooth, continuous margin).

6.4.5.2 Undulate (wavy margin).

6.4.6 Cross sectional appearance of leaflets

The leaflets were cross-sectioned at about the middle and observed for appearance. The genotypes were classified into three:-

6.4.6.1 Straight (cross sectional view a straight line on either side of midrib).

6.4.6.2 'V' shaped (lamina inclined upwards on either side of the midrib).

6.4.6.3 Boat shaped (lamina with a flat middle portion, either sides bending upwards).

6.4.7 Leaflet tip

Tips of the leaflets were observed visually and the genotypes were assigned to four groups.

6.4.7.1 Aristate (apical portion of leaflet tapering very narrow to an elongated apex).

6.4.7.2 Apiculate (leaflets terminating by an *apicula*, into a sharp point).

6.4.7.3 Cuspidate (apex of leaflets somewhat abruptly and sharply concavely constricted into a sharp pointed tip).

6.4.7.4 Accuminate (acute apex whose sides are somewhat concave and taper to a protracted point)

6.4.8 Lateral appearance

Lateral appearance of the lamina, when placed on a flat surface.

6.4.8.1 Flat (leaflets being flat, when placed on a flat surface).

6.4.8.2 Convex (convex shaped lateral view, when placed on a flat surface).

6.4.8.3 'S' shaped ('S' shaped lateral view, when placed on a flat surface).

6.4.9 Orientation

Disposition of the leaflets was ascertained by examining dorsally the entire leaf in position. The genotypes were classified into three classes.

6.4.9.1 Margin touching (margins of leaflets just touching each other).

6.4.9.2 Overlapping (margins of leaflets overlapping each other).

6.4.9.3 Separated (margins of leaflets separated and not touching each other).

6.4.10 Vein colour

Colour of the midrib and veins was observed externally and the genotypes were classified into two groups.

6.4.10.1 Yellow (yellow in colour or with yellowish tinge).

6.4.10.2 Light green (pale green in colour).

6.4.11 Nature of veins

Visual appearance of the veins on the leaflets in terms of their prominence was examined and the genotypes were assigned to:

6.4.11.1 Prominent (very prominent or protruding leaf veins).

6.4.11.2 Not prominent (not protruding or less prominent veins).

6.4.12 Lamina texture

Texture of the lamina was examined by touching and rubbing the leaf surface. The genotypes were grouped into:

6.4.12.1 Smooth (smooth dorsal side, without any wrinkles or waviness)

6.4.12.2 Irregular (wavy rough or irregular dorsal surface)

2.3.2 Morphological characters

(i) Girth of the plants

Girth of all the plants was recorded, at a height of 15 cm from the bud union, in the first four quarters from the sixth month after planting and also at the end of third year. The data were recorded as the diameter of the stem, using vernier caliper, and the measured data was converted as girth (circumference) in centimetres.

(ii) Height of the plants

Height of all the plants was recorded as the length of the main stem, from the bud union to the terminal bud of the plant, in centimetres. The data was recorded four times in the first year of observations, at quarterly intervals.

(iii) Total number of leaf flushes per plant

The total number of leaf flushes per plant was recorded four times, from all the plants, during the first year of observations, at quarterly intervals.

(iv) Total number of leaves per plant

Total number of leaves per plant was recorded by counting the number of nodes of both fallen and retained leaves. The data was recorded four times, during the first year of observations, at quarterly intervals from all the plants.

(v) Inter flush distance

The distance between two successive leaf flushes was recorded in centimetres, in the fourth quarter of the first year observations from all the plants.

(vi) Petiole length

The average length of the petiole was recorded in centimetres, as the average of four petioles of fully mature leaves in two whorls each from two plants in each replication.in the fourth quarter, in the first year of observations.

(vii) Total leaf area per plant

Total leaf area per plant of each genotype was estimated in cm^2, in the fourth quarter, during the first year of observations. The total leaf area was estimated as the product of the average single leaflet area in cm^2 and the total number of leaflets per plant, both recorded in the fourth quarter in the first year of recording observation.

(viii) Leaf area index (LAI)

Leaf area index was estimated in the fourth quarter of the first year of observations, as a unit free measurement. LAI was derived as follows:

$$LAI = \frac{\text{Total leaf area of the plant } (cm^2)}{\text{Land area occupied by one plant } (cm^2)}$$

(ix) Test tap yield

Test tap yield of the wild genotypes was recorded annually for three years from 1993, when the plants were 18 months old to 1995 when they were 42 months old. The data were recorded by conducting micro tapping in the fourth quarter in the first year by giving a uniform micro cut on the bark, 20 cm above the bud union. The latex that oozed out was collected in pre-weighed blotting paper. In the second year and third year end, the trees were test tapped using a special tapping knife, by giving half spiral cut, 20 cm above the bud union. Micro tapping was carried out three times at alternate days interval and test tapping was carried out for 10 alternate days (1/2S d/2 system) and the rubber yield was recorded for all the three micro tappings and for the last five tappings in the case of test tappings. The latex obtained was dried at 50^0 C in hot air oven and the weight of the dry rubber recorded in grams per tree per tap ($g\ t^{-1}\ t^{-1}$).

2.3.3 Stomatal characters

Stomatal characters were recorded in the third year of observations from mature sun leaves collected in pairs, from two plants in each plot. Epidermal peelings from both abaxial and adaxial surface of the leaf lamina were prepared and were examined microscopically. Leaf bits were taken out from the middle portion of the leaflets. The samples were boiled for 7-8 minutes in 3 percent KOH and washed in several changes of water as suggested by Senanayake (1969). The peelings were stained in Saffranin. Following characters were

recorded.

(i) Number of stomata per unit area.

Stomatal frequency was ascertained by counting the number of stomata per square millimeter of lamina surface by means of a calibrated CCD colour camera system attached to a phase contrast microscope. Ten camera fields per plant were scored for calculating stomatal density.

(ii) Number of epidermal cells per unit area.

This character was observed from the same peelings used for recording the stomatal count. The number of epidermal cells, in one mm^2 of the lamina, was recorded.

(iii) Stomatal index

Stomatal index was estimated in the third year of recording observations, based on the number of stomata and number of epidermal cells in unit area of the abaxial epidermis (Salisbury, 1927).

$$\text{Stomatal index} = \frac{\text{Number of stomata / unit area} \times 100}{\text{Number of stomata/unit area} + \text{Number of epidermal cells/unit area}}$$

2.3.4 Leaf anatomical investigations.

The middle leaflet of two randomly chosen mature sun leaves from the topmost mature whorl was collected from all the plants in all the replications. The leaf samples collected were preserved in 1:1:18 formalin-acetic-alcohol (FAA). Leaf bits of one cm^2 size, covering the midrib and either side of the lamina, were prepared and subjected to aspiration. The dehydration and infiltration was performed using Reichert-Jung Histokinette rotary tissue processor. The infiltrated samples were embedded in paraffin wax by means of Jung Histoembedder and the blocks were prepared. Serial sections, at cross sectional plane of these processed samples were taken at 5 μm thickness using semi automatic multicut rotary microtome. Sections were stained in Safranin-Fast green and made permanent following standard procedures. Observations on microscopic characters were taken with an

Aristoplan trinocular research microscope attached to CCD TV camera. The following characters were recorded:-

(i) Thickness of the lamina (μm)

(ii) Thickness of the midrib (mm)

(iii) Thickness of palisade layer (μm)

(iv) Thickness of spongy layer (μm)

(v) Number of cells in 1 mm distance of palisade layer

(vi) Number of cells in 1 mm distance of spongy layer

(vii) Thickness of cuticle ((μm).

(viii) Single leaflet area (cm^2)

The single leaflet area was measured as the average of the area of two middle leaflets from two mature leaves from two separate whorls in one plant. Two such plants were selected from each of the four plots. The single leaflet area was recorded using LI-COR 3100 area meter, in the third year of recording the data.

2.3.5 Bark anatomical investigations

Bark samples (1 x 1cm) were collected from two test tapped trees per plot, from the four replications for each treatment at 25 cm height above the bud union, using a bark sampler and fixed in 1:1:18 formalin-acetic-alcohol (FAA). Bark sections at 30-60 μm thickness were taken at cross sectional (CS), tangential longitudinal (TLS) and radial longitudinal (RLS) planes (Fig 37-39) using a Reichert Jung Sledge microtome. Four sections for each of the two trees in each replicate were stained in Sudan III and Sudan IV and mounted in glycerine gelly for microscopic observations.

Observations were taken with the help of an Aristoplan trinocular research microscope and Wild M.8 Stereo zoom microscope. Quantitative anatomical measurements were done using a calibrated CCD – TV attached to the Aristoplan microscope. The following characters were recorded for bark anatomical traits:

(i) Total bark thickness (mm).

Bark thickness was recorded using a Schlippers' gauge, for all the test tapped trees at tapping panel height, in the third year of recording observations prior to bark sampling.

(ii) Soft bark thickness (mm).

Soft bark thickness was measured as the distance from the cambial zone outward up to the zone of initiation of sclerified cells using the bark sections at cross sectional and radial longitudinal planes.

(iii) Hard bark thickness (mm).

Hard bark thickness was recorded as the distance from the initiation of the stone cell zone upto the inner boundary of the periderm.

(iv) Soft bark thickness in percentage.

Percentage of the soft bark was estimated as the proportion of the soft bark in total bark thickness.

(v) Hard bark thickness in percentage.

Percentage of the hard bark was estimated as the proportion of the hard bark in total bark thickness.

(vi) Number of latex vessel rows in the soft bark region

Number of functional latex vessel rows in the soft bark region was counted.

(vii) Number of latex vessel rows in the hard bark region

The number of latex vessel rows, in the stone cell occupied zone was counted.

(viii) Total number of latex vessel rows

Total number of latex vessel rows was computed as the sum of the number of latex vessel rows in the soft and hard bark regions.

(ix) Average distance between latex vessel rows in the soft bark region (mm).

Average distance between the functional latex vessel rows in the soft bark regior was measured.

(x) Density of latex vessels per row per mm circumference of the plant

Density of latex vessels per row per mm circumference of the plant was measurec from the tangential longitudinal sections.

(xi) Diameter of latex vessels (μm).

Diameter of latex vessels was measured from the tangential longitudinal sections.

(xii) Total cross sectional area of latex vessels (mm^2)

The total cross sectional area of the latex vessels (Laticifer Area Index) was computed as per the following formula:

Total cross sectional area = $n f G \Pi r^2$

Where n = total number of latex vessel rows,

f = density of latex vessels per row per mm circumference of the plant,

G = girth of the plant in mm

r = radius of the latex vessels in μm

(xiii) Frequency of phloic rays.

Frequency of phloic rays per 0.01 mm^2 area was counted in random fields of the bark sections at the tangential longitudinal plane.

(xiv) Height of phloic rays (mm)

Height of phloic rays was measured from the bark sections at the tangential longitudinal plane.

(xv) Width of phloic rays (mm)

Width of the phloic rays was measured from the bark sections at the tangential longitudinal plane.

(xvi) Height / width ratio of phloic rays.

Height / width ratio of phloic rays was worked out from the height and width recorded.

2.3.6 Photography

Photomicrographs were taken with a Wild MPA 46/52 Photoautomat attached to a Leitz Aristoplan Research microscope, using Kodak plus 100 GA 135-36 colour filim.

2.4 Statistical methods

2.4.1 Genetic variability

2.4.1.1 Analysis of variance

Analysis of variance (ANOVA) was carried out for all the characters studied, as per the procedures prescribed for a simple lattice design (Panse and Sukhatme, 1985), mainly (a) to test whether there exists significant differences between the wild genotypes studied, with respect to the various characters (b) to estimate the coefficients of variation and the genetic parameters. The test of significance was carried out with reference to the standard 'F' Table (Fisher and Yates, 1963).

2.4.2 Genetic parameters

2.4.2.1 Phenotypic and genotypic variance

Phenotypic and genotypic variances for the various characters were estimated as per Singh and Chaudhary (1985).

$$\text{Genotypic variance } (\sigma^2 g) = \frac{\text{MSS for treatment} - \text{MSS for error}}{\text{No of replications}}$$

where, MSS = mean sum of squares

$$\text{Phenotypic variance } (\sigma^2 p) = \sigma^2 g + \sigma^2 e$$

where $\sigma^2 e$ = error variance.

2.4.2.2 Coefficients of variation

For all the characters, genotypic and phenotypic coefficients of variation were estimated following Burton and Devane (1953).

(a) Genotypic coefficient of variation (GCV)

$$GCV = \frac{\sigma g \times 100}{\overline{X}}$$

where σg = genotypic standard deviation for a particular character

$\overline{X}$ = grand mean for a particular character

(b) Phenotypic coefficient of variation (PCV)

where σp = phenotypic standard deviation for a particular character

$$PCV = \frac{\sigma p \times 100}{\overline{X}}$$

$\overline{X}$ = grand mean for the particular character

2.4.2.3 Heritability (H^2) in the broad sense.

Heritability in the broad sense ie, the fraction of the total variance which is heritable, was estimated as a percentage following Jain (1982) as –

$$H^2 = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

where $\sigma^2 g$ = genotypic variance

$\sigma^2 p$ = phenotypic variance

2.4.2.4 Genetic advance under selection

Genetic advance (G.A.) was calculated employing the formula:-

$$G.A = \frac{K H^2 \sigma p}{\overline{X}}$$

where H^2 = heritability in the broad sense

σp = phenotypic standard deviation

K = selection differential which is 2.06 at 5% intensity of selection in large samples (Allard, 1960)

$\overline{X}$ = grand mean for the character x

2.4.3 Correlation

Phenotypic, genotypic and environmental correlation coefficients were worked out among all the characters studied, using the variance and covariance components, as suggested by Singh and Chaudhary (1985). Phenotypic correlation coefficient between characters x and y was estimated as:

$$rp\ (x,y) = \frac{\sigma p\ (x.y)}{\sqrt{\sigma^2 p(x)\ \sigma^2 p(y)}}$$

where, $\sigma p\ (x.y)$ = phenotypic covariance between x and y

$\sigma^2 p(x)$ = phenotypic variance of the character x and

$\sigma^2 p(y)$ = phenotypic variance of the character y.

Genotypic correlation coefficient between characters x and y was estimated as:

$$rg\ (x,y) = \frac{\sigma g\ (x,y)}{\sqrt{\sigma^2 g\ (x)\ \sigma^2 g\ (y)}}$$

where, $\sigma g\ (x,y)$ = genotypic covariance between x and y

$\sigma^2 g\ (x)$ = genotypic variance of the character x, and

$\sigma^2 g\ (y)$ = genotypic variance of the character y

Similarly, environmental correlation coefficient between characters x and y was worked out as:

$$re\ (x,y) = \frac{\sigma e\ (x,y)}{\sqrt{\sigma^2 e\ (x)\ \sigma^2 e\ (y)}}$$

where, $\sigma e\ (x,y)$ = environmental covariance between the characters x and y

$\sigma^2 e\ (x)$ = environmental variance for the character x, and

$\sigma^2 e\ (y)$ = environmental variance for the character y

2.4.4 Factor Analysis

For identifying the most important characters that contributes to genetic divergence from a larger set of characters, factor analysis was done, thereby reducing the num-

ber of characters to be studied further. The basic factor analysis model written in matrix notation is as,

$$X = (x1, x2, x3.....xp)$$

Where, x1, x2, x3.....xp are the variables.

$$x1 - \mu 1 = l_{11} F_1 + ...+ l_{1m} F_m + E_1$$

.....

.....

$$x_p - \mu p = l_{p1} F_1 + ... l_{pm} F_m + E_p$$

where, $F_1, F_2 ..... F_m$ are the common factors.

$E_1, E_2 .....E_p$ is the error.

$\mu 1, \mu 2 .....\mu p$ is the mean of the variables, x1, x2, ...xp.

2.4.5 Genetic divergence

Genetic divergence of the wild genotypes was estimated by D^2 Statistic as per Mahalanobis (1928, 1936)and computed as :

$$D_x^2 = \sum_{I}^{p} \sum_{j}^{p} (\lambda^{ij}) di\ dj$$

Where, x = number of metric traits in point,

p = number of genotypes

di and dj = the differences between the mean values of two genotypes, for i^{th} and

j^{th} characters respectively.

λ^{ij} = dispersion matrix reciprocal to the common dispersion matrix.

After computing the relative genetic distance between the clones, they were clus-

tered into genetically divergent clusters as per iterative relocation algorithm suggested by Friedman and Rubin (1967) and modified by Suresh and Unnithan (1996). The mean intra cluster distances were computed using the formula

$$\Sigma (d_{ij})^2 / n$$

where d_{ij}^2 is the distance between i^{th} and j^{th} genotypes in the same cluster.

n = number of values

The mean inter cluster distances were worked out by using the distances between all possible combinations of the clusters obtained. For this purpose, the sum of distances between all possible combinations of the clones in a pair of clusters was taken. The sum of D^2 values divided by the product of the number of genotypes in each cluster gave the inter cluster distance between the particular pair of clusters. The mean inter and intra cluster distances were then tabulated.

2.4.6 Performance index

Performance index of the genotypes was computed based on the 16 characters viz., girth of the plants, inter-flush distance, length of petiole, total number of leaves per plant, thickness of leaf blade, thickness of cuticle, single leaflet area, total bark thickness, total number of latex vessel rows, average distance between latex vessel rows in the soft bark, frequency of phloic rays, height of phloic rays, width of phloic rays, diameter of latex vessels, density of latex vessels, and test tap yield.

Application of discriminant function as a basis for making selection on several characters simultaneously is aimed at discriminating the desirable genotypes from undesirable ones on the basis of their phenotypic performance. Smith (1936) defined the genetic worth (H) of an individual as :

$$H = a_1 G_1 + a_2 G_2 + \ldots\ldots\ldots + a_n G_n$$

Where, $G_1, G_2, \ldots\ldots\ldots G_n$ are the genotypic values on individual characters and a_1, a_2, $\ldots\ldots a_n$ signify their relative economic importance. Another function (I) based on the

phenotypic performance of various characters, is defined as :

$$I = b_1p_1 + b_2p_{2+} \ldots\ldots\ldots\ldots + b_np_n$$

Where, b_1, $b_{2,} \ldots\ldots\ldots\ldots, b_n$ are to be estimated such that the correlation between H and I, ie, r(H, I) becomes maximum. Once such function is obtained, descrinination of good genotypes from the undesirable ones will be possible on the basis of phenotypic performance, ie, P_1, P_2, ..., P_n directly.

The maximization of r(H,I) leads ot a set of simultaneous equations which upon solvinggive the desired estimate of b_i values. Considering the 16 characters in this study, the simultaneous equations are as follows :

$$b_1x_{11} + b_2x_{12} + \ldots\ldots\ldots b_{16}x_{116} = a_1G_{11} + a_2G_{12} + \ldots\ldots\ldots a_{16}G_{116}$$

$$b_1x_{21} + b_2x_{22} + \ldots\ldots\ldots b_{16}x_{216} = a_1G_{21} + a_2G_{22} + \ldots\ldots\ldots a_{16}G_{216}$$

....

$$b_1x_{161} + b_2x_{162} + \ldots\ldots b_{16}x_{1616} = a_1G_{161} + a_2G_{162} \ldots\ldots a_{16}G_{1616}$$

which in matrix form become :

$$\begin{pmatrix} x_{11} & x_{12} \ldots\ldots\ldots\ldots & x_{116} \\ x_{21} & x_{22} \ldots\ldots\ldots\ldots & x_{216} \\ \ldots\ldots & \ldots\ldots & \ldots\ldots \\ x_{161} & x_{162} \ldots\ldots\ldots & x_{1616} \end{pmatrix} \begin{pmatrix} b_1 \\ b_2 \\ .. \\ b_{16} \end{pmatrix}$$

$$= \begin{pmatrix} G_{11} & G_{12} \ldots\ldots\ldots & G_{116} \\ G_{21} & G_{22} \ldots\ldots\ldots & G_{216} \\ \ldots\ldots & \ldots\ldots & \ldots\ldots \\ G_{161} & G_{162} \ldots\ldots\ldots & G_{1616} \end{pmatrix} \begin{pmatrix} a_1 \\ a_2 \\ .. \\ a_{16} \end{pmatrix}$$

The solution of these equations give the estimates of b_i values in the following manner :

$$b = X^{-1} G a$$

where, b is the column vector, X^{-1} is the inverse of the phenotypic variance and covariance matrix, G is the genotypic variance and covariance matrix and a is the column vector for economic weights. We take *a* as a unit vector assuming equal economic importance for all characters. The genotypes were ranked based on their performance indices.

CHAPTER 3

Results

The results of this study are presented in detail below under the following titles:

1. Juvenile characterisation
2. Genetic variability
3. Genetic parameters
4. Correlations
5. Factor analysis
6. Genetic divergence
7. Performance index

3.1 Juvenile characterisation

Juvenile characterisation of the wild genotypes for describing their morphological characteristics was done using a standard descriptor prepared for *Hevea*. Of the 80 wild genotypes characterised, 25 belonged to the Acre provenance, 27 to Rondonia and 28 to the provenance of Mato Grosso. The frequency distribution and the detailed genotype-wise description of the morphological traits of the wild genotypes along with that of the control are given in Tables 2 and 3 respectively.

Habit of the plants was catalogued under three classes- dwarf, medium tall and tall. Of the 25 Acre genotypes 12 genotypes were characterised as medium tall and 13 were dwarf in stature. Fifteen of the 27 Rondonian genotypes were found to be medium tall, while five genotypes were dwarf and a seven genotype had a tall habit. Majority of the Mato Grosso genotypes (14 among 28 accessions) had a dwarf habit, while 11 genotypes were medium tall and three were tall in stature. The popular Wickham clone used as control, RRII 105, had a dwarf habit, compared to the highly vigorous wild clones (Tables 2 and 3).

In the wild population studied, 17, 13 and 11 genotypes each from the three provenances Acre, Rondonia and Mato Grosso had average girth values. Three genotypes from Acre, nine from Rondonia and three from Mato Grosso had above average girth values. Poor growth, as indicated by the below average girth, was observed in five Acre, five Rondonia and 14 Mato Grosso genotypes. Control clone RRII 105, was found to have a below average girth of 6.06 cm compared to the wild genotypes. Of the 80 wild genotypes and RRII 105, observed for their branching habit at the juvenile phase, none of them showed any early branching habit (Tables 2 and 3).

All the 80 wild genotypes along with RRII 105, were observed for nodal characteristics and all had normal axillary buds irrespective of the provenance. Majority of the Acre genotypes had their leaf scars with pronounced margin (20 genotypes), while the remaining five Acre genotypes had normal margin of the leaf scars. Even though 15 of the Rondonian genotypes had their leaf scars with normal margin, 12 of them had pronounced margin for their leaf scars. Mato Grosso genotypes were in general having normal leaf scars (20 genotypes) while eight genotypes had pronounced margin of the leaf scars. The popular control clone was characterized by leaf scars with normal margin. Nature of leaf scars for 20 Acre, 24 Rondonia and 28 Mato Grosso genotypes and the control clone was found to be normal, flush with the bark while sunken leaf scars were observed in five Acre and three Rondonian genotypes (Tables 2 and 3).

The shape, separation and external appearance of the topmost leaf flush of the wild genotypes were characterised. It was seen that 23 of the 25 Acre genotypes, 24 of the 27

Rondonian and 25 of the Mato Grosso genotypes, along with RRII 105, had a hemispherical leaf flush at the top, while one genotype each from Acre had truncate and bow shaped leaf flushes. Among the Rondonian provenance, one genotype each exhibited conical, truncate and bow shaped leaf flushes. Two genotypes from Mato Grosso had truncate leaf flushes and a single Mato Grosso genotype had a bow shaped leaf flush. Well separated leaf flushes were noted in two, five and five genotypes from Acre, Rondonia and Mato Grosso genotypes respectively. Intermediate separation between leaf flushes, were recorded in 9, 14 and 12 genotypes from the three provenances Acre, Rondonia and Mato Grosso in that order. Closely placed leaf flushes were seen in 14, eight and 11 genotypes of Acre, Rondonia and Mato Grosso, as well as the control. All the genotypes including the control, except for two Rondonian genotypes, had open leaf flushes with the individual leaves in each flush spaced well apart (Tables 2 and 3).

Detailed characterisation of the leaves was done by defining the pulvinus, petiole, petiolule, extra floral nectary, colour, lustre, shape, size, margin, cross sectional appearance, leaf tip, lateral appearance, orientation of leaflets, colour and nature of vein and lamina texture (Tables 2 and 3).

Except for a single genotype each in Acre and Rondonia and three genotypes from Mato Grosso, which had a normal pulvinus, all the others including RRII 105 had a swollen pulvinus. It was seen that 17 Acre genotypes had a concave petiole, while 7 genotypes had straight petioles and one genotype had an 'S' shaped petiole. Similarly 18 Rondonian genotypes had concave petioles, while straight and 'S' shaped petioles were seen in four genotypes each. One Rondonian genotype had an arched petiole. Straight petioles were the characteristic of majority of the Mato Grosso genotypes (19 numbers), while concave petioles were seen in eight genotypes and one genotype had an arched petiole. Petioles of the control clone were found to be straight (Tables 2 and 3).

Nineteen out of the 25 Acre genotypes had their petiole of medium length, while three genotypes each had long and short petioles. Of the Rondonian genotypes, 15 out of 27 genotypes had petioles of medium length, while seven genotypes had long petioles and

five had short petioles. Only seven Mato Grosso genotypes had their petioles of medium length while 20 genotypes from this provenance had short petioles and a single one had long petioles. Compared to the wild genotypes, RRII 105 had short petioles (Tables 2 and3).

Majority of the wild genotypes, and the control RRII 105, irrespective of their provenances, had their petioles placed at acute angle to the stem axis. Twenty-two Acre genotypes, 24 Rondonian and 27 Mato Grosso genotypes had acute angled petioles while horizontal petioles were seen in three genotypes each in Acre and Rondonia and a single genotype in Mato Grosso (Tables 2 and 3).

Petiolules, with an upward orientation were seen in 14 Acre genotypes while two genotypes had a horizontal orientation and nine had a downward orientation. In the Rondonian genotypes, 17 had an upward orientation, three had horizontal and seven had a downward orientation for their petiolules. Upwardly oriented petiolules were seen in 16 Mato Grosso genotypes while seven genotypes had horizontal and five had downward oriented petiolules. Petiolules of RRII 105 were also upwardly oriented. Eighteen genotypes of Acre had medium long petiolule with a single genotype with long and six genotypes with short petiolules. Petiolules with medium length, was observed in the majority of the Rondonian genotypes (18 accessions), whereas eight genotypes had long petiolules and a single genotype had short petiolule. Similarly, majority of the Mato Grosso accessions also (22 genotypes) had medium long petiolules, while two genotypes had longer petiolules and four had shorter petiolules. The control clone had a medium long petiolule (Tables 2 and 3).

Extra floral nectary was found to be prominent in 14 out of the 25 Acre genotypes while the remaining genotypes had less prominent nectaries. Of the Rondonian genotypes, extra floral nectaries were less prominent in 17 genotypes while it was prominent only in 10 genotypes. In the Mato Grosso accessions, nectaries were prominent in 21 genotypes while it was less prominent in seven genotypes. The nectaries were less prominent in RRII 105 (Tables 2 and 3).

Majority of the wild genotypes from all the three provenances and RRII 105, had green coloured leaves. Out of the Acre genotypes, 20 had green leaflets, and five geno-

types dark green leaflets. Green leaflets were observed for 21 Rondonian genotypes, whereas six genotypes had dark green leaflets. Twenty-two Mato Grosso genotypes had green leaflets while six had dark green lamina. Except for four Rondonian and five Mato Grosso genotypes and the control clone RRII 105, which were characterised with glossy leaflets, all of the Acre genotypes, 23 each of the Rondonian and Mato Grosso genotypes had a dull lustre for their leaflets. Except for a single genotype from Acre, six from Rondonia and two from Mato Grosso with obovate leaflets, all the remaining genotypes including the control clone, had elliptical leaflets (Tables 2 and 3).

Of the 25 Acre genotypes studied, only three genotypes had large leaflets, 13 had medium and nine genotypes had small sized leaflets. Medium sized leaflets were recorded for 18 Rondonian genotypes while, two genotype had large and seven had small sized leaflets. Among the Mato Grosso collections, 12 genotypes had medium sized leaflets while two had large sized and remaining 14 had small leaflets. Medium sized leaflets were characteristic of RRII 105 as well. Margin of the leaflets was found to be entire for 14 Acre genotypes and undulate for 11 genotypes. Nineteen Rondonian genotypes had an undulate margin while another 8 genotypes had entire margin. In the case of Mato Grosso genotypes, 15 genotypes had leaflets with entire margin and 13 with undulating margin. The control clone had an entire and smooth margin for its leaflets (Tables 2 and 3).

Appearance of the leaflets in cross sectional view was observed. Eleven Acre genotypes had straight appearance while 12 had boat shaped and two genotypes 'V' shaped cross sectional appearance. Boat shaped cross sectional appearance of leaflets was recorded for 14 Rondonian genotypes, while 12 had straight shape and a single genotype had 'V' shape in cross section. Of the Mato Grosso accessions, 24 out of 28 genotypes had a straight cross sectional view with a single genotype having 'V' shape and another 3 with boat shaped leaflets. The leaflets of RRII 105 had a straight cross sectional appearance (Tables 2 and 3).

Accuminate tip of the leaflet was characteristic of 22 genotypes each in the three provenances of Acre, Rondonia and Mato Grosso, as well as that of RRII 105. One genotype each of the Acre and Mato Grosso provenance had aristate foliage tip. Two genotypes

each from Acre and Rondonia and five from Mato Grosso had apiculate laminae while three Rondonian and one Mato Grosso genotype had cuspidate tip (Tables 2 and 3).

Lateral appearance of the leaflets was of flat shape for 16 Acre genotypes, while eight genotypes had a 'S' shaped appearance and a single one had convex shaped lateral appearance. Fifteen Rondonian genotypes had a flat lateral appearance for their leaflets, while the remaining 12 had a 'S' shape. Majority of the Mato Grosso (21 genotypes) had a flat shaped lateral view while remaining seven genotypes had a 'S' shaped appearance. RRII 105 had a flat lateral appearance (Tables 2 and 3).

The individual leaflets in a leaf was found to be well separated in the case of 21 Acre genotypes while four genotypes had their leaflet margins touching each other. Among the Rondonian genotypes, 17 had well separated leaflets while six had their margins touching each other and another four had their leaflets overlapping over one another. Out of the Mato Grosso genotypes, except for a single genotype with overlapping leaflets, 20 had well separated leaflets and seven genotypes had their leaf margins touching each other. Leaflets of RRII 105 were found to be well separated, their margins not touching each other (Tables 2 and 3).

Except for two genotypes each from Acre and Rondonia with light green coloured veins, all the remaining wild genotypes irrespective of the provenances, and the control clone RRII 105, had yellow coloured leaf veins. Sixteen of the Acre genotypes, 15 Rondonian and 24 Mato Grosso genotypes had less prominent leaf veins while nine Acre, 12 Rondonian and four Mato Grosso genotypes as well as the control had prominent veins (Tables 2 and 3).

The dorsal side of the leaf blade was found to be smooth for all the Acre genotypes. Among the Rondonian clones, 25 genotypes had smooth dorsal surface while two of them had an irregular dorsal surface. In the case of Mato Grosso accessions, smooth lamina texture were found in 22 genotypes and the remaining six genotypes had an irregular dorsal surface. The leaflets of RRII 105 had smooth dorsal surface (Tables 2 and 3). A mosaic view of the morphological variability in the wild germplasm is given in Figs 1-12.

Table 2. Descriptors and frequency of distribution of the wild genotypes

Sl. No	Characters	Acre	Rondonia	Mato Grosso
1	**Height of the plants**			
1.1	Dwarf	13	5	14
1.2	Medium tall	12	15	11
1.3	Tall	0	7	3
2	**Girth of the plants**			
2.1	Below average	5	5	14
2.2	Average	17	13	11
2.3	Above average	3	9	3
3	**Branching**			
3.1	Branching	0	0	0
3.3	No branching	25	27	28
4	**Nodes**			
4.1	**Axillary buds**			
4.1.1	Protruding	0	0	0
4.1.2	Sunken	0	0	0
4.1.3	Normal	25	27	28
4.2	**Leaf scars**			
4.2.1	Pronounced margin	20	12	8
4.2.2	Normal margin	5	15	20
4.3	**Nature of leaf scars**			
4.3.1	Sunken	5	3	0
4.3.2	Normal	20	24	28
5	**Leaf storey**			
5.1	**Shape**			
5.1.1	Conical	0	1	0
5.1.2	Truncate	1	1	2
5.1.3	Bow shaped	1	1	1
5.1.4	Hemispherical	23	24	25
5.2	**Separation**			
5.2.1	Closely placed	14	8	11
5.2.2	Intermediately separated	9	14	12
5.2.3	Well separated	2	5	5
5.3	**External appearance**			
5.3.1	Open	25	25	28
5.3.2	Close	0	2	0
6	**Leaves**			
6.1	**Pulvinus**			
6.1.1	Swollen	24	26	25
6.1.2	Normal	1	1	3

Table 2. Continued.

Sl. No	Characters	Acre	Rondonia	Mato Grosso
6.2	**Petiole**			
6.2.1	**Shape**			
6.2.1.1	Arched	0	1	1
6.2.1.2	Concave	17	18	8
6.2.1.3	Straight	7	4	19
6.2.1.4	S' shaped	1	4	0
6.2.2	**Size**			
6.2.2.1	Short	3	5	20
6.2.2.2	Medium	19	15	7
6.2.2.3	Long	3	7	1
6.2.3	**Angle**			
6.2.3.1	Acute	22	24	27
6.2.3.2	Horizontal	3	3	1
6.2.3.3	Optuse	0	0	0
6.3	**Petiolule**			
6.3.1	**Orientation**			
6.3.1.1	Upward	14	17	16
6.3.1.2	Horizontal	2	3	7
6.3.1.3	Downward	9	7	5
6.3.2	**Size**			
6.3.2.1	Long	1	8	2
6.3.2.2	Medium	18	18	22
6.3.2.3.	Short	6	1	4
6.3.3	**Extra floral nectary**			
6.3.3.1	Prominent	14	10	21
6.3.3.2	Less prominent	11	17	7
6.4	**Leaflets**			
6.4.1	**Colour**			
6.4.1.1	Green	20	21	22
6.4.1.2	Dark green	5	6	6
6.4.2	**Lustre**			
6.4.2.1	Glossy	0	4	5
6.4.2.2	Dull	25	23	23
6.4.3	**Shape**			
6.4.3.1	Elliptic	24	21	26
6.4.3.2	Lanceolate	0	0	0
6.4.3.3	Obovate	1	6	2

Table 2. Continued

Sl. No	Characters	Acre	Rondonia	Mato Grosso
6.4.4	**Size**			
6.4.4.1	Small	9	7	14
6.4.4.2	Medium	13	18	12
6.4.4.3	Large	3	2	2
6.4.5	**Margin**			
6.4.5.1	Entire	14	8	15
6.4.5.2	Undulate	11	19	13
6.4.6	**Cross sectional appearance**			
6.4.6.1	Straight	11	12	24
6.4.6.2	V' shaped	2	1	1
6.4.6.3	Boat shaped	12	14	3
6.4.6.4	Convex shaped	0	0	0
6.4.7	**Leaflet tip**			
6.4.7.1	Aristate	1	0	1
6.4.7.2	Apiculate	2	2	5
6.4.7.3	Cuspidate	0	3	1
6.4.7.4	Accuminate	22	22	22
6.4.8	**Lateral appearance**			
6.4.8.1	Flat	16	15	21
6.4.8.2	Convex	1	0	0
6.4.8.3	S' shaped	8	12	7
6.4.9	**Orientation**			
6.4.9.1	Margin touching	4	6	7
6.4.9.2	Overlapping	0	4	1
6.4.9.3	Separated	21	17	20
6.4.10	**Vein colour**			
6.4.10.1	Yellow	23	25	28
6.4.10.2	Light green	2	2	0
6.4.11	**Nature of vein**			
6.4.11.1	Prominent	9	12	4
6.4.11.2	Not prominent	16	15	24
6.4.12	**Lamina texture**			
6.4.12.1	Smooth	25	25	22
6.4.12.2	Irregular	0	2	6

Table 3. Description of the wild genotypes along with control as per the descriptor.

Sl No	Genotype	Height	Girth	Branch-ing	4.0 Nodes			5.0 Leaf storey		
					Axillary buds	Leaf scars	Nature of scars	Shape	Separa-tion	Appear-ance
		1	**2**	**3**	**4.1**	**4.2**	**4.3**	**5.1**	**5.2**	**5.3**
(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)	(11)
1	AC 426	1	1	2	3	1	2	4	1	1
2	AC 453	2	2	2	3	1	2	4	1	1
3	AC 604	2	2	2	3	1	2	4	1	1
4	AC 626	1	2	2	3	2	2	4	1	1
5	AC 627	2	2	2	3	2	2	4	3	1
6	AC 629	1	1	2	3	1	2	4	1	1
7	AC 632	2	2	2	3	1	2	4	1	1
8	AC 644	1	1	2	3	1	2	4	2	1
9	AC 647	1	2	2	3	1	2	4	2	1
10	AC 650	2	2	2	3	1	2	4	2	1
11	AC 654	2	3	2	3	1	2	4	1	1
12	AC 657	2	3	2	3	1	2	4	1	1
13	AC 694	2	2	2	3	1	2	4	1	1
14	AC 706	1	1	2	3	1	2	4	1	1
15	AC 733	1	2	2	3	1	1	3	1	1
16	AC 754	1	2	2	3	1	2	4	1	1
17	AC 953	1	2	2	3	1	1	4	2	1
18	AC 959	1	2	2	3	2	2	4	2	1
19	AC 963	1	1	2	3	1	1	4	1	1
20	AC 966	2	2	2	3	1	1	4	2	1
21	AC 979	1	2	2	3	1	2	4	3	1
22	AC 986	2	2	2	3	2	2	4	2	1
23	AC 995	1	2	2	3	2	2	2	1	1
24	AC 1043	2	3	2	3	1	2	4	2	1
25	AC 1090	2	2	2	3	1	1	4	2	1
26	RO 254	2	1	2	3	1	1	4	2	1
27	RO 255	2	2	2	3	1	2	4	2	1
28	RO 256	1	2	2	3	1	2	3	2	1
29	RO 257	1	1	2	3	1	2	4	1	1
30	RO 287	2	2	2	3	1	2	4	2	1
31	RO 311	2	2	2	3	1	2	2	3	1
32	RO 316	2	2	2	3	1	2	4	1	1
33	RO 317	2	3	2	3	2	2	4	2	1
34	RO 319	3	3	2	3	1	2	4	2	1
35	RO 322	3	3	2	3	1	2	4	2	1
36	RO 328	3	3	2	3	2	2	4	3	1
37	RO 330	2	2	2	3	2	2	4	3	1

Table 3. Continued

(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)	(11)
38	RO 338	3	3	2	3	2	2	4	2	1
39	RO 352	3	2	2	3	2	2	4	2	1
40	RO 364	3	2	2	3	2	2	4	2	1
41	RO 369	1	1	2	3	1	2	4	1	1
42	RO 380	2	2	2	3	2	2	4	2	1
43	RO 381	1	1	2	3	2	2	4	2	1
44	RO 395	3	3	2	3	1	1	4	2	1
45	RO 399	1	1	2	3	1	1	4	1	1
46	RO 859	2	3	2	3	2	2	4	1	1
47	RO 868	2	2	2	3	2	2	4	1	1
48	RO 876	2	2	2	3	2	2	4	2	1
49	RO 879	2	3	2	3	2	2	1	3	1
50	RO 883	2	2	2	3	2	2	4	1	2
51	RO 886	2	2	2	3	1	2	4	3	1
52	RO 894	2	3	2	3	2	2	4	1	2
53	MT 899	2	2	2	3	1	2	4	2	1
54	MT 901	2	2	2	3	2	2	4	3	1
55	MT 906	1	1	2	3	2	2	4	3	1
56	MT 920	2	2	2	3	2	2	4	2	1
57	MT 922	1	1	2	3	2	2	3	1	1
58	MT 929	1	1	2	3	2	2	4	1	1
59	MT 931	2	1	2	3	2	2	4	1	1
60	MT 935	2	3	2	3	1	2	2	2	1
61	MT 944	3	3	2	3	2	2	2	3	1
62	MT 945	1	1	2	3	2	2	4	1	1
63	MT 947	2	2	2	3	1	2	4	1	1
64	MT 948	2	2	2	3	2	2	4	3	1
65	MT 1005	1	1	2	3	1	2	4	2	1
66	MT 1007	1	1	2	3	1	2	4	1	1
67	MT 1008	1	1	2	3	2	2	4	2	1
68	MT 1011	1	1	2	3	2	2	4	2	1
69	MT 1021	1	2	2	3	2	2	4	1	1
70	MT 1024	2	2	2	3	1	2	4	2	1
71	MT 1025	3	3	2	2	2	2	4	1	1
72	MT 1028	2	2	2	3	2	2	4	2	1
73	MT 1029	1	1	2	3	1	2	4	2	1
74	MT 1030	3	2	2	3	2	2	4	2	1
75	MT 1031	1	2	2	3	2	2	4	1	1
76	MT 1055	1	2	2	3	2	2	4	3	1
77	MT 1057	1	1	2	3	1	2	4	1	1
78	MT 1063	1	1	2	3	2	2	4	1	1
79	MT 1064	2	1	2	3	2	2	4	2	1
80	MT 1077	2	1	2	3	2	2	4	2	1
81	RRII 105	1	1	2	3	2	2	4	1	1

Table 3. Continued

Sl No	Genotype	6.0 Leaves						
		Pulvinus	6.2 Petiole			6.3 Petiolule		
			Shape	Size	Angle	Orientation	Size	Nectary
		6.1	**6.2.1**	**6.2.2**	**6.2.3**	**6.3.1**	**6.3.2**	**6.3.3**
(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)
1	AC 426	1	2	2	1	2	2	1
2	AC 453	1	2	2	2	1	2	1
3	AC 604	1	2	2	1	3	3	1
4	AC 626	1	3	2	1	3	3	2
5	AC 627	1	2	2	1	1	2	2
6	AC 629	1	3	2	1	3	3	2
7	AC 632	1	3	2	1	3	2	2
8	AC 644	1	2	3	2	3	2	2
9	AC 647	1	2	2	1	1	3	2
10	AC 650	1	3	2	1	1	3	2
11	AC 654	1	2	2	2	1	2	1
12	AC 657	1	2	2	1	1	2	1
13	AC 694	1	2	2	1	3	2	1
14	AC 706	1	3	1	1	3	3	2
15	AC 733	1	2	2	1	1	2	2
16	AC 754	1	2	2	1	1	2	1
17	AC 953	1	3	2	1	3	2	1
18	AC 959	2	2	1	1	1	2	1
19	AC 963	1	2	2	1	1	2	1
20	AC 966	1	2	3	1	1	2	1
21	AC 979	1	4	2	1	3	2	1
22	AC 986	1	2	2	1	1	1	1
23	AC 995	1	3	1	1	1	2	2
24	AC 1043	1	2	3	1	2	2	1
25	AC 1090	1	2	2	1	1	2	2
26	RO 254	1	2	2	2	3	2	2
27	RO 255	1	2	2	2	1	2	1
28	RO 256	1	2	3	1	1	2	1
29	RO 257	1	1	1	1	1	2	2
30	RO 287	1	2	3	1	3	2	2
31	RO 311	1	2	3	1	3	1	2
32	RO 316	1	3	2	1	1	1	1
33	RO 317	1	2	2	1	3	2	1
34	RO 319	1	2	3	1	1	1	2
35	RO 322	1	2	3	1	3	2	2
36	RO 328	1	2	1	1	1	2	2
37	RO 330	1	2	2	1	1	1	2

Table 3. Continued

(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)
38	RO 338	1	2	2	1	1	1	1
39	RO 352	1	2	2	1	2	1	2
40	RO 364	1	2	2	1	1	3	1
41	RO 369	1	3	2	1	3	2	2
42	RO 380	2	3	1	1	3	2	2
43	RO 381	1	2	2	1	2	2	1
44	RO 395	1	4	2	1	1	1	1
45	RO 399	1	2	1	1	2	2	2
46	RO 859	1	4	2	1	1	2	2
47	RO 868	1	3	2	1	1	2	2
48	RO 876	1	2	3	1	1	1	1
49	RO 879	1	4	2	2	1	2	2
50	RO 883	1	2	1	1	1	2	2
51	RO 886	1	4	3	1	1	2	2
52	RO 894	1	2	2	2	1	2	1
53	MT 899	1	3	1	1	1	2	2
54	MT 901	1	2	1	1	1	2	1
55	MT 906	1	2	1	1	1	1	1
56	MT 920	1	3	1	1	2	2	1
57	MT 922	1	3	1	1	2	2	1
58	MT 929	1	3	1	1	2	2	2
59	MT 931	2	3	1	1	3	2	1
60	MT 935	1	3	1	1	1	2	2
61	MT 944	1	3	1	1	2	2	2
62	MT 945	1	3	2	1	2	2	1
63	MT 947	1	3	2	1	3	2	1
64	MT 948	1	3	2	1	1	2	1
65	MT 1005	1	2	1	2	1	3	1
66	MT 1007	1	3	1	1	2	2	2
67	MT 1008	1	3	1	1	1	2	1
68	MT 1011	1	3	1	1	2	2	1
69	MT 1021	1	2	1	1	1	2	1
70	MT 1024	1	3	2	1	1	2	1
71	MT 1025	1	3	1	1	1	2	1
72	MT 1028	1	2	2	1	3	3	1
73	MT 1029	1	1	1	1	1	2	2
74	MT 1030	1	2	3	1	1	1	1
75	MT 1031	1	2	2	1	3	2	1
76	MT 1055	1	3	1	1	1	2	1
77	MT 1057	1	2	2	1	1	2	1
78	MT 1063	1	3	1	1	1	3	1
79	MT 1064	2	3	1	1	1	3	2
80	MT 1077	2	3	1	1	3	2	1
81	RRII 105	1	3	1	1	1	2	2

Table 3. Continued

Sl no	Genotype	6.0 Leaves 6.4 Leaflets					
		Colour	Lustre	Shape	Size	Margin	Appearance (CS)
		6.4.1	**6.4.2**	**6.4.3**	**6.4.4**	**6.4.5**	**6.4.6**
(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)
1	AC 426	1	2	1	2	1	1
2	AC 453	1	2	1	1	2	3
3	AC 604	1	2	1	2	2	4
4	AC 626	1	2	3	2	1	1
5	AC 627	1	2	1	2	1	3
6	AC 629	2	2	1	2	2	3
7	AC 632	1	2	1	2	2	3
8	AC 644	1	2	1	2	2	1
9	AC 647	1	2	1	2	1	1
10	AC 650	1	2	1	2	2	3
11	AC 654	1	2	1	2	1	1
12	AC 657	2	2	1	2	2	3
13	AC 694	1	2	1	2	1	1
14	AC 706	1	2	1	2	1	1
15	AC 733	1	2	1	2	2	2
16	AC 754	2	2	1	2	1	1
17	AC 953	1	2	1	2	2	3
18	AC 959	2	2	1	2	1	1
19	AC 963	1	2	1	2	1	3
20	AC 966	1	2	1	2	1	1
21	AC 979	2	2	1	2	2	3
22	AC 986	1	2	1	2	1	1
23	AC 995	1	2	1	2	2	3
24	AC 1043	1	2	1	2	1	2
25	AC 1090	1	2	1	2	2	3
26	RO 254	1	2	1	2	2	1
27	RO 255	1	2	1	2	1	1
28	RO 256	1	2	1	2	1	1
29	RO 257	1	2	1	2	1	3
30	RO 287	2	2	1	2	2	3
31	RO 311	1	2	1	1	2	3
32	RO 316	2	2	3	2	2	3
33	RO 317	1	2	1	2	2	3
34	RO 319	2	2	1	2	2	3
35	RO 322	1	2	1	2	1	3
36	RO 328	1	1	1	2	2	1
37	RO 330	1	1	1	2	2	1

Table 3. Continued

(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)
38	RO 338	1	2	1	2	2	3
39	RO 352	1	2	1	2	2	3
40	RO 364	1	1	1	2	2	3
41	RO 369	1	2	1	2	2	3
42	RO 380	1	2	1	2	2	2
43	RO 381	1	2	3	2	2	1
44	RO 395	1	2	1	2	2	1
45	RO 399	1	2	1	2	1	3
46	RO 859	2	1	1	2	2	1
47	RO 868	1	2	1	2	2	3
48	RO 876	1	2	3	2	1	1
49	RO 879	1	2	3	2	1	1
50	RO 883	2	2	1	2	2	1
51	RO 886	2	2	1	2	2	3
52	RO 894	1	2	3	2	1	1
53	MT 899	1	2	1	3	2	1
54	MT 901	2	2	1	2	1	1
55	MT 906	1	2	1	2	2	3
56	MT 920	1	1	1	2	1	1
57	MT 922	1	2	1	2	1	1
58	MT 929	2	2	1	3	2	1
59	MT 931	1	2	1	3	1	1
60	MT 935	2	1	1	3	1	1
61	MT 944	2	1	1	2	1	1
62	MT 945	1	2	1	2	1	1
63	MT 947	1	2	1	3	2	1
64	MT 948	1	2	3	2	1	3
65	MT 1005	2	2	1	2	1	2
66	MT 1007	1	2	1	3	2	1
67	MT 1008	1	2	1	2	1	1
68	MT 1011	1	2	1	2	1	1
69	MT 1021	1	1	1	3	2	1
70	MT 1024	1	2	1	2	2	1
71	MT 1025	2	2	1	2	2	1
72	MT 1028	1	2	1	2	2	1
73	MT 1029	1	1	1	3	1	3
74	MT 1030	1	2	1	2	2	1
75	MT 1031	1	2	1	2	2	1
76	MT 1055	1	2	1	2	2	1
77	MT 1057	1	2	1	3	1	1
78	MT 1063	1	2	1	2	1	1
79	MT 1064	1	2	3	2	2	1
80	MT 1077	1	2	1	3	1	1
81	RRII 105	1	1	1	3	2	1

Table 3. Continued

Sl no	Genotype	6.0 Leaves 6.4 Leaflets Leaf apex **6.4.7**	Lateral appearance **6.4.8**	Arrangement **6.4.9**	Vein colour **6.4.10**	Nature of vein **6.4.11**	Lamina texture **6.4.12**
(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)
1	AC 426	4	1	3	1	2	1
2	AC 453	1	1	3	1	1	1
3	AC 604	4	1	1	1	1	1
4	AC 626	4	1	3	1	1	1
5	AC 627	4	3	3	1	2	1
6	AC 629	4	1	3	1	1	1
7	AC 632	4	2	3	1	1	1
8	AC 644	4	1	3	1	2	1
9	AC 647	4	1	3	1	2	1
10	AC 650	4	3	3	1	1	1
11	AC 654	4	1	1	1	1	1
12	AC 657	4	3	1	1	1	1
13	AC 694	4	3	3	1	1	1
14	AC 706	4	3	3	1	2	1
15	AC 733	4	1	3	1	2	1
16	AC 754	4	1	3	1	2	1
17	AC 953	4	1	1	1	2	1
18	AC 959	4	1	3	2	2	1
19	AC 963	2	1	3	1	2	1
20	AC 966	4	1	3	2	2	1
21	AC 979	4	3	3	1	2	1
22	AC 986	2	1	3	1	2	1
23	AC 995	4	1	3	1	2	1
24	AC 1043	4	3	3	1	2	1
25	AC 1090	4	3	3	1	2	1
26	RO 254	4	1	3	1	2	1
27	RO 255	4	1	1	1	1	1
28	RO 256	4	1	1	1	2	1
29	RO 257	4	1	1	1	2	1
30	RO 287	4	1	1	2	2	1
31	RO 311	2	1	3	1	1	1
32	RO 316	3	3	3	1	1	1
33	RO 317	3	3	3	1	1	1
34	RO 319	4	3	3	1	1	1
35	RO 322	4	1	2	1	1	1
36	RO 328	4	1	3	1	2	1
37	RO 330	4	1	3	1	2	1

Table 3. Continued

(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)
38	RO 338	4	3	3	1	2	1
39	RO 352	4	3	3	2	2	1
40	RO 364	4	1	3	1	2	1
41	RO 369	4	1	3	1	1	1
42	RO 380	4	1	3	1	2	1
43	RO 381	4	3	1	1	2	1
44	RO 395	2	1	3	1	2	1
45	RO 399	4	1	3	1	1	1
46	RO 859	4	3	2	1	2	1
47	RO 868	4	3	1	1	1	1
48	RO 876	4	3	3	1	1	1
49	RO 879	4	3	3	1	1	1
50	RO 883	4	3	1	1	1	2
51	RO 886	4	3	2	1	2	2
52	RO 894	3	1	2	1	1	1
53	MT 899	4	1	3	1	2	1
54	MT 901	2	1	1	1	2	1
55	MT 906	2	1	3	1	2	2
56	MT 920	4	3	1	1	2	1
57	MT 922	4	1	3	1	2	1
58	MT 929	2	1	3	1	1	1
59	MT 931	4	1	3	1	2	1
60	MT 935	4	1	1	1	2	1
61	MT 944	4	1	1	1	2	2
62	MT 945	4	1	3	1	2	1
63	MT 947	2	3	3	1	1	1
64	MT 948	4	1	3	1	2	1
65	MT 1005	4	1	1	1	2	1
66	MT 1007	4	1	3	1	2	1
67	MT 1008	4	1	1	1	2	1
68	MT 1011	4	1	3	1	2	1
69	MT 1021	4	3	3	1	2	1
70	MT 1024	4	1	3	1	1	1
71	MT 1025	4	3	1	1	2	1
72	MT 1028	2	3	3	1	2	1
73	MT 1029	4	1	3	1	2	2
74	MT 1030	3	1	3	1	1	1
75	MT 1031	4	3	3	1	2	1
76	MT 1055	4	1	3	1	2	1
77	MT 1057	4	1	3	1	2	2
78	MT 1063	4	1	3	1	2	2
79	MT 1064	4	3	3	1	2	1
80	MT 1077	4	1	2	1	2	2
81	RRII 105	4	1	3	1	2	1

Keys to the characters

1 **Height of the plants**

1. Dwarf
2. Medium tall
3. Tall

2 **Girth of plants**

1. Below average
2. Average
3. Above average

3 **Branching**

1 Branching
2. No branching

4 **Nodes**

4.1 Axillary buds

1. Protruding
2. Sunken
3. Normal

4.2 Leaf scars

1. Pronounced margin
2. Normal margin

4.3 Nature of leaf scars

1. Sunken
2. Normal

5 **Leaf storey**

5.1 Shape

1. Conical
2. Truncate
3. Bow shaped
4. Hemispherical

5.2 Separation

1. Closely placed
2. Intermediate
3. Well separated

5.3 External appearance

1 Open
2. Close

6 **Leaves**

6.1 Pulvinus

1. Swollen
2. Normal

6.2 Petiole

6.2.1 Shape

1. Arched
2. Concave
3. Straight
4. 'S'shape

6.2.2 Size

1. Short
2. Medium
3. Long

6.2.3 Angle

1. Acute
2. Horizontal
3. Optuse

6.3 Petiolule

6.3.1 Orientation

1. Upward
2. Horizontal
3. Downward

6.3.2 Size
1. Long
2. Medium
3. Short

6.3.3 Extra floral nectary
1. Prominent
2. Less prominent

6.4 Leaflets

6.4.1 Colour
1. Green
2. Dark green
3. Yellowish green

6.4.2 Luster
1. Glossy
2. Dull

6.4.3 Shape
1. Elliptic
2. Lanceolate
3. Obovate

6.4.4 Size
1. Large
2. Medium
3. Small

6.4.5 Margin
1. Entire
2. Undulate

6.4.6 Cross Sectional appearance
1. Straight
2. 'V' shaped
3. Boat shaped

6.4.7 Leaflet tip
1. Aristate
2. Apiculate
3. Cuspidate
4. Accuminate

6.4.8 Lateral appearance
1. Flat
2. Convex
3. 'S' shape

6.4.9 Orientation
1. Margin touching
2. Overlapping
3. Separated

6.4.10 Vein colour
1. Yellow
2. Light green

6.4.11 Nature of vein
1. Prominent
2. Not prominent

6.4.12 Lamina texture
1. Smooth
2. Irregular

3.2 Genetic variability

3.2.1 Analysis of variance

Analysis of variance was carried out for the mean values of all the characters studied in three stages. **Stage 1**: At the end of each quarter during the first year of observations, girth of the plant, height of the plant, number of leaf flushes per plant and total number of leaves per plant was recorded. Inter flush distance, petiole length, total leaf area of the plant, leaf area index, and micro tap yield were recorded at the end of the fourth quarter (18 months after planting) in addition to the above four characters. **Stage 2**: In the fourth quarter of the second year of recording observations, (30 months after planting), test tap yield was recorded. **Stage 3**: At the end of third year of recording observations (42 months after planting), leaf stomatal characters, structural characters of leaf and bark, girth and dry rubber yield by test tapping were recorded. Stomatal characters included number of stomata per mm^2 of the leaf, number of epidermal cells per mm^2 of the lamina and stomatal index along with the single leaflet area. The leaf structural characters studied were thickness of the lamina, thickness of the midrib, thickness of the palisade layer, thickness of the spongy layer, number of cells per mm of palisade layer, number of cells per mm of spongy layer and thickness of the cuticle. Bark anatomical structures for which the analysis of variance was carried out were total bark thickness, soft bark thickness, hard bark thickness, percentage of soft bark in the total bark thickness, percentage of hard bark in the total bark thickness, number of laticifer rows in the soft bark region, number of laticifer rows in the hard bark region, total number of laticifer rows, density of latex vessels per row per mm circumference, diameter of latex vessels, total cross sectional area of the laticifers, average distance between the laticifer rows in the soft bark, frequency of phloic rays, height, width and height/width ratio of phloic rays.

Analysis of variance carried out in all the above characters revealed that there was highly significant genetic variation among the wild genotypes studied at one percent selection level (Tables 4 to 7). This is a clear evidence of the genetic potential of this collection of wild genotypes for their genetic improvement based on selected secondary characters like number of leaves, number of stomata / unit area, total bark thickness, total number of latex vessel rows and diameter of latex vessels etc.

Table 4. ANOVA for the growth characters during the first year

Character		Treatment adjusted mean square	MSE	Computed F	Critical Difference
Girth-	first quarter (cm)	0.78	0.11	7.09**	0.48
	second quarter (cm)	1.52	0.22	7.03**	0.67
	third quarter (cm)	3.33	0.46	7.31**	0.97
	fourth quarter (cm)	6.11	0.87	7.02**	1.34
Height-	first quarter (cm)	914.54	160.12	5.71**	18.31
	second quarter (cm)	2114.8	300.34	7.04**	25.18
	third quarter (cm)	3674.9	601.2	6.11**	34.96
	fourth quarter (cm)	7579.35	1440.4	5.26**	55.00
No of leaf whorls-	first quarter	0.42	0.13	3.27**	0.52
	second quarter	1.2	0.22	5.34**	0.66
	third quarter	2.06	0.36	5.78**	0.86
	fourth quarter	4.07	0.63	6.46**	1.14
Total no of leaves-	first quarter	84.06	19.93	4.22**	6.44
	second quarter	286.5	43.27	6.63**	9.65
	third quarter	559	86.62	6.45**	13.42
	fourth quarter	1226.04	190.24	6.44**	19.89
Total leaf area-fourth quarter(cm^2)		85810125.42	17628738.57	4.87**	6045.73
Leaf area index-fourth quarter		0.022	0.005	4.84**	0.11
Inter flush DS-	fourth quarter (cm)	35.32	9.29	3.80**	4.49
Petiole length-	fourth quarter (cm)	65.37	28.81	2.27**	7.69

** Significant at $P < 0.01$ $F = 1.53$

DS = distance

Tabel 5. ANOVA for test tap yield for the first three years.

Character	Treatment adjusted mean square	MSE	Computed F	Critical Difference
Dry rubber yield ($g\ t^{-1}\ t^{-1}$)				
First year	0.0117	0.0005	23.98**	0.03
Second year	0.0393	0.0091	4.32**	0.14
Third year	1.1403	0.1269	8.99**	0.50

** - Significant at $P < 0.01$ $F = 1.53$

Table 6. ANOVA for leaf structural characters in the third year

Character	Treatment adjusted mean square	MSE	Computed F	Critical Difference
No of stomata/mm^2 leaf area	16025.72	1042.82	15.37**	45.05
No of epidermal cells/mm^2 LA	444473.34	6186.4	71.85**	112.79
Stomatal Index	44.08	1.9441	22.67**	1.94
Single leaflet area (cm^2)	1525.23	554.76	2.75**	33.28
Thickness of the lamina (µm)	841.73	18.69	45.40**	6.00
Thickness of leaf midrib (mm)	0.0502	0.0003	148.05**	0.04
Thickness of palisade layer (µm)	260.39	3.12	84.10**	2.45
Thickness of spongy layer (µm)	359.39	57.15	6.30**	10.52
No of cells/mm of palisade layer	191.45	8.11	23.59**	4.05
No of cells/mm of spongy layer	6433.6	98.51	66.53**	13.67
Thickness of cuticle (µm)	1.52	0.0157	100.42**	0.20

** - Significant at P< 0.01 F = 1.53

LA = Leaf area

Table 7. ANOVA for bark structural characters in the third year

Character	Treatment adjusted mean square	MSE	Computed F	Critical Difference
Total bark thickness (mm)	0.7943	0.0048	164.30**	0.10
Soft bark thickness (mm)	0.1358	0.0028	49.31**	0.08
Hard bark thickness (mm)	0.5854	0.0077	76.00**	0.14
Soft bark thickness in %	183.75	4.68	39.29**	3.06
Hard bark thickness in %	183.75	4.67	39.31**	3.06
No of LV rows in soft bark	6.74	0.085	79.43**	0.39
No of LV rows in hard bark	2.26	0.082	27.55**	0.39
Total no of latex vessel rows	12.05	0.1487	81.93**	0.53
Density of LV per row /mm	38.73	0.2647	146.34**	0.70
Diameter of latex vessels (µm)	56.9	1.0207	58.63**	1.40
Total CSA of LV (mm^2)	1844903.71	48358.41	38.20**	53061.40
AD. between LVR in SB (mm)	0.0566	0.0002	392.97**	0.02
FQ. of PR /.01 mm^2 area	3.6	0.0894	41.18**	0.42
Height of phloic rays (mm)	0.0059	0.00008	77.98**	0.01
Width of phloic rays (mm)	0.0003	0.00001	23.10**	0.01
Height/width ratio of PR	6.46	0.1017	63.58**	0.44

** - Significant at P < 0.01 F = 1.53

SB = Soft bark; CSA = Cross sectional area; LV = Latex vessels; AD = Average distance; FQ=Frequency; PR = Phloic rays

3.2.2 General performance of the wild genotypes

3.2.2.1 Morphological characters

The range and general mean for the growth characters studied during the first four quarters of the first year of recording observations in the wild genotypes in comparison to the control clone RRII 105 is shown in Table 8 and the mean individual performance of the 80 genotypes for these characters in comparison with the control is shown in Table 9.

Girth of the plants in the first quarter (nine months after planting), showed a wide range of variation among the 80 wild genotypes. Maximum girth of 3.94 cm was recorded by the genotype RO 322 followed by the genotypes MT 935 (3.83 cm), RO 395 (3.75 cm), RO 319 (3.67 cm) and MT 1025 (3.66 cm) whereas the genotype MT 929 showed the minimum girth value of 1.88 cm. The control clone, RRII 105 had an average girth of 2.06 cm. Of the 80 wild genotypes, 60 accessions were found to be significantly different from the control with higher girth values, while the rest of the genotypes were statistically on par with the control clone (Tables 8 and 9).

During the second quarter, RO 395 had the maximum girth of 5.56 cm while the genotypes RO 322, RO 319, MT 1025 and RO 317 followed in the order their mean girths being 5.37 cm, 5.14 cm, 4.93 cm and 4.79 cm respectively. The minimum girth was recorded by the genotype MT 929 (2.51cm). Fifty-four wild genotypes showed their superiority in girth over the control clone (2.81 cm) in the analysis, while the remaining 26 genotypes were statistically on par with the control (Tables 8 and 9).

The maximum girth in the third quarter was in RO 322 with 7.62 cm followed by RO 395 (7.49 cm), RO 319 (7.28 cm), MT 1025 (6.99 cm) and AC 1043 (6.95 cm). MT 929 continued to show poor growth in terms of girth (3.38 cm). Forty-nine wild genotypes had their girth values significantly different from the control clone, which had a mean girth of 4.05 cm while the rest of the genotypes were on par with the control (Tables 8 and 9).

RO 322 retained its superiority in girth in the fourth quarter also with the maximum girth in the population (10.41 cm), while MT 929 continued to be the weakest with the minimum girth of 4.72 cm (Table 8). RO 322 was followed by RO 395 with an average girth of 9.98 cm, RO 319 with a girth of 9.53 cm, MT 1025 with a girth of 9.45 cm and AC 654 with a girth of 9.44 cm. Thirty-seven genotypes were found to be superior for their significantly higher girth values, compared to the control clone RRII 105, which had an average girth of 6.06 cm. All the other genotypes were found to have their girth statistically on par with that of the control (Table 9).

Height of the plants recorded at the end of first quarter was the maximum for the genotype RO 395 (125.77 cm) with minimum height recorded by MT 929 (41.76 cm) (Table 8). The genotypes MT 1025, RO 322, RO 352 and RO 364 followed RO 395 in that order with their heights being 105.31 cm, 104.17 cm, 101.79 cm and 101.69 cm respectively. 62 genotypes were significantly taller than the control clone (43.43 cm). Rest of the genotypes was found to be on par (Table 9).

During the second quarter, RO 395 was the tallest (189.35 cm), followed by RO 319 (165.47 cm), RO 328 (163.07 cm), RO 322 (160.77 cm) and MT 1025 (152.74 cm). The minimum height was shown by MT 929 (59.75 cm), while the control clone had a height of 73.48 cm. Fifty-six genotypes were found to be significantly taller than the control while the rest of the genotypes were on par with it (Tables 8 and 9).

The maximum height of 235.82 cm was recorded by the genotype RO 395, with the genotypes RO 328 (210.85 cm), RO 322 (202.07 cm), RO 319 (200.39 cm) and MT 1025 (197.78 cm) following in that order with MT 929 continuing to be the shortest with 71.72 cm height in the third quarter. The control clone was 87.69 cm tall with 57 wild genotypes significantly taller than the control. The remaining 23 genotypes were found to be statistically on par with control (Tables 8 and 9).

The genotype RO 395 continued to be tallest of all the genotypes in this population, during the fourth quarter also with a height of 322.99 cm followed by RO 328, RO 322, MT 1030 and MT 1025 with their heights 316.09cm, 280.73cm, 272.19 cm, 270.72 cm

respectively. The minimum height of 100.89 cm was recorded by the genotype MT 929. Twenty-eight genotypes were found to be statistically different by being taller than the control clone whose height was 145.70 cm. Rest of the genotypes had their height statistically comparable with that of the control (Tables 8 and 9).

The total number of leaf flushes per plant recorded over four quarters in the first year (Table 9) were found to be comparable with the control for most of the wild genotypes. During the first quarter, maximum number of leaf flushes per plant was produced by the genotype RO 395 with an average number of 3.85 flushes (Table 8) followed by RO 317 (3.75 flushes), RO 319 (3.72 flushes), MT 1025 (3.56 flushes) and RO 254 (3.53 flushes), while MT 929 had the lowest number of 2.20 flushes (Table 9) which was significantly different from the control clone also. Only six genotypes were found to have a significantly higher number of leaf flushes compared to the 2.94 flushes of the control clone while all the remaining clones (except 3 clones with significantly lower number of flushes) were found to be statistically on par with the control.

During the second quarter RO 319 showed the maximum number of leaf flushes (5.97 flushes), followed by RO 395 (5.87), RO 317 (5.58 flushes), RO 894 (5.52 flushes) and RO 859 (5.39 flushes), with the lowest number being recorded in AC 1090 (3.33 flushes). The control clone had an average of 4.13 flushes with 61 wild genotypes having their number of flushes on par with it. Only 17 genotypes had a significantly higher number of leaf flushes than the control while two clones were in the other extreme with very low values (Tables 8 and 9).

RO 319 continued to have the maximum number of leaf flushes in the third quarter also (7.40 flushes) with RO 317, RO 395, RO 894 and RO 859 following in the descending order with mean values of 7.33, 7.32, 7.12 and 7.05 respectively. The lowest number of leaf flushes was recorded by AC 1090 (4.07) and the control clone had 5.58 flushes. Ten genotypes had significantly higher number of leaf flushes and nine genotypes had significantly lower number of flushes compared to the control. All the remaining genotypes were found to be on par with the control (Tables 8 and 9).

In the fourth quarter, the number of leaf flushes per plant had the maximum mean value of 9.12 flushes for the genotype RO 894 followed by 9.08 flushes for RO 395, 9.02 for RO 859, 8.98 for RO 319 and 8.92 for RO317. The genotype MT 906 had the minimum value of 4.89 leaf flushes per plant. When the control clone RRII 105 had an average of 6.78 flushes, only 12 genotypes had a significantly higher number of leaf flushes, while 11 genotypes were found to have very low number of leaf flushes compared to the control. The rest of the genotypes were on par with control (Tables 8 and 9).

In the first quarter, RO 395 recorded the maximum number of leaves with 35.34 leaves per plant followed by RO 322, RO 311 and RO 317 all with 32.20 leaves and MT 1025 with 31.70 leaves. MT 929 had the lowest number of 12.80 leaves and the control clone had a mean value of 19.60 leaves. Nineteen genotypes had significantly higher number of leaves compared to the control while all the remaining genotypes were on par with it (Tables 8 and 9).

The maximum number of leaves per plant in the second quarter was recorded in RO 322 (61.60 leaves), with the genotypes RO 395, RO 319, RO 894 and RO 352 following with their mean values 59.70, 57.10, 56.30 and 55.10 in that order. MT 929 had the lowest number of 22.50 leaves, while the control clone had an average of 30.10 leaves. Twenty-nine genotypes were having significantly higher number of leaves compared to the control while the rest of the genotypes were on par with it (Tables 8 and 9).

In the third quarter also RO 322 had the maximum number of leaves (83.60). RO 894 with 80.50 leaves, RO 395 with 78.50 leaves, RO 317 with 74.40 leaves and MT 1025 with 73.40 leaves followed. The lowest value (29.70) was recorded in the genotype MT 929 again, while the control had an average of 44.52 leaves. Twenty-one genotypes had their average number of leaves significantly higher than the control while the rest of the genotype except one (MT 929) had their mean values on par with the control (Tables 8 and 9).

RO 322 continued to have the maximum number of leaves per plant in the fourth quarter also (119.80 leaves) followed by the genotypes RO 894 (116.20), RO 395 (107.00), AC 654 (100.30) and RO 859 (99.20) while the genotype MT 929 had the minimum number of leaves per plant (41.20). Seventeen genotypes were found to have significantly higher number of leaves per plant than that of the control clone which had an average of 62.80 leaves per plant. Apart from MT 929, genotypes AC 627 and MT 906 also had very low number of leaves per plant. Number of leaves in the other genotypes was on par with that of the control clone (Tables 8 and 9).

The majority of the wild genotypes had their leaf flushes placed more distantly than the popular control clone RRII 105 as evidenced by the higher average inter-flush distance of 19.81 cm in the wild genotypes compared to that of the control clone (12.74 cm). The inter-flush distance of sixteen wild clones were on par with the control. The rest of the genotypes had a higher inter flush distance significantly different from that of the control clone. Among the wild genotypes RO 399 had the minimum inter flush distance of 13.86 cm while MT 901 had the maximum distance between the leaf flushes (28.46 cm) followed by RO 328 (25.37cm), MT 906 (25.09 cm), RO 879 (25.01 cm) and MT 1055 (24.99 cm) (Tables 8 and 9).

The petiole length was found to be the maximum in the genotype RO 886 with 32.47 cm, while the shortest petiole of 13.03 cm was for the genotype MT 1064 (Table 8). The genotype RO 886 was followed, in the order, by RO 256, RO 311, RO287 and RO 876 with their petiole lengths 32.34 cm, 31.96 cm, 29.82 cm and 29.47 cm respectively. While 32 genotypes had a significantly higher petiole length than that of the control clone (14.59 cm), rest of the genotypes were on par with the control (Table 9).

The total leaf area was the highest for the genotype RO 322 (28683.45 cm^2) followed by RO 395 (22780.31 cm^2), MT 1025 (21571.29 cm^2), AC 1043 (21248.44 cm^2) and MT 944 (21036.32 cm^2), while the genotype MT 929 had the lowest total leaf area (4583.39cm^2). Twenty three genotypes had a significantly higher total leaf area than the control clone which had a total leaf area of 7675.35 cm^2. The total leaf area of all the other clones was not significantly different from the control (Tables 8 and 9).

Table 8. Range and general mean of growth characters in comparison with control.

Character	Range				General mean	Control RRII 105
	Minimum	Genotype	Maximum	Genotype		
Girth- first quarter (cm)	1.88	MT 929	3.94	RO322	2.84	2.08
second quarter (cm)	2.51	MT929	5.56	RO395	3.87	2.81
third quarter (cm)	3.38	MT929	7.62	RO322	5.37	4.05
fourth quarter (cm)	4.72	MT929	10.41	RO322	7.38	6.06
Height- first quarter (cm)	41.76	MT929	125.77	RO395	71.99	43.43
second quarter (cm)	59.75	MT929	189.35	RO395	112.51	73.48
third quarter (cm)	71.72	MT929	235.82	RO395	140.84	87.69
fourth quarter (cm)	100.89	MT929	322.99	RO395	191.98	145.70
No of LW - first quarter	2.20	MT929	3.85	RO395	2.95	2.94
second quarter	3.33	AC1090	5.97	RO319	4.36	4.13
third quarter	4.07	AC1090	7.40	RO319	5.53	5.58
fourth quarter	4.89	MT906	9.12	RO894	6.73	6.78
T. no of leaves-first quarter	12.80	MT 929	35.34	RO395	22.70	19.60
second quarter	22.45	MT929	61.60	RO322	38.20	30.10
third quarter	29.70	MT 929	83.60	RO322	51.60	44.50
fourth quarter	41.20	MT 929	119.80	RO322	69.80	62.80
Total leaf area (cm^2) *	4583.39	MT929	28683.5	RO322	11836.97	7675.35
Leaf area index *	0.08	MT929	0.46	RO322	0.19	0.13
Inter flush distance (cm) *	13.86	RO399	28.46	MT901	19.81	12.74
Petiole length (cm) *	13.03	MT1064	32.47	RO886	21.86	14.59

* - fourth quarter only

LW = Leaf whorls; T = Total

Table 9. Mean genotypic performance for the growth characters during the first year.

Sl.No	Genotype	Character: Girth (cm)				Height (cm)			
		Quarter 1	Quarter 2	Quarter 3	Quarter 4	Quarter 1	Quarter 2	Quarter 3	Quarter 4
(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)
1	AC 426	2.49	3.26	4.16	5.44	54.98	76.11	94.33	121.22
2	AC 453	3.48	4.40	6.31	8.31	78.62	116.73	131.33	187.37
3	AC 604	2.62	3.41	4.94	7.09	56.72	86.4	118.17	181.19
4	AC 626	2.72	3.48	4.85	6.78	62.29	85.38	113.87	160.39
5	AC 627	2.85	3.80	5.05	7.37	64.72	102.1	114.3	177.87
6	AC 629	2.55	3.59	4.60	5.79	56.2	90.62	106.93	147.06
7	AC 632	2.87	3.99	5.27	7.31	67.1	109.07	128.75	198.75
8	AC 644	2.27	3.01	4.14	6.05	63.99	97.39	117.92	150.07
9	AC 647	2.65	3.60	4.94	6.86	56.51	91.51	113.4	156.92
10	AC 650	2.73	4.07	5.63	7.66	57.87	103.75	137.99	183.45
11	AC 654	3.41	4.74	6.77	9.44	86	129.2	162.71	235.21
12	AC 657	3.36	4.79	6.49	8.67	64.92	107.01	143.85	196.83
13	AC 694	2.86	3.82	5.10	7.73	71.43	121.28	137.8	183.93
14	AC 706	2.71	3.64	4.79	6.44	58.13	90.58	109.44	144.05
15	AC 733	2.64	3.77	5.10	7.19	58.1	95.41	114.37	154.56
16	AC 754	2.56	3.58	4.72	6.93	64.25	100.48	127.73	162.83
17	AC 953	3.09	4.18	5.55	7.90	76.22	101.58	124.02	169.63
18	AC 959	3.11	3.96	5.37	7.08	65.23	87.91	125.82	171.84
19	AC 963	2.70	3.14	4.24	5.98	58.36	77.9	89.21	123.21
20	AC 966	2.62	3.48	5.07	7.22	70.56	112.11	136.76	195.61
21	AC 979	2.82	3.80	5.22	6.92	64.76	113.93	134.92	170.77
22	AC 986	2.51	3.48	4.62	7.07	58.6	97.95	132.93	188.51
23	AC 995	3.16	4.25	5.76	7.62	66.98	114.67	131.6	167.9
24	AC 1043	3.58	4.71	6.95	9.31	82.38	128.85	159.3	234.89
25	AC 1090	3.17	4.20	5.63	7.18	66.46	122.13	137.44	184.25
26	RO 254	2.92	3.84	5.07	6.45	85.15	135.8	165.44	218.65
27	RO 255	3.22	4.19	5.99	8.42	90.19	140.77	170.34	221.06
28	RO 256	2.99	4.06	5.80	7.35	68.83	121.03	134.33	153.66
29	RO 257	2.76	3.58	4.71	5.56	66.99	94.99	103.42	121.83
30	RO 287	2.88	3.96	5.96	8.17	76.41	128.31	163.73	217.67
31	RO 311	3.39	4.58	6.11	8.08	92.36	138.37	173.86	237.78
32	RO 316	3.20	4.54	6.13	8.07	84.87	129.18	164.22	194.59
33	RO 317	3.49	4.79	6.85	9.20	98.4	149.36	189.76	242.26
34	RO 319	3.67	5.14	7.28	9.53	96.71	165.47	200.39	260.43
35	RO 322	3.94	5.37	7.62	10.41	104.17	160.77	202.07	280.73
36	RO 328	3.43	4.74	6.19	9.39	100.4	163.07	210.85	316.09
37	RO 330	2.61	3.77	5.33	7.92	74.47	110.54	142.42	214.03
38	RO 338	3.09	4.49	6.29	8.90	90.22	144.44	176.83	257.12

Table 9. Continued

(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)
39	RO 352	3.33	4.58	6.36	8.29	101.79	144.23	175.37	253.55
40	RO 364	3.36	4.53	6.33	8.38	101.69	152.44	192.02	262.87
41	RO 369	2.14	3.18	4.45	6.40	64.18	100.3	134.07	167.98
42	RO 380	2.90	4.11	5.61	7.18	71.63	109.89	129.06	182.29
43	RO 381	2.26	3.25	4.65	6.35	58.29	97.11	115.53	148.31
44	RO 395	3.75	5.56	7.49	9.98	125.77	189.35	235.82	322.99
45	RO 399	2.43	3.16	4.56	6.38	64.59	89.73	107.38	159.99
46	RO 859	2.74	3.99	5.94	8.65	76.13	116.01	154.03	243.34
47	RO 868	2.89	3.87	5.24	7.63	65.47	102.98	138.97	200.46
48	RO 876	2.77	3.84	5.45	7.90	63.68	120.1	150.69	223.24
49	RO 879	3.06	4.27	6.08	8.79	85.93	136.8	170.16	239.81
50	RO 883	2.93	4.08	5.66	7.68	63.55	116.62	152.96	213.57
51	RO 886	3.18	4.26	5.90	8.04	70.26	122.99	148.54	187.24
52	RO 894	2.84	4.01	6.04	9.01	59.4	109.7	145.79	219.58
53	MT 899	2.62	3.52	5.35	7.39	67.81	110.83	143.69	199.11
54	MT 901	2.82	4.35	6.04	8.02	87.24	128.26	174.96	213.57
55	MT 906	2.65	3.66	4.92	6.58	73.28	120.85	134.04	164.79
56	MT 920	3.00	3.86	5.72	7.66	71.18	112.16	136.17	188.57
57	MT 928	2.41	3.06	4.57	6.33	64.48	92.73	131.26	164.74
58	MT 929	1.88	2.51	3.38	4.72	41.76	59.75	71.72	100.89
59	MT 931	2.39	3.41	4.78	6.55	71.55	110.45	136.83	206.19
60	MT 935	3.83	4.75	6.69	9.02	89.15	128.92	174.34	236.3
61	MT 944	3.52	4.56	6.38	9.03	96.72	139.13	179.21	249.36
62	MT 945	1.96	2.61	3.77	5.47	50.93	76.31	101.16	138.17
63	MT 947	3.27	4.66	6.70	8.41	81.15	118.22	155.95	197.77
64	MT 948	2.61	3.46	5.27	7.83	70	104.09	137.57	210.35
65	MT 1005	2.36	3.21	4.46	6.43	60.41	95.98	120.66	161.41
66	MT 1007	2.38	3.17	4.07	4.84	84.54	115.09	134.13	143.29
67	MT 1008	2.24	3.17	3.89	4.83	56.89	89.32	104.19	139.51
68	MT 1011	2.37	3.19	4.33	6.08	58.68	85.21	105.8	142.88
69	MT 1021	2.37	3.23	4.63	6.66	53.64	84.75	113.25	149.38
70	MT 1024	2.95	3.95	5.45	7.78	70.40	112.39	145.6	215.03
71	MT 1025	3.66	4.93	6.99	9.45	105.31	152.74	197.78	270.72
72	MT 1028	2.58	3.59	4.80	6.90	65.17	114.82	131.15	183.73
73	MT 1029	2.59	3.24	4.17	5.19	63.73	99.39	115.36	143.98
74	MT 1030	3.19	4.37	6.42	8.46	72.08	132.22	188.85	272.19
75	MT 1031	2.49	3.33	4.64	6.80	62.24	94.72	121.97	155.21
76	MT 1055	2.52	3.46	4.69	6.66	82.55	118.28	152.77	171.5
77	MT 1057	2.38	3.29	4.36	6.05	62.87	90.33	119.61	153.93
78	MT 1063	2.69	3.35	4.49	6.27	57.96	87.18	108.3	165.17
79	MT 1064	2.44	3.45	5.06	6.50	71.3	108.09	147.62	178.39
80	MT 1077	2.35	3.49	4.76	6.27	61.9	107.15	143.18	179.28
81	RRII 105	2.06	2.81	4.05	6.06	43.43	73.48	87.69	145.70
	Gl mean	2.84	3.87	5.37	7.38	71.99	112.51	140.84	191.98

Table 9. Continued

Sl.No.	Genotype	Character							
		Number of leaf flushes per plant				Total number of leaves per plant			
		Quarter 1	Quarter 2	Quarter 3	Quarter 4	Quarter 1	Quarter 2	Quarter 3	Quarter 4
(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)
1	AC 426	2.62	3.61	4.58	5.42	18.10	26.80	36.90	49.80
2	AC 453	3.38	4.93	5.82	7.15	27.10	45.10	54.30	72.90
3	AC 604	3.09	4.51	5.85	7.22	20.20	36.10	52.60	78.10
4	AC 626	3.25	4.70	5.59	6.61	21.50	34.40	45.20	61.40
5	AC 627	2.52	3.65	4.58	5.15	17.70	29.10	35.10	42.60
6	AC 629	3.25	4.19	5.16	6.41	19.00	29.50	40.10	59.70
7	AC 632	2.74	3.96	5.08	6.60	22.10	35.20	46.60	70.30
8	AC 644	2.63	3.74	4.63	5.46	15.80	26.20	36.10	46.70
9	AC 647	2.64	3.83	4.81	5.69	19.60	33.30	44.20	59.00
10	AC 650	2.71	3.85	5.07	6.10	20.50	35.40	51.30	74.30
11	AC 654	3.11	4.76	6.02	7.56	29.80	49.90	67.60	100.30
12	AC 657	2.91	4.11	5.18	6.61	25.90	40.90	57.40	84.80
13	AC 694	2.69	4.11	5.28	6.67	24.30	39.70	52.70	72.90
14	AC 706	3.02	4.15	5.33	6.14	20.40	30.50	42.40	54.10
15	AC 733	2.85	4.37	5.36	6.15	23.80	41.10	52.50	64.90
16	AC 754	3.00	4.42	5.21	6.21	23.80	38.20	47.40	62.00
17	AC 953	2.93	4.00	5.00	6.06	22.20	32.80	41.50	59.00
18	AC 959	2.87	4.14	5.23	6.32	22.20	36.70	48.60	71.10
19	AC 963	2.70	3.75	4.65	5.77	17.40	27.20	33.80	46.60
20	AC 966	2.66	4.02	5.36	6.55	20.10	36.10	52.30	70.00
21	AC 979	2.55	3.79	4.78	5.80	18.20	32.60	42.00	57.70
22	AC 986	2.82	3.81	5.16	6.42	21.10	30.60	47.30	65.00
23	AC 995	2.85	4.06	4.92	5.67	21.40	31.20	41.50	54.80
24	AC 1043	3.14	4.63	5.94	7.40	30.50	50.80	70.40	97.70
25	AC 1090	2.24	3.33	4.07	5.03	17.80	29.00	35.60	48.50
26	RO 254	3.53	4.88	6.32	7.70	27.70	42.10	55.00	71.70
27	RO 255	2.90	4.60	5.83	6.96	21.20	39.90	55.20	74.00
28	RO 256	2.74	4.07	5.35	5.57	24.70	39.00	52.40	63.30
29	RO 257	2.97	4.08	4.54	5.45	22.20	31.40	34.60	43.90
30	RO 287	2.86	4.29	5.61	6.99	19.30	35.50	48.90	66.60
31	RO 311	3.03	4.28	5.36	6.60	32.20	50.20	64.60	77.90
32	RO 316	3.05	4.37	5.90	7.53	27.20	43.60	60.10	85.80
33	RO 317	3.75	5.58	7.33	8.92	32.20	52.10	74.40	97.30
34	RO 319	3.72	5.97	7.40	8.98	29.80	57.10	72.60	96.80
35	RO 322	3.34	5.17	6.40	7.91	33.20	61.60	83.60	119.80
36	RO 328	3.08	4.76	6.11	8.15	23.30	42.70	62.10	89.70
37	RO 330	2.95	4.10	5.14	6.46	23.80	38.30	51.90	73.70
38	RO 338	3.22	4.81	6.25	7.98	26.30	48.10	64.30	92.50

Table 9. Continued

(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)
39	RO 352	3.31	5.35	6.83	8.36	30.10	55.10	71.40	94.40
40	RO 364	3.38	5.32	6.59	8.14	28.50	50.80	64.30	86.80
41	RO 369	2.83	4.09	5.37	6.23	20.10	35.10	49.10	61.40
42	RO 380	2.97	4.23	5.03	5.89	21.70	35.60	43.40	57.10
43	RO 381	2.44	4.44	5.41	6.56	18.30	37.70	45.60	59.60
44	RO 395	3.85	5.87	7.32	9.08	35.30	59.70	78.50	107.00
45	RO 399	3.17	4.52	5.61	6.95	26.00	40.40	55.40	73.20
46	RO 859	3.50	5.39	7.05	9.02	28.20	50.90	68.90	99.20
47	RO 868	2.97	4.76	6.11	7.59	22.30	38.60	54.60	78.70
48	RO 876	3.17	5.07	6.18	7.92	19.80	40.00	54.70	77.80
49	RO 879	3.05	4.71	5.78	6.99	23.70	39.10	51.50	70.50
50	RO 883	3.09	5.22	6.81	8.39	21.20	40.60	58.50	80.70
51	RO 886	3.11	4.84	5.62	6.65	24.70	46.70	55.70	71.40
52	RO 894	3.30	5.52	7.12	9.12	26.90	56.30	80.50	116.20
53	MT 899	2.70	4.09	5.51	6.64	18.80	35.20	50.80	65.70
54	MT 901	2.87	4.00	5.22	6.44	23.30	37.10	52.50	72.90
55	MT 906	2.64	3.69	4.54	4.89	18.40	28.60	36.30	41.60
56	MT 920	3.09	4.57	5.89	6.83	25.60	42.30	59.60	73.40
57	MT 928	3.15	4.51	5.87	6.81	21.20	33.20	48.80	62.90
58	MT 929	2.20	3.37	4.25	5.19	12.80	22.50	29.70	41.20
59	MT 931	2.85	4.20	5.35	6.81	19.60	32.90	44.10	64.10
60	MT 935	3.10	4.63	5.76	7.50	29.90	48.00	62.30	82.70
61	MT 944	3.11	4.61	5.72	7.25	24.60	44.70	60.50	82.70
62	MT 945	2.74	3.87	4.85	5.86	16.50	26.90	37.60	49.40
63	MT 947	3.29	4.90	6.45	7.80	29.50	48.90	68.50	88.20
64	MT 948	3.15	4.36	5.38	6.75	17.50	27.40	36.90	65.30
65	MT 1005	2.54	3.62	4.61	5.52	18.30	32.10	39.30	51.30
66	MT 1007	2.70	3.91	4.92	5.56	20.90	33.90	44.00	51.50
67	MT 1008	2.89	3.92	4.98	5.92	18.80	30.50	39.30	49.30
68	MT 1011	2.55	3.85	5.04	5.70	20.20	29.10	38.10	47.10
69	MT 1021	2.47	3.67	5.09	6.37	16.10	27.80	41.80	60.30
70	MT 1024	3.19	4.42	5.60	6.90	22.50	36.90	56.00	79.60
71	MT 1025	3.56	5.01	6.66	8.31	31.70	51.90	73.40	99.00
72	MT 1028	2.78	3.98	5.00	6.32	23.30	39.00	51.50	72.10
73	MT 1029	2.50	3.83	5.45	6.26	22.40	33.60	44.00	52.10
74	MT 1030	3.25	4.90	6.43	8.14	25.50	46.30	67.30	96.30
75	MT 1031	2.77	4.20	5.35	6.33	20.00	32.60	45.40	58.70
76	MT 1055	2.53	3.74	4.80	5.09	19.80	32.70	44.00	47.50
77	MT 1057	3.29	4.50	5.59	6.57	22.90	37.40	50.70	63.30
78	MT 1063	2.81	4.16	5.32	6.42	16.70	28.00	39.20	55.60
79	MT 1064	2.76	4.03	5.08	6.05	20.00	31.70	43.90	58.50
80	MT 1077	2.39	3.88	4.99	5.73	14.90	29.20	40.60	46.20
81	RRII 105	2.94	4.13	5.58	6.78	19.60	30.10	44.50	62.80
	Gl. Mean	2.95	4.36	5.54	6.73	22.70	38.20	51.60	69.80

Table 9. Continued

Character						
Sl.No	Genotype	Inter flush distance Quarter 4 (cm)	Petiole length Quarter 4 (cm)	Total leaf area Quarter 4 (cm^2)	Leaf area index Quarter 4	Test tap yield Quarter 4 ($g\ t^{-1}\ t^{-1}$)
(1)	(2)	(3)	(4)	(5)	(6)	(7)
1	AC 426	15.27	24.09	4965.50	0.08	0.082
2	AC 453	15.35	25.61	15367.08	0.25	0.037
3	AC 604	15.39	23.99	10162.55	0.16	0.033
4	AC 626	15.57	19.60	8563.85	0.14	0.087
5	AC 627	24.87	23.26	7378.90	0.12	0.032
6	AC 629	16.60	21.96	9824.53	0.16	0.032
7	AC 632	17.28	20.40	12432.90	0.20	0.048
8	AC 644	21.20	29.22	5235.31	0.09	0.030
9	AC 647	19.03	21.85	9161.88	0.15	0.127
10	AC 650	22.12	21.88	14391.99	0.23	0.065
11	AC 654	17.67	21.33	17517.75	0.28	0.083
12	AC 657	17.52	22.94	14963.75	0.24	0.075
13	AC 694	18.27	21.70	11563.93	0.19	0.042
14	AC 706	16.85	15.70	11116.02	0.18	0.035
15	AC 733	17.88	25.04	6508.01	0.10	0.035
16	AC 754	16.81	25.34	9270.87	0.15	0.088
17	AC 953	19.18	25.38	10026.65	0.16	0.010
18	AC 959	19.85	19.43	12812.21	0.20	0.070
19	AC 963	18.12	23.13	5027.23	0.08	0.052
20	AC 966	19.98	26.36	10547.04	0.17	0.020
21	AC 979	24.24	25.75	8788.23	0.14	0.050
22	AC 986	20.10	22.31	10797.79	0.17	0.013
23	AC 995	20.14	19.49	7782.94	0.13	0.017
24	AC 1043	19.27	26.19	21248.44	0.35	0.028
25	AC 1090	22.69	22.61	8457.28	0.14	0.062
26	RO 254	22.65	22.07	14103.35	0.23	0.017
27	RO 255	19.18	21.29	14886.57	0.24	0.082
28	RO 256	21.64	32.34	12433.44	0.20	0.077
29	RO 257	18.46	14.94	6032.72	0.10	0.028
30	RO 287	21.91	29.82	10819.68	0.18	0.140
31	RO 311	23.71	31.96	15131.70	0.24	0.065
32	RO 316	18.70	24.67	11960.11	0.19	0.050
33	RO 317	19.82	23.93	18598.09	0.30	0.045
34	RO 319	23.28	27.10	19068.81	0.31	0.007
35	RO 322	18.82	26.69	28683.45	0.46	0.063
36	RO 328	25.37	16.94	17678.40	0.28	0.068
37	RO 330	24.44	22.41	11636.89	0.19	0.030
38	RO 338	22.07	22.93	17571.33	0.28	0.195

Table 9. Continued

(1)	(2)	(3)	(4)	(5)	(6)	(7)
39	RO 352	19.27	22.88	17133.77	0.28	0.010
40	RO 364	19.35	23.25	12354.60	0.20	0.020
41	RO 369	18.25	21.93	9373.65	0.15	0.070
42	RO 380	20.02	19.45	7355.42	0.12	0.045
43	RO 381	19.27	21.82	8905.16	0.14	0.043
44	RO 395	22.84	21.64	22780.31	0.37	0.047
45	RO 399	13.86	19.31	11402.49	0.19	0.233
46	RO 859	15.16	19.52	17294.27	0.28	0.075
47	RO 868	15.87	24.72	10856.27	0.18	0.010
48	RO 876	21.34	29.47	12607.24	0.20	0.030
49	RO 879	25.01	22.29	10102.45	0.16	0.045
50	RO 883	18.54	14.25	13301.54	0.21	0.093
51	RO 886	23.70	32.47	13720.69	0.22	0.020
52	RO 894	14.99	19.84	18195.28	0.29	0.017
53	MT 899	23.13	16.91	10866.25	0.18	0.162
54	MT 901	28.46	19.25	12379.56	0.20	0.127
55	MT 906	25.09	19.25	6668.35	0.11	0.127
56	MT 920	19.70	19.04	14080.92	0.23	0.068
57	MT 928	17.46	18.46	7425.08	0.12	0.165
58	MT 929	18.26	16.64	4583.39	0.08	0.038
59	MT 931	18.51	18.82	8811.77	0.14	0.093
60	MT 935	19.50	18.52	14105.15	0.23	0.183
61	MT 944	24.49	19.16	21036.32	0.34	0.088
62	MT 945	17.64	21.37	7114.99	0.12	0.078
63	MT 947	16.26	19.56	16764.69	0.27	0.105
64	MT 948	23.79	20.17	11287.81	0.18	0.132
65	MT 1005	19.79	19.35	8279.90	0.13	0.158
66	MT 1007	17.33	18.88	6541.79	0.11	0.027
67	MT 1008	18.90	18.28	5355.63	0.09	0.033
68	MT 1011	20.58	14.69	6562.29	0.11	0.05
69	MT 1021	16.14	19.24	10232.98	0.17	0.115
70	MT 1024	20.89	19.93	8951.08	0.14	0.155
71	MT 1025	18.71	18.48	21571.29	0.35	0.078
72	MT 1028	19.36	19.68	12688.63	0.21	0.038
73	MT 1029	20.06	17.38	5705.37	0.09	0.032
74	MT 1030	22.58	28.55	15817.36	0.25	0.015
75	MT 1031	17.12	24.36	8514.06	0.14	0.065
76	MT 1055	24.99	17.10	7337.86	0.12	0.075
77	MT 1057	15.52	19.99	7831.67	0.13	0.225
78	MT 1063	17.16	17.40	7665.97	0.13	0.003
79	MT 1064	20.60	13.03	7870.94	0.13	0.190
80	MT 1077	21.54	16.90	6838.36	0.11	0.135
81	RRII 105	12.74	14.59	7675.35	0.13	0.163
	Gl.Mean	19.81	21.86	11836.97	0.19	0.070

Leaf area index was found to be the highest for the clone RO 322 with a value of 0.46 followed by RO 395 (0.37), MT 1025 (0.35), AC 1043 (0.35), and MT 944 (0.34) whereas the lowest index of 0.08 was exhibited by the genotype MT 929. Control clone had a leaf area index of 0.13. Twenty-three genotypes had a significantly higher leaf area index than the control clone and the rest was on par with the control (Tables 8 and 9)

3.2.2.2 Test tap yield over three years

The range and general mean values of the test tap yield recorded in the wild genotypes over three years compared to the control, is depicted in Table 10 and the individual mean yield of the 80 wild genotypes is given in Table 11.

The majority of the wild genotypes showed very low and significantly lower test tap yield. At the end of 18 months after planting, it was found that only two genotypes had significantly higher dry rubber yield than the control clone RRII 105. Genotype RO 399 had an yield of 0.2327 g t^{-1} t^{-1}, while MT 1057 had the second highest yield in the population with 0.2251 g t^{-1} t^{-1}. The control clone recorded a test tap yield of 0.1626 g t^{-1} t^{-1} and it was seen that 10 wild genotypes had their dry rubber yield on par with the control clone.

During the second year also, the test tap yield of majority of the wild clones was significantly lower than the control. Only two genotypes showed their superiority for yield

Table 10. Range and general mean of test tap yield of wild genotypes and control.

Character	Range				General mean	Control RRII 105
	Minimum	Genotype	Maximum	Genotype		
Dry rubber yield						
First year (g t^{-1} t^{-1})	0.0027	MT 1063	0.2327	RO 399	0.0716	0.1626
Second year (g t^{-1} t^{-1})	0.0208	RO 254	0.6358	MT 1057	0.1206	0.2986
Third year (g t^{-1} t^{-1})	0.0480	RO 257	4.2711	MT 1057	0.5273	2.3547

Table 11.Mean test tap yield of the wild genotypes and the control (g t^{-1} t^{-1})

Sl No	Genotype	First year	Second year	Third year
(1)	(2)	(3)	(4)	(5)
1	AC 426	0.0823	0.1042	0.1135
2	AC 453	0.0373	0.0491	0.1879
3	AC 604	0.0325	0.0425	0.2346
4	AC 626	0.0871	0.0992	0.8620
5	AC 627	0.0324	0.0825	0.2194
6	AC 629	0.0324	0.1143	0.1377
7	AC 632	0.0476	0.0573	0.3987
8	AC 644	0.0298	0.0478	0.0549
9	AC 647	0.1274	0.1556	0.7132
10	AC 650	0.0647	0.0971	0.1198
11	AC 654	0.0828	0.1250	0.2748
12	AC 657	0.0750	0.0893	0.3218
13	AC 694	0.0422	0.0662	0.5559
14	AC 706	0.0350	0.0515	0.1452
15	AC 733	0.0348	0.0523	0.1764
16	AC 754	0.0875	0.1205	0.3445
17	AC 953	0.0099	0.0214	0.0882
18	AC 959	0.0702	0.1454	0.1770
19	AC 963	0.0524	0.1170	0.1973
20	AC 966	0.0197	0.0340	0.0769
21	AC 979	0.0497	0.1370	0.3640
22	AC 986	0.0131	0.0215	0.3252
23	AC 995	0.0173	0.0385	0.3384
24	AC 1043	0.0276	0.0733	0.2268
25	AC 1090	0.0624	0.0943	0.2674
26	RO 254	0.0174	0.0208	0.0714
27	RO 255	0.0824	0.1234	0.3777
28	RO 256	0.0773	0.0984	0.3602
29	RO 257	0.0276	0.0328	0.0480
30	RO 287	0.1400	0.1808	1.0502
31	RO 311	0.0649	0.0893	0.5495
32	RO 316	0.0498	0.0714	0.1829
33	RO 317	0.0449	0.1036	0.8900
34	RO 319	0.0073	0.0301	0.1071
35	RO 322	0.0630	0.1550	1.2259
36	RO 328	0.0675	0.0835	0.5587
37	RO 330	0.0300	0.0335	0.2409
38	RO 338	0.1947	0.2676	0.7169
39	RO 352	0.0102	0.0624	0.2960
40	RO 364	0.0199	0.0455	0.3689

Table 11. Continued

(1)	(2)	(3)	(4)	(5)
41	RO 369	0.0700	0.0774	0.3516
42	RO 380	0.0449	0.0734	0.8515
43	RO 381	0.0427	0.0564	0.5727
44	RO 395	0.0473	0.0747	0.4773
45	RO 399	0.2327	0.2439	1.2785
46	RO 859	0.0753	0.1094	0.3809
47	RO 868	0.0099	0.0209	0.1348
48	RO 876	0.0304	0.0783	0.2421
49	RO 879	0.0449	0.0690	0.1254
50	RO 883	0.0925	0.1196	0.2839
51	RO 886	0.0196	0.0248	0.0548
52	RO 894	0.0172	0.0445	0.3542
53	MT 899	0.1624	0.2023	0.6088
54	MT 901	0.1273	0.1705	0.5516
55	MT 906	0.1274	0.1560	0.8114
56	MT 920	0.0680	0.1199	0.7776
57	MT 928	0.1651	0.2095	0.5156
58	MT 929	0.0375	0.0539	0.6719
59	MT 931	0.0926	0.1239	0.6238
60	MT 935	0.1828	0.2161	0.6100
61	MT 944	0.0878	0.1361	0.3628
62	MT 945	0.0776	0.0924	0.4070
63	MT 947	0.1051	0.1332	0.3925
64	MT 948	0.1322	0.1632	0.6941
65	MT 1005	0.1578	0.1641	0.8448
66	MT 1007	0.0274	0.0551	0.1158
67	MT 1008	0.0326	0.1861	0.8875
68	MT 1011	0.0503	0.2526	0.5080
69	MT 1021	0.1153	0.5606	2.0905
70	MT 1024	0.1550	0.2582	1.1251
71	MT 1025	0.0777	0.2624	1.1793
72	MT 1028	0.0375	0.0507	0.3355
73	MT 1029	0.0323	0.0510	0.1787
74	MT 1030	0.0149	0.1465	1.0045
75	MT 1031	0.0651	0.1173	0.3650
76	MT 1055	0.0751	0.1079	0.1588
77	MT 1057	0.2251	0.6358	4.2711
78	MT 1063	0.0027	0.0583	0.4180
79	MT 1064	0.1902	0.2188	0.8019
80	MT 1077	0.1351	0.1419	0.6930
81	RRII 105	0.1626	0.2986	2.3547
	Gl mean	0.0716	0.1206	0.5273

over the control with MT 1057 giving a dry rubber yield of 0.6358 g t^{-1} t^{-1} and MT 1021 an yield of 0.5606 g t^{-1} t^{-1}, compared to the yield of the control (0.2986 g t^{-1} t^{-1}). Fourteen other genotypes showed better yield which were statistically on par with the control clone.

In the third year of test tapping, done 42 months after planting, the wild genotypes showed a similar trend in their dry rubber yield, with the majority of the genotypes giving a very low yield compared to the control. Only one genotype, MT 1057 yielded a significantly higher dry rubber yield of 4.2711 g t^{-1} t^{-1}, almost double the yield of the control clone RRII 105 (2.3547 g t^{-1} t^{-1}). The genotype MT 1021 however with its dry rubber yield of 2.094 g t^{-1} t^{-1} was statistically on par with RRII 105.

3.2.2.3 Leaf structural characters

The range and general mean values for the leaf structural characters including single leaflet area, in comparison with the control are shown in Table 12 while Table 13 gives the individual mean of the wild genotypes for these characters.

The number of stomata per mm^2 on the abaxial epidermis of the leaflet, 42 months after planting, showed that the majority of the wild genotypes had a significantly lower value than the control clone. Only two genotypes showed significantly higher stomatal counts than the control, with the genotype MT 928 showing a count of 612.67 per mm^2 followed by AC 754 (587.59). The stomatal count of genotypes RO 255, MT 1005, AC 627, MT 1077, RO 317, MT 1055, AC 1090, AC 644, AC 966, AC 733, AC 706, MT 920 and MT 944 was on par with that of the control (Tables 12 and 13).

Number of epidermal cells per mm^2 of the abaxial epidermis also showed a similar trend. The genotypes, RO 369 (2741.23), MT 928 (2539.73), AC 453 (2433.21), MT 944 (2376.31), MT 1005 (2348.96) showed a higher significant difference than the control clone, with 2237.76 cells per mm^2 of the epidermis. Number of epidermal cells for the genotypes MT 1031 (2159.05) and RO 399 (2225.00) was on par with RRII 105, the control clone (Tables 12 and 13).

Stomatal index of the wild genotypes studied showed significant differences from the control clone for 38 genotypes while the rest of the genotypes were on par with the control,

which had an index of 19.26. The genotype AC 966 had the highest stomatal index of 27.43 followed by MT 1077 (27.14), RO 883 (26.70), AC 706 (26.43) and AC 986 (25.94). RO 369 had the lowest stomatal index of 10.81 (Tables 12 and 13).

The single leaflet area of the wild genotypes, showed that about half of the genotypes had significantly larger leaves than the control clone. Forty-one genotypes showed their single leaflet area to be significantly higher than the control clone, which had a single leaflet area of 60.83 cm^2. The rest of the genotypes were on par with the control clone. Largest single leaflet was seen in RO 311 (189.58 cm^2) and the smallest leaflet with an area of 59.94 cm^2 was in MT 1057. AC 453 (157.62 cm^2), RO 876 (133.77 cm^2), RO 322 (121.88 cm^2) and AC 1043 (121.88 cm^2) followed RO 311, in that order for their single leaflet area (Tables 12 and 13).

The thickness of lamina in wild genotypes studied had a maximum value of 0.1760 mm for AC 953 followed by the genotypes MT 944 with 0.1675 mm, MT 945 with 0.1660 mm, MT 1008 with 0.1620 mm and RO 876 with 0.1613 mm thickness. The minimum thickness was shown by the genotype RO 380 (0.1107 mm). A total of 13 genotypes showed their mean lamina thickness statistically higher than that of the control clone (0.1490 mm). Twelve wild genotypes had their mean leaf blade thickness statistically on par with the control clone. Rest of the wild genotypes had a significantly lower lamina thickness than the control (Tables 12 and 13).

Thickness of the leaflet midrib, measured from the cross section, showed the maximum thickness of 1.3220 mm for the genotype AC 754 followed by 1.0380 mm for AC 953, 0.9930 mm for AC 995, 0.9530 mm for AC 650 and 0.9500 mm for AC 1090. The genotype MT 901 recorded the minimum thickness of 0.6300 mm. The control clone had a mean thickness of 0.6950 mm. 27 genotypes were on par with the control for this character. Forty-seven genotypes had significantly higher values compared to the control. Six genotypes had their leaflet midrib thickness significantly lower from the control (Tables 12 and 13).

Thickness of the palisade layer was the maximum in RO 369 (81.00 μm) followed by the genotypes MT 1008 (79.70 μm), RO 395 (77.64 μm), AC 654 (74.62 μm) and AC

632 (74.26 μm). Only these five genotypes had a statistically significant difference on the higher side than the control clone, while only another 6 genotypes had their mean palisade thickness on par with the control. Rest of the genotypes had a much thinner palisade than the control clone (70.87 μm) with the minimum value of 42.57 μm for the genotype RO 380 (Tables 12 and 13).

In the case of thickness of the spongy tissue also majority of the genotypes, were having significantly lower values than the control clone. The maximum value was shown by the genotype AC 966 (93.50 μm) followed by AC 754 (86.25 μm), MT 947 (82.50 μm), RO 876 (81.00 μm) and MT 935 (76.50 μm). Of this, only the genotypes AC 966 and AC 754 had a significantly higher spongy tissue thickness than the control, while 25 genotypes showed their mean thickness on par with their control (75.49 μm). The genotype RO 859 had the minimum value of 45.00 μm as the thickness of its spongy tissue (Tables 12 and 13).

Number of cells per mm of palisade layer was found to be the highest for the genotype RO 352 (134.34) followed by the genotypes RO 859 (132.66), RO 399 (132.58), RO 330 (130.16) and AC 986 (129.35). The genotype RO 257 had the minimum number (100.62) of cells per mm length of palisade layer. Twenty wild genotypes had significantly higher and 24 genotypes had significantly lesser number of cells per unit length of palisade layer, compared to the control (117.24). 36 genotypes were on par with the control (Tables 12 and 13).

Number of cells per mm length of spongy layer was the maximum for the genotype AC 650 (417.06) followed by RO 338 (379.11), AC 986 (368.76), MT 944 (365.21) and RO 330 (351.22). The minimum value was recorded for the genotype AC 706 (189.24). The control clone had a value of 232.24. 16 genotypes had significantly lower number of cells. But the majority of the genotypes (64 genotypes) had significantly higher values than the control (Tables 12 and 13).

Thickness of the cuticle was found to vary from the maximum value of 4.27 μm for the genotype MT 945 to a minimum of 1.22 μm for MT 935. Four clones, MT 1025 (3.72 μm), AC 963 (3.70 μm), AC 647(3.70 μm) and MT 1031 (3.63 μm) followed the genotype

Table 12. Range and general mean of leaf structural characters in the third year.

Character	Range				Gl. Mean	Control RRII 105
	Minimum	Genotype	Maximum	Genotype		
No of stomata / mm^2 leaf area	281.16	MT1028	612.67	MT 928	433.87	525.30
No of epidermal cells/mm^2 LA	1132.84	MT1028	2741.23	RO369	1711.50	2237.76
Stomatal Index	10.81	RO369	27.43	AC966	20.63	19.26
Single leaflet area (cm^2)	59.94	MT1057	189.58	RO311	95.23	60.83
Thickness of lamina (mm)	0.1107	RO380	0.1760	AC953	0.1371	0.1490
Thickness of leaf midrib (mm)	0.6300	MT901	1.3220	AC754	0.7850	0.6950
Thickness of palisade L. (µm)	42.57	RO380	81.01	RO369	60.58	70.87
Thickness of spongy L. (µm)	45.00	RO859	93.50	AC966	61.71	75.49
No of cells / mm palisade L.	100.62	RO257	134.34	RO352	117.03	117.24
No of cells / mm spongy L.	189.24	AC706	417.06	AC650	273.95	232.24
Thickness of cuticle (µm)	1.22	MT935	4.27	MT945	2.57	3.67

LA = Leaf area; L = layer

Table 13. Mean values for the leaf structural characters in the third year.

Sl No.	Genotype	No of stomata per mm^2 leaf area	No of epidermal cells per mm^2 leaf area	Single leaflet area (cm^2)	Stomatal index
(1)	(2)	(3)	(4)	(5)	(6)
1	AC 426	362.42	1224.07	100.36	22.76
2	AC 453	443.72	2433.21	157.62	15.47
3	AC 604	393.68	1184.70	97.00	24.87
4	AC 626	375.05	1240.40	90.72	23.18
5	AC 627	481.27	1984.05	100.01	19.55
6	AC 629	387.45	1273.51	94.45	23.32
7	AC 632	362.41	1539.94	94.21	19.02
8	AC 644	531.24	1800.75	91.16	22.77
9	AC 647	312.40	1694.32	90.49	15.50
10	AC 650	456.32	1543.00	92.43	22.84
11	AC 654	381.38	1552.41	89.59	20.27
12	AC 657	468.73	2072.02	100.15	18.41
13	AC 694	399.97	1334.70	110.10	23.04
14	AC 706	493.86	1372.02	90.13	26.43
15	AC 733	487.48	1655.69	97.00	22.80
16	AC 754	587.59	2060.35	100.47	22.19
17	AC 953	399.95	1768.75	110.83	18.43
18	AC 959	456.18	1682.74	96.41	21.41
19	AC 963	437.41	1702.90	104.03	20.39
20	AC 966	493.76	1280.13	106.54	27.43
21	AC 979	431.37	1473.78	95.42	22.74
22	AC 986	424.94	1218.09	85.92	25.94
23	AC 995	474.93	1530.69	100.64	23.76
24	AC 1043	456.36	2119.30	121.88	17.70
25	AC 1090	487.54	1704.10	98.78	22.28
26	RO 254	368.79	1649.17	100.06	18.23
27	RO 255	500.23	2016.87	107.49	20.32
28	RO 256	412.55	1832.37	108.05	18.33
29	RO 257	368.62	1751.49	93.76	17.45
30	RO 287	437.40	1498.51	111.56	22.65
31	RO 311	337.46	1627.25	189.58	17.16
32	RO 316	431.18	1647.95	88.87	20.66
33	RO 317	531.10	2124.63	95.43	20.18
34	RO 319	462.59	1868.56	96.68	19.90
35	RO 322	468.71	1973.51	121.88	19.14
36	RO 328	450.02	1551.96	82.26	22.61
37	RO 330	362.61	1945.06	85.43	15.94
38	RO 338	425.17	1374.16	94.63	23.68

Table 13. Continued

(1)	(2)	(3)	(4)	(5)	(6)
39	RO 352	456.18	1422.20	91.38	24.22
40	RO 364	443.75	1288.90	101.11	25.75
41	RO 369	331.28	2741.23	82.86	10.81
42	RO 380	381.19	1319.68	90.97	22.43
43	RO 381	393.70	1281.91	98.97	23.35
44	RO 395	462.45	1481.91	113.62	23.89
45	RO 399	381.27	2225.00	118.44	14.68
46	RO 859	412.40	1958.86	113.73	17.40
47	RO 868	387.55	1321.65	111.91	22.55
48	RO 876	406.09	1538.43	133.77	20.83
49	RO 879	475.04	1730.59	94.16	21.58
50	RO 883	537.33	1471.83	112.09	26.70
51	RO 886	431.36	1747.02	120.71	19.78
52	RO 894	412.53	1430.69	89.03	22.40
53	MT 899	449.91	1395.06	70.14	24.43
54	MT 901	456.23	1456.64	90.59	23.67
55	MT 906	431.25	2050.94	82.28	17.55
56	MT 920	531.11	1909.05	83.81	21.79
57	MT 928	612.67	2539.73	61.39	19.76
58	MT 929	425.00	1882.56	68.45	18.36
59	MT 931	337.50	1973.98	70.79	14.73
60	MT 935	462.53	1481.90	85.30	23.88
61	MT 944	549.94	2376.31	120.34	18.93
62	MT 945	456.27	1535.65	73.43	22.78
63	MT 947	443.62	1881.25	91.46	19.23
64	MT 948	400.02	2085.65	95.01	16.05
65	MT 1005	500.21	2348.96	84.93	17.67
66	MT 1007	437.41	1374.81	68.14	24.16
67	MT 1008	450.21	2000.92	78.18	18.85
68	MT 1011	443.98	2085.62	80.61	18.44
69	MT 1021	399.92	1757.00	77.56	18.54
70	MT 1024	356.44	1662.86	95.10	18.17
71	MT 1025	412.54	1486.67	99.72	21.67
72	MT 1028	281.16	1132.84	90.14	19.81
73	MT 1029	418.84	1925.29	73.08	17.96
74	MT 1030	306.10	1816.89	89.63	14.41
75	MT 1031	418.70	2159.05	89.78	16.27
76	MT 1055	481.22	1753.45	80.88	21.53
77	MT 1057	437.47	1364.46	59.94	24.19
78	MT 1063	368.71	1448.51	82.79	20.19
79	MT 1064	343.60	1761.20	80.29	16.33
80	MT 1077	549.95	1479.29	64.58	27.14
81	RRII 105	525.30	2237.76	60.83	19.26
	Gl mean	433.87	1711.50	95.23	20.63

Tabel 13. Continued.

Sl No.	Genotype	Thickness of lamina (mm)	Thickness of leaf midrib (mm)	Thickness of palisade tissue (µm)	Thickness of spongy tissue (µm)
(1)	(2)	(3)	(4)	(5)	(6)
1	AC 426	0.1217	0.7400	53.4410	60.5310
2	AC 453	0.1333	0.7950	57.3810	56.0100
3	AC 604	0.1330	0.8900	56.2710	69.5100
4	AC 626	0.1213	0.7120	58.8890	50.0320
5	AC 627	0.1359	0.7600	53.6280	54.7540
6	AC 629	0.1305	0.8750	58.1350	64.2600
7	AC 632	0.1530	0.7120	74.2570	67.4920
8	AC 644	0.1165	0.7730	42.7590	59.2750
9	AC 647	0.1437	0.7130	67.3200	66.9990
10	AC 650	0.1470	0.9530	56.0450	73.7190
11	AC 654	0.1585	0.8400	74.6240	68.7420
12	AC 657	0.1240	0.7900	60.0230	50.4980
13	AC 694	0.1201	0.8750	55.6890	56.5020
14	AC 706	0.1335	0.9320	61.6670	73.2490
15	AC 733	0.1312	0.7920	64.3030	56.5030
16	AC 754	0.1600	1.3220	63.1820	86.2500
17	AC 953	0.1760	1.0380	67.6930	74.7520
18	AC 959	0.1340	0.8270	60.5730	56.5050
19	AC 963	0.1332	0.6500	45.3740	64.4750\
20	AC 966	0.1305	0.7830	44.9960	93.4970
21	AC 979	0.1364	0.7180	54.1880	68.0260
22	AC 986	0.1498	0.8220	53.4190	65.7490
23	AC 995	0.1520	0.9930	68.9830	69.7170
24	AC 1043	0.1342	0.6550	66.5610	66.7490
25	AC 1090	0.1225	0.9500	52.8670	47.5040
26	RO 254	0.1253	0.7100	56.4650	54.5050
27	RO 255	0.1213	0.7150	63.1960	51.0000
28	RO 256	0.1345	0.6600	58.8710	61.2480
29	RO 257	0.1290	0.7300	56.8040	53.4940
30	RO 287	0.1480	0.7150	62.4500	58.2530
31	RO 311	0.1438	0.6780	69.7630	66.4940
32	RO 316	0.1320	0.8730	58.3000	56.9750
33	RO 317	0.1308	0.8570	63.5540	62.0010
34	RO 319	0.1487	0.7950	58.1300	69.0040
35	RO 322	0.1150	0.7050	52.8420	53.2480
36	RO 328	0.1337	0.6330	60.0320	61.2540
37	RO 330	0.1462	0.7650	69.3890	65.2480
38	RO 338	0.1604	0.7880	56.6120	70.4980
39	RO 352	0.1275	0.7320	58.1420	56.4960

Table 13. Continued

(1)	(2)	(3)	(4)	(5)	(6)
40	RO 364	0.1292	0.6780	55.5090	55.7190
41	RO 369	0.1573	0.9470	81.0070	64.7770
42	RO 380	0.1107	0.7250	42.5660	51.0240
43	RO 381	0.1280	0.7880	56.8080	56.0050
44	RO 395	0.1525	0.6470	77.6420	52.2600
45	RO 399	0.1600	0.7920	71.6460	64.5000
46	RO 859	0.1158	0.7320	47.7960	44.9970
47	RO 868	0.1265	0.7550	56.6180	55.2770
48	RO 876	0.1613	0.7550	63.3530	81.0020
49	RO 879	0.1500	0.7080	64.1130	73.7460
50	RO 883	0.1433	0.7100	59.2570	68.7590
51	RO 886	0.1203	0.6620	46.6880	53.5040
52	RO 894	0.1282	0.7100	46.7060	62.2820
53	MT 899	0.1361	0.9200	56.2470	62.7460
54	MT 901	0.1172	0.6300	67.8740	52.2150
55	MT 906	0.1335	0.7030	57.7720	54.0000
56	MT 920	0.1300	0.6420	56.9780	59.4950
57	MT 928	0.1360	0.7180	67.8420	45.4940
58	MT 929	0.1360	0.9150	60.5530	59.7460
59	MT 931	0.1355	0.8530	68.0730	50.7460
60	MT 935	0.1590	0.8600	60.9110	76.4970
61	MT 944	0.1675	0.8550	60.7420	58.7530
62	MT 945	0.1660	0.9280	67.8710	60.4960
63	MT 947	0.1588	0.8950	69.5580	82.5020
64	MT 948	0.1165	0.6800	63.9550	52.2500
65	MT 1005	0.1395	0.7080	67.1270	57.496
66	MT 1007	0.1345	0.9130	58.1260	69.2540
67	MT 1008	0.1620	0.8580	79.7010	65.0000
68	MT 1011	0.1397	0.8730	62.2380	66.4960
69	MT 1021	0.1200	0.7750	65.7820	55.4680
70	MT 1024	0.1555	0.6750	69.5530	64.9650
71	MT 1025	0.1372	0.8750	61.5070	57.7500
72	MT 1028	0.1375	0.7580	66.7670	64.7530
73	MT 1029	0.1259	0.6800	66.7540	49.2440
74	MT 1030	0.1368	0.7770	62.9960	63.5090
75	MT 1031	0.1363	0.8520	55.3120	61.5060
76	MT 1055	0.1295	0.7370	49.8550	64.2480
77	MT 1057	0.1378	0.8270	63.7350	72.7560
78	MT 1063	0.1178	0.7570	48.7380	46.0030
79	MT 1064	0.1255	0.6800	57.5690	53.7510
80	MT 1077	0.1196	0.7100	55.6820	50.7480
81	RRII 105	0.1490	0.6950	70.8700	75.4940
	Gl mean	0.1371	0.7850	60.5800	61.7100

Tabel 13. Continued.

Sl No.	Genotype	No of cells/mm length of palisade layer	No of cells/mm length of spongy layer	Thickness of the cuticle (μm)
(1)	(2)	(3)	(4)	(5)
1	AC 426	118.25	250.25	2.48
2	AC 453	112.24	250.58	3.35
3	AC 604	123.33	287.74	2.40
4	AC 626	111.79	281.11	3.36
5	AC 627	117.91	284.55	2.74
6	AC 629	108.53	241.55	2.20
7	AC 632	114.30	271.06	3.12
8	AC 644	123.22	274.07	2.51
9	AC 647	103.08	266.33	3.70
10	AC 650	124.34	417.06	1.80
11	AC 654	114.78	255.83	2.88
12	AC 657	120.66	286.87	2.68
13	AC 694	116.13	227.40	2.85
14	AC 706	113.08	189.24	2.32
15	AC 733	121.95	306.95	2.15
16	AC 754	115.40	328.82	1.98
17	AC 953	108.51	243.37	2.05
18	AC 959	116.81	246.76	2.95
19	AC 963	118.72	258.04	3.70
20	AC 966	120.65	282.62	2.21
21	AC 979	120.61	273.18	2.85
22	AC 986	129.35	368.76	1.78
23	AC 995	116.79	270.32	2.80
24	AC 1043	123.08	328.05	3.10
25	AC 1090	124.58	268.43	1.47
26	RO 254	118.99	275.55	2.48
27	RO 255	111.15	234.30	3.03
28	RO 256	110.90	236.25	2.83
29	RO 257	100.62	227.05	2.07
30	RO 287	114.66	235.83	2.90
31	RO 311	101.41	250.30	3.23
32	RO 316	118.76	288.02	2.68
33	RO 317	114.40	250.44	1.80
34	RO 319	114.89	331.13	1.55
35	RO 322	104.37	217.85	1.65
36	RO 328	122.70	265.35	2.62
37	RO 330	130.16	351.22	2.52
38	RO 338	117.28	379.11	1.89
39	RO 352	134.34	283.80	2.30

Table 13. Continued

(1)	(2)	(3)	(4)	(5)
40	RO 364	127.07	269.25	2.15
41	RO 369	124.60	269.38	2.71
42	RO 380	124.40	269.43	2.68
43	RO 381	125.43	262.25	2.30
44	RO 395	107.13	224.89	3.45
45	RO 399	132.58	345.86	2.70
46	RO 859	132.66	307.05	2.63
47	RO 868	112.12	269.25	3.10
48	RO 876	127.69	335.96	1.90
49	RO 879	110.50	199.16	2.67
50	RO 883	120.63	281.92	2.45
51	RO 886	111.19	263.60	1.28
52	RO 894	114.71	272.47	2.15
53	MT 899	115.85	246.93	3.20
54	MT 901	108.21	256.90	3.33
55	MT 906	113.59	307.69	1.87
56	MT 920	116.66	308.27	1.45
57	MT 928	115.56	260.08	2.78
58	MT 929	110.52	297.63	2.77
59	MT 931	110.20	240.54	3.13
60	MT 935	115.60	334.67	1.22
61	MT 944	115.56	365.21	1.65
62	MT 945	117.25	243.53	4.27
63	MT 947	118.61	283.04	3.03
64	MT 948	110.28	244.45	2.70
65	MT 1005	117.32	297.97	3.41
66	MT 1007	117.82	247.44	1.78
67	MT 1008	117.98	258.48	2.28
68	MT 1011	121.64	263.46	2.75
69	MT 1021	117.20	277.70	2.05
70	MT 1024	112.59	257.68	3.08
71	MT 1025	115.03	267.21	3.72
72	MT 1028	120.38	248.99	1.82
73	MT 1029	111.29	236.13	2.52
74	MT 1030	103.86	271.67	1.68
75	MT 1031	126.62	269.32	3.63
76	MT 1055	120.76	268.67	3.25
77	MT 1057	109.84	261.77	2.85
78	MT 1063	127.87	298.07	2.78
79	MT 1064	111.15	255.02	2.20
80	MT 1077	119.96	233.64	2.55
81	RRII 105	117.24	232.24	3.67
	Gl mean	117.03	273.95	2.57

MT 945 for their thickness of cuticle, in that order and were statistically on par with the control, which had a cuticle of 3.67 μm thickness. Rest of the genotypes had significantly lower values. In the whole of the population, only MT 945 had a significantly higher cuticle thickness compared to the control (Tables 12 and 13).

3.2.2.4 Bark structural characters.

The range and the general mean value for the population for the bark structural characters are shown in Table 14 and Table 15 depicts the individual mean values for the 80 wild genotypes, together with the corresponding values of the control clone RRII 105.

Total bark thickness of the wild germplasm was found to be the maximum for the genotype RO 395 with 4.00 mm thickness followed by AC 733 (3.93 mm), MT 944 (3.64 mm), AC 650 (3.53 mm) and AC 979 (3.50 mm). The control clone had a mean bark thickness of 3.06 mm and the genotype RO 886 had the least bark thickness of 2.00 mm. Twenty-one genotypes had significantly higher bark thickness than the control clone. Fourteen genotypes had their average bark thickness on par with the control, while the rest of the genotypes had significantly lower values (Tables 14 and 15).

Soft bark thickness was found to be the maximum for the genotype RO 311 with 1.75 mm followed by RO 868 (1.69 mm), AC 650 (1.58 mm), AC 647 (1.56 mm) and MT 944 (1.53 mm) while the minimum soft bark thickness of 0.87 mm was recorded by AC986. Twenty eight genotypes had their soft bark thickness significantly higher than the control which had a thickness of 1.16 mm. Twenty six genotypes were on par with the control while rest of the genotypes had significantly lower soft bark thickness (Tables 14 and 15).

Hard bark thickness was the maximum for RO 395 (2.53mm) and minimum for AC 654 (0.84 mm). AC 733 with 2.49 mm, RO 257 with 2.29 mm, AC 995 with 2.27 mm and MT 947 with 2.20 mm hard bark thickness followed, in that order. The control clone had an average thickness of 1.90 mm. While 47 genotypes had a significantly lower hard bark thickness than the control, 19 genotypes were on par with it. Rest of the genotypes had significantly higher values for hard bark thickness (Tables 14 and15).

The percentage of soft bark zone in the total bark was found to be the highest for the genotype RO 868 (64.88%) followed by AC 654 (60%), RO 311 (57.66%), MT 1021 (56.69%) and AC 1043 (56.14%). The control clone had 38.01% of its bark occupied by the soft bark zone. Genotype RO 287 had the minimum soft bark percentage of 31.26. Forty-one genotypes had significantly higher values than the control, while 29 genotypes were on par with the control. Soft bark percentage for the rest of the genotypes was found to be significantly lower than the control (Tables 14 and 15).

Percentage of hard bark region in the sampled bark was the maximum for RO 287 (68.74%) and the minimum for the genotype RO 868 (35.12%). The percentage of hard bark in the control clone was 61.99 of the total bark thickness. 28 genotypes were statistically on par with the control. Only 10 genotypes were found to have a statistically different with higher percentage of hard bark. Rest of the genotypes had lower percentage of hard bark than that of the control (Tables 14 and 15).

The number of laticifer rows in the soft bark was the maximum in the genotype RO 399 with 8.01 rows, followed by MT 1057 with 6.25 rows, RO 255 with 6.00 rows, AC 754 with 5.76 rows and the minimum number of rows was observed in the genotype MT 947 (1.74 rows). The control clone occupied the fifth position in the ranking with 5.75 rows. Only two genotypes, RO 399 and MT 1057 had significantly higher number of laticifer rows in the soft bark region, while three genotypes RO 255, RO 328 and AC 754 were on par with the control. Rest of the genotypes had significantly lower number of laticifer rows in the soft bark (Tables 14 and 15).

Number of laticifer rows in the hard bark was the maximum in AC 733 with an average of 5.01 rows and the minimum in AC 959 with only a single row. The control clone had an average of 2.25 rows of laticifers in its hard bark region. Nineteen genotypes had their laticifer rows in hard bark significantly higher than the control, while 44 genotypes were on par with control. Seventeen genotypes had their average number of laticifer

significantly higher width than the control, while 18 genotypes had significantly lower values and 42 genotypes were on par with the control. The control clone had an average phloic ray width of 0.053μm (Tables 14 and 15).

The height / width ratio of the phloic rays was the maximum for the genotype RO 254 (9.95) followed by 9.95 for RO 287, 9.17 for RO 883, 8.45 for RO 380and 8.28 for AC 644. The minimum ratio was for MT 1008 (3.33) and the control clone showed a ratio of 3.96. Seventy-four genotypes had their length/ width ratio of phloic rays significantly higher than the control while six of them were on par with the control (Tables 14 and 15).

3.2.3 Provenance-wise comparison of performance

3.2.3.1 Morphological characters

The wild genotypes studied represents more or less equally in number, the three provenances of Brazil- Acre, Rondonia and Mato Grosso- representing three distinct geographic localities from where they were originally collected. Most of the morphological characters recorded at the end of 18 months after planting showed a generally higher vigour for the genotypes from the provenance of Rondonia and the results are shown in Table 16.

The genotypes from the provenance of Rondonia were found to have the maximum provenance-wise mean value for girth of the plants, with the Acre and Mato Grosso genotypes following, during all the four quarters of observation. In the first quarter, Rondonian genotypes had an average girth of 3.04 cm, followed by 2.86 cm for the Acre and 2.66 cm for the Mato Grosso genotypes while the control had an average girth of 2.08 cm. In the second quarter, the average provenance-wise mean of the genotypes from Rondonia, Acre and Mato Grosso were 4.21 cm, 3.85 cm and 3.60 cm respectively with 2.81 cm for the control. In the third quarter, Rondonian genotypes had an average girth of 5.89 cm, with the Acre genotypes (5.25 cm) and Mato Grosso genotypes (5.03 cm) following with the control having a mean girth of 4.05 cm. Rondonian genotypes, in the fourth quarter had an

average girth of 8.08 cm followed by the genotypes from Acre (7.25 cm), and Mato Grosso (6.86 cm) while the control clone RRII 105 had an average girth of 6.06 cm only (Table 16).

Height of the plants was the maximum for the Rondonian genotypes in the first quarter (81.53 cm), followed by the Mato Grosso (69.82 cm) and Acre genotypes (65.25 cm) with a height of 43.43 cm for the control. In the second, third and fourth quarters also the wild genotypes showed the same trend in the provenance-wise performance, with mean values of 129.27 cm, 106.76 cm and 102.40 cm for the second quarter, 161.04 cm, 136.68 cm and 125.80 cm for the third quarter and 220.78 cm, 181.98 cm and 173.93 cm for the fourth quarter for the Rondonian, Mato Grosso and Acre genotypes respectively. The control clone was always shorter than the wild genotypes with an average height of 73.48 cm, 87.69 cm and 145.69 cm for the second, third and fourth quarters (Table 16).

Number of leaf flushes per plant recorded in the first quarter was the maximum for the Rondonian genotypes (3.16 flushes) followed by Acre and Mato Grosso genotypes having the same average number of leaf flushes (2.85 flushes) while the control had an average of 2.94 flushes. In the second, third and fourth quarters Rondonian genotypes had the maximum value with Mato Grosso and Acre genotypes following. In the second quarter the mean values were 4.82, 4.16 and 4.10 in that order, while the third quarter mean values were 6.09, 5.35 and 5.15 and for the fourth quarter the mean values were 7.48, 6.43 and 6.25 for the Rondonian, Mato Grosso and Acre provenances respectively. The control clone had an average of 4.13, 5.58 and 6.78 flushes in the second, third and fourth quarters (Table 16).

The total number of leaves per plant was the maximum for the Rondonian genotypes (25.56) followed by Acre (21.62) and Mato Grosso (21.13) with 19.60 leaves for the control. In the second quarter also the Rondonian genotypes had the maximum value of 44.74 with both Acre and Mato Grosso genotypes having almost equal values of 35.12 and

35.01 respectively with 30.10 leaves for the control. The trend slightly reversed in the third quarter with the Mato Grosso and Acre genotypes with 48.07 and 47.01 leaves respectively following the Rondonian genotypes which still had the maximum mean value of 59.69 leaves. In the fourth quarter Rondonian genotypes had the maximum number of leaves (81.01) with the Acré (64.96) and the Mato Grosso genotypes (63.53) following, while the control had and average of 62.83 leaves (Table 16).

In the fourth quarter, the genotypes from the provenance of Rondonia had their leaf flushes placed at the maximum distance of 20.28 cm closely followed by the Mato Grosso genotypes (20.13cm), while the genotypes from Acre had their leaf flushes placed at a distance of 18.85 cm. The leaf flushes of the control clone were still closer at an average distance of 12.74 cm. The length of the petiole showed a different trend, where the Rondonian genotypes still showed the maximum mean value of 23.33 cm. The Mato Grosso genotypes had the shortest petiole with a length of 18.94 cm while the genotypes from Acre fell between the two other provenances with an average petiole length of 22.98 cm. The petiole length of the control clone was 14.59cm (Table 16).

The total leaf area per plant of the wild genotypes in the fourth quarter was the highest for the genotypes from Rondonia (14221.77 cm^2) followed by the genotypes from Acre (10556.5 cm^2) and Mato Grosso (10103.19 cm^2) whereas the control clone had an average total leaf area of 7675.35 cm^2. The leaf area index also followed the same pattern with Rondonia, Acre and Mato Grosso genotypes in that order with 0.23, 0.17 and 0.16 as their index respectively with 0.13 for the control clone RRII 105 (Table 16).

3.2.3.2 Test tap yield over three years

Table 17 gives the provenance-wise comparison of the wild genotypes for their average test tap yield over the first three years. The yield at the end of the first year was

rows in the hard bark significantly lower than the control (Tables 14 and 15).

The total number of laticifer rows in the bark (the sum of laticifer rows in the soft and hard bark regions) was the highest for the genotype RO 399 with 11.01 rows, followed by AC 733 (10.01 rows), AC 754 (8.77 rows), AC 632 (8.51) and MT 901 (8.26 rows). MT 1031 recorded the minimum number of vessel rows (3.00). The control had an average of eight laticifer rows with 13 genotypes statistically on par with it. Rest of the genotypes had their total number of laticifer rows significantly lower than the control (Tables 14 and 15).

The density of the latex vessels per row per mm distance was the maximum for RO 894 with 25.00 rows followed by MT 1055 (23.99) and the control clone (23.76). Only one genotype, RO 894 had a significantly higher value than the control clone, while MT 1055 was on par. All the remaining genotypes had their density of latex vessel significantly lower than the control (Tables 14 and 15).

Genotype MT 899 with a latex vessel diameter of 34.00 μm ranked first in the population followed by the genotypes AC 632, RO 886, AC 1043 and RO 381 with their respective vessel diameters 30.45 μm, 28.96 μm, 27.79 μm and 27.68 μm. The diameter of latex vessels was minimum for MT 906 with 13.44 μm while that of the control was 16.30 μm. Sixty-four genotypes had significantly higher vessel diameter than the control, while 14 genotypes were on par whereas, the diameter of 2 genotypes, MT 906 and AC 657 were significantly lower than that of the control clone (Tables 14 and 15).

The total cross sectional area of the laticifers estimated was the maximum for AC 1043 (17.77 mm^2) followed by RO 255 (17.33 mm^2), AC 733 (15.82 mm^2), MT 1025 (15.72 mm^2) and AC 632 (15.26 mm^2), with the minimum value recorded for MT 929 (1.33 mm^2). Twenty genotypes had their total cross sectional area of laticifers significantly higher and 25 genotypes had their values on par, with the control. The remaining 35 genotypes had significantly lower cross sectional areas than the control clone RRII 105 (Tabels 14 and 15).

The average distance between laticifer rows in the soft bark region of the wild genotypes showed a maximum value (0.75 mm) for the genotype AC 647 followed by AC 959, MT 1029, AC 995 and MT 947 with 0.58 mm, 0.58 mm, 0.54 mm and 0.52 mm respectively, in that order. The laticifer rows in the soft bark region were the closest in AC 644 with only an average distance of 0.12 mm. The control clone had an average distance of 0.20 mm between its latex vessel rows in the soft bark. A total of 60 wild genotypes had their latex vessel rows in the soft bark placed at a significantly higher distance than the control clone while this distance was on par with the control for seven genotypes. The average distance in the rest of the 13 genotypes were significantly lower than the values recorded for the control (Tables 14 and 15).

Frequency of the phloic rays per 0.01mm^2 area, was found to be the highest for the genotype AC 629 with 7.75 rays followed by 7.01 rays for MT 1005, 6.26 rays for MT 1011, 5.99 rays for RO 328 and 5.74 rays for MT 1008, while MT 935 had the least frequency of phloic rays (2.50). Only 12 genotypes had a significantly higher frequency of phloic rays compared to the value of 4.0 for the control. Thirty-one genotypes had their frequency of phloic rays statistically on par with the control while the remaining genotypes had significantly lower phloic frequencies (Tables 14 and 15).

The maximum height of phloic rays was 0.41μm for the genotype AC 644 followed by 0.40 μm for RO 254, 0.38 μm for AC 963, 0.37 μm for MT 947 and 0.36 μm for RO 330, while the shortest phloic rays were recorded by MT 1024 (0.18 μm) which was the only genotype with a significantly lesser height than the control. The control clone with phloic rays of 0.21 μm height had the genotype MT 1008 statistically on par with it. The majority of 78 genotypes had their phloic ray height significantly higher than the control (Tables 14 and 15).

The width of the phloic rays was the maximum for the genotype MT 947 (0.08 μm) followed by the genotypes MT 899, MT 1011, MT 1007 and AC 453 with the mean values being 0.080 μm, 0.070 μm, 0.065 μm and 0.065 μm respectively. Twenty genotypes had a

Table 14. Range and general mean of bark structural characters in the third year.

Genotype	Range				Gl. Mean	Control RRII 105
	Minimum	Genotype	Maximum	Genotype		
Total bark thickness (mm)	2.00	RO886	4.00	RO395	2.86	3.06
Soft bark thickness (mm)	0.87	AC986	1.75	RO311	1.19	1.16
Hard bark thickness (mm)	0.84	AC654	2.53	RO395	1.67	1.90
Soft bark thickness in %	31.26	RO287	64.88	RO868	42.17	38.01
Hard bark thickness in %	35.12	RO868	68.74	RO287	57.83	61.99
No of LV rows in soft bark	1.74	MT947	8.01	RO399	3.65	5.75
No of LV rows in hard bark	1.00	AC959	5.01	AC733	2.16	2.25
Total no of LV rows	2.99	MT1031	11.01	RO399	5.81	8.00
Density of LV/row/mm	11.50	RO399	25.00	RO894	17.15	23.76
Diameter of LV (µm)	13.44	MT906	34.00	MT899	21.46	16.30
Total CSA of LV(mm^2)	1.33	MT929	17.77	AC1043	6.96	7.14
AD. between LV in SB (mm)	0.12	AC644	0.75	AC647	0.31	0.20
FQ. of PR/ .01mm^2 area	2.50	MT935	7.75	AC629	3.78	4.00
Height of phloic rays (mm)	0.18	MT1024	0.41	AC644	0.29	0.21
Width of phloic rays (mm)	0.03	RO287	0.08	MT947	0.05	0.05
Height/width ratio of PR	3.33	MT1008	9.95	RO254	5.86	3.96

LV = Latex vessel; PR = Phloic rays; FQ = Frequency; CSA = Cross sectional area; AD = Average distance; SB = Soft bark

Table 15. Mean values for bark structural characters in the third year.

Sl.No.	Genotypes	Character				
		Total bark thickness (mm)	Soft bark thickness (mm)	Hard bark thickness (mm)	Soft bark thickness (%)	Hard bark thickness (%)
(1)	(2)	(3)	(4)	(5)	(6)	(7)
1	AC 426	2.21	0.93	1.29	41.91	58.09
2	AC 453	2.66	1.14	1.52	42.95	57.06
3	AC 604	2.50	1.19	1.32	47.16	52.84
4	AC 626	2.72	1.07	1.64	39.44	60.56
5	AC 627	3.02	1.17	1.85	38.69	61.32
6	AC 629	3.19	1.31	1.88	41.09	58.92
7	AC 632	2.28	1.08	1.20	47.68	52.32
8	AC 644	2.55	0.96	1.59	37.84	62.16
9	AC 647	3.44	1.56	1.89	45.84	54.16
10	AC 650	3.53	1.58	1.95	44.74	55.26
11	AC 654	2.10	1.25	0.84	60.00	40.00
12	AC 657	2.96	1.20	1.76	40.58	59.42
13	AC 694	3.08	1.38	1.70	44.99	55.02
14	AC 706	3.05	1.26	1.79	41.34	58.67
15	AC 733	3.93	1.44	2.49	36.59	63.42
16	AC 754	3.41	1.52	1.89	44.98	55.03
17	AC 953	2.79	1.04	1.76	37.21	62.79
18	AC 959	2.34	1.20	1.15	51.27	48.74
19	AC 963	2.83	1.14	1.69	40.43	59.57
20	AC 966	2.44	1.16	1.28	47.68	52.32
21	AC 979	3.50	1.33	2.18	37.91	62.09
22	AC 986	2.27	0.87	1.40	38.45	61.55
23	AC 995	3.48	1.22	2.27	34.96	65.04
24	AC 1043	2.47	1.37	1.11	56.14	43.86
25	AC 1090	3.43	1.45	1.97	42.60	57.40
26	RO 254	2.08	0.99	1.08	48.05	51.95
27	RO 255	2.69	1.16	1.53	43.52	56.48
28	RO 256	2.34	1.06	1.28	45.56	54.44
29	RO 257	3.35	1.06	2.29	31.94	68.06
30	RO 287	3.16	0.99	2.18	31.26	68.74
31	RO 311	3.05	1.75	1.29	57.66	42.34
32	RO 316	2.72	1.12	1.60	41.16	58.84
33	RO 317	2.31	1.24	1.07	53.69	46.31
34	RO 319	2.36	0.93	1.43	39.58	60.43
35	RO 322	3.38	1.35	2.03	40.12	59.88
36	RO 328	3.49	1.43	2.05	41.17	58.83
37	RO 330	3.25	1.36	1.89	42.50	57.50
38	RO 338	2.49	1.02	1.47	41.04	58.96
39	RO 352	2.17	1.16	1.02	53.72	46.28

Table 15. Continued

(1)	(2)	(3)	(4)	(5)	(6)	(7)
40	RO 364	3.34	1.17	2.17	35.15	64.85
41	RO 369	2.38	0.89	1.49	37.32	62.69
42	RO 380	2.24	1.17	1.07	52.71	47.29
43	RO 381	3.18	1.12	2.05	35.72	64.28
44	RO 395	4.00	1.47	2.53	36.80	63.20
45	RO 399	2.94	1.29	1.65	44.09	55.91
46	RO 859	2.56	1.08	1.48	42.32	57.68
47	RO 868	2.61	1.69	0.92	64.88	35.12
48	RO 876	2.44	1.11	1.34	45.47	54.53
49	RO 879	3.22	1.24	1.98	39.08	60.92
50	RO 883	2.69	1.11	1.59	41.22	58.78
51	RO 886	2.00	1.08	0.92	53.92	46.08
52	RO 894	3.35	1.17	2.18	34.84	65.16
53	MT 899	2.81	1.09	1.73	38.85	61.15
54	MT 901	2.76	1.29	1.47	48.99	51.01
55	MT 906	3.05	1.08	1.97	35.52	64.49
56	MT 920	2.58	1.26	1.33	48.73	51.27
57	MT 928	2.94	1.21	1.74	40.99	59.01
58	MT 929	2.61	0.90	1.72	34.32	65.69
59	MT 931	3.11	1.30	1.81	41.95	58.05
60	MT 935	2.97	1.31	1.67	43.96	56.04
61	MT 944	3.64	1.53	2.12	41.89	58.11
62	MT 945	3.06	1.23	1.83	40.37	59.63
63	MT 947	3.48	1.28	2.20	36.90	63.11
64	MT 948	3.01	1.02	2.00	33.76	66.25
65	MT 1005	2.81	1.20	1.62	42.88	57.12
66	MT 1007	3.12	1.06	2.08	33.66	66.34
67	MT 1008	3.00	1.03	1.98	34.03	65.97
68	MT 1011	2.50	1.11	1.39	46.23	53.77
69	MT 1021	2.50	1.42	1.08	56.69	43.31
70	MT 1024	2.86	0.97	1.89	34.34	65.66
71	MT 1025	2.71	1.03	1.67	38.17	61.84
72	MT 1028	3.08	1.09	2.00	35.24	64.76
73	MT 1029	2.31	1.06	1.25	47.07	52.93
74	MT 1030	2.56	0.94	1.63	36.51	63.49
75	MT 1031	2.20	0.93	1.28	42.02	57.99
76	MT 1055	2.94	1.25	1.69	42.65	57.35
77	MT 1057	3.02	1.22	1.80	40.25	59.75
78	MT 1063	3.29	1.11	2.17	34.06	65.94
79	MT 1064	2.66	0.99	1.68	37.11	62.89
80	MT 1077	2.98	1.00	1.99	33.47	66.53
81	RRII 105	3.06	1.16	1.9	38.01	61.99
	Gl mean	2.86	1.19	1.67	42.17	57.83

Table 15. Continued

Sl No	Genotypes	Character					
		No of LVR in soft bark	No of LVR in hard bark	Total No of LV rows	Density of LV	Diameter of LV (µm)	Total CSA of LV(mm^2)
(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)
1	AC 426	2.01	1.75	3.76	15.25	23.87	3.841
2	AC 453	1.99	1.99	3.98	15.25	21.29	3.970
3	AC 604	4.74	1.99	6.73	13.50	18.66	4.260
4	AC 626	4.75	3.00	7.75	17.24	18.36	6.585
5	AC 627	4.00	2.49	6.49	18.75	19.14	5.824
6	AC 629	3.99	2.00	5.99	23.01	25.70	10.631
7	AC 632	4.76	3.75	8.51	15.25	30.45	15.264
8	AC 644	4.01	1.99	6.00	19.00	26.29	11.021
9	AC 647	2.26	2.00	4.26	17.00	24.74	6.723
10	AC 650	5.00	2.76	7.76	21.50	19.38	11.325
11	AC 654	3.00	4.00	7.00	14.00	22.75	7.931
12	AC 657	5.00	2.24	7.24	12.00	14.79	2.961
13	AC 694	4.00	2.49	6.49	16.24	24.95	10.139
14	AC 706	4.00	2.01	6.01	14.75	19.51	4.334
15	AC 733	5.00	5.01	10.01	21.00	23.71	15.818
16	AC 754	5.76	3.01	8.77	18.76	20.98	10.957
17	AC 953	3.99	2.00	5.99	13.75	14.98	2.807
18	AC 959	2.01	1.00	3.01	16.50	21.02	3.228
19	AC 963	3.00	1.99	4.99	17.50	20.79	5.391
20	AC 966	3.01	2.00	5.01	15.50	23.28	5.520
21	AC 979	5.00	2.00	7.00	18.75	22.63	8.521
22	AC 986	2.25	1.01	3.26	18.50	19.52	3.437
23	AC 995	2.00	1.00	3.00	12.00	25.12	3.254
24	AC 1043	5.00	2.50	7.50	17.75	27.79	17.767
25	AC 1090	1.99	1.25	3.24	14.01	17.56	2.128
26	RO 254	2.00	1.00	3.00	21.25	16.10	2.077
27	RO 255	6.00	2.00	8.00	21.50	25.28	17.328
28	RO 256	2.00	1.25	3.25	14.00	20.39	2.690
29	RO 257	4.75	1.99	6.74	16.00	16.67	2.962
30	RO 287	3.00	2.24	5.24	20.25	24.80	9.647
31	RO 311	4.01	1.99	6.00	18.50	17.16	5.656
32	RO 316	3.00	2.00	5.00	15.00	22.83	5.769
33	RO 317	3.00	2.00	5.00	15.75	24.33	8.268
34	RO 319	2.49	1.01	3.50	15.76	19.11	3.817
35	RO 322	3.00	2.02	5.02	22.00	22.43	11.773
36	RO 328	5.74	2.00	7.74	17.00	21.39	10.720
37	RO 330	3.50	3.00	6.50	16.50	21.25	7.769
38	RO 338	4.00	2.01	6.01	15.51	18.10	5.350

LVR=Latex vessel rows; LV = Latex vessels; CSA = Cross sectional area

Table 15. Continued

(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)
39	RO 352	3.00	2.00	5.00	14.75	23.08	6.410
40	RO 364	4.00	3.25	7.25	17.00	22.27	10.409
41	RO 369	3.51	2.00	5.51	18.25	24.51	8.726
42	RO 380	4.00	2.00	6.00	19.00	17.21	4.472
43	RO 381	4.01	3.24	7.25	18.74	27.68	15.010
44	RO 395	5.00	2.99	7.99	14.99	21.25	8.841
45	RO 399	8.01	3.00	11.01	11.50	26.51	11.501
46	RO 859	3.00	2.01	5.01	17.25	18.68	4.980
47	RO 868	2.01	2.00	4.01	16.74	17.42	3.232
48	RO 876	3.00	1.52	4.52	14.25	21.01	4.543
49	RO 879	2.00	1.25	3.25	20.75	21.97	5.159
50	RO 883	5.01	2.24	7.25	17.75	20.26	7.640
51	RO 886	2.25	2.51	4.76	18.00	28.96	10.928
52	RO 894	5.25	3.00	8.25	25.00	19.64	13.883
53	MT 899	3.00	1.99	4.99	13.50	34.00	10.628
54	MT 901	5.26	3.00	8.26	14.50	22.65	8.756
55	MT 906	4.25	4.00	8.25	19.50	13.44	3.690
56	MT 920	2.99	1.76	4.75	17.25	20.34	4.664
57	MT 928	4.00	2.24	6.24	18.00	19.54	5.805
58	MT 929	2.00	1.01	3.01	18.51	17.05	1.334
59	MT 931	5.01	2.00	7.01	23.00	19.38	8.500
60	MT 935	2.99	1.52	4.51	18.00	19.89	4.325
61	MT 944	2.99	1.02	4.01	12.50	17.28	2.745
62	MT 945	4.76	3.00	7.76	15.00	23.79	7.882
63	MT 947	1.74	1.99	3.73	15.51	24.76	4.902
64	MT 948	4.01	2.00	6.01	14.75	21.60	6.553
65	MT 1005	3.51	2.00	5.51	11.50	17.68	2.514
66	MT 1007	4.00	1.99	5.99	15.25	25.10	5.182
67	MT 1008	2.99	2.75	5.74	21.00	20.07	5.541
68	MT 1011	3.00	2.75	5.75	22.25	16.84	2.789
69	MT 1021	2.00	1.02	3.02	14.50	16.92	1.945
70	MT 1024	4.25	3.25	7.50	11.50	17.33	6.016
71	MT 1025	4.51	2.00	6.51	21.25	24.41	15.719
72	MT 1028	2.01	2.00	4.01	17.00	24.74	5.171
73	MT 1029	3.51	2.00	5.51	17.00	20.87	3.341
74	MT 1030	4.00	2.75	6.75	19.01	21.55	10.902
75	MT 1031	2.00	1.00	3.00	15.01	21.32	2.747
76	MT 1055	2.25	2.25	4.50	23.99	17.63	3.545
77	MT 1057	6.25	2.00	8.25	15.00	22.85	8.593
78	MT 1063	4.74	2.01	6.75	20.00	22.37	7.446
79	MT 1064	3.00	1.99	4.99	17.25	26.59	8.651
80	MT 1077	2.01	0.99	3.00	14.00	24.72	3.311
81	RRII 105	5.75	2.25	8.00	23.76	16.30	7.144
	Gl mean	3.65	2.16	5.81	17.15	21.46	6.960

Table 15. Continued

Sl. No.	Genotypes	Character				
		AD between LVR in SB (mm)	Frequency of phloic rays	Height of phloic rays (mm)	Width of phloic rays (mm)	Height /width ratio
(1)	(2)	(3)	(4)	(5)	(6)	(7)
1	AC 426	0.13	3.75	0.270	0.060	4.467
2	AC 453	0.47	3.51	0.350	0.065	5.385
3	AC 604	0.22	2.74	0.313	0.060	5.217
4	AC 626	0.17	4.00	0.320	0.047	6.766
5	AC 627	0.23	4.50	0.285	0.050	5.700
6	AC 629	0.26	7.75	0.260	0.040	6.475
7	AC 632	0.35	2.99	0.293	0.053	5.528
8	AC 644	0.12	3.00	0.410	0.050	8.280
9	AC 647	0.75	4.00	0.280	0.050	5.600
10	AC 650	0.17	3.25	0.280	0.047	5.979
11	AC 654	0.33	4.00	0.275	0.060	4.583
12	AC 657	0.20	3.00	0.320	0.050	6.380
13	AC 694	0.29	4.00	0.323	0.065	4.969
14	AC 706	0.21	4.00	0.270	0.040	6.625
15	AC 733	0.30	3.00	0.350	0.050	7.060
16	AC 754	0.18	3.75	0.310	0.055	5.691
17	AC 953	0.31	4.99	0.298	0.045	6.622
18	AC 959	0.58	3.51	0.333	0.050	6.660
19	AC 963	0.18	2.75	0.376	0.057	6.596
20	AC 966	0.24	2.50	0.300	0.060	5.050
21	AC 979	0.25	3.99	0.320	0.047	6.702
22	AC 986	0.41	3.01	0.270	0.040	6.700
23	AC 995	0.54	4.00	0.241	0.050	4.820
24	AC 1043	0.27	5.01	0.248	0.058	4.276
25	AC 1090	0.40	3.00	0.280	0.048	5.875
26	RO 254	0.39	3.50	0.400	0.040	9.950
27	RO 255	0.30	5.01	0.268	0.055	4.873
28	RO 256	0.42	3.50	0.300	0.045	6.756
29	RO 257	0.34	3.00	0.323	0.060	5.383
30	RO 287	0.42	3.00	0.297	0.030	9.900
31	RO 311	0.16	4.00	0.312	0.047	6.638
32	RO 316	0.36	3.76	0.318	0.063	5.048
33	RO 317	0.25	3.26	0.303	0.045	6.733
34	RO 319	0.34	2.99	0.240	0.040	6.075
35	RO 322	0.35	4.00	0.270	0.055	4.945
36	RO 328	0.27	5.99	0.270	0.040	6.625
37	RO 330	0.24	2.99	0.360	0.060	6.033
38	RO 338	0.36	2.99	0.320	0.045	7.044

AD=Average distance; LVR= Latex vessel rows; SB= Soft bark

Table 15. Continued

(1)	(2)	(3)	(4)	(5)	(6)	(7)
39	RO 352	0.28	3.99	0.280	0.043	6.442
40	RO 364	0.16	5.00	0.290	0.050	5.800
41	RO 369	0.35	3.00	0.280	0.062	4.532
42	RO 380	0.26	4.00	0.340	0.040	8.450
43	RO 381	0.33	3.00	0.285	0.053	5.377
44	RO 395	0.15	3.50	0.251	0.047	5.340
45	RO 399	0.14	4.00	0.320	0.052	6.115
46	RO 859	0.37	3.00	0.270	0.050	5.380
47	RO 868	0.26	4.00	0.300	0.050	5.940
48	RO 876	0.34	4.01	0.260	0.050	5.200
49	RO 879	0.48	3.75	0.297	0.058	5.121
50	RO 883	0.35	3.01	0.275	0.030	9.167
51	RO 886	0.33	4.00	0.300	0.055	5.509
52	RO 894	0.24	2.99	0.320	0.043	7.512
53	MT 899	0.49	3.00	0.327	0.080	4.088
54	MT 901	0.31	4.00	0.301	0.057	5.281
55	MT 906	0.34	3.74	0.275	0.055	5.000
56	MT 920	0.38	3.00	0.250	0.052	4.712
57	MT 928	0.32	3.76	0.280	0.050	5.600
58	MT 929	0.34	2.99	0.340	0.060	5.717
59	MT 931	0.37	4.00	0.285	0.060	4.750
60	MT 935	0.45	2.50	0.260	0.045	5.711
61	MT 944	0.34	2.99	0.310	0.060	5.083
62	MT 945	0.24	3.50	0.279	0.060	4.650
63	MT 947	0.52	4.00	0.370	0.080	4.625
64	MT 948	0.31	3.25	0.278	0.057	4.877
65	MT 1005	0.48	7.01	0.256	0.050	5.120
66	MT 1007	0.17	4.01	0.270	0.065	4.092
67	MT 1008	0.22	5.74	0.200	0.060	3.333
68	MT 1011	0.34	6.26	0.315	0.070	4.500
69	MT 1021	0.39	3.00	0.240	0.052	4.673
70	MT 1024	0.26	3.01	0.183	0.042	4.357
71	MT 1025	0.27	4.50	0.240	0.047	5.043
72	MT 1028	0.46	4.00	0.290	0.050	5.860
73	MT 1029	0.58	3.99	0.265	0.052	5.096
74	MT 1030	0.17	5.01	0.310	0.048	6.354
75	MT 1031	0.28	3.76	0.307	0.058	5.293
76	MT 1055	0.21	4.00	0.322	0.058	5.552
77	MT 1057	0.18	3.01	0.259	0.050	5.180
78	MT 1063	0.20	4.00	0.270	0.052	5.096
79	MT 1064	0.21	4.00	0.320	0.060	5.333
80	MT 1077	0.46	3.01	0.325	0.040	8.125
81	RRII 105	0.20	4.00	0.210	0.053	3.962
	Gl mean	0.31	3.78	0.290	0.052	6.442

Table 16. Provenance-wise performance for growth characters in the first year.

Character		Provenance			Control RRII 105
		Acre	Rondonia	Mato Grosso	
Girth-	first quarter (cm)	2.86	3.04	2.66	2.08
	second quarter (cm)	3.85	4.21	3.60	2.81
	third quarter (cm)	5.25	5.89	5.03	4.05
	fourth quarter (cm)	7.25	8.08	6.86	6.06
Height-	first quarter (cm)	65.25	81.53	69.82	43.43
	second quarter (cm)	102.40	129.27	106.76	73.48
	third quarter (cm)	125.80	161.04	136.68	87.69
	fourth quarter (cm)	173.93	220.78	181.98	145.70
No of leaf whorls- first quarter		2.85	3.16	2.85	2.94
	second quarter	4.10	4.82	4.16	4.13
	third quarter	5.15	6.09	5.35	5.58
	fourth quarter	6.25	7.48	6.43	6.78
Total no of leaves- first quarter		21.62	25.56	21.13	19.60
	second quarter	35.12	44.74	35.01	30.10
	third quarter	47.01	59.69	48.07	44.50
	fourth quarter	64.96	81.01	63.53	62.80
Total leaf area- fourth quarter (cm^2)		10556.5	14221.77	10103.19	7675.35
Leaf area index-fourth quarter		0.17	0.23	0.16	0.13
Inter flush DS- fourth quarter (cm)		18.85	20.28	20.13	12.74
Petiole length- fourth quarter (cm)		22.98	23.33	18.94	14.59

maximum for Mato Grosso genotypes with 0.0986 g t^{-1} t^{-1} followed by the Rondonian genotypes with an average of 0.0601 g t^{-1} t^{-1} and the Acre genotypes with an yield of 0.0501 g t^{-1} t^{-1} while the control had an average of 0.1626 g t^{-1} t^{-1}. In the second year of test tapping, the maximum yield was given by the Mato Grosso genotypes (0.1801 g t^{-1} t^{-1}) followed by Rondonian (0.0885 g t^{-1} t^{-1}) and Acre genotypes (0.0815 g t^{-1} t^{-1}) with the control clone yielding 0.2986 g t^{-1} t^{-1}. In the third year also, the Mato Grosso genotypes retained their superiority in their average performance over Acre and Rondonia genotypes with an average

yield of 0.7602 g t^{-1} t^{-1} followed by 0.4501 g t^{-1} t^{-1} for the Rondonian and 0.2769 g t^{-1} t^{-1} for the Acre genotypes with an average yield of 2.3547 g t^{-1} t^{-1} for the control clone RRII 105. Table 17. Provenance-wise performance for test tap yield over three years,

Character		Provenance			Control
		Acre	Rondonia	Mato Grosso	RRII 105
Dry rubber yield					
(g t^{-1} t^{-1})	First year	0.0501	0.0601	0.0986	0.1626
	Second year	0.0815	0.0885	0.1801	0.2986
	Third year	0.2769	0.4500	0.7602	2.3547

3.2.3.3. Leaf structural characters

The provenance-wise comparison of the leaf structural characters with respect to the three provenances studied are given in Table 18. No stomata were observed in the adaxial surface of the lamina (Fig 57). The number of stomata per mm^2 of the abaxial surface (Fig 58) of the leaf was the highest for the genotypes from Acre (439.5) followed by the Mato Grosso genotypes (434.38) and the Rondonian genotypes (424.76) while the control clone had the highest average number of 525.3. Maximum number of epidermal cells per mm^2 of the abaxial epidermis was the highest for the Mato Grosso genotypes (1790.23) and the minimum for Acre (1617.82) while the genotypes from Rondonia (1697.09) was intermediary in position. The control clone had the highest epidermal cell count (2237.76) compared to all the three provenances. The stomatal index was the highest for the Acre genotypes (21.7) with the Rondonian and Mato Grosso genotypes following, with 20.47 and 19.87 as their indices followed by the control clone with an index of 19.26. The single leaflet area was however the maximum for the Rondonian genotypes with an average area of 105.5 cm^2 with the Acre genotypes having medium sized single leaflet (100.65 cm^2) and the Mato Grosso genotypes with the smallest single leaflet with an area of 81.73 cm^2. The single leaflet area of the control was still lower than that of all the three provenances (60.83 cm^2).

The thickness of the lamina of the Acre and Mato Grosso genotypes were the

same, the average thickness being 0.137 mm in both and was closely followed by the Mato Grosso genotypes (0.136 mm). The control clone had a comparatively thicker lamina with an average thickness of 0.149 mm (Figs 13-18). Thickness of the leaflet midrib was the maximum for the Acre genotypes (0.840 mm), with Mato Grosso and Rondonian genotypes following (0.790 and 0.740 mm respectively), while the control clone recorded a thickness of 0.700 mm (Table 18) (Figs 19-24).

Thickness of the palisade layer was the maximum for the genotypes from Mato Grosso (62.49 μm) and the minimum thickness of 58.89 μm was in Acre genotypes with the control clone having a thickness of 70.87 μm. The Rondonian genotypes fell in between with an average thickness of 59.79 μm (Figs 25-30). The thickness of the spongy layer showed the reverse trend with the Acre genotypes having the maximum thickness of 64.85 μm followed by the Rondonian genotypes (60.13 μm) and Mato Grosso genotypes (59.92 μm) (Figs 31-36). The control clone RRII 105 had a higher thickness of 75.49 μm for the spongy layer, compared to the genotypes from the three provenances (Table 18).

Table 18. Provenance-wise comparison for leaf structural characters in the third year.

Character	Provenance			Control
	Acre	Rondonia	Mato Grosso	RRII 105
No of stomata/mm^2 of LL.	439.50	424.76	434.38	525.30
No of epidermal cells/mm^2 of LL.	1617.82	1697.09	1790.23	2237.76
Stomatal Index	21.70	20.47	19.87	19.26
Single leaflet area (cm^2)	100.65	105.50	81.73	60.83
Thickness of lamina (mm)	0.137	0.136	0.137	0.149
Thickness of leaf midrib (mm)	0.84	0.74	0.79	0.700
Thickness of palisade layer (μm)	58.89	59.79	62.49	70.87
Thickness of spongy layer (μm)	64.85	60.13	59.92	75.49
No of cells/mm palisade layer	117.52	117.97	115.68	117.24
No of cells/mm spongy layer	278.36	273.95	271.5	232.24
Thickness of cuticle (μm)	2.62	2.43	2.63	3.67

LL = Leaf lamina

Rondonian and Acre genotypes had the maximum number of cells per mm length of palisade layer (117.97 and 117.52 respectively followed by Mato Grosso (115.68). The control clone showed a more or less similar value of 117.24 cells. The number of cells per mm spongy layer was the maximum for the Acre genotypes (278.36) followed by Rondonian (273.95) and Mato Grosso genotypes (271.5) with the control clone showing the lowest mean value of 232.24 compared to the three provenances (Table 18).

Thickness of cuticle was the same for the Acre and Mato Grosso genotypes with an average thickness of 2.62 μm and 2.63 μm with the Rondonian genotypes falling behind with a thickness of 2.43 μm. The control clone had a higher cuticular thickness of 3.67 μm (Table 18).

3.2.3.4 Bark structural characters

Provenance-wise comparison of the bark structural parameters of the wild genotypes in the third year is depicted in Table 19 and Figs 40-57. Total bark thickness in the wild genotypes from the three provenances of Acre, Rondonia and Mato Grosso were almost similar with an average thickness of 2.89 mm, 2.81 mm and 2.88 mm respectively while the control clone had a higher bark thickness of 3.06 mm. Soft bark thickness of the wild genotypes was the maximum in Acre genotypes with 1.23 mm followed by Rondonian genotypes (1.19 mm) and Mato Grosso genotypes (1.14 mm) with a soft bark thickness of 1.16 mm for the control. Hard bark thickness was the maximum with 1.74 mm for Mato Grosso genotypes with Acre and Rondonian genotypes following with 1.66 mm and 1.61 mm respectively while the control clone had a mean value of 1.90 mm.

The percentage of soft bark in the total bark thickness was similar for the Acre and Rondonian genotypes (43.30 and 43.50% respectively) with the Mato Grosso genotypes having 40.02% of its total bark as the soft bark. The control clone had a lower value of 38.01% compared to the three provenances. Proportion of the hard bark was the lowest for Acre and Rondonian genotypes (56.70% and 56.50% respectively) while Mato Grosso genotypes had a slightly higher percentage of hard bark zone (59.98%) and that of the control clone was 61.99% (Table 19).

Number of laticifer rows in the soft bark region was comparable for the genotypes from Rondonia (3.72) and Acre (3.70), with Mato Grosso genotypes following (3.46), compared to that of the control clone with an average of 5.75 vessels. Number of laticifer rows in the hard bark region was the maximum for Acre genotypes followed by Rondonian and Mato Grosso genotypes with their mean values being 2.29, 2.13 and 2.08 respectively with the control having 2.25 rows in its hard bark. The total number of laticiferous rows was comparable in the three provenances with 5.94, 5.79 and 5.46 vessel rows for Acre, Rondonia and Mato Grosso genotypes respectively. The control clone had the highest number of laticifer rows compared to any of the three provenances with an average of 7.75 rows (Table 19).

The mean values for the density of latex vessels per row per mm circumference was similar with 21.89, 21.49 and 21.23 for the Acre, Rondonia and Mato Grosso genotypes respectively with a lesser density of 16.30 for the control clone. The diameter of latex vessels was the maximum for Rondonian genotypes (17.52 μm) followed by the Mato Grosso (16.98 μm) and Acre genotypes (16.67 μm) while the control had a higher mean value of 23.75 μm (Table 19).

The total cross sectional area of laticifer rows was the highest for Rondonian genotypes (7.76 mm^2) followed by Acre (7.35 mm^2) and Mato Grosso genotypes (5.83 mm^2), compared to 7.14 mm^2 for the control. Average distance between laticifer rows in the soft bark region of the bark was the maximum for the Mato Grosso genotypes (0.33 mm), while the Acre and Rondonian genotypes had their rows placed at an equal distance of 0.30 mm. Unlike the wild genotypes the control clone had their laticifer rows placed still closely at 0.20 mm (Table 19).

Frequency of phloic rays was the maximum for Mato Grosso genotypes with Acre and Rondonian genotypes following with a frequency of 3.89, 3.76 and 3.67 per 0.01 mm^2 area, respectively. The control clone had a higher frequency of 4.0 per 0.01mm^2 area. Acre and Rondonian genotypes each had the maximum height of 0.30 mm for the phloic rays with the Mato Grosso genotypes having a mean value of 0.28 mm. The control had still

shorter phloic rays with 0.21mm height. Width of phloic rays was the maximum for 0.06 mm for the Mato Grosso genotypes with the Acre and Rondonian genotypes immediately following with a width of 0.05 mm. The control clone also had the same width as the Rondonan and Mato Grosso genotypes. The height/ width ratio of phloic rays in the wild genotypes was the highest for the Rondonian genotypes (6.51) with the lowest ratio for Mato Grosso (5.22) and the Acre genotypes having an intermediate ratio of 5.96. The ratio was the lowest (4.12) for the control clone RRII 105 (Table 19).

3.3 Genetic Parameters

Estimates of variability and the genetic parameters were worked out for all the traits studied ie, growth characters during the first year of growth, leaf and bark anatomical characters during the third year and the average dry rubber yield over the three years of tapping.

Table 19. Provenance-wise performance for bark structural characters in the third year.

Character	Provenance			Control
	Acre	Rondonia	Mato Grosso	RRII 105
Total bark thickness (mm)	2.89	2.81	2.88	3.06
Soft bark thickness (mm)	1.23	1.19	1.14	1.16
Hard bark thickness (mm)	1.66	1.61	1.74	1.90
Soft bark thickness in %	43.30	43.50	40.02	38.01
Hard bark thickness in %	56.70	56.50	59.98	61.99
No of LVR in soft bark	3.70	3.72	3.46	5.75
No of LV rows in hard bark	2.29	2.13	2.08	2.25
Total no of latex vessel rows	5.94	5.79	5.46	7.75
Density of LV/row/mm	21.89	21.49	21.23	16.30
Diameter of latex vessels (μm)	16.67	17.52	16.98	23.75
Total CSA of LV (mm^2)	7.35	7.76	5.83	7.14
AD between LVR in SB (mm)	0.30	0.30	0.33	0.20
Frequency of PR/.01 mm^2 area	3.76	3.67	3.89	4.00
Height of phloic rays (mm)	0.30	0.30	0.28	0.21
Width of phloic rays (mm)	0.05	0.05	0.06	0.05
Height/width ratio of PR	5.96	6.51	5.22	4.12

LVR= Latex vessel rows; LV=Latex vessels; CSA= Cross sectional area; AD= Average distance; PR= Phloic rays; SB= Soft bark.

3.3.1 Phenotypic and genotypic coefficients of variation

3.3.1.1 Morphological characters

The phenotypic and genotypic coefficients of variation of the growth characters observed in the first year are given in Table 20. Among the various morphological traits depicting the growth characteristics of the wild genotypes, maximum genotypic coefficient of variation (GCV) was exhibited by the total leaf area of the plant (35.63) with a similar value of 35.34 for leaf area index. Total number of leaves in the fourth quarter had the second highest GCV of 23.06 followed by the same character in the third quarter (21.07), second quarter (20.40) and first quarter (17.61). The height of the plants recorded during the four quarters showed their GCV in the next order with 20.41,19.68, 19.08 and18.93 in

Table 20. Coefficients of variation, heritability and genetic advance for growth characters in the first year.

Character	Coefficients of variation (%)		Heritability in broad sense (%)	Genetic advance as % over mean
	Phenotypic	Genotypic		
Girth- first quarter (cm)	18.51	14.38	60.37	23.02
second quarter (cm)	19.03	14.75	60.11	23.57
third quarter (cm)	20.18	15.79	61.20	25.44
fourth quarter (cm)	20.02	15.52	60.08	24.78
Height- first quarter (cm)	25.94	19.08	54.08	28.90
second quarter (cm)	24.41	18.93	60.16	30.25
third quarter (cm)	26.28	19.68	56.08	30.36
fourth quarter (cm)	28.41	20.41	51.58	30.19
No of leaf whorls- first quarter	15.13	9.10	36.16	11.27
second quarter	15.68	11.31	52.06	16.81
third quarter	15.97	11.78	54.44	17.91
fourth quarter	18.13	13.78	57.71	21.56
Total no of leaves- first quarter	26.37	17.61	44.58	24.22
second quarter	26.69	20.40	58.42	32.12
third quarter	27.74	21.07	57.69	32.97
fourth quarter	30.37	23.06	57.65	36.06
Total leaf area- fourth quarter (cm^2)	50.82	35.63	49.16	51.47
Leaf area index-fourth quarter	50.48	35.34	48.99	50.95
Inter flush DS- fourth quarter (cm)	20.18	12.95	41.18	17.12
Petiole length- fourth quarter (cm)	28.52	13.4	24.08	14.15

DS = distance

the fourth, third, first and second quarter respectively. The girth of the plant in the first four quarters followed, the GCV being 15.79, 15.52, 14.75 and 14.38 for the third, fourth, second and first quarter respectively. The GCV for the number of leaf flushes produced in the four quarters varied in an ascending order 9.1, 11.31, 11.78 and 13.78 respectively. Inter flush distance and petiole length taken in the fourth quarter had a GCV of 12.95 and 13.4 respectively (Table 20).

The phenotypic coefficient of variation (PCV) was also the highest for the characters total leaf area in the fourth quarter and leaf area index (50.82 and 50.48 respectively). Total number of leaves in the fourth quarter had a high PCV of 30.37, followed by petiole length in the fourth quarter (28.52), total number of leaves in the third, second and the first quarters (27.74, 26.69 and 26.37 respectively), height of the plants in the fourth, third, first and second quarters (28.41, 26.28, 25.94 and 24.41 respectively), girth of the plants in the third, fourth, second and first quarters (20.18, 20.02, 19.03 and 18.51 respectively) and number of leaf flushes in the fourth, third, second and first quarters (18.13, 15.97, 15.68 and 15.13 respectively) (Table 20).

3.3.1.2 Test tap yield over three years

Dry rubber yield on test tapping over the three years, recorded the highest GCV in the third year (95.54) followed by the first year yield (74.15) and the second year yield (72.15). Phenotypic coefficient of variation was the highest for the third year (117.01) followed by the second year (106.91) and the first year (80.35). (Table 21)

Table 21. Coefficients of variation, heritability and genetic advance for test tap yield over three years

Character		Coefficients of variation (%)		Heritability in broad sense (%)	Genetic advance as % over mean
		Phenotypic	Genotypic		
Dry rubber yield ($g\ t^{-1}\ t^{-1}$)	First year	80.35	74.15	85.17	140.98
	Second year	106.91	72.15	45.5	100.3
	Third year	117.01	95.54	66.67	160.7

3.3.1.3 Leaf structural characters

Table 22 gives the coefficients of variation of the leaf structural characters in the wild genotypes in the third year. The genotypic coefficients of variations estimated for the stomatal characters varied from 14.1 to 19.34. Maximum GCV of 19.34 was recorded for the number of epidermal cells per mm^2 of the abaxial leaf surface, followed by the stomatal index (15.73) and number of stomata per mm^2 of the abaxial surface of the leaves (14.1). Single leaf area had a GCV of 16.36. Phenotypic coefficient of variation was the maximum for the character number of epidermal cells per mm^2 of the leaf lamina (19.88) followed by stomatal index (17.13) and number of stomata per mm^2 of the leaf surface (15.95). Whereas, the single leaflet area had the highest PCV of 29.65 compared to all the leaf structural characters.

Leaf structural characters studied had their GCV ranging from 5.78 to 23.86. Among

Table 22. Coefficients of variation, heritability and genetic advance for leaf structural characters in the third year.

Character	Coefficients of variation (%)		Heritability in broad sense (%)	Genetic advance as % over mean
	Phenotypic	Genotypic		
No of stomata/ mm^2 of leaf area	15.95	14.10	78.22	25.7
No of epidermal cells/ mm^2 of LA	19.88	19.34	94.65	38.76
Single leaflet area (cm^2)	29.65	16.36	30.43	18.59
Stomatal Index	17.13	15.73	84.42	29.78
Thickness of lamina (mm)	10.93	10.46	91.67	20.64
Thickness of leaf midrib (mm)	14.41	14.22	97.34	28.9
Thickness of palisade layer (µm)	13.56	13.24	95.38	26.64
Thickness of spongy layer (µm)	18.67	14.09	56.95	21.9
No of cells/mm palisade layer	6.28	5.78	84.96	10.98
No of cells/mm spongy layer	14.97	14.53	94.15	29.05
Thickness of cuticle (µm)	24.35	23.86	96.01	48.16

LA = Leaf area

these characters, thickness of cuticle had a very high GCV of 23.86. Other characters, number of cells per mm spongy layer, thickness of leaf midrib, thickness of spongy layer, thickness of palisade layer, thickness of the lamina and the number of cells per mm of palisade layer had a GCV of 14.53, 14.22, 14.09, 13.24, 10.46 and 5.78 respectively. Thickness of cuticle had the highest PCV value of 24.35. It was followed by the characters-thickness of spongy layer (18.67), number of cells per mm spongy layer (14.97), thickness of leaf midrib (14.41), thickness of palisade layer (13.56), thickness of lamina (10.93) and the number of cells per mm palisade layer (6.28).

3.3.1.4 Bark structural characters

The phenotypic and genotypic coefficients of variation for the bark structural characters in the third year are depicted in Table 23. The GCV for the 16 bark structural characters studied ranged from 11.57 to 55.62. Maximum GCV was estimated for the total cross sectional area of latex vessels (55.62), followed by the average distance between latex vessel rows in the soft bark region (38.13), number of latex vessel rows in the soft bark (35.35), total number of latex vessel rows (30.01), frequency of phloic rays (24.79), thickness of the hard bark (22.69), height-width ratio of phloic rays (21.51), density of latex vessels (18.08), diameter of latex vessels (17.42), width of phloic rays (16.88), soft bark thickness in percentage (15.87), total bark thickness (15.53), soft bark thickness (15.38), height of phloic rays (13.01) and hard bark thickness in percentage (11.57).

Phenotypic coefficient of variation was maximum for the character total cross sectional area of latex vessels (58.53), followed by average distance between latex vessel rows in the soft bark (38.34), number of latex vessel in the hard bark (36.57), number of latex vessel in the soft bark (36.24), total number of latex vessel rows (30.75), frequency of phloic rays (26.02), hard bark thickness (23.28), height / width ratio of phloic rays (22.19), width of phloic rays (18.39), density of latex vessels (18.33), diameter of latex vessels (18.05), soft bark thickness in percentage (16.68), soft bark thickness in mm (16.0), total bark thickness (15.73), height of phloic rays (13.34) and hard bark thickness in percentage (12.16).

Table 23. Coefficients of variation, heritability and genetic advance for bark structural characters in the third year.

Character	Coefficients of variation (%)		Heritability in broad sense (%)	Genetic advance as % over mean
	Phenotypic	Genotypic		
Total bark thickness (mm)	15.73	15.53	97.61	31.62
Soft bark thickness (mm)	16.00	15.38	92.35	30.44
Hard bark thickness (mm)	23.28	22.69	94.96	45.55
Soft bark thickness in %	16.68	15.87	90.50	31.10
Hard bark thickness in %	12.16	11.57	91.00	22.68
No of LVR in soft bark	36.24	35.35	95.15	71.03
No of LVR in hard bark	36.57	34.10	86.90	65.48
Total no of latex vessel rows	30.75	30.01	95.24	60.34
Density of LV per row per mm	18.33	18.08	97.32	36.75
Diameter of latex vessels (µm)	18.05	17.42	93.20	34.65
Total CSA of LV (mm^2)	58.53	55.62	90.29	108.86
AD. between LVR in SB (mm)	38.34	38.13	98.95	78.14
FQ of PR/ 0.01mm^2 area	26.02	24.79	90.76	48.66
Height of phloic rays (mm)	13.34	13.01	95.06	26.13
Width of phloic rays (mm)	18.39	16.88	84.30	31.93
Height/width ratio of PR	22.19	21.51	94.00	42.96

LVR= Latex vessel rows; AD= Average distance; FQ= Frequency; LV= Latex vessels; CSA= Cross sectional area; SB= Soft bark; PR= Phloic rays.

3.3.2 Heritability (broad sense)

Heritability estimated in the broad sense, along with the genetic advance expected, expressed over mean values were estimated for all the characters studied and is presented in Tables 20-23.

3.3.2.1 Morphological characters

Among the various growth characters indicating the early vigour of the plants (Table 20), very high heritability estimates (in the broad sense) was recorded for the characters girth of the plants in first four quarters (60.37%, 60.11%, 61.20% and 60.08% respec-

tively) and height of the plants in the second quarter (60.16%). Medium estimates of heritability were recorded for the characters height of the plants in the first third and fourth quarters (54.08%, 56.08% and 51.58% respectively), number of leaf flushes per plant in the four quarters (36.16%, 52.06%, 54.44% and 57.71% respectively), total number of leaves per plant in the four quarters (44.58%, 58.42%, 57.69% and 57.65% respectively), inter flush distance (41.18%), total leaf area in the fourth quarter (49.16%) and leaf area index in the fourth quarter (48.99%). Petiole length recorded in the fourth quarter had a low estimate of heritability (24.08).

3.3.2.2 Test tap yield over three years

Dry rubber yield (Table 21) had a very high heritability estimate in the first and third year (85.17% and 66.67% respectively) followed by that in the second year yield with a medium heritability (45.5%).

3.3.2.3 Leaf structural characters

Among the leaf stomatal characters, (Table 22) number of epidermal cells per mm^2 area of the leaf abaxial surface had a high heritability estimate of 94.65%, followed by the stomatal index (84.42%) and the number of stomata per mm^2 area (78.22%) while the single leaflet area showed only a medium heritability estimate of 30.43%. Very high heritability estimates were recorded for the thickness of the leaf midrib (97.34%), followed by the thickness of the cuticle (96.01%), thickness of the palisade layer (95.38%), number of cells per mm spongy layer (94.15%), thickness of the lamina (91.67%) and number of cells per mm palisade layer (84.96%). Thickness of the spongy layer had a medium heritability estimate of 56.95%.

3.3.2.4 Bark structural characters

Very high heritability estimates were recorded by all the bark structural characters studied (Table 23). The average distance between the latex vessels in the soft bark region recorded the highest heritability estimate (98.95%). It was followed by the characters total bark thickness (97.61%), density of latex vessels per row per mm circumference (97.32%),

number of latex vessels in the soft bark (95.15%), height of phloic rays (95.06%), height / width ratio of phloic rays (94%), thickness of the hard bark (94.96%), diameter of latex vessels (93.2%), thickness of the soft bark (92.35%), frequency of phloic rays (90.76%), soft bark thickness in percentage (90.50%), hard bark thickness in percentage (91.00%), total cross sectional area of latex vessels (90.29%), number of latex vessel rows in the hard bark (86.90%) and width of phloic rays (84.30%).

3.3.3 Genetic advance

Genetic advance as percentage of mean was estimated for all the characters studied.

3.3.3.1 Morphological characters

Among the growth characters studied in the first year of recording observation (Table 20) maximum genetic advance expressed as percentage over mean was recorded by the character total leaf area (51.47) followed by leaf area index (50.95). Medium genetic advance values were recorded for the growth characters total number of leaves in the fourth, third and second quarters (36.06, 32.97 and 32.12 respectively), height of the plants in the third, second, fourth and first quarters (30.36, 30.25, 30.19 and 28.9 respectively), girth in the third and fourth quarters (25.44 and 24.78 respectively), total number of leaves in the first quarter (24.22), girth in the second and first quarters (23.57 and 23.02 respectively) and number of leaf flushes in the fourth quarter (21.56). The number of leaves in the first quarter (11.27), number of leaf flushes in the second and third quarters (16.81 and 17.91 respectively), inter-flush distance (17.12) and petiole length (14.15), recorded a low genetic advance compared to the other characters.

3.3.3.2 Test tap yield over three years

Test tap yield recorded as dry rubber, over three years showed very high genetic advance of 140.98, 100.30 and 160.7 respectively (Table 21).

3.3.3.3 Leaf structural characters

Medium estimates of genetic advance were recorded for the stomatal characters,

number of stomata per mm^2 area of the leaf lamina (25.70), number of epidermal cells per mm^2 of leaf lamina (38.76) and stomatal index (29.78). The single leaflet area recorded a low genetic advance of 18.59. Maximum genetic advance of 48.16 was recorded for the characters thickness of cuticle, followed by number of cells per mm of spongy layer (29.05), thickness of leaf midrib (28.90), thickness of palisade layer (26.64), thickness of spongy layer (21.90) and thickness of lamina (20.64). Number of cells per mm palisade layer had a low genetic advance of 10.98 (Table 22).

3.3.3.4 Bark structural characters

Very high genetic advance of 108.86 was recorded by the total cross sectional area of latex vessels. Average distance between latex vessel rows in the soft bark had a genetic advance of 78.14 followed by number of latex vessel rows in soft bark (71.03); number of latex vessel rows in the hard bark (65.48), total number of latex vessel rows (60.34); frequency of phloic rays (48.66); thickness of the hard bark (45.55); height/width ratio of phloic rays (42.96); density of latex vessels per row per mm distance (36.75); diameter of latex vessels (34.65); width of phloic rays (31.93); total bark thickness (31.62); thickness of soft bark in percentage (31.10); thickness of soft bark (30.44); height of phloic rays (26.13) and thickness of hard bark in percentage (22.68) (Table 23).

3.4 Character associations

The phenotypic, genotypic and environment correlation coefficients of the yield with a set of morphological characters at the age of 18 months and leaf and bark structural characters at the age of 42 months, were worked out. In general all the characters showed negligible correlation coefficients with the dry rubber yield while significant inter correlations were recorded between certain characters.

3.4.1 Morphological characters

The phenotypic, genotypic and environmental correlation coefficients of the morphological characters at the end of first year are depicted in Table 24. Test tap yield recorded a negative genotypic correlation with girth (-0.0667); number of leaf flushes(-0.0905);

Table 24. Correlation coefficients of growth characters with yield in the first year

Character		Yield	Girth	No of leaf flushes	Total no of leaves	LAI
Yield ($g\ t^{-1}\ t^{-1}$)	P	1	-0.0322	-0.0411	-0.0318	-0.0396
	G	1	-0.0667	-0.0905	-0.0810	-0.1075
	E	1	0.0593	0.0858	0.0949	0.1039
Girth (cm)	P		1	0.6862	0.8211	0.8013
	G		1	0.7387	0.8717	0.9050
	E		1	0.6164	0.7550	0.6946
No of leaf flushes	P			1	0.8702	0.7200
	G			1	0.9193	0.8095
	E			1	0.8074	0.6288
Total no of leaves	P				1	0.8785
	G				1	0.9310
	E				1	0.8286
Leaf area index (LAI)	P					1
	G					1
	E					1

P=Phenotypic correlation coefficient
G=Genotypic correlation coefficient
E=Environmental correlation coefficient

total number of leaves (-0.0810) and leaf area index (-0.1075), whereas very high positive genotypic correlation coefficients were recorded between girth and number of leaf flushes (0.7387), total number of leaves (0.8717) and leaf area index (0.9050). Similarly number of leaf flushes had a very high positive genotypic correlation with total number of leaves (0.9193) and leaf area index (0.8095) and the total number of leaves per plant had a high positive genotypic correlation with leaf area index (0.9310).

Dry rubber yield also showed low negative phenotypic correlation with the morpho-

logical characters girth, number of leaf flushes, total number of leaves and leaf area index (-0.0322, -0.0411, -0.0318 and -0.0396 respectively). Very high positive phenotypic correlations were observed for the characters- number of leaf flushes, total number of leaves and leaf area index with the girth of the plants (0.6862, 0.8211 and 0.8013 respectively). Number of leaf flushes per plant had a high positive phenotypic correlation of 0.8702 with the total number of leaves and 0.7200 with the leaf area index. Total number of leaves also had a high positive phenotypic correlation with leaf area index (0.8785).

The environmental correlation coefficients were also negligible between yield and the four morphological characters. Girth had a high positive environmental correlation coefficient of 0.6164 with the number of leaf flushes; 0.7550 with total number of leaves; and 0.6946 with leaf area index. Number of leaf flushes had a high positive environmental correlation with total number of leaves (0.8074) and leaf area index (0.6288). Total number of leaves had a high positive environmental correlation coefficient of 0.8286 with leaf area index.

3.4.2 Leaf structural characters

In general all the structural characters studied showed negligible correlation coefficients with dry rubber yield, but several structural characters showed significant inter correlations among themselves as given in Table 25.

Dry rubber yield recorded at 42 months after planting, had only negligible correlation values with almost all the leaf structural characters. Yield at this stage was found to have a negative genotypic correlation with single leaflet area (-0.4176) and a positive genotypic correlation with thickness of palisade tissue (0.2526). Number of stomata per mm^2 of the leaf area had a positive genotypic correlation with stomatal index (0.4085) but had a negligible negative association (-0.1580) with single leaflet area at the genotypic level. All the other leaf structural characters had a low and insignificant degree of genotypic association with the number of stomata. Stomatal index had a negative and low genotypic correlation with single leaflet area (-0.1512) and had genotypic correlation of -0.3833 with

thickness of palisade tissue, while all the other structural characters had only a negligible genotypic correlation with stomatal index.

Single leaflet area had a positive but very low degree of genotypic association with thickness of leaf blade (0.0827) and a negative and weak genotypic association with thickness of leaf midrib (-0.1651), thickness of palisade tissue (-0.0872) and thickness of cuticle (-0.0173). Thickness of lamina had a strong positive genotypic correlation with thickness of leaf midrib (0.4127), thickness of palisade tissue (0.6074), thickness of spongy tissue (0.6803) and number of cells per mm length of spongy layer (0.3056). Thickness of lamina had a weak negative genotypic correlation with number of cells per mm length of palisade layer (-0.0152) and a weak positive genotypic relation with the thickness of cuticle (0.0286). Positive genotypic correlation of the thickness of leaf midrib was observed with the characters thickness of palisade layer (0.1352), thickness of spongy layer (0.4459), number of cells per mm of palisade layer (0.0939), number of cells per mm length of spongy layer (0.1744), but had a negative correlation with the thickness of cuticle (-0.1611). Thickness of palisade layer had a positive genotypic correlation with the thickness of spongy layer (0.1927) and thickness of cuticle (0.2569) while it recorded negative genotypic association with the number of cells per mm length of palisade layer (-0.2397) and with the number of cells per mm length of spongy layer (-0.1049).

Thickness of spongy layer had a weak positive genotypic relation with number of cells per mm length of palisade layer (0.0361) and with number of cells per mm of spongy layer (0.2480) and a weak negative genotypic correlation with thickness of cuticle (-0.1363). Number of cells per mm length of palisade layer had a strong positive genotypic correlation with the number of cells per mm spongy layer (0.4994) but had a weak negative genotypic association of –0.0981 with the thickness of cuticle. Number of cells per mm spongy layer and the thickness of cuticle had a negative genotypic association of –0.3472.

The test tap yield had only negligible phenotypic correlation with the leaf structural characters. Number of stomata per mm^2 of the leaf lamina had a positive phenotypic correlation with stomatal index (0.4874) and a negligible but negative phenotypic correlation

with the single leaflet area (-0.0660) while there was only a negligible phenotypic association with the other leaf structural characters. Stomatal index had a weak and negative phenotypic association with single leaflet area (-0.0735) and similar weak phenotypic associations with the rest of the structural characters except with thickness of palisade tissue, which had a negative phenotypic association of –0.3498.

Single leaflet area had only negligible phenotypic correlation with most of the leaf structural characters viz- thickness of lamina, thickness of leaf midrib, thickness of palisade layer, thickness of spongy layer, number of cells per mm of palisade layer, number of cells per mm spongy layer and thickness of cuticle. Thickness of lamina had a high and positive phenotypic correlation with the thickness of leaf midrib (0.3851), thickness of palisade layer (0.5670), thickness of spongy layer (0.4935) and a lesser degree of positive association with number of cells per mm spongy layer (0.2869) and negligible relation with thickness of cuticle (0.0208). Negligible and negative phenotypic correlation existed between thickness of lamina and number of cells per mm of palisade layer (-0.0111). Thickness of leaf midrib had a positive phenotypic association with thickness of spongy layer (0.3317), number of cells per mm of spongy layer (0.1681), thickness of palisade layer (0.1316) and a very weak association with the number of cells per mm of palisade layer (0.0817). A negative, but weak association was recorded with thickness of cuticle (-0.1513). Thickness of palisade layer had a positive phenotypic association with thickness of spongy layer (0.1427) and thickness of cuticle (0.2492). Similar, but negative phenotypic correlation was recorded for this character with number of cells per mm palisade layer (-0.2033) and number of cells per mm of spongy layer (-0.1056). Thickness of spongy layer had very negligible positive phenotypic correlation with number of cells per mm palisade layer (0.0362) and number of cells per mm spongy layer (0.1884) and a weak negative phenotypic association with thickness of cuticle (-0.0848). Number of cells per mm palisade layer had a positive phenotypic association with number of cells per mm spongy layer (0.4542) and a weak negative association with thickness of cuticle (-0.0881). Number of cells per mm spongy layer had a negative phenotypic association with the thickness of cuticle (-0.3303).

Table 25. Correlation coefficients of leaf structural characters with yield in the third year.

Character Code		1	2	3	4	5	6	7	8	9	10	11
1	P	1	-0.0327	-0.0925	-0.0116	0.0157	-0.0793	0.2023	0.0129	-0.1313	-0.0604	-0.1111
	G	1	-0.0138	-0.0793	-0.4176	0.0147	-0.1029	0.2526	0.0128	-0.1730	-0.0797	-0.1461
	E	1	-0.0847	-0.1450	0.1479	0.0258	0.0421	0.0028	0.0133	-0.0028	-0.0213	-0.0545
2	P		1	0.4874	-0.0660	0.0411	0.1327	-0.1262	0.0582	0.1142	0.0662	-0.0965
	G		1	0.4085	-0.1580	0.0208	0.1603	-0.1334	0.0913	0.1223	0.0811	-0.1082
	E		1	0.8439	0.0273	0.1747	-0.0961	-0.1093	-0.0090	0.0797	-0.0308	-0.0298
3	P			1	-0.0735	-0.1034	0.0785	-0.3498	0.1360	0.1591	-0.0216	-0.1404
	G			1	-0.1512	-0.1251	0.0943	-0.3833	0.2325	0.1834	-0.0129	-0.1506
	E			1	0.0082	0.0590	-0.1105	-0.0685	-0.0976	0.0235	-0.1070	0.0608
4	P				1	0.0284	-0.0834	-0.0485	0.0151	-0.0619	0.0234	-0.0105
	G				1	0.0827	-0.1651	-0.0872	0.0902	-0.1539	0.0791	-0.0173
	E				1	-0.0628	0.0447	-0.0101	-0.0406	0.0501	-0.0934	-0.0072
5	P					1	0.3851	0.5670	0.4935	-0.0111	0.2869	0.0208
	G					1	0.4127	0.6074	0.6803	-0.0152	0.3056	0.0286
	E					1	-0.1080	-0.0215	0.0088	0.0210	0.0405	-0.1080
6	P						1	0.1316	0.3317	0.0871	0.1681	-0.1513
	G						1	0.1352	0.4459	0.0939	0.1744	-0.1611
	E						1	0.0382	-0.0054	0.0264	0.0271	0.1464
7	P							1	0.1427	-0.2033	-0.1056	0.2492
	G							1	0.1927	-0.2397	-0.1049	0.2569
	E							1	0.0041	0.1549	-0.1209	0.0747
8	P								1	0.0362	0.1884	-0.0848
	G								1	0.0361	0.2480	-0.1363
	E								1	0.0441	0.0419	0.1242
9	P									1	0.4542	-0.0881
	G									1	0.4994	-0.0981
	E									1	0.0729	0.0086
10	P										1	-0.3303
	G										1	-0.3472
	E										1	0.0034
11	P											1
	G											1
	E											1

1. Yield (g t^{-1} t^{-1})
2. No of stomata/ mm^2 of leaf area
3. Stomatal index
4. Single leaflet area (cm^2)
5. Thickness of lamina (μm)
6. Thickness of leaf midrib (mm)
7. Thickness of Palisade layer (μm)
8. Thickness of spongy layer (μm)
9. No of cells/mm palisade layer
10. No of cells/mm spongy layer
11. Thickness of cuticle(μm)

P=Phenotypic correlation coefficient
G=Genotypic correlation coefficient
E=Environmental correlation coefficient

Dry rubber yield on test tapping showed a similar trend of weak association at the environmental level with the various leaf structural characters as in the case of genotypic and phenotypic correlation coefficients. No of stomata per mm^2 area of leaf surface had a positive environmental correlation coefficient with stomatal index (0.8439) whereas it had a weak degree of association with other leaf structural characters. For all the other leaf structural characters the inter-correlation coefficients among themselves were very weak and thus insignificant.

3.4.3 Bark structural characters

The phenotypic, genotypic and environmental correlation coefficients of the dry rubber yield at 42 months after planting, with the various bark structural characters of the wild genotypes studied are shown in Table 26, 27 and 28 respectively.

Phenotypic correlation coefficients between the test tap yield of the wild genotypes and the bark structural characters studied showed weak associations with most of the characters (Table 26). Moderately strong and positive correlations of the test tap yield with number of latex vessel rows in soft bark region (0.2567), total number of latex vessel rows (0.1868) and the total cross sectional area of latex vessels (0.1176) were recorded. Test tap yield had a moderate and negative phenotypic correlation with height of phloic rays (-0.2799) while it had weak correlation with other structural characters.

Total bark thickness had a high positive phenotypic correlation with soft bark thickness (0.5033) and hard bark thickness (0.9054) and a moderate association with the characters number of latex vessel rows in the soft bark (0.3032), number of latex vessel rows in the hard bark (0.2334), total number of latex vessel rows (0.3028) and total cross sectional area of latex vessels (0.1940). The rest of the characters had only a weak association with the bark thickness. Soft bark thickness had a moderate degree of association at the phenotypic level with number of latex vessel rows in the soft bark region (0.1802), number of latex vessel rows in the hard bark (0.1476), total number of latex vessel rows (0.1930) and

the total cross sectional area of latex vessels (0.1323), while the rest of the characters had only a weak phenotypic correlation with soft bark thickness. Hard bark thickness had a positive phenotypic correlation with number of latex vessels in the soft bark (0.2614), number of latex vessels in the hard bark (0.1967), total number of latex vessel rows (0.2547), density of latex vessels (0.1455) and total cross sectional area of latex vessels (0.1581). The phenotypic correlation between hard bark thickness and the remaining characters were found to be negligible.

Number of latex vessels in the soft bark had a positive phenotypic correlation with the number of latex vessels in the hard bark (0.4908), total cross sectional area of latex vessels (0.5506) with a high correlation coefficient of 0.9098 with the total number of latex vessel rows. This character showed a high but negative phenotypic association with average number of latex vessel rows in the soft bark (-0.5199) and weaker associations with the remaining structural traits. Number of latex vessel row in the hard bark had a high positive phenotypic correlation with the total number of latex vessel rows (0.7613) and total cross sectional area of latex vessels (0.5218) and a negative correlation with average distance between latex vessels in the soft bark (-0.3393). Total number of latex vessel rows had a high positive phenotypic correlation with the total cross sectional area of latex vessels (0.6149) and had a high negative correlation with average distance between the latex vessels in the soft bark (-0.5122). Weak associations were recorded for the remaining characters with the total number of latex vessel rows.

Average distance between the latex vessel rows in the soft bark region had a negative phenotypic association with the total cross sectional area of the latex vessels (-0.2780) and had very weak phenotypic correlation with the remaining characters. Frequency of phloic rays had a positive phenotypic correlation with the density of latex vessels per mm circumference (0.2037) and with the total cross sectional area of latex vessels (0.1226) and a negative association with the height of phloic rays (-0.2314). The remaining characters exhibited only weak correlation with the frequency of phloic rays. Height of

phloic rays had a positive phenotypic association with the width of the phloic rays (0.2169) and height/width ratio (0.5500) with negligible correlation coefficients with rest of the characters. Width of the phloic rays had a high negative phenotypic correlation with the height/width ratio (-0.6477) and a positive but lesser degree of association with the diameter of latex vessels (0.2721) with the rest of the characters showing only a weak association with it. Height / width ratio of phloic rays had a positive correlation of 0.1972 with the density of latex vessels per mm circumference and a negative association with the diameter of latex vessels (-0.1542) with very weak correlation with total cross sectional area of latex vessels. Density of latex vessels had a positive association with the total cross sectional area of the latex vessels (0.3388), while the diameter of latex vessels had a high positive phenotypic correlation with the total cross sectional area of the latex vessels (0.6075).

Test tap yield recorded a very weak genotypic correlation coefficient, with most of the bark structural characters studied (Table 27), except with number of latex vessels in the soft bark region (0.2990), total number of latex vessel rows (0.2237) and with similar but negative associations with height of phloic rays (-0.3568) and height / width ratio of phloic rays (-0.2156).

Bark thickness of the wild genotypes had a high positive genotypic correlation with the characters- soft bark thickness (0.5307), hard bark thickness (0.9120), number of latex vessel rows in the soft bark (0.3180), number of latex vessel rows in the hard bark region (0.2492), total number of latex vessel rows (0.3129) and total cross sectional area of latex vessels (0.2080). All the other bark structural traits exhibited only negligible genotypic correlation with bark thickness. Soft bark thickness had weak but positive genotypic correlation coefficient with most of the bark structural characters like hard bark thickness (0.1365), number of latex vessel rows in the soft bark region (0.1955), number of latex vessel rows in the hard bark region (0.1699), total number of latex vessel rows (0.2119) and the total cross sectional area of latex vessels (0.1467). Rest of the characters had only

a negligible degree of genotypic correlation with the soft bark thickness. Hard bark thickness also showed the same trend with the characters number of latex vessel rows in the soft bark region, number of latex vessel rows in the hard bark region and the total number of latex vessels rows recording positive genotypic correlation coefficients of 0.2775, 0.2109 and 0.2636 respectively, while the rest of the characters had only a weak genotypic correlation with the hard bark thickness.

Number of latex vessel rows in the soft bark region had a high and positive genotypic correlation with number of latex vessel rows in hard bark (0.5438), total number of latex vessel rows (0.9308) and total cross sectional area of latex vessels (0.5802). It had a significant but negative genotypic correlation with average distance between latex vessel rows in the soft bark region (-0.5352). Number of latex vessel rows in the soft bark had only a very weak genotypic correlation with the rest of the characters. Whereas the number of latex vessel rows in the hard bark had a high and positive genotypic correlation with total number of latex vessel rows (0.8068) and total cross sectional area of latex vessels (0.5697). It had a negative genotypic association with the average distance between latex vessel rows in the soft bark region (-0.3667) while the association with the rest of the characters was negligible. Total number of latex vessels rows of the wild genotypes had a negative and high degree of genotypic correlation with the average distance between the latex vessel rows in the soft bark (-0.5285), but had a high positive genotypic correlation with the total cross sectional area of latex vessels (0.6445).

Average distance between latex vessel rows in the soft bark had a negative genotypic correlation with the total cross sectional area of latex vessels (-0.2965) and had only a negligible association with all the other bark structural traits. Frequency of phloic rays had a positive genotypic correlation of 0.2159 with the density of latex vessel rows per mm circumference and a less stronger and positive association with the total cross sectional area of latex vessels (0.1310). It had a negative association with the height of phloic rays

(-0.2460), with weak associations with the rest of the characters. Height of phloic rays had a high and positive genotypic correlation with the height/width ratio of phloic rays (0.5535) and a lesser degree of positive association with the width of phloic rays (0.2376). Other characters had only a negligible association with the height of phloic rays. Width of phloic rays had a high negative genotypic correlation with height / width ratio of phloic rays (-0.6586) and a positive association with the density of latex vessels per mm circumference (0.2989) with very weak associations with other traits. Height / width ratio had a positive genotypic correlation with the density of latex vessels (0.2035) and a negative correlation with diameter of latex vessels (-0.1587) and a very weak association with the total cross sectional area of latex vessels. Density of latex vessels had a negative and weak genotypic association with the diameter of latex vessels (-0.0752) and a positive association with the total cross sectional area of latex vessels (0.3589). Diameter of latex vessels had a high positive genotypic correlation coefficient of 0.6284 with the total cross sectional area of latex vessels.

Test tap yield had a positive environmental (Table 28) correlation with the total cross sectional area of latex vessels (0.2981). Bark thickness had a high environmental correlation of 0.7901 with the hard bark thickness; soft bark thickness had a high negative environmental correlation with the hard bark thickness (-0.6078); number of latex vessel rows in the soft bark had a positive environmental association with total number of latex vessel rows (0.4940); number of latex vessel rows in the hard bark had a positive correlation with the total number of latex vessel rows (0.3420); total number of latex vessel rows had a positive phenotypic correlation with the total cross sectional area of the latex vessels (0.2535); height of phloic rays had a high positive correlation with the height/width ratio (0.4952); a high negative association of width of phloic rays with the height/width ratio of phloic rays (-0.5820); and a positive association of 0.3792 between the diameter of latex vessels and total cross sectional area of latex vessels. All the other environmental inter-correlations were found to be of insignificant nature.

Table 26. Phenotypic correlation coefficients of bark structural characters with yield in the third year

Character	Code	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
Yield (g t^{-1} t^{-1})	1	1	0.0546	0.0133	0.0564	0.2567	0.0145	0.1868	-0.0859	-0.0256	-0.2799	-0.0200	-0.1748	0.0106	-0.0495	0.1176
Total BT (mm)	2		1	0.5033	0.9054	0.3032	0.2334	0.3028	-0.0593	0.0564	-0.0537	0.0545	-0.1175	0.1362	-0.0249	0.1940
Soft BT (mm)	3			1	0.0890	0.1802	0.1476	0.1930	-0.0343	0.0972	-0.0240	0.0000	-0.0639	0.0225	-0.0853	0.1323
Hard BT (mm)	4				1	0.2614	0.1967	0.2547	-0.0513	0.0180	-0.0508	0.0628	-0.1052	0.1455	0.0128	0.1581
No of LVR in SB	5					1	0.4908	0.9098	-0.5199	0.1147	-0.1358	-0.0954	-0.0569	0.1084	0.0339	0.5506
No of LVR in HB	6						1	0.7613	-0.3393	0.0932	-0.0088	0.0947	-0.1230	0.1429	0.1427	0.5218
TLVR	7							1	-0.5122	0.1279	-0.1012	-0.0247	-0.1007	0.1310	0.0825	0.6149
AD between LVR in SB	8								1	-0.0631	-0.0061	0.0655	0.0026	-0.1401	0.0835	-0.2780
Frequency of phloic rays/ 0.01mm^2 area	9									1	-0.2314	0.0182	-0.1245	0.2037	0.0221	0.1226
Height of phloic rays (mm)	10										1	0.2169	0.5500	0.0569	0.0654	-0.0401
Width of phloic rays (mm)	11											1	-0.6477	-0.1025	0.2721	0.0055
Height/width ratio of phloic rays	12												1	0.1972	-0.1542	-0.0529
Density of latex vessels per row per mm	13													1	-0.0710	0.3388
Diameter of latex vessels (µm)	14														1	0.6075
Total CSA of latex vessels (mm^2)	15															1

BT = Bark thickness; LVR=Latex vessel rows; SB=Soft bark; HB=Hard bark:CSA=Cross sectional area; AD = Average distance

Table 27. Genotypic correlation coefficients of bark structural characters with yield in the third year

Character	Code	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
Yield ($g\ t^{-1}\ t^{-1}$)	1	1	0.0655	0.0095	0.0716	0.2990	0.0212	0.2237	-0.1022	-0.0183	-0.3568	-0.0356	-0.2156	0.0129	-0.0616	0.0826
Total BT (mm)	2		1	0.5307	0.9120	0.3180	0.2492	0.3129	-0.0607	0.0584	-0.0540	0.0536	-0.1180	0.1390	-0.0241	0.2080
Soft BT (mm)	3			1	0.1365	0.1955	0.1669	0.2119	-0.0364	0.0961	-0.0202	0.0129	-0.0734	0.0241	-0.0948	0.1467
Hard BT (mm)	4				1	0.2775	0.2109	0.2636	-0.0531	0.0228	-0.0540	0.0564	-0.1034	0.1503	0.0175	0.1720
No of LVR in soft bark	5					1	0.5438	0.9308	-0.5352	0.1220	-0.1486	-0.1073	-0.0611	0.1103	0.0311	0.5802
No of LVR in hard bark	6						1	0.8068	-0.3667	0.1053	-0.0073	0.1165	-0.1340	0.1620	0.1446	0.5697
TLVR	7							1	-0.5285	0.1301	-0.1098	-0.0263	-0.1072	0.1354	0.0858	0.6445
AD between LVR in SB	8								1	-0.0654	-0.0063	0.0703	0.0005	-0.1437	0.0890	-0.2965
Frequency of phloic rays/ $0.01 mm^2$ area	9									1	-0.2460	0.0306	-0.1411	0.2159	0.0223	0.1310
Height of phloic rays (mm)	10										1	0.2376	0.5535	0.0600	0.0755	-0.0434
Width of phloic rays (mm)	11											1	-0.6586	-0.1057	0.2989	0.0040
Height/width ratio of phloic rays	12												1	0.2035	-0.1587	-0.0551
Density of latex vessels per row per mm	13													1	-0.0752	0.3589
Diameter of latex vessels (µm)	14														1	0.6284
Total CSA of latex vessels (mm^2)	15															1

BT = Bark thickness; LVR=Latex vessel rows; TLVR Total no. of latex vessel rows: AD = Average distance

Table 28. Environmental correlation coefficients of bark structural characters with yield in the third year

Character	Code	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
Yield ($g\ t^{-1}\ t^{-1}$)	1	1	0.0178	0.0370	-0.0058	0.1424	-0.0082	0.0645	-0.0478	-0.0652	0.0411	0.0448	-0.0262	0.0014	-0.0054	0.2981
Total BT (mm)	2		1	0.0053	0.7901	-0.0949	0.0676	0.0321	0.0363	0.0290	-0.0480	0.0904	-0.1204	0.0280	-0.0480	-0.0278
Soft BT (mm)	3			1	-0.6078	-0.0446	-0.0172	-0.0879	0.0156	0.1096	-0.0823	-0.1164	0.0643	-0.0075	0.0370	-0.0155
Hard BT (mm)	4				1	-0.0483	0.0627	0.0805	0.0192	-0.0472	0.0127	0.1076	-0.1352	0.0290	-0.0653	-0.0167
No of LVR in soft bark	5					1	-0.0493	0.4940	-0.0146	0.0186	0.1199	0.0219	0.0169	0.0642	0.0806	0.1875
No of LVR in hard bark	6						1	0.3420	0.0292	-0.0035	-0.0309	-0.0546	-0.0200	-0.1043	0.1337	0.1506
TLVR	7							1	0.0551	0.1040	0.0729	-0.0082	0.0158	0.0175	0.0253	0.2535
AD between LVR in SB	8								1	-0.0343	0.0000	0.0000	0.0844	0.0557	-0.0789	0.0776
Frequency of phloic rays/ $0.01 mm^2$ area	9									1	-0.0378	-0.0855	0.0812	0.0101	0.0200	0.0420
Height of phloic rays (mm)	10										1	0.0000	0.4952	-0.0260	-0.1056	0.0023
Width of phloic rays (mm)	11											1	-0.5820	-0.0858	0.0225	0.0179
Height/width ratio of phloic rays	12												1	0.0641	-0.0867	-0.0280
Density of latex vessels per row per mm	13													1	0.0188	0.0472
Diameter of latex vessels (µm)	14														1	0.3792
Total CSA of latex vessels (mm^2)	15															1

BT = Bark thickness; LVR=Latex vessel rows; TLVR Total no. of latex vessel rows: AD = Average distance

3.5 Factor analysis

A pooled factor analysis of 33 characters representing morphological and anatomical traits of both leaf and bark viz. girth, height, number of leaf flushes, total number of leaves, total leaf area, leaf area index, inter-flush distance, length of petiole, number of stomata and epidermal cells per mm^2 of leaf area, stomatal index, single leaflet area, thicknesses of lamina, midrib, palisade and spongy layers, number of cells per unit length of palisade layer and spongy layer, thickness of cuticle, total bark thickness, soft bark and hard bark thicknesses, number of latex vessels in the soft and hard bark, total number of latex vessel rows, density of latex vessels per mm circumference, diameter of latex vessels, total cross sectional area of latex vessels, average distance between latex vessels in soft bark, frequency, height, width and height / width ratio of phloic rays, was carried out. The factors were subjected to varimax rotation. Twelve factors influencing 12 groups of characters out of the total 33 characters, were identified based on their factor loadings. The rotated factor matrix with the factor loadings and communalities for each of the 33 characters are given in Table 29.

The rotated factor matrix identified 12 factors that accounts for 82.3% of the total variability in the 33 variables. Factor one was associated with the characters- girth of the plant, height, number of leaf flushes per plant, total number of leaves per plant, total leaf area and leaf area index with a factor loading of 0.8439, 0.8793, 0.9067,0.9630, 0.9482 and 0.9475 respectively. Factor two was associated with the characters latex vessels in the hard bark (0.7759 factor loading), latex vessels in the soft bark (0.8861 factor loading), total number of latex vessel rows (0.9531 factor loading), average distance between the latex vessel rows with a negative correlation with the factor loading (-0.6477) and the total cross sectional area of laticifers. (0.6400 factor loading).

The characters total bark thickness with a factor loading of 0.9409, thickness of soft bark with a loading of 0.5214 and thickness of hard bark with a loading of 0.8427 were associated with factor number 3. Factor number 4 was associated with only two characters number of epidermal cells per unit area of leaf lamina and a negatively correlated stomatal

Table 29. Factor loadings and communalities of the pooled characters.

Slno	Character	Communality	Factor loadings											
			F1	F2	F3	F4	F5	F6	F7	F8	F9	F10	F11	F12
1	Girth of the plants (cm)	0.8159	0.8439											
2	Height of the plants (cm)	0.8876	0.8793											
3	Number of leaf flushes/plant	0.8828	0.9067											
4	Total number of leaves/plant	0.9575	0.9630											
5	Total leaf area (cm^2)	0.9341	0.9482											
6	Leaf area index	0.9318	0.9475											
7	Inter flush distance (cm)	0.8077										0.8208		
8	Petiole length (cm)	0.7515						0.7530						
9	No of stomata/mm^2 of leaf area	0.9340												0.9501
10	No of epidermal cells/mm^2 of leaf area	0.9445				0.9266								
11	Stomatal index	0.9535				-0.8758								
12	Single leaflet area (cm^2)	0.7512						0.7590						
13	Thickness of leaf blade (µm)	0.9082					0.9045							
14	Thickness of midrib (mm)	0.6785					0.5597							
15	Thickness of palisade layer (µm)	0.8353					0.5530							
16	Thickness of spongy layer (µm)	0.7525					0.7795							
17	No of cells /mm of palisade tissue	0.5884							0.5930					
18	No of cells /mm of spongy tissue	0.7639							0.7706					
19	Thickness of cuticle (µm)	0.6785							-0.7021					
20	Total bark thickness (mm)	0.9514			0.9409									
21	Soft bark thickness (mm)	0.6714			0.5214									
22	Hard bark thickness (mm)	0.8438			0.8427									
23	No of latex vessels in hard bark	0.6895		0.7759										
24	No of latex vessels in soft bark	0.8435		0.8861										
25	Total no of latex vessel rows	0.9414		0.9531										
26	Density of latex vessels/mm circumference	0.8032											0.849	
27	Diameter of latex vessels (µm)	0.8844								0.8917				
28	Total CSA of latex vessels (mm^2)	0.9162		0.6400										
29	Av. distance between latex vessels (mm)	0.6275		-0.6477										
30	Frequency of phloic rays/ 0.01mm^2 area	0.5972											0.4916	
31	Height of phloic rays (mm)	0.8666									0.8515			
32	Width of phloic rays (mm)	0.8507								0.6111				
33	Height /width ratio of phloic rays	0.9305									0.7154			

index with a factor loadings of 0.9266 and -0.8758 respectively. Four leaf structural traits - thickness of lamina, thickness of leaf midrib, thickness of palisade layer and thickness of spongy layer- were associated with the factor number 5, the respective factor loading being 0.9045, 0.5597,0.5530 and 0.7795. Factor six was associated with two distinct characters- length of the petiole and single leaflet area- where the factor loading were almost equal (0.7530 and 0.7590 respectively).

Factor seven was identified with another set of leaf structural characters - number of cells per unit length of palisade layer, number of cells per unit length of spongy layer and thickness of cuticle with factor loadings of 0.5930, 0.7706 and-0.7021 respectively. Characters width of phloic rays with a loading of 0.6111 and diameter of latex vessels with a loading of 0.8917 were associated with the next factor. Factor nine was associated with height of phloic rays (0.8515 factor loading) and height/width ratio of phloic rays (0.7154 factor loading).

The inter-flush distance was the lone character associated with the factor 10, with a factor loading of 0.8208. Frequency of phloic rays and density of latex vessels with a factor loadings of 0.4916 and 0.8490 were identified with the factor number 11. Factor 12 was associated with a single character number of stomata per unit area of leaf lamina with a factor loading of 0.9501. Thus the 12 factors could identify 12 groups of characters, which are related and can be expected to show likeness in their inheritance pattern.

3.6 Genetic divergence - D^2 analysis

Genetic divergence existing in the population of wild genotypes was assessed in terms of 'generalized group distance' using the Mahalanobis D^2 analysis. The genetic distance between the 81 treatments were determined by means of the values of uncorrelated linear combinations for 16 selected variables- girth of the plants, inter-flush distance, petiole length, total number of leaves per plant, thickness of lamina, thickness of cuticle, single leaflet area, total bark thickness, total number of latex vessel rows, average distance between latex vessel rows in the soft bark, frequency of phloic rays, height of phloic rays, width of phloic rays, diameter of latex vessels, density of latex vessels and test tap yield.

All the 81 genotypes were taken in all possible paired combinations to derive D^2 values.

The clustering of the genotypes was done by the by iterative relocation algorithm suggested by Friedman and Rubin (1967) and modified by Suresh and Unnithan (1996). Accordingly, the wild genotypes including the control clone, was grouped into 9 divergent clusters. The distribution of the genotypes in these clusters is presented in Table 30.

Table 30. Distribution of wild genotypes in divergent clusters

Cluster no	No of genotypes	Genotypes included
1	20	MT 948, MT 901, RO 381, AC 604, AC 627, MT 1064, RO 257, AC 694, MT 1007, AC 626, RO 868, AC 966, AC 979, RO 380, RO 364, RO 330, RO 328, AC 657, AC 706, MT 1063.
2	17	AC 654, RO 883, AC 953, RO 317, RO 316, MT 1031, RO 352, RO 886, RO 256, RO 338, RO 319, MT 929, AC 986, RO 876, RO 859, MT 1021, MT 920.
3	8	RO 311, AC 963, MT 1055, RO 894, AC 644, AC 733, AC 754, AC 650.
4	4	AC 647, AC 995, MT 899, MT 947.
5	8	MT 928, MT 1011, RO 255, AC 1043, MT 931, MT 906, RO 369, RO 322.
6	7	RO 287, MT 1077, RO 879, AC 1090, MT 1028, MT 944, MT 935.
7	6	MT 1024, MT 945, AC 632, RO 395, MT 1057, RO 399.
8	5	MT 1005, MT 1029, AC 959, AC 453, RO 254.
9	6	MT 1008, RRII 105, MT 1030, AC 629, AC 426, MT 1025.

Table 31. Inter and Intra cluster distances in D^2 analysis in the wild genotypes.

Cluster No	1	2	3	4	5	6	7	8	9
1	**281.07**	488.12	472.24	1448.45	545.02	677.88	531.4	1060.55	517.69
2		**312.31**	873.12	1164.29	515.62	533.7	838.92	645.63	695.78
3			**439.50**	2005.33	716.37	1046.26	772.79	542.21	627.44
4				**555.41**	1328.06	763.89	1774.35	827.84	1957.38
5					**339.09**	724.3	934.26	798.68	555.90
6						**391.64**	1087.1	686.16	1038.75
7							**541.58**	1529.07	789.61
8								**550.44**	1353.79
9									**504.31**

Intra cluster distances in bold letters

Maximum number of 20 genotypes was found in the first cluster with the genotypes MT 948, MT 901, RO 381, AC 604, AC 627, MT 1064, RO 257, AC 694, MT 1007, AC 626, RO 868, AC 966, AC 979, RO 380, RO 364, RO 330, RO 328, AC 657, AC 706 and MT 1063 included in the cluster. There were 17 genotypes in the second cluster. They were AC 654, RO 883, AC 953, RO 317, RO 316, MT 1031, RO 352, RO 886, RO 256, RO 338, RO 319, MT 929, AC 986, RO 876, RO 859, MT 1021 and MT 920. Eight genotypes each clustered together in the third (RO 311, AC 963, MT 1055, RO 894, AC 644, AC 733, AC 754 and AC 650) and in the fifth (MT 928, MT 1011, RO 255, AC 1043, MT 931, MT 906, RO 369 and RO 322) clusters. Fourth cluster included AC 647, AC 995, MT 899 and MT 947. Seven genotypes- RO 287, MT 1077, RO 879, AC 1090, MT 1028, MT 944 and MT 935 formed the sixth cluster. Seventh and ninth clusters had six genotypes each (MT 1024,MT 945, AC 632, RO 395, MT 1057, RO 399 and MT 1008, RRII105, MT 1030, AC 629, AC 426, MT 1025 respectively). Five genotypes viz., MT 1005, MT 1029, AC 959, AC 453 and RO 254 grouped together to form the eighth cluster.

The mean inter and intra cluster distances are given in Table 31. The intra cluster distances varied from 281.07 in the 1st cluster to 555.41 in 4th cluster. The inter cluster distances varied from a minimum of 472.24 between the clusters one and three, to a maximum of 2005.33 between 3rd and 4th clusters.

3.7 Performance Index

Performance index was worked out for the wild genotypes based on a set of 16 selected characters, viz., girth of the plants, inter-flush distance, length of petiole, total number of leaves per plant, thickness of lamina, thickness of cuticle, single leaflet area, total bark thickness, total number of latex vessel rows, average distance between latex vessel rows in the soft bark, frequency of phloic rays, height of phloic rays, width of phloic rays, diameter of latex vessels, density of latex vessels, and test tap yield. The genotypes ranked according to the performance index are presented in Table 32. Thirty-eight genotypes were found to have an index greater than the mean index value of 247.10. The popular control clone RRII 105 was ranked 65th with 64 wild genotypes ranked above it for the

set of characters pooled for this analysis. By selecting the best 10 per cent of the wild genotypes the following eight genotypes can be considered superior ones for the overall performance of several characters- RO 395, AC 953, AC 1043, RO 876, AC 654, MT 944, RO 399 and RO 894. Character wise mean values for the eight genotypes selected, shows the general dominance of morphological characters determining the high vigour of the wild genotypes along with the accountable contribution of other structural characters (Table 33).

Table 32. Wild genotypes ranked on the basis of Performance index.

Sl no	Genotype	Index	Ranking
(1)	(2)	(3)	(4)
1	RO 395	293.27	1
2	AC 953	288.02	2
3	AC 1043	286.90	3
4	RO 876	286.32	4
5	AC 654	285.97	5
6	MT 944	285.31	6
7	RO 399	285.19	7
8	RO 894	285.02	8
9	AC 754	283.78	9
10	RO 338	283.55	10
11	RO 319	283.32	11
12	RO 883	282.81	12
13	AC 632	282.08	13
14	RO 311	279.22	14
15	AC 650	278.23	15
16	MT 1025	274.34	16
17	RO 287	273.12	17
18	RO 328	271.40	18
19	MT 947	271.24	19
20	MT 1030	267.03	20
21	MT 935	266.73	21
22	RO 364	266.66	22
23	RO 317	263.86	23
24	RO 352	263.59	24
25	MT 945	262.71	25
26	MT 1024	261.90	26
27	RO 369	261.73	27
28	RO 330	261.00	28
29	AC 995	258.29	29
30	RO 879	258.22	30
31	AC 453	257.37	31
32	AC 986	256.15	32
33	RO 322	255.72	33
34	RO 868	254.33	34
35	AC 733	253.35	35
36	AC 629	251.43	36
37	RO 886	251.14	37
38	RO 859	247.83	38
39	AC 647	246.32	39
40	RO 316	245.58	40

Table 32. Continued

(1)	(2)	(3)	(4)
41	MT 1028	245.36	41
42	RO 381	244.85	42
43	AC 959	244.77	43
44	AC 979	244.66	44
45	AC 706	244.33	45
46	RO 255	243.17	46
47	AC 604	241.03	47
48	AC 657	240.85	48
49	AC 966	240.38	49
50	AC 694	240.30	50
51	AC 963	238.27	51
52	MT 1008	237.46	52
53	AC 644	236.56	53
54	MT 899	234.00	54
55	AC 627	232.16	55
56	MT 1031	231.53	56
57	RO 254	230.75	57
58	MT 931	230.65	58
59	MT 1064	230.41	59
60	RO 256	230.29	60
61	MT 928	228.76	61
62	AC 626	228.55	62
63	MT 920	227.02	63
64	MT 948	225.85	64
65	RRII 105	223.18	65
66	MT 901	223.10	66
67	MT 1005	221.91	67
68	AC 426	220.97	68
69	MT 1007	216.91	69
70	RO 380	216.61	70
71	AC 1090	215.08	71
72	MT 1063	213.80	72
73	MT 1077	210.08	73
74	MT 906	209.49	74
75	RO 257	209.17	75
76	MT 1011	205.64	76
77	MT 1055	205.33	77
78	MT 1029	200.16	78
79	MT 1057	198.88	79
80	MT 929	192.79	80
81	MT 1021	189.61	81

Table 33. Mean values of selected characters for the selected genotypes.

Character	Genotypes selected								Control RRII 105	Gl. Mean
	RO 395	AC 953	AC 1043	RO 876	AC 654	MT 944	RO 399	RO 894		
Inter-flush D.(cm)	22.84	19.18	19.27	21.34	17.67	24.49	13.86	14.99	12.74	19.81
Petiole length (cm)	21.64	25.38	26.19	29.47	21.33	19.16	19.31	19.84	14.79	21.86
Total no of leaves	107.00	59.00	97.70	77.80	100.3	82.70	73.20	116.20	62.80	69.80
Thickness of lamina (µm)	0.15	0.18	0.13	0.16	0.16	0.17	0.16	0.13	0.15	0.14
Thickness of LC (µm)	3.45	2.05	3.10	1.90	2.88	1.65	2.70	2.15	3.67	2.57
Single leaflet area (cm^2)	113.62	110.83	121.88	133.70	89.50	120.34	118.34	89.03	60.83	95.23
Total BT (mm)	4.00	2.79	2.47	2.44	2.10	3.64	2.94	3.35	3.06	2.86
Total no of LVR	7.99	5.99	7.50	4.52	7.00	4.01	11.01	8.25	8.00	5.81
AD.between LV in SB (mm)	0.15	0.31	0.27	0.34	0.33	0.34	0.14	0.24	0.20	0.31
FQ. of PR /0.01mm^2	3.50	4.99	5.01	4.01	4.00	2.99	4.00	2.99	4.00	3.78
Height of PR (mm)	0.25	0.30	0.25	0.26	0.28	0.31	0.32	0.32	0.21	0.29
Width of PR (mm)	0.05	0.05	0.06	0.05	0.06	0.06	0.05	0.04	0.05	0.05
Diameter of LV (µm)	21.25	14.98	27.79	21.01	22.75	17.28	26.51	19.64	16.30	21.46
Density of latex vessels	14.99	13.75	17.75	14.25	14.00	12.50	11.50	25.00	23.76	17.15
Girth (cm)	16.92	19.27	19.72	18.08	19.57	17.84	15.92	21.99	22.35	18.53
Yield ($g\ t^{-1}\ t^{-1}$)	0.48	0.09	0.23	0.24	0.27	0.36	1.28	0.35	2.35	0.53

D = distance; AD = Average distance; LC = Leaf Cuticle; BT = Bark thickness; LVR = Latex vessel rows; LV = Latex Vessels; SB = Soft bark; FQ = frequency; PR = Phloic Rays.

Discussion

Hevea brasiliensis is a highly heterozygous perennial, plantation crop species. Substantial amount of work has been done in this crop in the existing Wickham clones, over the decades, which resulted in remarkable genetic improvement. But very little work has been done in India in the wild germplasm of the crop, introduced from its centre of origin, in order to genetically evaluate this unexploited material for the benefit of utilizing them in the breeding programmes. Except for certain preliminary studies (Varghese *et al.*, 1988,1989; Abraham *et al.*, 1992,1995; Mercy *et al.*, 1993a, 1995; Madhavan *et al.*, 1993, 1996; Reghu *et al.*, 1996 and Rao *et al.*, 1999 in the estimation of variability, character associations and genetic divergence in the wild germplasm of *H. brasiliensis*, from India, this is the first detailed study in the wild germplasm of this crop, in the first three years of its growth in a statistically laid out field evaluation trial, from this country.

Morphological description as well as agronomic assessment of the wild germplasm has very high significance in the best utilization of this material for the genetic improvement of this crop. Rubber yield in *H. brasiliensis* is a manifestation of various morphological, anatomical, biochemical and physiological characters of the tree. These factors are ultimately manifested in the volume of latex obtained by tapping and the quantum of rubber it contains (Pollinere, 1966). Girth is considered as the most important morphological parameter of growth and vigour in

rubber. Yield and vigour in *H. brasiliensis* are hardly separable (Simmonds, 1989). A very vigorous growth in the early growth phase of the tree can be expected to produce good yield even in the initial years of tapping. The increase in girth during the first three years is relatively small which is greatly accelerated once the tree branches and the crown takes shape.

Rubber yield in *H. brasiliensis* is highly heritable and the potentiality of a clone is expressed early during the nursery stage. Growth rate during the pre-exploitation phase and that after opening of the tree are equally important factors influencing yield of *H. brasiliensis* (Premakumari *et al.*, 1988). Tan (1998) reported that the nursery yield was significantly correlated with mature yield over 5 years of tapping, which can be considered as a reasonable predictor for mature yield. Thus the yield recorded in the juvenile phase of the crop gives a satisfactory comparison of the large collection of wild germplasm. Other morphological growth characters like girth and foliar characters like number of leaves, rate of production of leaves, inter flush distance, length of the petioles etc in the initial stage of plant growth, give a fair indication of the vigour of the clones in its juvenile phase helping the breeder to apply appropriate selection index for yield and yield contributing morphological characters.

4.1 Juvenile characterisation

Morphological characterisation of a sample of 80 genotypes, representing a reasonable collection of the wild germplasm of *H. brasiliensis*, from three provenances-Acre, Rondonia and Mato Grosso, was carried out in this study. Characterisation forms the first important aspect in the evaluation, cataloguing and the successful utilization of the wild germplasm for broadening the narrow genetic base of the crop. The hitherto undescribed wild genotypes have been described for easily distinguishable and highly heritable morphological traits using a set of descriptors prepared for the purpose adopting the terminologies suggested by Dijkman (1951); Jayasekera *et al.*, (1984); Lawrence (1967) and Mercykutty *et al.*, (1991) in rubber.

In India, Varghese *et al.*, (1989) has described a set of wild genotypes based on their juvenile morphological characters like branching habits, variability in leaf size and shape, leaf margins, leaf scars, arrangement of leaves, presence of pulvinus, separation of leaf flushes, num-

ber of leaves and habit of the plants. Very few reports are there from other countries on detailed morphological characterization of the wild genotypes. Clement-Demange *et al.*, (1997) described the Brazilian germplasm to show some morphological distinctness among the three provenances and observed that Acre and Rondonia genotypes were tall and straight trees with very few branches growing at a high level of the trunk. Mato Grosso genotypes were more similar to Wickham clones with abundant branches growing at a low level of the trunk. Huasun and Shaofu (1990) have reported the attempts for early stage prediction by means of identification of morphological characters of high yielding and cold resistant clones. They reported high yielding clones to have medium to long petioles and yellowish green leaves and leaf vein colour. Cold resistance was related to short to relatively short petioles, blue green to dark green leaves and leaf vein colour.

Mohd. Noor and Ibrahim (1986) from Malaysia had described a descriptor for characterization and evaluation of the wild *Hevea* germplasm, where the characterization was categorized into three sets viz. plant characteristics, latex and rubber properties and diseases. Some of the descriptors which was in agreement with the present study was growth vigour, habit of the stem, inter node length, shape of leaves, length of petioles and petiolules, angle of petiolules, shape of leaf storey and foliage density. Ong *et al.*, (1983) also from Malaysia, reported on the variations in leaf characters like shape, margin, length of petioles and petiolules and inter-node length, among the wild genotypes. In Ivory Coast, Clement-Demange *et al.*, (1990a) reported that leaf morphological characters of the genotypes from Rondonia were intermediate between Acre and Mato Grosso in accordance with the geographical position of the provenances.

Of the 80 wild genotypes, 25 belonged to the state of Acre, 27 belonged to the state of Rondonia and 28 to Mato Grosso. The genotypes showed considerable variation for most of the characters recorded (Table 2). In general, individual plants within a genotype showed similar character expressions, as is naturally expected in vegetatively propagated populations. There was no specific pattern noted in the expression of traits between the three states. The variation in the expression of the characters were thus distributed over the 80 genotypes for the characters like height, girth, separation of leaf storey, shape and size of petiole, size and orientation of the

petiolule, prominence of extra floral nectary, shape, size and colour of leaves, nature of leaf margin, cross sectional appearance of leaf blade, leaf tip, lateral appearance of leaves, leaflet arrangement and prominence of veins. However, characters like branching habit, nature of axillary buds and leaf scars, leaf storey shape, external appearance of leaf flushes, prominence of pulvinus, petiole angle, luster of leaves, leaf vein colour and lamina texture exhibited very little variation and had more of a similar trend over the entire genotypes (Table 3).

The general habit of the genotypes showed that majority of Acre, Rondonia and Mato Grosso genotypes were either dwarf or medium tall, while seven Rondonian and three Mato Grosso genotypes had a tall stature. Schultes (1977) reports the occurrence of the *Hevea brasiliensis* usually in low areas subjected to annual floods and also reported a general superiority of the mature Acre genotypes based on the growth and rubber quality as partially due to the ecological factors, because the trees grow on high, well-drained soil. In this study at the juvenile phase, the vigour of the plants was found to be more for Rondonian genotypes as indicated by their above average girth for nine genotypes, while only three each of the Acre and Mato Grosso genotypes had an above average girth. Seventeen Acre genotypes, 13 Rondonian and 11 Mato Grosso genotypes had an average girth indicating the generally good growing habit of these genotypes (Tables 2 and 3). Ong *et al.*, (1983) also reports a highly vigorous growth habit for the genotypes from the provenances of Acre and Rondonia, supporting the vigourous growth nature of Rondonian genotypes followed by Acre in this study.

Dijkman (1951) and Polhamus (1962) have reported the relevance of the axillary buds and leaf scars for clonal identification. In this study, the entire population characterised, had normal axillary buds. Majority of the Acre genotypes followed by 12 Rondonian genotypes, showed prominent leaf scars with pronounced margin while majority (20 genotypes) of the genotypes from Mato Grosso had normal leaf scars. Nature of leaf scars can serve as identifying trait in the juvenile stage, as in the case of the genotypes AC 963, AC 953, AC 1090, AC 966, AC 733, RO 395, RO 254 and RO 399, which possesses sunken leaf scars (Table 3).

One of the most easily identified character in the genotypes studied was the shape of the mature top most leaf flushes which provides several valuable diagnostic characters as reported

by Dijkman (1951); Silva and Satchuthananthavale (1961) and Mercykutty *et al.*, (1991) in Wickham clones of *Hevea.* Here, most of the genotypes showed hemispherical leaf flushes while a few genotypes from the three provenances had specificity for this character with conical, truncate and bow shaped flushes. The topmost mature leaf flush was used for the description of axillary buds, leaf storey and leaves. It was noted that majority of the Rondonian and Mato Grosso genotypes followed by Acre had intermediately separated flushes except for two Acre, five Rondonia and five Mato Grosso genotypes which had well separated flushes and 14 Acre, eight Rondonia and 11 Mato Grosso genotypes had closely placed leaf flushes. This clearly shows the wide variation in the canopy architecture of the wild germplasm, which is of great breeding value. In general, the genotypes expressed open flushes except for two Rondonian genotypes (Table 3).

In leaf characters, there were marked variation for the petiole shape and size, where majority of the Acre and Rondonia genotypes (17 and 18 genotypes respectively) had concave and majority of the Mato Grosso genotypes (19 genotypes) had straight petioles. Four of the Rondonian genotypes and one Acre genotype had long 'S'shaped petioles and one genotype each from Rondonia and Mato Grosso, showed arched petioles. Considerable variation was noticed in the petiole length with majority of the Acre and Rondonian genotypes having medium sized petioles. Majority of the Mato Grosso (20 genotypes) had short petioles. Three Acre genotypes, seven Rondonian genotypes and one Mato Grosso genotype had long petioles. Short petioles were noted for three and five genotypes each from Acre and Rondonia (Table 3).

Majority of the plants had petioles with acute angle and only a few, three each of Acre and Rondonia and a single Mato Grosso genotype, had a perpendicularly placed petioles. Petiolule orientation and its size were also found to be distributed over the entire class; with the majority of the genotypes possessing upwardly oriented medium size petiolules. In a limited number of genotypes, leaflets were easily distinguishable by specificity in the colour, lustre, size, shape, leaf margin, lateral appearance, leaflet orientation, cross sectional appearance, leaf apex, nature and colour of vein and lamina texture. However, majority of the genotypes were found to have green coloured leaves with dull luster, elliptic leaf shape, medium sized leaflets (except for majority of

the Mato Grosso genotypes which had small sized leaves), accuminate leaf tip, flat lateral appearance, well separated leaflets, yellowish and less prominent veins and with smooth surfaced leaf blades. The entire and undulate nature of leaf margin was distributed over the two classes.

The observations thus reveal that there are enough variation in the genotypes studied for many of the characters and also that some of them like height of the trees, leaf flush arrangement petiolar architecture, specific traits like boat shaped cross sectional appearance of leaflets, orientation of leaflets etc are of breeding value. Genotypes with very tall stem and less or no normal branching will be desirable for the breeders in look out for clones suitable for timber breeding. Arrangement of leaf flushs and petiolar architecture ensures better leaf orientation and finally efficient leaf canopy architecture along with photosynthetic efficiency. Size, shape other leaflet related traits plays significant roles in the light use efficiency and also in conservation of leaf water indicating their drought or cold tolerance capacities. Such characters help the breeders when hybridizations are programmed for specific non-conventional objectives like breeding for better leaf orientation, well structured canopy, leaves with optimum size, trees with optimum leaf area index and drought and cold tolerance.

4.2 Genetic Variability

Exploitation of the available natural genetic variability within a species is the first step in all selection and breeding work. The breeder should be in a position to separate the genetic component of variation from the phenotypic variation, so as to make a correct assessment of the true worth of the genotype. With the hybridization and clonal selection getting popular in the improvement of the Wickham clones of *Hevea*, several studies have been reported in this population on the estimation of genetic variability in the different stages of growth of the crop. Clonal variations were reported by Simmonds (1969); Markose and George (1980); Liu (1980); Nazeer *et al.*, (1986); Mydin *et al.*, (1992b) and other workers. Very high genetic variability had also been reported in the populations of wild *Hevea* germplasm in other countries by Anonymous (1986) and Ong *et al.*, (1983) from Malaysia; Jayasekera *et al.*, (1992) from Sri Lanka; Nicolas (1992) and Clement-Demange (1988) from the Ivory Coast and in India by Varghese *et al.*, (1988, 1989); Abraham *et al.*, (1992); Mercy *et al.*, (1993); Madhavan *et al.*, (1993); Reghu

et al., (1996); and Rao and Reghu (1999) in the nursery stage of growth of the wild genotypes.

4.2.1 Analysis of Variance

The analysis of variance carried out in this study in the first three years of growth, in the wild genotypes, revealed very high significant genetic variation at 1% level of probability for all the characters studied- morphological, leaf and bark structural characters and test tap yield (Tables 4-7). The results revealed the presence of inherent genetic variability in this population, which will enhance selection programmes and enable the breeder to apply enough selection pressure for these characters. Mydin *et al.*, (1992a) reported similar results of significant genetic variation for the characters juvenile yield, total bark thickness, number of leaf flushes and number of leaves per plant, in Wickham seedling progenies. In another report (Mydin *et al.*, 1990) on 10 Wickham clones involving 6 parental and 4 progeny clones, at 18 months of growth, significant genetic variation was reported for the number of leaf flushes per plant and number of leaves per plant. Significant genetic variation was also reported for the characters girth, height and number of leaf flushes per plant, in 14 month old Wickham clones (Goncalves *et al.*, 1994) and for the characters yield, girth, length of the petiole, leaf area and leaf area index in 36 month old Wickham clones (Boock *et al.*, 1995). Moreti *et al.*, (1994) had reported similar results for girth, leaf area and petiole length in juvenile Wickham clones, while Jayasekera *et al.*, (1992) reported significant genetic variation for girth of the plants in another set of Wickham clones in the juvenile phase. Varghese *et al.*, (1988, 1989) and Varghese (1992) have reported wide variability in the young wild germplasm with respect to growth parameters like plant height, girth, number of leaves and number of flushes. The observations made in the present study are in agreement with these reports.

Significant genetic differences were observed among the wild genotypes for the number of stomata/mm^2 of the leaf, number of epidermal cells/mm^2 of the leaf and stomatal index. Slack (1974) in apple and Senanayake (1969) in *Hevea* have reported significant differences between different species in stomatal number per unit area of the leaf. Gomez and Hamzah (1980) have reported significant differences for the number of stomata and number of epidermal cells, in unit

area of leaf lamina, in Wickham clones of *Hevea*, in agreement with the present study. Significant differences in stomatal density between cultivars of *H. brasiliensis* have also been reported by Premakumari *et al.*, (1979), which also supports the present observations.

Leaf structural characters such as the thickness of lamina, leaf midrib, palisade layer, spongy layer and cuticle and number of cells per unit length of the palisade and spongy layers also showed significant genetic differences among the wild genotypes studied. Similar results of significant clonal differences were reported by Gomez and Hamzah (1980) for all these characters and for thickness of cuticle by Premakumari (1992).

This study has revealed significant genetic variation for all the bark structural characters studied in the wild germplasm, at 42 months age. Several workers mainly in mature Wickham clones of *Hevea* have reported significant genetic differences for various bark structural characters. Characters like total bark thickness and number of latex vessel rows of *Hevea* clones at the juvenile stage, have been reported as clonal characteristics (Ho *et al.*, 1973); Narayanan *et al.*, 1974; Licy and Premakumari, 1988; and Mydin 1992a). They also reported significant differences for total bark thickness in young *Hevea* plants. Premakumari (1992) had reported the proportion of soft bark to differ significantly in a study on drought tolerant and susceptible Wickham clones. Significant genetic variation was reported for the characters height and width of phloic rays (Premakumari *et al.*, 1985; Premakumari, 1992) and for the bark structural characters like density of latex vessels, diameter of latex vessels and frequency of phloic rays (Premakumari *et al.*, 1985) among mature trees of 10 clones and for the characters height / width ratio of phloic rays, number of latex vessel rows and total cross sectional area of latex vessels, in a set of Wickham clones of *Hevea* (Premakumari, 1992). Moreti *et al.*, (1994) had reported significant differences for total bark thickness, total number of latex vessel rows, density of latex vessels per 5 mm circumference of the plant, diameter of the latex vessels and average distance between latex vessels among clones at the juvenile stage. Licy *et al.*, (1992) reported significant variance ratios in four year old hybrid progenies, for total bark thickness and total number of latex vessel rows. Varghese *et al.*, (1988, 1989) have reported wide variability in young wild germplasm for the characters total bark thickness and total number of latex vessel rows. All these reports are in

conformity with the results of this study. However, Nazeer *et al.*, (1992) could not get statistical significance for the characters total bark thickness and total number of latex vessels in a set of 15 Wickham clones, also studied at the age of four years, even though they observed slight numerical differences between the clones.

4.2.2 Performance of the wild genotypes

4.2.2.1 Morphological characters

Wild genotypes of any crop can be expected to possess a wide range of inherent genetic variability mainly because of its genetically unexploited and unaltered nature. Wild germplasm of *H. brasiliensis* also exhibited a wide range in their phenotypic expression, for all the characters studied. The initial vigour and rate of growth of the wild genotypes were closely monitored by means of the growth characters girth, height, number of leaf flushes per plant, total number of leaves, inter-flush distance, length of the petioles, total leaf area and the leaf area index.

In general, it was noticed that the wild genotypes had a vigorous growth during the first year with a wide range of values for most of the parameters. Pollinere (1966) reported that among the morphological components of yield, girth is considered as the most important parameter of growth and vigour in rubber. It is seen that the genotype MT 929 maintained a very poor growth rate throughout the four quarters with the minimum girth, whereas the genotype RO 322 was seen to have the maximum girth, among all the wild genotypes studied, in the first, third and fourth quarters of recording observation (3.94cm, 7.62 cm and 10.41 cm respectively), except for the second quarter where only one genotype (RO 395) marginally surpassed the girth of this clone. Genotypes RO 395, RO 319, MT 1025, MT 935, RO 317, AC 1043, AC 654 etc. were some of the genotypes which showed superiority for their girth values, in the first year. It can be seen that the general mean for the girth of the wild genotypes was higher than that of the control clone, RRII 105 (Table 8). Out of the 80 genotypes, 60 genotypes in the first quarter, 54 genotypes in the second quarter, 49 genotypes in the third quarter and 37 genotypes in the fourth quarter, recorded an average girth significantly above that of the control (Table 9).

Height of the plants, which is another indicator of the rate of growth, also exhibited a

wide range of variability in the wild population. The range in the height of the plants was seen to increase by each quarter with the maximum variability in the fourth quarter (100.89 cm-322.99 cm). Mydin *et al.*, (1990) reported a lesser range (294.47-385.86 cm) for the height of the plants recorded in 10 Wickham clones of the same age. The genotype MT 929 was found to be shortest of the wild genotypes with the minimum height in all the quarters whereas RO395, which was one of the very vigorous clone as evidenced by its higher girth values also, recorded the maximum height (Table 8) in all the four quarters (125.77 cm, 189.35 cm, 235.80 cm and 322.99 cm respectively). Genotypes MT 1025, RO 322, RO 328, RO 319, MT 1030, RO 352 and RO 364 were some of the accessions, which exhibited very active growth during the first year, in terms of the height of the plants. The general mean for this character in all the four quarters (71.99 cm, 112.51 cm, 140.84 cm and 191.98 cm respectively) were higher than that of the control clone (42.43 cm, 73.48 cm, 87.69 cm and 145.70 cm respectively), with 62 genotypes, 56 genotypes, 57 genotypes and 2837 genotypes, being significantly taller than the control clone, in the four quarters respectively (Table 9). Varghese *et al.*, (1988) had also reported similar results where the mean height of wild genotypes, were much higher than the control clone, in a set of wild genotypes at nine months age.

Rate of production of leaves is another indicator of the vigour of the plants in the active growth phase. The evaluation of germplasm involves biometric study of descriptors of leaf and flush morphology (Lesprit, 1984). The number of leaf flushes per plant and the total number of leaves per plant were monitored in the four quarters of the first year. In the first quarter, the genotype RO 395 had the highest number of leaf flushes per plant (3.85), while RO 319 had the maximum leaf flushes in the second (5.97) and third quarter (7.40) and RO 894 had the maximum number of flushes in the fourth quarter (9.12) (Table 8). The average number of flushes reported by Varghese *et al.*, (1988) in another set of wild genotypes at the age of 9 months was in accordance with the results of this study at the same age. Genotypes RO 317, RO 859 and MT 1025 were certain other genotypes with a larger number of leaf flushes in this study. MT 929 continued to be a weak clone with respect to this character also with the minimum number of flushes. In general, the number of leaf flushes per plant in all the four quarters of the first year, had a general mean comparable to the popular clone RRII 105 (Table 8), except the few genotypes

mentioned above. Similar reports were also available from Indonesia (Alwi and Suhendry, 1992) in 24 months old wild germplasm with an average of 7.87 flushes per plant, comparable with 6.73 flushes in this study at 18 months age, while Mydin *et al.*, (1990) in a study in 18 month old Wickham clones had reported an average of only 4.82 leaf flushes per plant.

The total number of leaves produced, which is a reliable indicator of the vigour of the plants, showed a wide range of variation in all the four quarters. In the first quarter, RO 395 and in the following three quarters RO 322 had the highest number of leaves produced (35.34, 61.60, 83.60 and 119.80 respectively). MT 929 had the minimum number of leaves produced in all the four quarters, indicating to be the least vigorous genotype in the population (Table 8). Several genotypes such as RO 317, RO 311, RO 859, RO 319, RO 352, MT 1025 and AC 654 produced much higher number of leaves compared to the control. The general mean for this character was higher compared to the control, in all the four quarters thus indicating the higher vigour of the wild genotypes (Table 8). Varghese *et al.*, (1988) in a study of 100 wild genotypes from Rondonia and Mato Grosso provenance, has reported a higher average number of leaves produced (34.35) at the age of 9 months compared to a lower average value of 22.70 in the present study, which comprises of genotypes from all the three provenances, at the same age.

Well-separated leaf flushes are desirable for efficient trapping of sun light. In the fourth quarter, it was observed that except for 16 genotypes, which had their inter-flush distance comparable with the popular clone RRII 105, all the remaining genotypes had their average inter-flush distance higher than that of the control (Table 9). MT 901, RO 328, MT 906, RO 879 and MT 1055 were some of the genotypes, which had a higher inter-flush distance compared to the control clone. MT 901 showed the maximum inter-flush distance (28.46 cm) while RO 399 had the minimum inter-flush distance of 13.86, which was still higher than the popular control clone (12.74 cm).

The general mean for petiole length was 21.86 cm, in the wild genotypes, which was higher than the control clone RRII 105 (14.59). Maximum length of the petiole was observed in the genotype RO 886 (32.47 cm) and the shortest petiole (13.03 cm) was recorded in MT 1064 (Table 8). Thirty-two of the wild genotypes showed a significantly higher length of the petiole

than the control clone. RO 256, RO 311, RO 287, RO 876 etc were some of the other genotypes which had longer petioles thus contributing to a light efficient canopy. Total leaf area of the wild genotypes was estimated from the total number of leaves and average single leaflet area. It was found that the genotype RO 322, which was found to be a highly vigorous clone with respect to many of the growth characters studied, had the maximum total leaf area (28683.45 cm^2). The general mean of the total leaf area of the wild genotypes (11836.97 cm^2) was also much higher than that of the control clone (7675.35 cm^2). Another 22 genotypes also had their total leaf area significantly higher than the control (Tables 8 and 9).

Leaf area index (LAI) was calculated for the wild germplasm, in the fourth quarter. Leaf area index and leaf orientation have been identified as two important factors, which determine growth in pre-exploitation stage by Sethuraj (1985). Ishii (1998) had also considered leaf area index as one of the major contributing parameters of canopy photosynthesis. High growth rate is usually associated with high leaf area index in crop plants, and hence high LAI indicates a high rate of photosynthesis (Wang *et al.*, 1991). However, there is an optimum index where crop growth rate reaches maximum level. Rate of growth increases concomitantly with the increase of LAI, attains the maximum level and then decreases with increasing LAI. In the present study, (Table 8) leaf area index was the maximum for the genotype RO 322 (0.46) which was only natural because of its higher total number of leaves while it was the minimum for MT 929 (0.08). The average leaf area index of the population (0.19) was slightly higher than that of the control clone RRII 105 (0.12). All these growth indicators, thus clearly points out the higher vigour of the wild germplasm compared to the genetically improved control clones.

4.2.2.2 Test tap yield over three years

It has been reported that the nursery yield in rubber at the age of 24 months, was significantly associated with mature yield over five years of tapping, which can be considered as a satisfactory predictor for mature yield (Tan, 1998). Test tapping in the early growth phase of the wild germplasm, was done to get a comparative assessment and indication on the yielding potential of each genotype. Tan (1983) cautioned that the nursery yield should be viewed only as an

early guide in selection, which has to be confirmed in the mature phase. Ong *et al.*, (1997) suggested that the yield potential of clonal genotypes could be expected, to express in the early growth phase.

Micro tapping done at the end of the fourth quarter at 18 months and test tappings done at 30 and 42 months age exhibited a wide range of variability for the yield collected. Maximum variability was observed for this character by Abraham *et al.*, (1992); Mercy *et al.*, (1993b, 1995); Rao *et al.*, (1999) and Rao and Reghu (1999). In general, the average test tap yield recorded in the three years was very low compared to that of the popular clone, RRII 105. In the first year, the wild genotypes had the test tap yield ranging from 0.0027 g $t^{-1}t^{-1}$ for MT 1063 to a maximum of 0.2327 g t^{-1} t^{-1} (RO 399) with a general mean of 0.0716 g t^{-1} t^{-1} while the control had 0.1625 g t^{-1} t^{-1} of yield. Besides RO 399, MT 1057 had a significantly higher yield than the control while another ten genotypes had a comparable yield with the control. In the second year, RO 254 recorded the minimum test tap yield of 0.0212 g t^{-1} t^{-1} and MT 1057 was the highest yielder with 0.6358 g t^{-1} t^{-1}, followed by MT 1021 (0.5607 g t^{-1} t^{-1}), while the general mean was 0.1205 g t^{-1} t^{-1} and that of the control clone was 0.2986 g t^{-1} t^{-1}. Fourteen genotypes had a comparable yield with the control. The test tap yield in the third year showed the maximum variability with RO 257 recording the minimum yield of 0.0480 g t^{-1} t^{-1} whereas MT 1057 continued to be the highest yielder with an average yield of 4.2711 g t^{-1} t^{-1} and MT 1021 had a comparable yield (2.0905 g t^{-1} t^{-1}) with the control. The population mean was only 0.5273 g t^{-1} t^{-1} while the control had a yield of 2.3547 g t^{-1} t^{-1} (Tables 10 and 11).

The very low yield in this wild population may be due to the fact that these genotypes were brought directly from the jungle where they had not been subjected to selection for yield. The average test tap yield of the wild population in the second year (0.1206 g t^{-1} t^{-1}) was in accordance with the earlier reports from Indonesia by Alwi and Suhendry (1992) in two year old, Amazonian germplasm (0.1500 g t^{-1} t^{-1}). Lam *et al.*, (1997) from Vietnam opined that the photosynthetic partitioning in these wild germplasm seems to favour growth, leading to low yield but with good girth on tapping, based on the high girth increment on tapping observed by them. The generally low yielding nature of the 1981 IRRDB germplasm has already been reported

from India (Varghese *et al.*, 1988, 1989; Abraham *et al.*, 1992; Mercy *et al.*, 1993a; Madhavan *et al.*, 1993 and Rao and Reghu, 1999); Malaysia (Ong and Othman, 1992); Ivory Coast (Clement-Demange *et al.*, 1990b, 1997); Vietnam (Lam *et al.*, 1997) and Sri Lanka (Anonymous, 1995), in agreement with the results of this study.

4.2.2.3 Leaf structural characters

The green leaves of plants are photosynthetically active organs, which are able to store absorbed solar energy in reduced organic compounds. Leaf structural characters influence the net leaf photosynthesis to a large degree and thus cause great differences in light use efficiency. Stomatal pores, which are minute intercellular openings bounded by two kidney-shaped guard cells plays significant role in the exchange of water vapour, CO_2 and O_2 between the internal and external atmosphere of the leaves ultimately controlling the photosynthetic efficiency of the plants (Bolhar- Nordenkampf and Draxler, 1993). Frequency of stomata is one of the most important factors determining the rate of transfer of atmospheric CO_2 to the carboxylation sites within the leaf (Leech and Baker, 1983) and the regulation of water loss from the plant, another critical factor, which is controlled by the plant by the powerful means of stomatal conductance. The rate of evaporation per unit area of exposed wall is greater from the guard cells and the subsidiary cells than the mesophyll cells, because they are closest to the stomatal pore (Tanton and Crowdy, 1972). As such the stomatal conductance directly influences the leaf ψ by determining 'leaf demand' for transpiration, even though the stomatal conductance may be affected by the bulk leaf ψ, particularly when the leaf experiences water stress (Cowan, 1977, Terry *et al.*, 1983). It is the response of the stomata, through the regulation of stomatal conductance, to various environmental parameters that determine the environmental demand on the leaf to supply water for evaporation (Rachel and Baker, 1983). Ceulemans *et al.*, (1978) have shown the existence of a relationship between stomatal frequency and water diffusion process, which in turn reflects the growth rate in poplars. Stomatal density is thus an important parameter, determining the water use efficiency of the leaf and in turn, that of the plant. As the stomatal density of leaves is usually variable and influenced by various environmental factors, the correlation between number of stomata per unit area and the number of epidermal cells in the same unit area is used to compute

stomatal index (Ticha, 1985; Salisbury, 1927). Stomatal characteristics are species specific and may vary according to the habitat, leaf age and insertion level (Ticha *et al.*, 1982).

Stomata in *H. brasiliensis* belong to the paracytic type (Panikkar, 1974 and Premakumari, 1992) and in the wild genotypes also the same type of stomata was observed. The majority of the wild genotypes studied had a significantly lower number of stomata per unit area, with a population mean of 433.87/mm^2, compared to the higher value of the control clone (525.30/ mm^2). The frequency of stomata ranged from 281.16/mm^2 of leaf lamina for MT 1028 to 612.67/ mm^2 for the genotype MT 928 (Table 12). Besides MT 928, only one genotype (AC 754) had a significantly higher value (587.59/mm^2) than the control while 15 genotypes had their stomatal frequencies comparable to the control clone (Table 13). In all the wild genotypes studied, as well as in control, stomata were present only in the lower epidermis of the leaves. This was in agreement with the earlier reports of Gomez (1982); Premakumari *et al.*, (1984, 1989); Rao (1963); Senanayake (1969) and Senanayake and Samaranayake (1970) in elite cultivars of *H. brasiliensis*.

Carpenter and Smith (1975) had reported in several tree species, a range of 65-910 stomata per mm^2 of the leaf area, and Slack (1974) had reported a range of 170-510 stomata per mm^2 area, in apple. Gomez and Hamzah (1980) had reported a range of 280-370 stomata per mm^2 in 11 Wickham clones of *Hevea*. The number of epidermal cells per mm^2 area of the leaf was also found to have a wider range in the wild genotypes. Except for the genotypes MT 1005, AC 453, RO 369, MT 944 all the remaining 76 wild genotypes had their frequency of epidermal cells per mm^2 of leaf area, statistically on par with the control clone (Table 13). The general mean of the population for this character was lower (1711.50/mm^2) compared to the control (2218.75/ mm^2). MT 1028 had the minimum value of 1132.84/mm^2, while the maximum number of epidermal cells (2741.23/mm^2), was recorded by RO 369 (Table 12).

Stomatal index worked out based on the number of stomata and number of epidermal cells per unit area of the leaf lamina, showed a wide range of variation in the wild genotypes studied. Thirty-eight genotypes had significantly higher stomatal index values compared to the control clone, with 31 genotypes on par with the control (Table 13). The genotype RO 369 with

the maximum number of epidermal cells per unit area had the lowest value of stomatal index (10.81), while the maximum index was recorded by AC 966 (27.43). The general mean value for this character (20.63) was comparable to the control clone (19.26) (Table 12).

Leaf area is another important character to ascertain the photosynthetic capacity of the plants. The total leaf area is sometimes referred to as its photosynthetic potential (Ticha, 1985). In the improvement of plantation crops like rubber, effort have to be to bring light interception to 100% but without making the lower leaves parasitic. A plant having large leaves at the top could intercept almost all the light but would result in so much shading that the efficiency of lower leaves would be reduced. Therefore selection for smaller leaves may provide a better plant canopy for higher photosynthetic efficiency. It has been reported that a small leaf size and greater leaf thickness are correlated to higher photosynthetic rate (Swaminathan, 1977). The single leaflet area of the wild genotypes varied from 59.94 cm^2 to 189.58 cm^2 in the genotypes MT 1057 and RO 311 respectively. The generally smaller single leaf size of the Mato Grosso genotypes can be assumed to be contributing to the photosynthetic capacity of Mato Grosso genotypes compared to the other two provenances. This is very evident in MT 1057 with the smallest leaflet size and highest yield in two subsequent years. The general mean of this character in wild population was 95.23 cm^2, which was higher than the average single leaflet area of the control clone, RRII 105 (60.83 cm^2) (Table 12).

It is well established that a close relationship exists between leaf structure and photosynthetic activity in mature leaves. Internal architecture of the leaf is complex and varies considerably from species to species. Leaf structure has also a critical role in the water relations of the plant. In rubber, where vegetative growth is important it is necessary to know the relationship between leaf area, leaf structure and leaf photosynthesis (Swaminathan, 1977). Important leaf structural traits contributing directly or indirectly on the water relations and gaseous exchange of the plant were recorded in this study viz., thickness of the lamina and midrib, thickness of the palisade and spongy layers, number of cells in unit length of palisade and spongy layer and thickness of the cuticle layer. Thickness of lamina is a character of great importance due its association with photosynthetic capacity. Leaf thickness increases, along with the leaf area, which involves both cell division and cell enlargement (Ticha, 1985). There is plenty of experimental evidence to

suggest that both adaptive and genetic differences in the rate of photosynthesis per unit leaf area are associated with differences in leaf thickness (Nobel *et al.*, 1975 in *Plectranthus* sp.; Doley, 1978 in Eucalyptus; Charles, 1983 and Pearcy, 1998). Changes in leaf thickness might be expected to affect movement of CO_2 in the gaseous phase. There appears to be concomitant changes in the anatomy (stomatal density and distribution) and structure (mesophyll cell size) of the leaf with changes in leaf thickness, which tend to minimize the effects of these changes on the photosynthetic functioning of the leaf (Charles, 1983). Leaf thickness is a character, which changes itself to adapt to the available light intensity for best light interception. Plants growing in weak light conditions have large and thin leaves (Ishii, 1998).

Out of the 80 wild genotypes studied, 13 had significantly higher leaf blade thickness than the control clone (0.1490 mm) whereas the rest of the 67 genotypes had their leaf blade thickness comparable to that of the control clone. RO 380 recorded the minimum leaf thickness (0.1107 mm) while, the maximum lamina thickness was recorded by AC 953 (0.176 mm) (Table 12). Those genotypes with thicker leaf blades than that of the control clone and those, which had comparable thickness with it, can be expected to be having higher photosynthetic capacity. These results are in agreement with the study on 11 Wickham clones by Gomez and Hamzah (1980) where the leaf blade thickness varied from 0.100 mm for the clone IRC 110 to 0.143 mm for the clone SS2 with a general mean of 0.115 mm.

The midrib was very prominent and abuts the lower surface. It was semicircular in the cross sectional view. This was in agreement with the earlier report of Panikkar (1974) in Wickham clones of *Hevea*. The thickness of the leaf midrib assumes importance in relation to the translocation of photosynthates from the sites of their production. Wide variation was noticed for this character among the wild genotypes with the genotype MT 901 having a minimum thickness of 0.6300 mm and AC 754 with the maximum thickness of 1.3220 mm in their cross section. While the general mean for this character was 0.7850 mm, the control clone had a thickness of 0.6950 mm (Table 12). In general, most of the wild genotypes (47 genotypes) had a significantly thicker midrib than the control clone with another 27 genotypes having comparable midrib thickness with that of the control. Only 6 genotypes had a significantly thinner leaf midrib than the control

(Table 13). The thicker leaf midrib of the wild genotypes, thus provide better translocation ability for the clones.

Mesophyll is a specialized photosynthetic tissue consisting of the palisade and spongy tissues. Both these tissues offer distinct functions in the plant's activities. Palisade tissue has the unique function of photosynthetic activity due to the presence of chloroplast in them. The lacunose structure of mesophyll enables smooth gaseous exchange between the outside air and the photosynthetic tissue. Even though spongy parenchyma has a much larger intercellular space than the palisade tissue, the palisade tissue has a larger free surface exposed to the internal atmosphere. Studies in the leaves of several species of dicots showed that per unit volume of leaf tissue, the palisade tissue exposes to the intercellular air, 1.6-3.5 times the surface exposed by spongy parenchyma (Turrel, 1936; Easau, 1965). In view of this report the high ratio on internal to external surface in sun leaves can be explained by the higher proportion of palisade cells in such leaves. The high ratio of internal to external surface may be accompanied by a high concentration of chlorophyll (Turrel, 1939). The ratio of internal to external surface is strongly and positively correlated with the rate of transpiration (Turrel, 1944). Thus the structure favourable for photosynthesis induces at the same time a high loss of water from the plants (Stalfelet, 1956).

The cells of the palisade parenchyma are elongated and regularly oriented with their long axes at right angles to the leaf surface, with no intercellular spaces. Palisade parenchyma is believed to be the major site of CO_2 fixation for its large surface area (Ticha, 1985). Palisade cells in sun leaves are closely associated with the adaxial epidermis so that much of the incident light can enter the leaf without interruption by the intercellular air spaces (Terashima and Hikosako, 1995). The palisade parenchyma of the leaf of *Hevea* is composed of a single row of cells, which are elongated and lie so closely together that no intercellular spaces are formed. Spongy parenchyma consists of rounded or irregular cells, which result in the formation of large intercellular spaces between them. The upper and lower epidermis, contains no chlorophyll in the case of *Hevea* (Bobilioff, 1923). This characteristic structure of the leaves seen in the wild *Hevea* is suggestive of the fact that these wild clones would have developed in their original habitat in abundant sunlight. These anatomical characters are by and large fixed early in leaf development

and well before full expansion of the lamina so that any later transfers between light environments have limited effect on leaf structure (Terasimha and Hikosaka, 1995).

Out of the 80 wild genotypes studied, five genotypes had a significantly thicker palisade layer than the control clone, along with another six genotypes, which had a comparable palisade thickness to that of the control. All the remaining 69 genotypes had a palisade layer of lesser thickness than that of the control clone. The generally higher thickness of the palisade layer of these 11 genotypes is a good indicator of the possible photosynthetic potential of the clones (Table 13). The minimum thickness of the palisade layer was recorded by RO 380 (42.57 μm) and the maximum value was recorded by RO 369 (81.01 μm) while the control clone had a thickness of 70.87 μm (Table 12). This is in agreement with the finding of Gomez and Hamzah (1980) who reported comparable values for this character in 11 Wickham clones. The average palisade layer thickness in these 11 clones was 51.59 μm while the range was from 42.83 μm (IRCI 10) to 70.19 μm (SS2).

Spongy parenchyma appears to be less regular and has conspicuous inter cellular spaces. It acts as an intermediate conducting tissue for the movement of photosynthates to the veins, as well as photosynthetic tissues and also helps in the smooth gaseous exchange in the leaves. Two genotypes, AC 966 and AC 754 had a significantly higher thickness for the spongy layer and 27 genotypes had their spongy layer thickness comparable to the control clone. The remaining genotypes had a significantly lower thickness, than the control clone (Table 13). AC 966 had the maximum thickness of 93.50 μm followed by AC 754 (86.25 μm). The minimum thickness was recorded by RO 859 (45.0 μm). Control clone had a thickness of 75.49 μm while the general mean of the population for this character was 61.71μm (Table 12). Gomez and Hamzah (1980) reported comparable results in 11 Wickham clones of *Hevea* where the range of the spongy layer thickness varied from a minimum of 40.27 μm (IRCI10) to 55.08 μm (SS2) while the population mean was 45.90 μm).

Number of cells per unit length of the palisade layer had a range of 100.62 for the genotype RO 257 to 134.34 for RO 352. The general mean was 117.03 while that of the control was 117.24 (Table 12). Twenty wild genotypes had a significantly higher number of cells per unit

length of the palisade layer while 36 of the genotypes were on par with the control. Remaining genotypes had a significantly lower value for this character (Tabel 13). The studies conducted by Gomez and Hamzha (1980) revealed similar results for this character with a range of 126-194 cells per mm distance of palisade layer for the Wickham clones ES 4 and RRIM 614 respectively. The greater number of cells in a cross section of sun leaves results in more chloroplasts per unit area in sun as compared to shade developed leaves, although the chloroplasts in shade leaves are typically larger and contain more chlorophyll (Terasimha and Hikosaka, 1995).

Number of cells per unit length of spongy layer also exhibited a wide range in their values and majority of them had higher number of cells compared to the control. The genotype AC 706 had the minimum number of 189.24 and AC 650 had the maximum number of cells per unit length of spongy layer (417.06), while the control clone had 232.24 cells and the general mean for this character was 273.95 (Table 12). Sixty-six of the wild genotypes had a significantly higher number of cells while the remaining 14 genotypes were on par with the control (Table 13). Similar results were obtained in a study of 11 Wickham clones of *Hevea* (Gomez and Hamzha, 1980). They reported a minimum value of 195.85 for the clone SS2 while the maximum number of cells per mm of spongy layer was 262.65 in RRIM 614 with a population mean of 232.2 cells.

The restriction of transpiration by the epidermis largely results from the presence of fatty substances present as a separate layer called the cuticle (Frey-Wyssling and Muhlethaler, 1959) along with epicuticular wax. Several attempts were reported to separate the two components of stomatal conductance - stomatal and cuticular, by transpiration curve analysis or artificial stomata closing (Catsky *et al.*, 1985). Cuticle has an important role as a structural element holding the cellular tissues compact and firm and serving as the bounding layer between plant body and its environment. Its main functions are conservation of water in the plant, prevention of loss of plant components by leaching and the protection of the plant from injuries due to wind and physical abrasion by frost, radiation, etc and attack by fungi, insects or pathogens. Some plants may benefit from the possession of a poorly developed leaf cuticle, either overall or in localized areas, by absorbing water from rain or dew. It is generally believed that transpiration through cuticle is relatively unimportant compared to the loss of water through stomata. Ketellapper (1963) ech-

oes this belief by stating that at least 90% of the water loss from a leaf occurs by diffusion through the stomata while Easau (1965) suggests a larger role for cuticular transpiration. It is possible to demonstrate excretion of water through cuticle and its aggregation into droplets which occurs without any evidence of submicroscopic pores in the cuticle (Bancher *et al.*, 1960). Comparatively little is known about the gaseous exchange through cuticle in contrast to the wealth of information available on exchange through stomata. The extent and mechanism of cuticular penetration of CO_2 is of special interest in relation to photosynthesis. Dorokov (1963) reported that at the normal concentration of CO_2 in the air, the astomatous adaxial cuticle of the apple leaf transmits 20-30% of the total quantity absorbed. This uptake, he described as responsible for the "extra-stomatal cuticular photosynthesis".

In the wild genotypes studied, a wide range of variability was noticed for the thickness of the cuticle. The minimum thickness was recorded by MT 935 (1.22 μm), while the maximum cuticular thickness was recorded by MT 945 (4.27 μm). The control clone had a thickness of 3.67 μm while the general mean value was only 2.57 μm (Table 12). The cuticular thickness of the majority of the wild genotypes was found to be very less than that of the control. Only one genotype, MT 945 had a higher cuticular thickness while another four genotypes had their cuticular thickness on par with the control (Table 13). Cuticle thickness in general does not influence water loss from plants significantly, as atleast 90% of the water loss from a leaf occurs by diffusion through stomata (Ketellaper, 1963). But in general, cuticle serves as the bounding layer between the body of the plant and its environment besides other important functions like protection of plants from injuries due to wind and physical abrasion, frost and radiation (Martin and Juniper, 1970).

4.2.2.4 Bark structural characters

Latex is produced in the laticifers, which form the laticiferous system, distributed in the bark tissue. Latex vessels originate from the cells initiated by the cambium and along with the phloem is pushed to the outside while the cambium generates wood and xylem vessels to the inside (Auzac, 1997). The vessels, which are arranged in rows, run at an inclination varying from 2-7^0, in an anticlockwise direction in the form of articulated anastomising tubes (Bobilioff, W.

1923; Dijkman, 1951; Anonymous, 1980). There is a characteristic zonation in the whole bark tissue in *H. brasiliensis* where there is an inner zone with soft tissue and an outer zone of hard bark. The inner zone contains the functional elements including normal latex vessels while the outer hard bark zone comprising of a superficial layer of the periderm and the sclerified portion of the cortex, affords protection. Numerous studies on the quantitative features of the laticiferous system over the last few decades have advanced the knowledge of the productivity of *Hevea* (Gomez *et al.*, 1972; Gomez, 1982; Ho, *et al.*, 1973; Narayanan and Ho, 1973; Narayanan *et al.*, 1974; Ho, 1975 and Sethuraj, 1981). The importance of the bark structural parameters as yield-contributing factors are well established, especially in the Wickham clones of *Hevea*. In this study, the detailed bark anatomical characters were studied to characterise the genotypes for these traits and also to assess the extent and nature of variability available and their relationships and contribution to the genetic divergence in this wild population, as reports in these line are very few in the wild germplasm.

Earlier studies on the relationship between various bark structural characters and yield in *H. brasiliensis* had revealed that the number of latex vessel rows was the most important single factor related to yield (Premakumari *et al.*, 1985). This was reported to vary greatly with the age and type of the clone (Riches and Gooding, 1952). Gomez *et al.*, (1972) considered in detail the factors affecting the quantitative determination of laticiferous tissue. In addition to the number of laticifer rows, density and diameter of latex vessels and distance between the latex vessel rows were determined as factors influencing the quantity of laticiferous tissue. There are reports on the influence of various laticifer characters such as number of latex vessel rows (Gomez *et al.*, 1972; Gomez, 1982; Ho, 1975 and Premakumari *et al.*, 1988); latex vessel diameter (Ashplant 1927; 1928 a,b,c) and latex vessel density (Premakumari *et al.*, 1988) on yield of *Hevea* clones.

The wild germplasm clones irrespective of their geographical origin in the three states of Brazil, recorded lower values for almost all the anatomical characters of virgin bark, especially in the case of number of latex vessel rows (Lam *et al.*, 1997). This can be substantiated partially by the suggestion of Wycherley (1969) that selection for high yield in the Wickham clones over the years resulted in a corresponding increase in the number of latex vessel rows in the bark.

Even though similar trends were noted in this study also, there were several individual genotypes as exceptions for several characters either being superior or comparable to the popular control clone, RRII 105. Compared to RRII 105, which had a total latex vessel row of 8.00, certain genotypes had a higher value for this character in the population studied viz. RO 255 (8.00), MT 1057 (8.25), RO 894 (8.25), MT 906 (8.25), MT 901 (8.26), AC 632 (8.51), AC 754 (8.77), AC 733 (10.01) and RO 399 (11.01). For the character diameter of latex vessels it was noted that all the wild genotypes except four genotypes had their diameter higher than the control clone RRII 105 (Table 15).

Total bark thickness of *Hevea* clones at juvenile stage has been reported as clonal character (Ho *et al.*, 1973; Narayanan *et al.*, 1974 and Licy and Premakumari 1988). The general mean of total bark thickness of the wild genotypes (2.86 mm) was lower than the popular control clone (3.06 mm), whereas a maximum total bark thickness of 4.00 mm was recorded by the genotype RO 395 (Table 14). Similar trend of a wide range for this character (1.67 – 4.44 mm) was also reported by Varghese *et al.*, (1988) in another set of two year old wild *Hevea* germplasm. A range of 1.83-3.08 mm was reported by Abraham *et al.*, (1992) in a set of two year old wild genotypes. The general mean of soft bark thickness of the wild genotypes studied was comparable to that of the control (1.19 mm and 1.16 mm respectively), while this character had a range of 0.87 mm to 1.75 mm for the genotypes AC 986 and RO 311 respectively. In the case of hard bark thickness wild genotypes had a lesser average thickness (1.67 mm) compared to that of the control (1.90 mm). RO 395, which had the highest total bark thickness (4.00 mm), had the maximum hard bark thickness also (2.53 mm), thus reducing the advantage of a high total bark thickness, even though it still possessed a comparatively higher soft bark thickness of 1.47 mm. The minimum hard bark thickness was recorded by AC 654 (0.84 mm) but had only a soft bark thickness of 1.25 mm. RO 868 had the maximum soft bark zone expressed in percentage (64.88 %), while the same clone recorded the lowest hard bark zone thickness expressed in percentage (35.12 %). RO 287 had the maximum hard bark thickness (68.74%) and the same clone had the minimum proportion of soft bark (31.26%) (Table14). High proportion of soft bark was reported to be related to the drought susceptibility of the clones and vice versa (Premakumari, 1992).

The stone cell formation is influenced by environmental and seasonal factors and is often identified as a clonal character. (Bobilioff, 1923; Gomez, 1982; Premakumari *et al.*, 1990; and Premakumari, (1992). Drought tolerant clones showed high sclerification resulting in low proportion of soft bark thickness indicating the potentiality of such clones to resist drought conditions. It is important to note that drought tolerant and susceptible groups of clones differ significantly for certain bark anatomical characters like phloem ray width, height / width ratio of phloic rays and proportion of soft bast (Premakumari, 1992). Ten of the wild genotypes, which had a significantly higher proportion of hard bark region and another 28 wild genotypes, which had hard bark proportion comparable to the control clone, are indicative of their possible drought tolerance potential.

Number of latex vessel rows forms the most important structural trait in the bark of *Hevea* clones in terms of the latex production and has been identified as another clonal character at the juvenile stage. (Ho, *et al.*, 1973; Narayanan *et al.*, 1974 and Licy and Premakumari, 1988). The number of latex vessel rows in the soft bark zone and in the hard bark zone were counted separately in this study which adds up to the total number of latex vessel rows in the genotypes studied. Wide variation was noted for these characters. The average numbers of latex vessel rows, in the soft bark zone ranged from a minimum of 1.74 to a maximum of 8.01 for the wild clones MT 947 and RO 399 respectively. The population average of this character was expectedly lower (3.65) than the popular Wickham clone RRII 105 (5.75) (Table 14). Except for the clones RO 399 and MT 1057 with significantly higher values and three genotypes AC 754, RO 328 and RO 255, which had a comparable number of latex vessels rows in the soft bark with the control clone, all the remaining 75 wild genotypes had a significantly lower number of latex vessel rows in their soft bark (Table 15). Reghu *et al.*, (1996) had reported a lower average number of latex vessel rows in a study on two-year old wild genotypes, compared to the control, which is in agreement with this study.

Number of latex vessel rows in the hard bark zone of the wild genotypes, varied from a minimum of a single latex vessel row in AC 959 to an average of 5.01 in AC 733. The population mean for this character (2.16) was comparable to that of the control clone (2.25) (Table 14).

Seventeen of the wild genotypes had a significantly higher number of latex vessel rows in the hard bark zone, compared to the control clone and 24 genotypes had their average number of latex vessel row in the hard bark, on par with that of the control. Thirty-nine genotypes had a significantly lower number of latex vessel rows in the hard bark zone (Table 15). Even though the hard bark zone can never be as productive as the soft bark zone, the discontinuous latex vessels rows (mainly due to the disruption exerted by stone cells) in this zone, can also contribute to the total yield. Thus the total number of latex vessel rows in the wild genotypes assumes importance in the final productivity, especially in the juvenile stage. There was a wide range of variation in the total number of latex vessel rows with a minimum of 2.99 vessel rows for MT 1021 and a maximum of 11.01 for RO 399. Understandably, the average number of total rows of the population was less (3.65) than the control clone (8.00) (Table 14).

The average distance between latex vessel rows is another factor affecting the total number of latex vessel rows in general and the number of productive latex vessels in the soft bark, in particular. Hence, the average distance between the latex vessel rows in the soft bark zone was given due consideration for the present study. The latex vessel rows of the genotype AC 644 were the closest in the soft bark zone (0.12 mm) while that of AC 647 had the maximum distance between rows (0.75 mm) (Table 14). AC 647 has thus very low number of latex vessel rows in the soft bark (2.26), while it had a total bark thickness of 3.44 mm and AC 644 which had the closest latex vessel rows had an average of 4.01 vessels in the soft bark, in a total bark thickness of 2.55 mm (Table 15). Reghu *et al.*, (1996) had reported a range of 0.256 - 0.790 mm distance between the latex vessels, with a population mean of 0.43 mm distance comparable to 0.47 mm of the control clone RRII 105, in a set of 100 wild genotypes at the age of 2 years, in agreement with the present study.

Metcalfe and Chalk (1950) has reported on the utility of phloem ray characters for identification of plant species. Premakumari (1992) had indicated that phloem ray characters would be useful for identification of *H.brasiliensis* at clonal level.. It has been reported that the density and width of phloic rays in the laticifer layer influences the yield of rubber clones (Premakumari *et al.*, 1988). The structural alignment of the bark tissues of *Hevea* has the laticifers running from

the base of the trunk upward, weaving the ray groups, and is distributed in rows alternating with sieve tube layers. Frequency, height and width of phloic rays in the laticiferous layer highly influences the orientation of laticifers in the extent of their waviness, which is a clonal character. As the frequency of phloic rays increases, it increases the number of deviations in the running directions of laticifers. Likewise, higher ray width will lead to wider angles of the deviations of latex vessels. Thus broad rays and their higher density will cause the most wavy direction of laticifers (Premakumari *et al.*, 1988). The rate of flow of latex will thus be significantly affected by the waviness of the vessels. The rate of flow of the latex coming out per unit length of the tapping panel in unit time has been described as a major component factor influencing the yield of *Hevea* clones (Sethuraj, 1981). Thus an increased width or smaller height / width ratio of the rays can be expected to be one factor reducing the yield expression of the wild genotypes. Maintenance of latex flow in rubber depends on maintenance of turgour pressure in the latex vessels by a dilution reaction which is the influx of water from the neighbouring cells into the latex vessels to restore equilibrium disturbed by tapping and this osmotic adjustment depends on the turgour pressure of surrounding cells also (Frey-Wyssling, 1932; Riches and Gooding, 1952 and Sethuraj 1977). Therefore small diameter of phloem rays, favours better turgour maintenance in latex vessels. This structure and function relationship influences the yield through dilution reaction and the extent of drainage area of bark, especially at conditions when water status in plant tissue is a limiting factor. Cell diameter is also a factor deciding the width of phloem rays and hence the orientation of latex vessels.

Frequency of phloic rays in a unit area of 0.01 mm^2 in the wild genotypes showed a minimum of 2.50 in MT 935 to a maximum of 7.75 in AC 629. The population mean was 3.78 comparable to that of the control clone (4.00) (Table 14). Twelve of the wild genotypes had a significantly higher frequency of phloic rays per unit area and 31 genotypes were on par with the control. Remaining genotypes had a significantly lower number of phloic rays per unit area compared to the control (Table 15).

Height of phloic rays was the minimum for the genotype MT 1024 (0.18 mm) and maximum for AC 644 (0.41 mm) while the population mean was 0.29 mm and that of the control was

0.21 mm (Table 14). Except for the genotype MT 1024, which had the minimum height of phloic rays and MT 1008 which had a phloic ray height on par with the control, all the remaining 78 wild genotypes had a significantly higher phloic ray height compared to the control (Table 15). Width of the phloic rays studied showed a range of 0.03-0.08 mm for the genotypes RO 287 and MT 947 respectively. The general mean of the population, was the same as that of the control (0.05 mm) (Table 14). 42 genotypes had their phloic ray width comparable to the control. Twenty genotypes had a significantly higher phloic ray width than the control while the rest of the genotypes had a significantly lower ray width (Table 15). Thus the sixty genotypes altogether with comparable and significantly lower width for their phloic rays can be expected to have a similar influence on the orientation of laticifers as that is in the control.

Height / width ratio of the phloic rays had a wide range for the wild genotypes studied. The genotype MT 1008 had the lowest ratio (3.33) while the genotype RO 254 had the highest ratio of 9.95. The population mean for this character was 5.86 compared to 3.96 of the control clone (Table 14). Six of the genotypes had their height / width ratio comparable to the control clone RRII 105 while the remaining 74 genotypes had a significantly higher ratio than the control clone, indicating the possible favourable influence in the orientation of laticifers.

The density of latex vessels per row per mm distance of the circumference of the plant was found to be lower (17.15) than that of the control (23.76). The genotype RO 399 showed the minimum density of latex vessels (11.50) and RO 894 had the maximum density of latex vessels (25.00) (Table 14). The genotype with maximum density had a lesser frequency of phloic rays (2.99) and a higher height/width ratio (7.512). The genotype RO 399 even though had the lowest density of latex vessels, it had the maximum number of latex vessel rows in the soft bark region (8.01), besides having the maximum number of latex vessel rows in the whole bark (11.01) (Table 15). Except for the genotype RO 894, which had the highest density of latex vessels and MT 1055, which had a comparable density with the control clone all the remaining 78 genotypes had a significantly lower density compared to that of the control. Similar trends of this character was reported by Reghu *et al.*, (1996) in a set of two-year old wild genotypes, where the density of latex vessels ranged from 10.17-23.83, with an average of 12.83 compared to 19.17 of the

control.

Another important structural character is the diameter of the latex vessels. It was also found to have a wide range of 13.44 μm (MT 906) to 34 μm (MT 899), while the general mean of the character (21.46 μm) was higher than that of the control (16.30 μm) (Table 14). Only two genotypes, MT 906 and AC 657 had significantly lower diameter of the latex vessels compared to the control clone. Fourteen genotypes had their vessel diameter on par with the control and the remaining 64 wild genotypes had significantly higher diameter for their latex vessels (Table 15). Reghu *et al.*, (1996) in two year old wild genotypes, had reported a range of 14.29 μm to 27.99 μm comparable to the range observed in this study and the general mean was similar to that of the control while in the present study it was greater than the control.

The total cross sectional area of the laticifers, as described by Gomez (1982); Premakumari (1992) and Reghu *et al.*, (1996), represents the total quantity of laticifer tissue to be cut under tapping in terms of cross sectional area. Number of latex vessel rows, density of latex vessels per unit distance and diameter of latex vessels contribute to this estimate. Premakumari *et al.*, (1988) emphasizes the importance of total cross sectional area of laticifers by its combined effect with the orientation of laticifers, which is influenced by the phloic rays, in the expression of yield in *H. brasiliensis*. This character has been identified as the best parameter by Premakumari *et al.*, (1993) for early prediction of drought tolerant clones in *Hevea*. MT 929 had the minimum cross sectional area of laticifers (1.33 mm^2) and AC 1043 had the maximum cross sectional area of 17.77 mm^2. The wild population had a general mean of 6.96 mm^2 compared to the control clone's 7.14 mm^2. Reghu *et al.*, (1996) had reported similar wide range in this character in a study on two year old wild germplasm. Goncalves (1982); Paiva (1982) and Premakumari *et al.*, (1989) have reported the importance of the juvenile characters in rubber viz., girth, total bark thickness, number of latex vessel rows, density of latex vessels and test tap yield over the first three years of growth, to be related with the yield potential and thus these characters can serve as early selection criteria in the evaluation of the wild germplasm.

4.2.3 Provenance-wise performance of the wild genotypes.

4.2.3.1 Morphological characters

Comparison of the general performance of the wild genotypes based on their provenances- Acre, Rondonia and Mato Grosso was carried out for all the characters studied. During the first four quarters of the first year, the wild genotypes from Rondonia showed superiority over the other two provenances, Acre and Mato Grosso, for all the morphological characters like girth, height, number of leaf flushes per plant, total number of leaves per plant, inter-flush distance, petiole length, total leaf area and leaf area index (Table 16). Earlier reports of Ong *et al.*, (1983, 1995) on the superiority of Rondonian genotypes along with Acre genotypes for the girth of the wild germplasm were in agreement with the present study. Ong *et al.*, (1983) in a study of one year old seedlings, had reported Rondonian genotypes to have the maximum average girth of 7.1 cm compared to the Acre and Mato Grosso in agreement with the present study. Mercy *et al.*, (1993a) had reported in a study of wild genotypes of 18 months age, the superiority of Rondonian genotypes for the characters, girth and number of leaf flushes and Rao and Reghu (1999) had reported similar results for girth of the plants in another set of wild genotypes.

4.2.3.2 Test tap yield over three years

The test tap yield of the wild genotypes over the three years was recorded. It was found that the wild genotypes from Mato Grosso recorded the maximum test tap yield in all the three years (0.0986 g t^{-1} t^{-1}, 0.1801 g t^{-1} t^{-1}, 0.7602 g $t^{-1}t^{-1}$ respectively) compared to the other two provenances of Acre and Rondonia (Table 17). This result was in agreement with Clement-Demange *et al.*, (1990b); Abraham *et al.*, (1992); Mercy *et al.*, (1995); Chapuset *et al.*, (1995) and Rao and Reghu (1999).

4.2.3.3. Leaf structural characters

Provenance-wise comparison of the wild genotypes for the stomatal and other leaf structural characters did not show any specific trend between the three provenances. Number of stomata per unit area of leaf was the highest in the Acre genotypes (439.5) immediately followed by Mato Grosso (434.38) and Rondonia (424.76) whereas the epidermal cells per unit area of leaf in wild genotypes was the highest in Mato Grosso (1790.23) followed by Rondonia (1697.09)

and Acre (1617.82). The differences in the stomatal density between the Acre and Rondonian genotypes, even though not of a wide range can influence the transpiration rates in Rondonian genotypes favourably. Stomatal index was invariably the highest for Acre genotypes (21.70) followed by Rondonia (20.47) and Mato Grosso (19.87). The average single leaflet area was the highest in Rondonia (105.50 cm^2) followed by Acre (100.65 cm^2) and Mato Grosso (81.73 cm^2) (Table 18).

Thickness of the lamina was the same in the three provenances of Acre, Rondonia and Mato Grosso (0.137, 0.136 and 0.137 mm respectively) indicating no significant differences between the provenances in the photosynthetic capacity as contributed by this character. But the Acre genotypes had a thicker midrib (0.84 mm) compared to the other two provenances of Rondonia and Mato Grosso (0.74 mm and 0.79 mm respectively), which may give a better translocation capacity for the Acre gentoypes. Mato Grosso genotypes had the maximum palisade layer thickness (62.49 μm) compared to the Rondonia (59.79 μm) and Acre (58.89 μm). The greater thickness of the palisade layer in Mato Grosso genotypes may be an important contributing factor for its superiority in the test tap yield compared to the other two provenances in this study and in many other studies elsewhere. Acre genotypes on the other hand had the thickest spongy tissue (64.85 mm), followed by Rondonia (60.13 mm) and Mato Grosso (59.92 mm) which should help in a better light scattering ability in the internal atmosphere of the leaves enabling maximum light absorption besides resulting in a better gas exchange. Number of cells per unit length of palisade layer was the same for Acre and Rondonian genotypes (117.52 and 117.97 respectively) closely followed by Matto Grosso (115.68), which was comparable with that of the control clone (117.24). The closeness of these values shows no significant contribution of this character in the photosynthetic capacity of the genotypes provenance-wise. Number of cells per unit length of spongy layer was the highest in Acre (278.36) followed by Rondonia (273.95) and Mato Grosso (271.50). Acre and Mato Grosso genotypes had the maximum cuticle thickness of 2.62 μm and 2.63 μm respectively, followed by the Rondonia with 2.43 μm cuticle thickness. Cuticle thickness in the wild genotypes from all the three provenances was lower than that of the control clone (3.67 μm) thus giving no significant contribution to the water control efficiency of the wild genotypes.

4.2.3.4 Bark structural characters

Average values of the bark structural characters for the genotypes from the three provenances were compared. It was found that the total bark thickness did not have any differences between the three provenances with Acre, Mato Grosso and Rondonia genotypes having 2.89 mm, 2.88 mm and 2.81 mm thickness respectively in agreement with Alwi and Suhendry (1992) from Indonesia, in two year old wild *Hevea* germplasm. Soft bark thickness was the highest in Acre (1.23 mm) with Rondonia and Mato Grosso genotypes closely following (1.19 mm and 1.14 mm respectively), whereas the hard bark thickness was the highest in Matto Grosso genotypes (1.74 mm), which had the minimum soft bark thickness (1.14 mm). Acre and Rondonian genotypes had very similar values for this character (1.66 mm and 1.61mm respectively) (Table 19). The thickness of the soft bark and hard bark zones in this study was in agreement with the results of Reghu *et al.*, (1996) in a set of wild *Hevea* genotypes.

Mato Grosso genotypes had their number of latex vessel rows in the soft bark (3.46) closely behind the Acre and Rondonian genotypes, which had similar number of vessels (3.7 and 3.72 respectively). Similar results of maximum number of latex vessel rows in the soft bark region in the Acre genotypes, in a set of two year old wild genotypes was reported by Reghu *et al.*, (1996) in accordance with this study. Same trend was noticed for the number of vessels in the hard bark zone with 2.08, 2.13, and 2.29 vessels for Mato Grosso, Rondonia and Acre and respectively. Total number of latex vessel rows was the maximum in Acre (5.94) closely followed by Rondonia and Mato Grosso genotypes (5.79 and 5.46 respectively). Total number of latex vessel rows reported by Abraham *et al.*, (1992) and Rao and Reghu (1999) in different sets of wild genotypes was the highest for Mato Grosso genotypes, which was not in agreement with the present study. But this cannot be considered as a trend, as in this study the total number of latex vessel rows between the three provenances was almost similar.

Density of the latex vessels per mm distance of the rows was the highest for Acre genotypes (21.89) followed by Rondonia (21.49) and Mato Grosso (21.23). Diameter of latex vessels was the highest in Rondonian genotypes (17.52 μm) while the lowest diameter was recorded in Acre genotypes (16.67 μm) with the Mato Grosso genotypes coming in between

with a vessel diameter of 16.98 μm. Total cross sectional area of laticifer rows was the highest for the genotypes from Rondonia (7.76 mm^2) with only a slight difference for the Acre genotypes (7.35 mm^2) and Matto Grosso genotypes having the minimum cross sectional area (5.83 mm^2). This low cross sectional area of the laticifer rows of the Matto Grosso genotypes along with the other major bark structural traits, is not substantiative of its superiority of the test tap yield over the other two provenances. It can be assumed that the higher yield expression of the Matto Grosso genotypes is not only the contribution of laticifer elements alone, but can also due to many other factors.

Average distance between the latex vessel rows in the soft bark recorded in this study was the same for Acre and Rondonian genotypes (0.30 mm) and there was only a very minor increase in the distance between the vessel rows in the Mato Grosso genotypes (0.33 mm). Reghu *et al.*, (1996) had reported the Acre genotypes to be having the maximum distance between the latex vessel rows compared to the other two provenances in another set of wild genotypes, not in agreement with this study. The genotypes from the Acre and Rondonia had a slightly lower average value for the character frequency of phloic rays (3.76 and 3.67 respectively), and height of phloic rays (0.30 mm each) with the Mato Grosso genotypes having 3.89 and 0.28 mm for these two characters respectively. Width of the phloic rays was similar in Acre and Rondonian genotypes (0.05 mm each) with a slight increase in Mato Grosso genotypes (0.06 mm) while the control had an average width of 0.05 mm. Height / width ratio of the rays was the highest for the Rondonian genotypes (6.51) closely followed by Acre (5.96) and Mato Grosso (5.22) while the control had a value of only 4.12. The slightly disadvantageous phloic ray characters of the Mato Grosso genotypes shows that the orientation of latex vessels in this group of genotypes may not have a significant influence in the higher latex yield expressed by these genotypes. Clone to clone differences for the size and distribution of phloem rays is in agreement with the observations of earlier studies by Premakumari *et al.*, (1985, 1988) and Premakumari, 1992. It general it can be concluded that the bark structural character do not exert any significant influence on the genotypes based on their provenances and that the performance variation between the genotypes has to be due to reasons beyond the influence of geographical origin

4.3 Genetic parameters

In rubber, the breeder has to deal with a polygenic system. A polygenic system was defined by Mather (1941) as one where the characters display quantitative variation mediated by the joint action of a number of supplementary genes, each having a small effect in relation to the total variation. Genetic variation available in any population, forms one of the fundamental aspects that a breeder should be aware of, in any crop improvement programme (Mather and Jinks, 1977). This is not directly measurable, and only phenotypic characters, which are external expressions of genetic values modified by the environment, are measurable. Gilbert *et al.*, (1973) was the first to report on application of biometrical analysis to rubber progeny data. Genetic parameters like phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in the broad sense (H^2) and genetic advance (GA), help in partitioning the genetic variability into heritable and non-heritable components (Johansen, 1909; Henderson, 1953 and King and Henderson, 1954). Several forest geneticists have discussed several methods for estimation of genetic parameters in perennial crops (Sakai *et al.*, 1963, 1967; Huhn, 1975 and Kedarnath, *et al.*, 1969).

4.3.1 Phenotypic and genotypic coefficients of variation

For all the characters studied in this experiment, the phenotypic coefficient of variation was always higher than the genotypic coefficient of variation. This is only natural as variability at the phenotypic level consists of both genotypic and environmental variabilities, besides the genotype-environment interaction (G x E). When the total variability for any character is contributed mainly by the genotypic variation and is less influenced by the environmental factors the scope for selection of this character increases.

4.3.1.1 Morphological characters

It was seen that among the morphological, leaf and bark structural characters studied, the effect of environment was the least for the leaf and bark structural characters and more but reasonable for the morphological characters. In general, the morphological characters like girth, height, number of leaf flushes per plant, total number of leaves per plant, inter-flush distance, total

leaf area and leaf area index exhibited medium to high estimates of PCV and GCV (Table 20) with the genetic components of the total variability contributing in the range of 60.14% to 78.25% to the total variation, except for petiole length (46.98%). This indicates a significant involvement of genetic factors in the expression of these characters, even though they were more influenced by the environmental factors than the structural characters. Petiole length was however, found to be more influenced by the environment where the GCV was low (13.40) compared to the PCV (28.52) with the genetic variation being 46.98% of the total variation. Moderate estimates of variability was reported by Chandrasekhar *et al.*, (1995) for height of the plants, and by Licy *et al.*, (1993) for girth of the plants in studies on immature Wickham clones. Low variability estimates were reported by Mydin *et al.*, (1996) for the characters girth, height and number of leaf flushes in two year old Wickham progenies which was not in agreement with the medium estimates of variability in this study. But Mydin (1992a) has reported high estimates of variability for number of leaf flushes in two-year-old seedling progenies. Abraham *et al.*, (1992) in studies in two-year old wild genotypes had reported moderate estimates of the coefficients of variation, for the girth and height of the plants, in agreement with the present study. Higher estimates of PCV and GCV were reported in another study, in a set of wild genotypes at 18 months age, for height of the plants and number of leaf flushes with medium estimates for the characters leaf area index and girth of the plants (Mercy *et al.*, 1993a). Medium estimates were recorded for these characters in this study.

4.3.1.2 Test tap yield over three years

The test tap yield over the first three years, recorded very high estimates of GCV and PCV. The environmental effect in the expression of yield was the least in the first and third year where the genetic component contributed 92.2% and 81.65% of the total variation. In the third year, test tap yield had the highest GCV of 95.54 and a PCV of 117.01. This high estimate of coefficient of variation demonstrates the wide variability for this character in the wild genotypes. Mydin *et al.*, (1992b, 1996) have reported the highest genotypic coefficient of variation of the juvenile rubber yield in two year old Wickham progenies while Abraham *et al.*, (1992) had reported very high estimates of PCV and GCV for the test tap yield in the second year (153.33

and 137.17 respectively) in a study in 2 year old wild genotypes.

4.3.1.3 Leaf structural characters

Stomatal characters- the number of stomata and number of epidermal cells/mm^2 of leaf and the stomatal index- recorded medium estimates of coefficient of variation. But the differences between PCV and GCV was very low for these characters with the genetic component contributing 88.4%, 97.35 and 91.8% respectively, thus highlighting the significant effect of the genotype in these characters rather than the environmental factors. But the single leaflet area had a greater difference between the PCV and GCV (29.65 and 16.36 respectively), which indicates higher influence of the environment in the expression of this character. Abraham *et al.*, (1992) had reported higher estimates of PCV (35.85) and GCV (31.24) for the character single leaflet area in two year old wild genotypes, compared to the medium estimates of coefficients for this character in this study whereas, Rao and Reghu (1999) had reported medium estimates of PCV (36.0) and GCV (23.95) for this character in a study on four year old wild germplasm, which was in agreement with this study.

Other leaf structural characters in the wild genotypes showed low to medium estimates of PCV and GCV. For the characters thickness of lamina and leaf midrib, thickness of the palisade and spongy layers, number of cells per unit length of palisade layer and spongy layer and thickness of the cuticle, the difference between the PCV and GCV was very less, thus indicating the higher involvement of genetic factors in the expression of these characters (Table 22).

4.3.1.4 Bark structural characters

For all the bark structural characters studied medium to high estimates of coefficients of variation were recorded (Table 23). The differences between PCV and GCV for these characters were very low, that the genetic contribution to the total phenotypic variation ranged from 91.79-99.4%. This showed the negligible influence of the environment in the expression of these characters. Chandrasekhar *et al.*, (1995) reported moderate estimates and Mydin (1992a) reported higher estimates of genotypic variability for the total number of latex vessel rings. Licy *et al.*, (1992) had medium estimates for the characters, total number of latex vessels and total

bark thickness in immature Wickham clones. Premakumari *et al.*, (1987) had reported moderate estimates of PCV and GCV for the diameter of latex vessels, frequency, height and width of phloic rays, in a set of mature Wickham clones, which was in agreement with this study. But, low estimates of the coefficients of variability reported for the density of latex vessels was not in agreement with the moderate estimates in this study. Reghu *et al.*, (1997) had reported medium estimates of PCV and GCV for the character total number of latex vessel rows (20.20 and 16.40 respectively) compared to the higher estimates for this character, in this study (30.75 and 30.01 respectively). Low estimates of PCV and GCV for total bark thickness and density of latex vessels, were also reported by the same authour, in 3 ½ year old Wickham clones, compared to the medium estimates of 15.73, 15.53 for total bark thickness, and 18.33 and 18.03 for density of latex vessels as PCV and GCV respectively, in this study. Abraham *et al.*, (1992) had reported in wild genotypes, medium estimates of PCV and GCV for total bark thickness, total number of latex vessels and density of latex vessels, which were in accordance with the results of this study. In four year old wild genotypes, Rao and Reghu (1999) had reported medium estimates of PCV and GCV for total bark thickness, in accordance with this study while the medium estimates for total number of latex vessel rows was not in agreement with the higher estimates in this study.

The narrow differences between the phenotypic and genotypic coefficients of variation for the leaf and bark structural characters including the stomatal characters are indicative of the comparatively stable nature of these characters due to the negligible influence of the environment on these characters. The medium to high estimates of variability recorded for the morphological, stomatal, leaf and bark structural characters suggests the possibility of genetic advancement for these characters through selection.

4.3.2 Heritabiltiy (broad sense)

Heritability of a character specifies the proportion of the total variability that is due to genetic causes, or the ratio of the genetic variance to the total variance (Allard, 1960). Lush (1937) has defined broad sense heritability (H^2) as the proportion of total genetic variance to the total or phenotypic variance. It refers to the functioning of the whole genotype as a unit and is

used in contrast with environmental sources of variation (Lerner and Michael, 1950). The estimation of heritable variation is not possible with the help of genotypic coefficient of variation alone. Burton (1952) suggested that genotypic coefficient of variation together with heritability estimates would give a better idea of selection advance to be expected. Selection acts on genetic differences and gains from selection for a specific character depends largely on the heritabiltiy of the character (Allard, 1960). Broad sense heritability reflects the proportion of additive plus non-additive genetic variance and is useful in predicting improvement achieved by cloning selected trees (Hogarth, 1971).

4.3.2.1 Morphological characters

Heritability in the broad sense was found to be medium to high for all the characters studied indicating that the expression of these characters are largely under the genetic influence rather than environmental influence. Morphological characters recorded in the four quarters of first year recorded medium estimate of heritability (Table 20). Maximum heritability was recorded for the girth of the plants in all the four quarters (60.37%, 60.11%, 61.20% and 60.08% respectively). Height of the plants recorded a maximum heritability of 60.16% in the second quarter, followed by 56.08%, 54.08% and 51.58% in the third, first and fourth quarters respectively. Medium heritability estimates were recorded for number of leaf flushes per plant in the four quarters (36.16%, 52.06%, 54.44% and 57.71% respectively), the total number of leaves in the four quarters (44.58%, 58.42%, 57.69% and 57.65% respectively) and inter-flush distance (41.18%). Petiole length recorded a low heritability (24.08%) showing the observed variance of this character to be non-heritable. Total leaf area and leaf area index recorded in the fourth quarter showed medium estimates of heritability (49.16% and 48.99% respectively).

High estimates of H^2 were reported for the character girth by Boock *et al.*, (1995); Moreti *et al.*, (1994) and Hoa and Nuong, (1997) and moderate to high H^2 for girth (Mydin *et al.*, 1996, in two year old Wickham clones) and for height in 3 ½ year old Wickham clones in rubber by Chandrasekhar *et al.*, (1995) in conformity with the results of this study. Mydin *et al.*, (1996) had also reported moderate heritability estimates for number of leaf flushes in agreement with the

results of this study while low heritabilty reported for height of the plants was not in agreement with the present study. In the wild genotypes, medium H^2 estimates have been reported for single leaf area in 4 ½ year old genotypes (Rao and Reghu, 1999), for height of plants in two year old wild genotypes (Abraham *et al.*, 1992 and Rao *et al.*, 1999), in accordance with the result of this study. Mercy *et al.*, (1993a) in a set of 18 month old wild genotypes had reported moderate H^2 estimates for height of the plants and number of leaf flushes per plant, while the high heritability for leaf area index and the moderate heritability for girth of the plants were not in agreement with the results of this study.

4.3.2.2 Test tap yield over three years

High heritability estimates were recorded for the test tap yield in the first and third year (85.17% and 66.67% respectively) with medium heritability estimates in the second year (45.50%) (Table 21). This is a clear indication of the possibility of good response to selection by this character. According to Ong *et al.*, (1997) yield in rubber is highly heritable and the potential is expressed early in the nursery stage itself. High estimates of H^2 were reported for yield by several workers (Boock *et al.*, 1995; Moreti *et al.*, 1994; Hoa and Nuong, 1997; Liang *et al.*, (1980); Licy *et al.*, (1992) in 4 ½ year old Wickham plants and Saraswathy Amma and Panikkar (1989) in a seedling progeny study in Wickham clones. All these reports were in conformity with the present study. In two year old Wickham clones, Mydin *et al.*, (1996) and Samsuddin *et al.*, (1985) have reported moderate heritability estimates for nursery yield in rubber. Abraham *et al.*, (1992) in two year old wild genotypes, Mercy *et al.*, (1993a) in a set of 18 month old wild genotypes and Rao *et al.*, (1999) in four year old wild genotypes, have reported high heritability for test tap yield in accordance with the results of this study,

4.3.2.3 Leaf structural characters

Stomatal characters –number of stomata and number of epidermal cells per mm^2 of leaf area and stomatal index – recorded high estimates of broad sense heritability (78.22%, 94.65% and 84.42% respectively) indicating the scope for inheritance of this character. Stomatal frequency has been reported earlier to be a heritable character in *Populus* (Pallardy and Kozlowski,

1979) and in *Hordeum* (Miskin *et al.*, 1972) and in *Zea* (Heichel, 1971) showed that a simple genetic system controlled the epidermal cell and stomatal frequency. Single leaf area however showed only medium heritability, in agreement with the report of Rao *et al.*, (1999), thus highlighting the influence of the environment in the expression of this character. All the other leaf structural characters studied recorded high to very high heritabilty – thickness of lamina (91.67 %), thickness of leaf midrib (97.34 %), thickness of palisade layer (95.38 %), thickness of spongy layer (56.95 %), number of cells per unit length of palisade layer (84.96 %) and spongy layer (94.15 %) and thickness of the cuticle (96.01 %) (Table 22). The high heritable values are indicative of the higher contribution of the genetic component in the expression of these characters.

4.3.2.4 Bark structural characters

High estimates of broad sense heritability were recorded for all the bark structural characters studied- viz, total bark thickness (97.61%), thickness of the soft bark (92.35%), thickness of the hard bark (94.96%), thickness of the soft bark and hard bark in percentage (90.50% and 91.00% respectively), number of latex vessel rows in the soft bark (95.15%), number of latex vessel rows in the hard bark (86.90%), total number of latex vessel rows (95.24%), average distance between the latex vessel rows in the soft bark (98.95%), frequency of phloic rays (90.76%), height of phloic rays (95.06%), width of phloic rays (84.3%), height / width ratio (94.00%), density of latex vessels per mm circumference (97.32%) and diameter of latex vessels (93.20%) and total cross sectional area of latex vessels (90.29%) (Table 23). The high heritability values are suggestive of the possible good response of these characters to selection. The high H^2 estimates of most of the economical characters studied, are in accordance with the similar observations on heritabilty of the economic characters in rubber by Simmonds (1989).

Moderate to high estimates of heritability were reported for the total number of latex vessel rows by Chandrasekhar *et al.*, (1995) in 3 ½ year old Wickham clones and by Licy *et al.*, (1993) in young Wickham clones. Premakumari *et al.*, (1987) had reported moderate to high H^2 estimates for the characters frequency of phloic rays, height of phloic rays, width of phloic rays, diameter of latex vessels and density of latex vessels. In two year old Wickham clones Mydin *et*

al., (1996) had reported moderate heritability estimates for total bark thickness and total number of latex vessel rows. Abraham *et al.*, (1992) had reported high H^2 for total number of latex vessel rows in a study in two year old wild genotypes of *Hevea.* All these studies were in agreement with the results of this study.

Premakumari (1992) had reported in mature Wickham clones that the bark anatomical characters in general showed very high heritability values when compared to latex flow characters studied, indicating the more dependability of structural parameters as selection criteria for yield. High heritability values for various structural traits like height, width and the height/width ratio of phloic rays were observed in a different population in an earlier study (Premakumari *et al.*, 1984) where the total number of latex vessel rows, a well established yield component and the laticifer area index, a more balanced system of laticifer trait were also reported to be highly heritable. These results were in agreement with the findings in this study.

4.3.3 Genetic advance

Even though heritability estimates are useful in the selection of superior genotypes on the basis of phenotypic performance of the characters, it does not give a clear picture on the extent of improvement that can be achieved. Hence, Johnson (1955) suggested that heritability estimates along with genetic advance (expressed in percentage of mean) furnishes a better picture than heritability alone. Ramanujam and Thirumalachar (1967) also suggested the reliability of expressing the broad sense heritability along with genetic advance. According to Panse (1957), the traits with high heritability and genetic advance are controlled by additive gene action and are therefore amenable to genetic improvement by selection.

4.3.3.1 Morphological characters

Moderate to high heritability accompanied by moderate to high genetic advance was recorded for the characters girth, height, total number of leaves per plant, total leaf area and leaf area index. Low genetic advance accompanying the high heritability estimates were observed for the characters number of leaf flushes, inter flush distance and petiole length (Table 20). Exploitation of heterosis for these traits with low genetic advance, could be possible if dominance is

involved in the non-additive gene effects (Singh and Choudhary, 1985). Mercy *et al.*, (1993a) in young wild genotypes had reported high genetic advance for leaf area index and moderate advance for height of the plants along with Rao *et al.*, (1999) who also reported moderate advance for height, in conformity with the results of this study. Medium genetic advance for the number of leaf flushes per plant and low advance for the girth of the plants, reported by Mercy *et al.*, (1993a) was not in agreement with the present study. High genetic advance had been reported by Moreti *et al.*, (1994) for girth and by Chandrasekhar *et al.*, (1995) for plant height in their studies in Wickham clones in the immature phase, in conformity with the results of the present study.

4.3.3.2 Test tap yield over three years

Very high genetic advance (140.98%, 100.30% and 160.70%) accompanying medium to very high heritability estimates (85.17%, 45.50% and 66.67%) were observed for the test tap yield in the three years respectively (Table 21). This highlights the scope of obtaining considerable genetic gain by applying selection pressure in this population for this character. High genetic advance recorded for test tap yield in this study was in accordance with similar reports for yield by Abraham *et al.*, (1992), Mercy *et al.*, (1993a) and Rao *et al.*, (1999) in different sets of wild genotypes in the nursery. High genetic advance has also been reported by Moreti *et al.*, (1994) for yield in Wickham clones of rubber.

4.3.3.3 Leaf structural characters

Most of the leaf structural characters recorded medium to high genetic advance along with very high estimates of heritablility indicating the preponderance of additive gene action in the genetic control of these characters. Characters number of stomata and number of epidermal cells per mm^2 of the leaf area, stomatal index, thickness of lamina and leaf midrib, thickness of palisade and spongy layers, number of cells per unit length of spongy layer and thickness of cuticle had moderate to high genetic advance along with high heritability indicating the additive gene action, while very low genetic advance with high heritability estimates were observed for single leaflet area and number of cells per unit length of palisade layer which should be the result of non-

additive gene action. In their studies in immature wild genotypes Rao and Reghu (1999) had reported medium genetic advance, and Abraham *et al.*, (1992) in a study in two year old wild genotypes, had reported high genetic advance for single leaflet area compared to the low genetic advance observed in this study.

4.3.3.4 Bark structural characters

In the present study, high heritability estimates accompanied with moderate to high estimates of genetic advance was recorded for the bark structural characters viz. total bark thickness, thickness of soft and hard bark, soft and hard bark thicknesses in percentages, number of latex vessel rows in the soft and hard bark, total number of latex vessel rows, frequency of phloic rays, height and width of phloic rays, height / width ratio of phloic rays, density and diameter of latex vessels and the total cross sectional area of laticiferous vessels (Table 23). The above findings points out the preponderance of additive gene action and hence the possibility of considerable genetic gain by including these characters in the selection programme.

Goncalves *et al.*, (1995b) had reported high genetic advance for the characters total bark thickness and total number of latex vessel rows in a set of Wickham clones at the age of three years. High genetic advance was reported by Moreti *et al.*, (1994) for the characters total bark thickness, total number of latex vessels rows, density and diameter of latex vessels and average distance between the latex vessel rows, and by Chandrasekhar *et al.*, (1995) for total number of latex vessel rows in their studies in Wickham clones in the immature phase. Premakumari (1992) in a set of Wickham clones reported, number of latex vessel rows, laticifer area index and height / width ratio of phloic rays to have high genetic advance associated with high heritability. Premakumari *et al.*, (1987) in another set of mature Wickham clones had reported additive gene action for height of phloic rays. All these studies were in support of the results obtained in this study. Premakumari *et al.*, (1987) had also reported low genetic advance for the characters-frequency of phloic rays, width of phloic rays, diameter and density of latex vessels indicating their non-additive nature, not in agreement with the present study in the immature phase.

There are similar reports in wild genotypes also. In a study in a set of immature wild

genotypes Abraham *et al.*, (1992) had reported high heritability and moderate genetic advance for the total number of latex vessel rows, which is comparable to the high genetic advance recorded in this study. Rao and Reghu (1999) had reported medium genetic advance for total bark thickness in agreement with this study and medium genetic advance for total number of latex vessel rows not in agreement with the high genetic advance observed in this study.

4.4 Character associations

When the breeder applies selection pressure for a trait, the population under selection is not only improved for that trait, but is also improved in respect of other characters associated with it. Correlations provide information on the nature and extent of relationship between characters in a population, thus facilitating effective selection and simultaneous improvement of two or more characters. Therefore, analysis of yield in terms of phenotypic, genotypic and environmental correlation coefficients of component characters, leads to the understanding of the characters that can form the basis of selection. Selection pressure can be exerted efficiently in any of these easily discernible characters having close associations with yield. This forms an essential prerequisite for formulating breeding programmes (Gilbert, 1961) aimed at achieving desirable combinations of various components of rubber yield. Genetic correlation between two characters is most relevant when determining the value of a secondary character; it may be caused by linkage and /or pleiotropy (Falconer, 1981). If caused by linkage, a correlation can be changed as a result of selection where a negative correlation can be broken. If the correlation is due to pleiotropy it cannot be changed or broken, in which one of the two linked characters can be considered as a physical marker of the other. Irrespective of its origin, genotypic correlation is dependent on the frequencies of genotypes in a population and thus can vary from one population to another (Gallais, 1984). In the context of plant breeding, a certain comprehension of genetic correlation is particularly useful for performing indirect artificial selection on characters that show low heritability and /or are difficult to measure (Gallais *et al.*, 1983). Thus the phenotypic, genotypic and environmental correlation coefficients worked out in this study will help to get an idea of the nature and extent of the association between the various characters in the wild genotypes in the early growth phase.

4.4.1 Morphological characters

The phenotypic, genotypic and environmental correlation coefficients worked out for the test tap yield at 18 months age with the selected growth characters like girth, number of leaf flushes, total number of leaves and leaf area index did not show any significant degree of association with any of these characters (Table 24). This might be due to the too early a growth stage for these characters to have any contribution to the test tap yield, which might have been contributed by other factors. Several significant and positive genotypic correlations were noted among the various characters studied viz. girth of the plants with number of leaf flushes (0.7387), total number of leaves (0.8717) and leaf area index (0.9050); number of leaf flushes with total number of leaves (0.9193) and leaf area index (0.8095) and total number of leaves with leaf area index (0.9310).

The test tap yield at the end of 18 months was found to have a negative but negligible genotypic and phenotypic correlation with the girth of the plants. There are several reports of a positive and significant correlation between these two characters (Madhavan *et al.*, 1996; Narayanan *et al.*, 1974 and Licy and Premakumari 1988). But there are also reports of insignificant correlation in the immature phase between yield and girth by Olapade (1992), Alika (1982) and Goncalves *et al.*, (1995a, 1996) who have reported non significant correlations between yield and girth in *Hevea* progenies which is in accordance with the results of this study. Premakumari (1992) and Olapade (1988) have reported negative correlation between girth and yield. This negative relation, can be explained as most probably a spurious one, i.e., the negative correlation between the yield and girth occurring due to an association with other characters (Olapade, 1988). Besides, Goncalves *et al.*, (1998) suggests that girth at the first year of growth is not a reliable predictor of future field performance.

Mydin (1992a) had reported negligible correlation between yield and number of leaf flushes and significant positive correlation for the characters girth vs number of leaf flushes, total number of leaves and number of leaf flushes vs total number of leaves, in one year old Wickham seedlings, in agreement with this study. Mercy *et al.*, (1993a) had reported insignificant correlations between yield and number of leaf flushes, and positive significant correlation of leaf area index

with girth of the plants and number of leaf flushes, in a set of 18 month old wild genotypes in conformity with the results in this study. Goncalves *et al.*, (1994) in two-year old Wickham clones from Brazil, and Mercy *et al.*, (1993a, 1995) in 18 and 21 months old wild genotypes respectively had reported positive and significant correlation between girth and number of leaf flushes, which were in agreement with the results of this study. Licy *et al.*, (1993) had reported high genotypic and phenotypic correlation coefficients between the girth and leaf area index in agreement with this study thus bringing out the possibility of obtaining vigorous plants by selecting for high leaf area index. The high and positive correlation of total number of leaves with girth and number of leaf flushes reported by Mercy *et al.*, (1993a) is in agreement with the results of this study.

Varghese *et al.*, (1989) reported that the morphological characters like girth, number of leaf flushes and total number of leaves contribute to the juvenile vigour which in turn determine the yield potential and Varghese *et al.*, (1993) points out that good immature vigour is one of the important attributes associated with yield potential in rubber. High correlations between nursery yield at different growth stages and mature yield (Ho, 1976) and Tan (1987) suggests that nursery yield could be used to select at least certain proportion of the genetically high yielders. Hence, even though these growth characters studied in the first year in this experiment did not show any significant correlation with the test tap yield, these characters definitely is of importance in the immediate years following as they contribute much to the general vigour of these genotypes and hence the yield expression.

4.4.2 Leaf structural characters

The phenotypic, genotypic and environment correlation coefficients worked out for the test tap yield at 42 months age with the stomatal and leaf structural characters showed negligible correlations with all these characters (Table 25). But certain significant inter-correlations were recorded for certain characters. Bobilioff (1923); Gomez (1982) and Gomez and Hamzah (1980) have reported that there is no relationship between anatomical structures of the leaves and the yield in their studies in *Hevea*. Gomez and Hamzah (1980) had reported negative and weak correlation of yield with number of stomata in the lower epidermis, negligible positive correlations

with thickness of lamina and thickness of spongy layer in agreement with this study, while a positive and medium correlation with number of cells per unit length of palisade and spongy layers was not in agreement with this study. Balasimha *et al.*, (1985) had reported no positive relations between stomatal frequencies and yield in a study on leaf characteristics in Cocoa as reported in this study.

Several significant inter-correlations were recorded in this study between the various structural traits (Table 25). Thickness of the lamina had a positive and high genotypic correlation with the thickness of leaf midrib (0.4127), thickness of palisade layer (0.6074) and spongy layer (0.6803) and with number of cells per unit length of spongy layer (0.3056) indicating a related response for these characters with an increase in the leaf thickness. Thickness of leaf midrib had a positive genotypic correlation with the thickness of spongy layer (0.4459). Thickness of palisade layer had a positive genotypic correlation with the thickness of spongy layer (0.1927), and a negative genotypic relation (-0.2397) with the number of cells per unit length of palisade layer, where the latter had a negative but negligible genotypic correlation (-0.0152) with the thickness of lamina. Number of cells per unit length of palisade layer was positively correlated with the number of cells per unit length of spongy layer (0.4994). Thus the thickness of the lamina becomes a reliable character among the various leaf structural traits due to its significantly high genotypic correlation with other important leaf structural traits.

4.4.3 Bark structural characters

Correlation coefficients at the phenotypic, genotypic and environmental level worked out for yield and bark structural characters and their inter correlations revealed interesting results in the wild genotypes at 42 months age (Tables 26, 27 and 28 respectively). Test tap yield recorded positive genotypic correlation with number of latex vessel rows in the soft bark (0.2990) and total number of latex vessel rows (0.2237). Yield recorded practically no correlation with other important traits like total bark thickness, density and diameter of latex vessels.

Several notable inter-correlations were recorded among the different structural traits studied. Positive genotypic correlations were recorded for the total bark thickness with soft bark thickness (0.5307), hard bark thickness (0.9120), number of latex vessel rows in soft bark and

hard bark (0.318 and 0.2492 respectively), total number of latex vessel rows (0.3129) and total cross sectional area of latex vessels (0.2080). Number of latex vessel rows in soft bark had positive genotypic correlations with number of latex vessel rows in hard bark (0.5438), total number of latex vessel rows (0.9308), total cross sectional area of latex vessels (0.5802) and negative but high genotypic correlation with average distance between the latex vessel rows in soft bark (-0.5352). Number of latex vessel rows in the hard bark had positive and high genotypic association with total number of latex vessel rows (0.8068) and total cross sectional area of latex vessels (0.5697). Total number of latex vessel rows had a negative and high genotypic correlation with average distance between latex vessel rows in soft bark (-0.5285) and a high positive genotypic correlation with total cross sectional area of latex vessels (0.6445).

Frequency of phloic rays had a negative genotypic association with length of phloic rays (-0.2460); height of phloic rays had a positive genotypic relation with width of phloic rays (0.2376) and its height / width ratio (0.5535); width of phloic rays had a high negative genotypic association with height/width ratio (-0.6586); density of latex vessels had a positive genotypic association with total cross sectional area of latex vessels (0.3589) and diameter of latex vessels had a high positive genotypic correlation with the total cross sectional area of latex vessels (0.6284).

Many workers reported significant correlation coefficients between the yield and total number of latex vessel rows both in mature and immature phase of *Hevea*. Licy and Premakumari (1988); Chandrashekar (1994); Tan and Subramaniyam (1975); Narayanan *et al.*, (1974) and Hamzah and Gomez (1982) in Wickham clones and Madhavan *et al.*, (1996) in wild genotypes, reported significant and positive correlation of yield with Total number of latex vessel rows in clonal studies, in immature phase, which was in agreement with the results of the present study. Goncalves *et al.*, (1995c, 1996) in nursery level studies reported significant correlation coefficients for the character yield with total number of latex vessel rows and density of latex vessels. Goncalves (1996) reported similar result between yield and diameter of latex vessels also. The significant correlation of yield with the total number of latex vessel rows was in agreement with the results of this study, while the correlation with density and diameter of latex vessels in these reports were not in accordance with that observed in this study. In another study in a set of two year old Wickham clones, Mydin *et al.*, (1996) reported a positive and significant correlation

with number of latex vessel rows in accordance with this study but the positive and significant correlation with total bark thickness and number of leaf flushes were not in agreement with this study. The importance of the number of latex vessel row in determining the yield in rubber, has been reported by Ho *et al.*, (1973) and Premakumari *et al.*, (1988) also. The negligible correlation observed between the yield and total bark thickness in this study was in line with several other reports (Tan,1998; Olapade, 1992; Alika, 1982, Goncalves *et al.*, 1995a; Licy and Premakumari 1988 in Wickham clones) and Madhavan *et al.*, (1996) in wild genotypes.

Madhavan *et al.*, (1996) had reported the absence of any degree of association between the yield and the average distance between latex vessel rows in conformity with the results of present study, whereas Ho, (1976) had reported low, but significant correlation for these characters not in agreement with this study. The positive correlation reported in a set of wild genotypes of *Hevea* by Madhavan *et al.*, (1996) and in Wickham clones by Narayanan *et al.*, (1974); Licy and Premakumari (1988) and Hamzah and Gomez (1982) for the characters number of latex vessel rows and total bark thickness was in agreement with the results of the present study. The high negative correlation observed in this study between the characters number of latex vessel rows and average distance between latex vessel rows in the soft bark was in conformity with the results of Narayanan *et al.*, (1974) in Wickham clones and Madhavan *et al.*, (1996) in wild genotypes. The insignificant relation observed in this study between the density of latex vessels and diameter of latex vessels is in accordance with similar results by Premakumari *et al.*, (1984); Narayanan *et al.*, (1974) and Hamzah and Gomez (1982). Weak associations of the average distance between the latex vessel rows with density and diameter of latex vessels; between the number of latex vessel rows and diameter of latex vessels; between the total bark thickness and density of latex vessels and diameter of latex vessels, was reported by Narayanan *et al.*, (1974) in a nursery level study, in conformity with the results of the present study.

Among all the characters studied total number of latex vessel rows exhibited the maximum genotypic correlation with the test tap yield among the bark structural characters at the age of 42 months after planting. None of the leaf structural characters seemed to have any significant association with the test tap yield at the same age. The selected growth characters at the age of 18

months also did not show any association with the test tap yield as it would have been too early to detect any sort of association of these characters for the expression of yield, as there can be many other factors contributing to and governing yield. Unfavorable associations between yield and other secondary characters have been a problem in rubber (Wycherley, 1969; Ho, 1972). Ho *et al.*, 1973 opined that relatively low correlations can be useful in early selections especially if the dependent variable (ie, mature yield) is correlated with two or more independent variables (ie, juvenile characters) which are not highly correlated with each other.

4.5 Factor analysis

Factor analysis refers to the statistical techniques whose common objective is to represent a set of variables in terms of a smaller number of hypothetical variables. Hence, the complexity of recording, analysing and interpreting a host of multivariate data in field experiments, especially in a perennial tree crop like rubber, can be lessened by adopting factor analysis whereby the breeder benefits from this character reduction technique, to concentrate on selected independent marker characters which also represents other characters related by their likeness in inheritance.

Factor analysis is the most common method used for identifying the factors of divergence in a multivariate data. In this study, a pooled set of 33 characters representing the morphological, leaf and bark anatomical characters in the wild *Hevea* germplasm was used for factor analysis to get a set of reduced number of new orthogonal variables. The characters used for factor analysis were girth, height, number of leaf flushes, total number of leaves, total leaf area, leaf area index, inter-flush distance, length of the petiole, number of stomata and epidermal cells per mm^2 of leaf area, stomatal index, single leaflet area, thicknesses of lamina, midrib, palisade and spongy layers, number of cells per unit length of palisade layer and spongy layer, thickness of cuticle, total bark thickness, soft bark and hard bark thicknesses, number of latex vessels in the soft and hard bark, total number of latex vessel rows, density of latex vessels per mm circumference, diameter of latex vessels, laticifer area index, average distance between latex vessels in soft bark, frequency, height, width and height / width ratio of phloic rays. Mydin (1992a) reported factor analysis in two genetically divergent clusters of Wickham clones where the yield factors comprising dry rubber yield, latex flow rate, volume of latex, length of tapping panel and plugging index

were identified as the main factors of divergence.

Factor analysis carried out in the above set of characters identified 12 factors, which accounted for 82.30 % variability in these 33 variables. It should be stressed that this method only estimates mathematical associations among the multi variates. The most important aspect is the biological interpretation of these associations, which should be done based on logics. It was seen that the first factor was associated with six of the growth characters- girth, height, number of leaf flushes/ plant, total number of leaves per plant, total leaf area and leaf area index. All these six characters can be expected to behave alike in their inheritance, as a single factor is believed to control the inheritance of these characters. Of these characters, the maximum factor loading was recorded for the total number of leaves per plant and hence could be treated as a marker character in this group, which can represent all the other five characters in any future study involving these characters. But, girth of the plants has to be singled out even though it comes along with the other five growth characters, as the uniqueness of girth, as the most reliable indicator of vigour in rubber has been proved beyond doubt (Table 29).

The second factor was found to be associated with a set of five bark structural characters - number of latex vessel rows in the hard bark and in the soft bark, total number of latex vessel rows in the total bark, average distance between the latex vessel rows in the soft bark and laticifer area index, of which the average distance between the latex vessel rows in the soft bark was found to be negatively associated with this factor. Total number of latex vessel rows was identified as the marker character to represent the remaining four structural traits, as it carried the maximum factor loading (0.9531). Factor three was associated with the characters related to the thickness of the bark ie, total bark thickness, thickness of the soft bark and hard bark. Here total bark thickness was found to have the maximum factor loading of 0.9409 and can represent the thickness of soft bark and hard bark in their inheritance studies.

Two leaf structural characters identified with the factor four were the number of epidermal cells per unit area of leaf lamina and stomatal index. Stomatal index was negatively correlated with this factor while the number of epidermal cells per unit area had a factor loading of 0.9266. Four of the important leaf structural traits - thickness of the lamina, thickness of leaf midrib,

thickness of palisade and thickness of spongy layers- were associated with the factor five. Thickness of the lamina could be identified as the marker trait in this group with its maximum factor loading (0.9045).

Factor six was associated with two morphological traits like petiole length and single leaflet area. These two traits carried almost equal factor loadings (0.7530 and 0.7590 respectively) and may be considered as two independent traits as the factor seems to have an equal control in their inheritance.

Three leaf structural traits were associated with the factor seven viz. number of cells per unit length of palisade layer and spongy layer and thickness of the cuticle. Thickness of the cuticle was negatively correlated with the factor. The maximum factor loading was for the number of cells per unit length of spongy layer (0.7706).

Factor eight was associated with the width of phloic rays and diameter of latex vessels, more factor loading (0.8917) being for the diameter of latex vessels. Height of phloic rays and the height / width ratio of phloic rays were associated together by the ninth factor with the height of phloic rays (0.8515) having more factor loading. Factor ten was associated with only a single character - the inter-flush distance with a loading of 0.8208, which can be considered as an independent trait. Frequency of phloic rays and density of latex vessels were associated together with the next factor and more factor loading was seen for density of latex vessels (0.8490). The last factor was associated with only a single factor, the number of stomata per unit area of the lamina, with a factor loading of 0.9501.

Out of the twelve factors identified three factors controlled the morphological characters, five factors controlled bark structural characters and four factors controlled leaf anatomical characters. Thus each factor can be identified with those characters with the maximum factor loadings in the respective groups namely girth of the plants, total number of leaves per plant, petiole length, number of stomata and number of epidermal cells per unit area of leaf lamina, thickness of lamina, number of cells per unit length of spongy layer, total bark thickness, total number of latex vessel rows, height of phloic rays, diameter and density of latex vessels. It can be seen that the

12 principal components or factors account for 82.30% of the total variance, which will sum up the information in the original data of the 33 selected characters in the set of 80 wild genotypes. So the dimension of the data can be reduced to the 12 variables, which can thus very well present the structure of the whole data from the complete set of variables.

4.6 Genetic divergence - D^2 analysis

Genetic divergence in a population, especially in respect of the characters in which improvement is sought, is an indispensable prerequisite for successful crop improvement programme. The D^2 statistics has found favour as a tool for estimating genetic divergence, which is the basis in choosing parents for hybridization. Progenies derived from diverse crosses are expected to show a broad spectrum of genetic variability providing greater scope for isolating high yielding segregates in the succeeding generations.

The narrow genetic base of the Wickham clones derived from a few seeds, have necessitated the introduction of a large number of wild germplasm from the primary center of origin of the crop expecting a large amount of variability available from the highly heterogenous wild population. Even though there has been a consistent narrowing down of the genetic base for of *H. brasiliensis* over the decades due to unidirectional selection for yield, there are reports of a workable genetic diversity existing among the Wickham clones. Mydin (1992a) has reported creation of eight genetically divergent clusters in 40 mature Wickham clones and Markose (1984) had reported eight genetically divergent clusters in another 20 Wickham clones. However the genetic base is still narrowing down due to the prominence of a very few genetically improved clones in the plantations exposing them to the threat of new diseases and pests and also succumbing to the extremes of climate. Hence, international attention was drawn to formulate long term strategies to broaden the narrow genetic base. Incorporation of superior genes identified and isolated from the highly potential wild germplasm could then be achieved by hybridization of highly divergent wild genotypes with popular cultivated clones, which can result in very high heterotic effects. In this perspective, study of genetic divergence existing in the wild gemplasm assumes great importance and the identification of divergent clones along with the genetic divergence they have with popular clones assumes a lot of practical significance.

Selection of parents on the basis of their genetic distance helps in a better realization of heterosis, but desirable and high magnitudes of heterosis are not directly related to extreme parental divergence as discussed by Arunachalam *et al.*, (1984) and Mydin (1992a). Parents with intermediate genetic divergence also have a higher chance of producing heterotic hybrids (Thakur and Zarger, 1989). Selection of parents will be more appropriate from those clusters separated by intermediate to high genetic distances (Mydin, 1992b) because strong positive relationship have been found between genetic distance and heterosis in a broad range of crop species (Balasch *et al.*, 1984; Shamsuddin, 1985). Employment of D^2 analysis successfully, has been reported in a number of perennials and annuals-viz, in Banana (Valsalakumari *et al.*, 1985); in Sugarcane (Punia *et al.*, 1983 and Ram and Hemaprabha, 1993); in Coconut (Balakrishnan and Namboodiri, 1987) and in rubber by Markose (1984) and Mydin (1992a) in mature Wickham clones and by Abraham *et al.*, (1995) in immature wild genotypes.

In the present study, 81 genotypes including the popular clone, RRII 105, were statistically clustered by iterative relocation algorithm suggested by Friedman and Rubin (1967) and modified by Suresh and Unnithan (1996) for clustering using any dissimilarity index. The genotypes were clustered into 9 divergent clusters revealing the very high amount of genetic divergence existing in this particular set of 80 wild genotypes (Table 30). A maximum of 20 genotypes were grouped in one cluster (Cluster 1), and 17 genotypes were grouped in cluster two. Third and fifth clusters had eight genotypes each while the seventh and ninth clusters had six genotypes each. Fourth cluster had four genotypes and eighth cluster had five genotypes grouped together. Sixth cluster had seven genotypes grouped. The popular Wickham clone RRII 105 used as the control was grouped along with five other wild genotypes from Mato Grosso and Acre provenances. This indicates a genetic similarity and thus a lesser genetic distance of these clones with the popular clone. Among the divergent clusters, maximum genetic divergence based on the magnitude of the genetic distance, was observed between the clusters 3 and 4 (2005.33), followed by 4 and 9 (1957.38) and 4and 7 (1774.35) indicating their suitability as parents in hybridization programmes depending upon the objective of the programme (Table 31).

Genotypes from the three provenances were seen distributed throughout the 9 clusters

and there was no specificity of genotypes from any particular geographical provenance (Acre, Rondonia or Mato Grosso) confining to any of the clusters separately. This lack of correlation between the geographic diversity with genetic diversity observed in this study is in agreement with studies in Wickham clones by Markose (1984); Mydin (1992a) and Paiva and Paiva, (1994). In a similar study for estimating genetic divergence, in a set of 100 wild genotypes in their second year of growth, Abraham *et al.*, (1995) reported the wild genotypes to be grouped into five divergent clusters based on the characters girth, height, total bark thickness, single leaflet area and total yield, thus in strong accordance with the present study. The distribution of the wild genotype between the clusters shows that there is a wide range of genetic diversity among the wild genotypes with the genetically improved popular control clone, RRII 105 which is a commonly used female parent in hybridization programmes in *H. brasiliensis* in India. Thus it is evident that there is a great scope of identifying suitable parents in the present sample of wild germplasm studied.

4.7 Performance Index

The 80 wild genotypes studied were ranked statistically, based on an index prepared by pooling the performance of these genotypes for 16 different variables. These variables were girth of the plants, inter-flush distance, petiole length, total number of leaves per plant, thickness of lamina, thickness of cuticle, single leaflet area, total bark thickness, total number of latex vessel rows, average distance between latex vessel rows in the soft bark, frequency of phloic rays, height of phloic rays, width of phloic rays, diameter of latex vessels, density of latex vessels and test tap yield.

The genotypes were ranked according to the performance index (Table 32). It was seen that 64 of the 80 wild genotypes studied, had an index above that of the popular control clone, RRII 105 and hence were ranked above it. Thirty-eight wild genotypes were ranked high as per their performance index being higher, than the average index value of 247.10. To make an efficient selection, the best 10 per cent of the population was selected based on their top rankings. Accordingly, eight genotypes were selected with the ranking from one to eight viz. RO 395, AC

953, AC 1043, RO 876, AC 654, MT 944, RO 399 and RO 894 in the order. Similar ranking of superior progenies have been reported in rubber where performance indices of 20 progenies were computed based on the contribution of test tapping yield, girth, number of latex vessel rows and number of leaf flushes (Mydin, 1992b). Performance indices were also worked out in young Wickham clones where it was found that in general, high yielders recorded higher values in comparison to medium and low yielders (Varghese *et al.*, 1993) thus highlighting the real potential of the superior wild genotypes identified in this study by performance index.

Out of the eight genotypes selected as the best, it was observed that four of them were Rondonian genotypes followed by three Acre genotypes and only one Mato Grosso genotype. The general superiority of the Rondonian genotypes followed by Acre genotypes for their vigorous growth in terms of the morphological characters in the first year of growth can be a major contributing factor for this ranking. The dominance of the Rondonian genotypes can be explicitly explained by the dominance of these genotypes for the various growth characters as seen in Table 33. Good immature vigour has been reported to be one of the important attributes associated with the yield potential in rubber (Varghese *et al.*, 1993).

All the eight genotypes were found to be highly genetically divergent, especially with the popular control clone RRII 105, with all of them in genetically divergent clusters with RRII 105, except AC 654, AC953 and RO 876 which grouped together in cluster two, and RO 395 and RO 399 which grouped together in cluster seven (Table 28). Thus the eight wild genotypes- RO 395, AC 953, AC 1043, RO 876, AC 654, MT 944, RO 399 and RO 894- ranked as the best from the eighty genotypes can be considered as potential parents in future hybridization programmes, involving the wild genotypes as one parent and an improved clone as the other parent.

Figures 1 - 59. *Hevea brasiliensis* (Willd.ex Adr. de Juss.) Muell. Arg.

Figures 1 - 59. *Hevea brasiliensis* (Willd.ex Adr. de Juss.) Muell. Arg.

Fig. 1. A wild genotype (AC 426) showing hemispherical, distantly placed leaf storeys.

Fig. 2. A wild genotype (AC 995) showing truncate, closely placed leaf storeys, with short petioles.

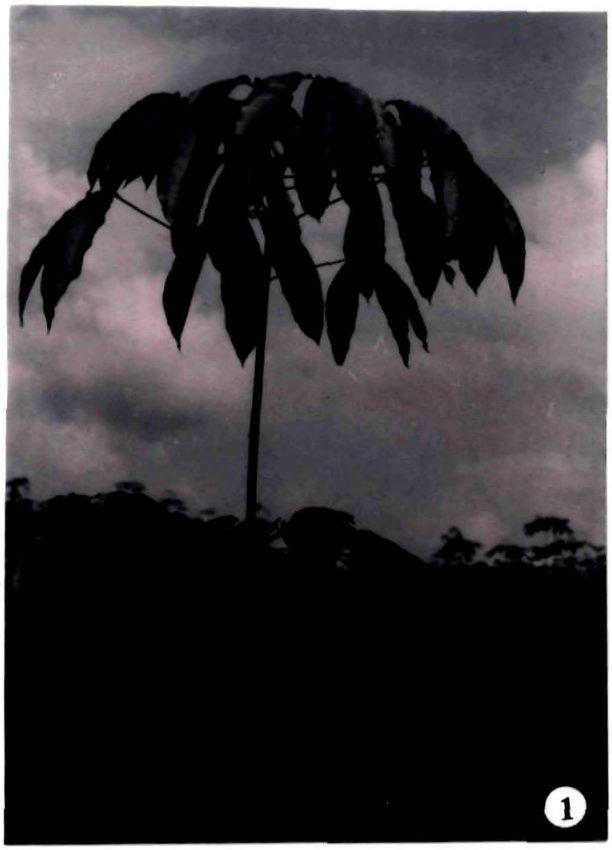
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Fig. 3. A wild genotype (AC 966) showing open leaf storey, with very long petioles placed at acute angles

Fig. 4. A wild genotype (RO 322) showing tall habit, with intermediately separated leaf storeys.

Fig. 5. Leaflets showing elliptical (AC 604) and obovate (RO 316) shape.

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Fig. 6. Leaflets showing variations in size.

Fig. 7. A wild genotype (MT 922) showing prominent extra floral nectaries.

Fig. 8. Leaflets of two genotypes (RO 322, RO 330) showing dull and glossy nature.

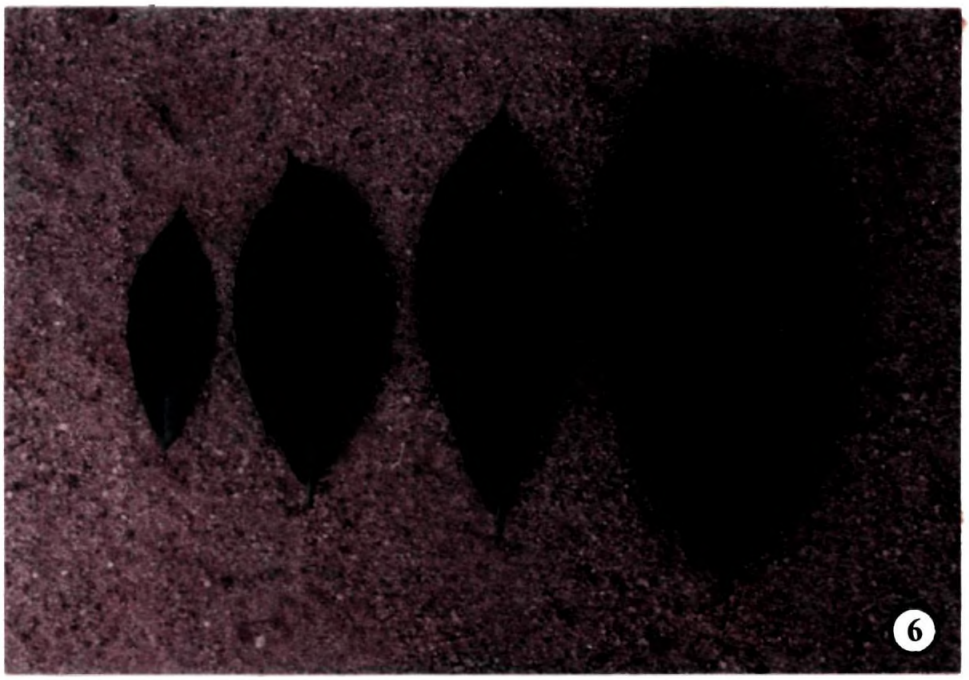
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Fig. 9. Leaflets showing irregular (RO 886) (below) and smooth (RO 879) (above) leaf laminae.

Fig. 10. Wild genotypes showing short, long and medium long petiolules.


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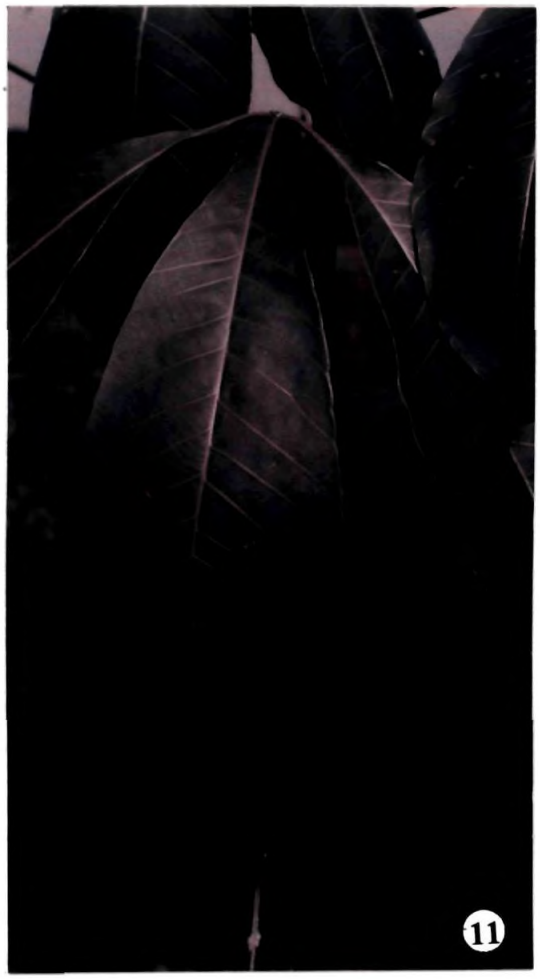
Fig. 11. A wild genotype (AC 979) showing well separated leaf laminae with downwardly oriented petiolules.

Fig. 12. Leaves of a wild genotype (AC 453) having curved leaflet margins (which gives boat shaped cross-sectional appearance of the leaflets).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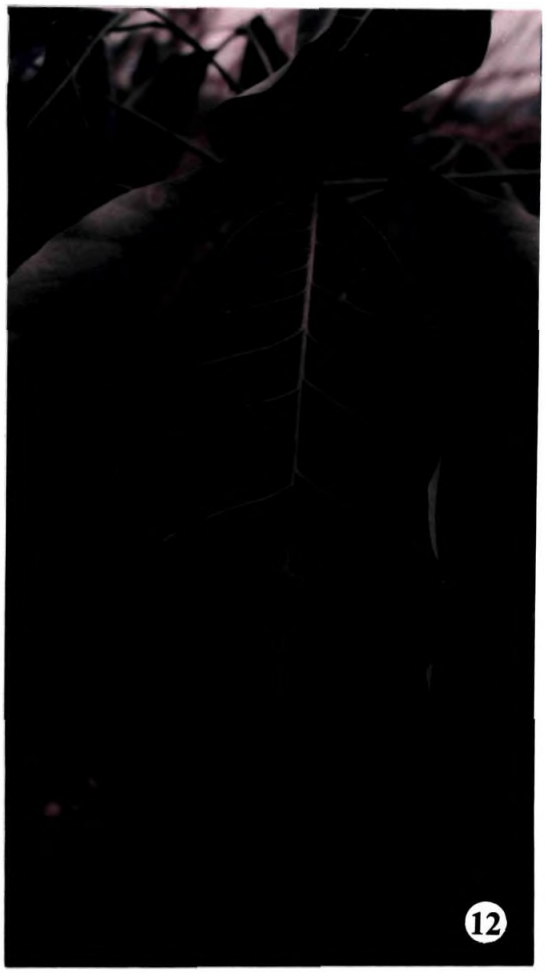
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Figs 13-14. Sectional view of laminae of two Acre genotypes.

13. Thin laminae (AC 644) x50.
14. Thick laminae (AC 953) x50

Figs. 15-16. Sectional view of laminae of two Rondonian genotypes.

15. Thin laminae (RO 380) x50.
16. Thick laminae (RO 876) x45.

Figs. 17-18. Sectional view of laminae of two Mato Grosso genotypes.

17. Thin laminae (MT 948) x50.
18. Thick laminae (MT 944) x50.

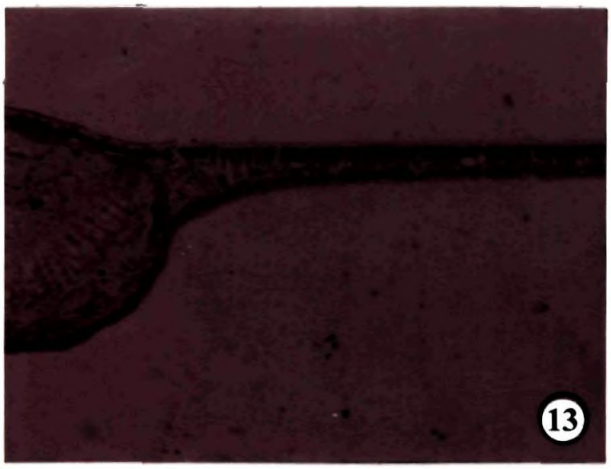
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Fig 19. Cross sectional view of the lamina of an Acre genotype (AC 963), having thin midrib x50.

Fig 20. Cross sectional view of the lamina of an Acre genotype (AC 754), having thick midrib x50.


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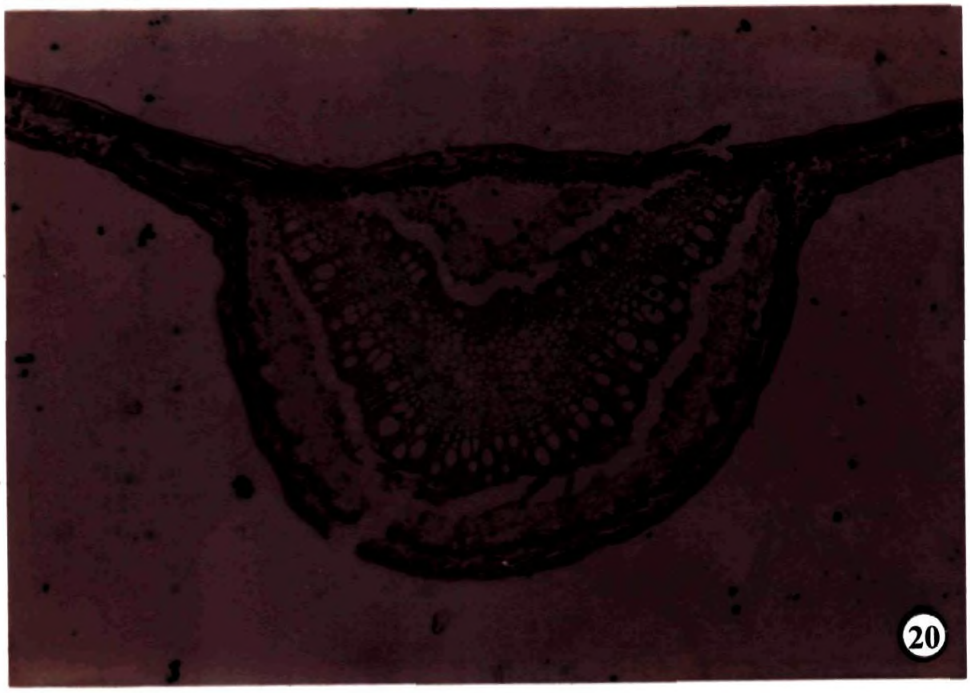
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Fig 21. Cross sectional view of the lamina of a Rondonian genotype (RO 328), having thin midrib x45.

Fig 22. Cross sectional view of the lamina of a Rondonian genotype (RO 369), having thick midrib x40.


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Fig 23. Cross sectional view of the lamina of a Mato Grosso genotype (MT 901), having thin midrib x45.

Fig 24. Cross sectional view of the lamina of a Mato Grosso genotype (MT 945), having thick midrib x48


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Figs 25-26. Cross sectional view of the laminae of two Acre genotypes.

25. AC 644 having thin palisade layer x360.

26. AC 654 having thick palisade layer x360.

Figs. 27-28. Cross sectional view of the laminae of two Rondonian genotypes.

27. RO 380 having thin palisade layer x360.

28. RO 369 having thick palisade layer x360.

Figs. 29-30. Cross sectional view of the laminae of two Mato Grosso genotypes.

29. MT 1063 having thin palisade layer x320.

30. MT 1008 having thick palisade layer x320.


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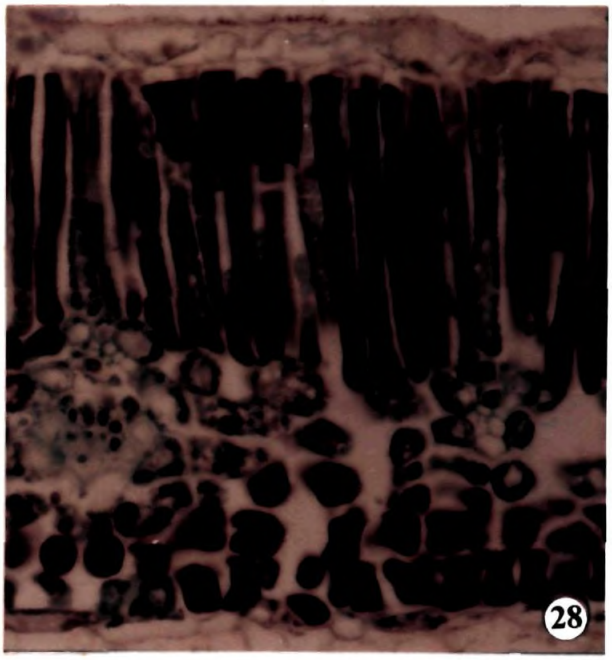
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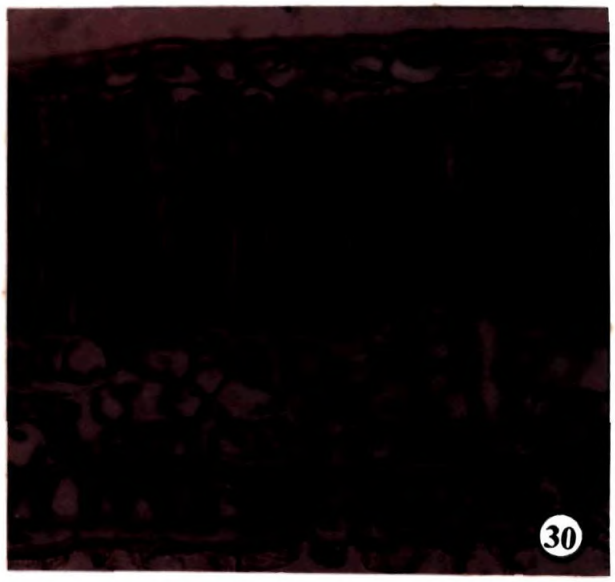
30

Figs. 31-32. Cross sectional view of the laminae of two Acre genotypes

31. AC 1090 having thin spongy tissues x320.

32. AC 966 having thick spongy tissues x320.

Figs. 33-34. Cross sectional view of the laminae of two Rondonian genotypes.

33. RO 255 having thin spongy layer x320.

34. RO 876 having thick spongy layer. x320

Figs. 35-36. Cross sectional view of the laminae of two Mato Grosso genotypes.

35. MT 928 having thin spongy layer x320.

36. MT 947 having thick spongy layer x320.


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Figs. 37-39. Sections of the bark of a wild genotype (AC 1090) showing the alignment of tissues.

37. Transverse section x 45.

38. Tangential longitudinal section through the soft bast x 45.

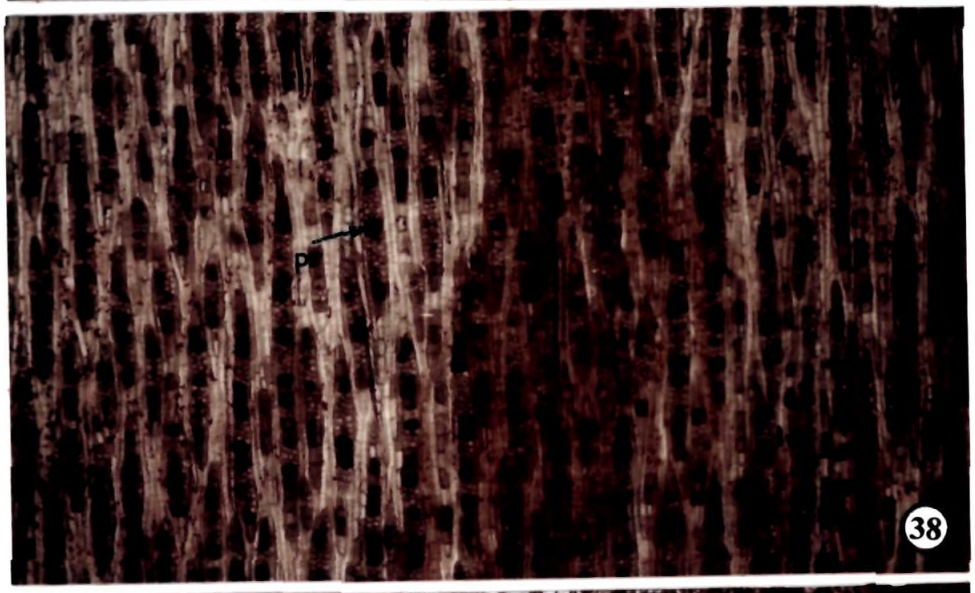
39. Radial longitudinal section x 45.

lv – latex vessels

pr – phloic rays

sc – sclereids

37



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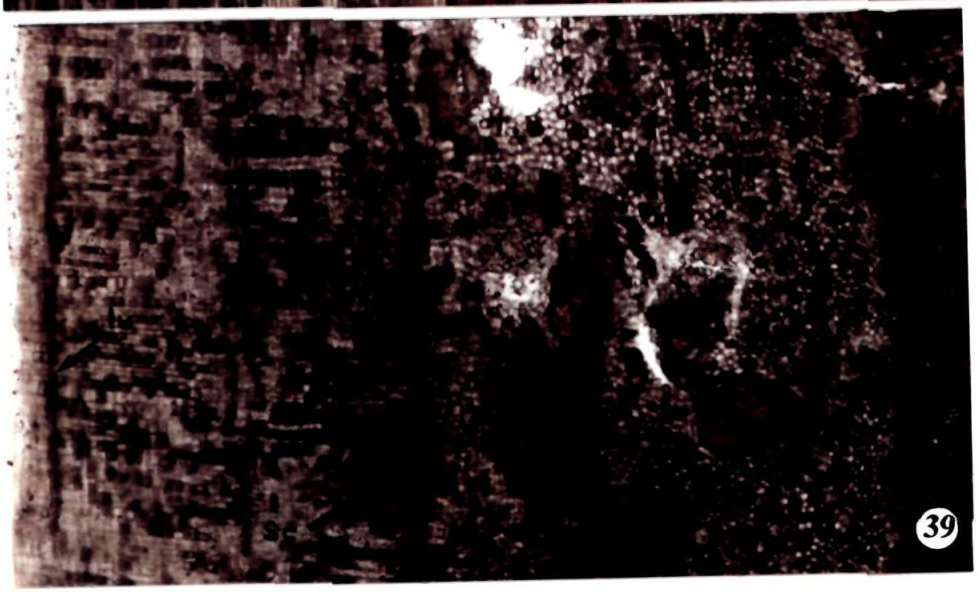
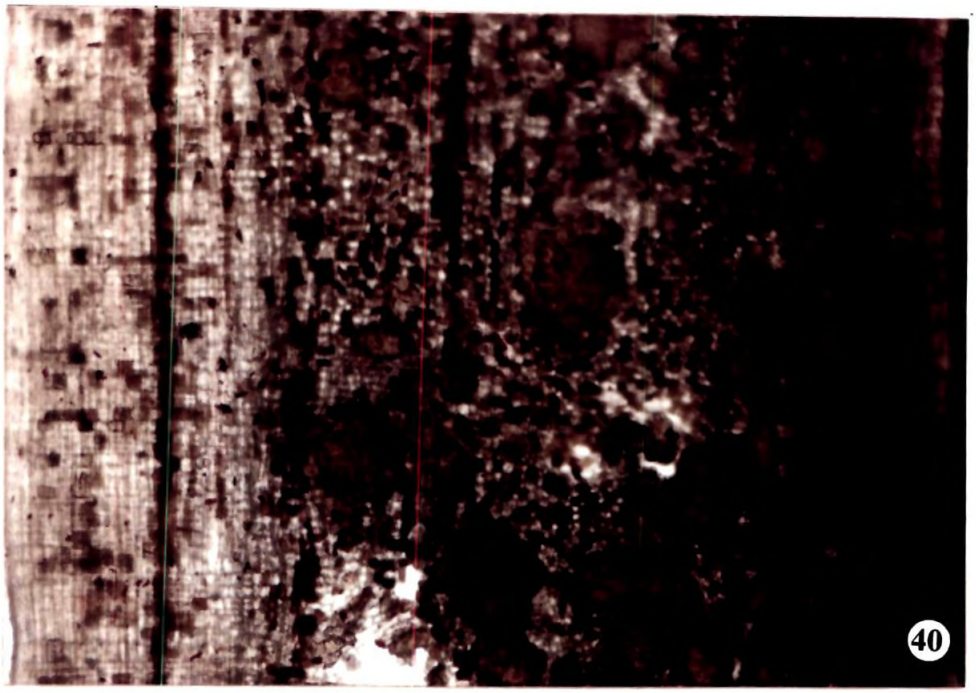


39

Figs 40-41. Radial longitudinal sections of the bark of two Acre genotypes.

40. AC 995 with low number of latex vessel rows distantly placed x 45.

41. AC 1043 with more number of latex vessel rows closely placed x 45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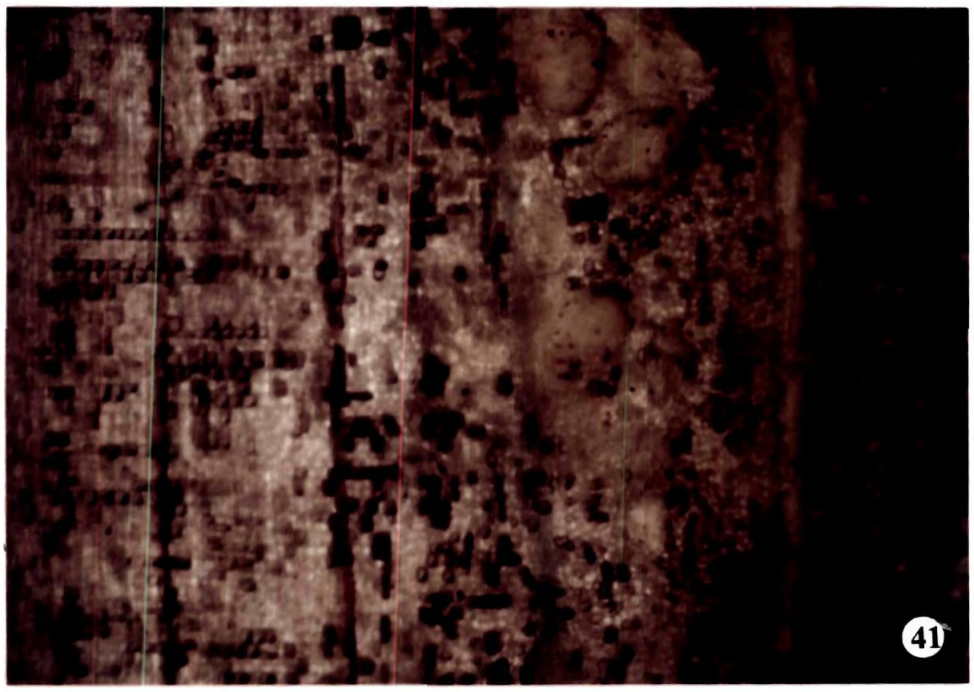

41

Figs. 42-43. Radial longitudinal sections of the bark of two Rondonian genotypes

42. RO 879 with low number of latex vessel rows distantly placed x50.

43. RO 328 with more number of latex vessel rows closely placed x45.


42

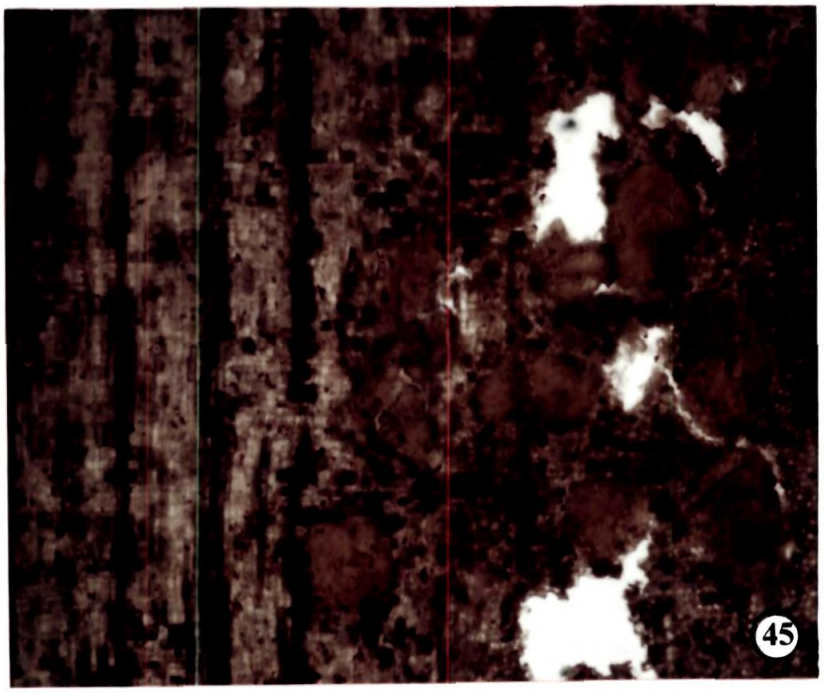

43

Figs 44 – 45. Radial longitudinal sections of the bark of two Mato Grosso genotypes.

44. MT 1077 with low number of latex vessel rows distantly placed x50.

45. MT 1057 with more number of latex vessel rows closely placed x50.


44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Figs 46-47. Laticifers of Acre genotypes.

46. AC 657 - Narrow laticifers x450.

47. AC 632 - Relatively large laticifers x450.


46

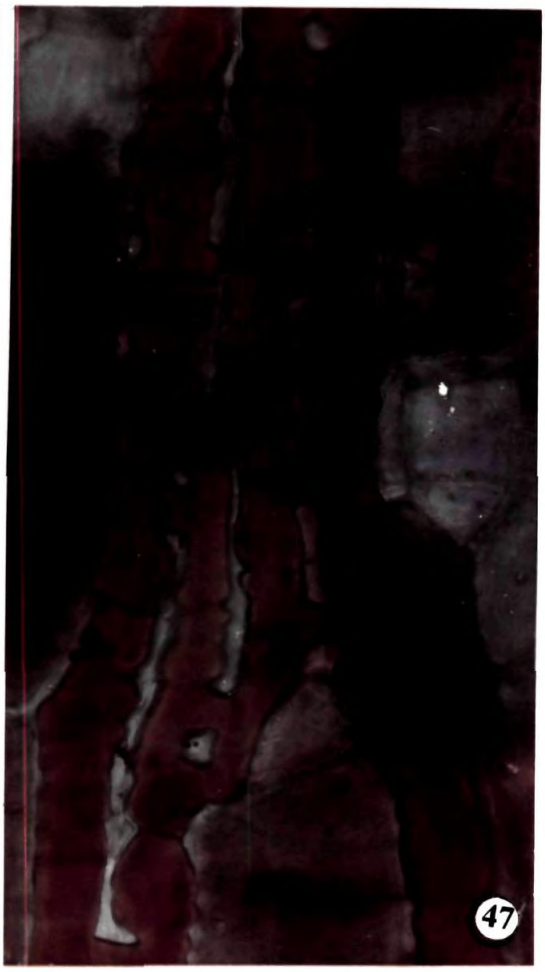
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Fig 48 – 49. Laticifers of Rondonian genotypes.

48. RO 254 - Narrow laticifers x512
49. RO 886 - Relatively large laticifers x512.


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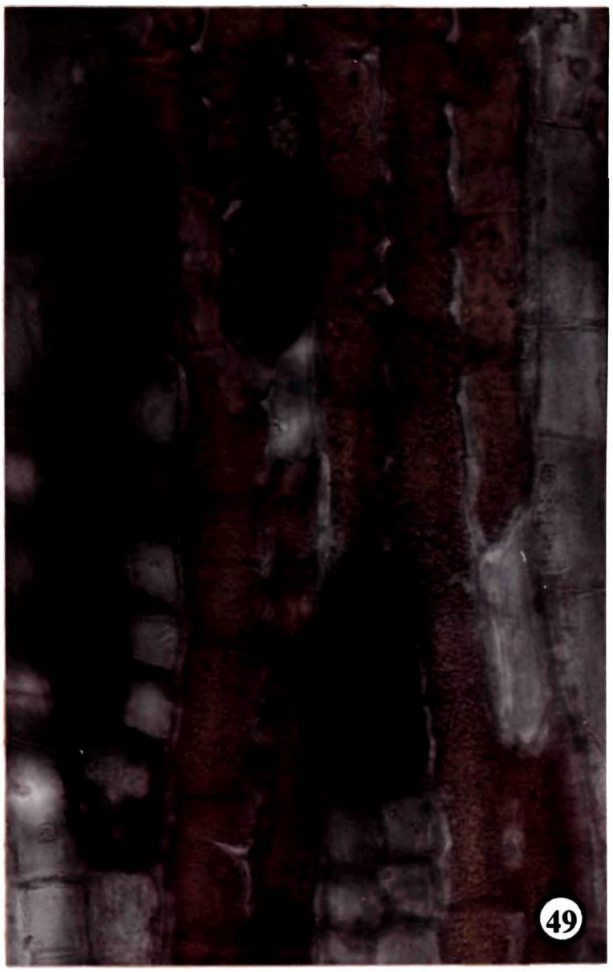
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Fig 50 – 51. Laticifers of Mato Grosso genotypes.

50. MT 906 - Narrow laticifers x512.

51. MT 899 - Relatively large laticifers x512. .


50


51

Fig 52 – 53. Tangential longitudinal sections of the bark of two Acre genotypes.

52. AC 995 with lesser number of laticifers x50.

53. AC 629 with more number of laticifers x50.

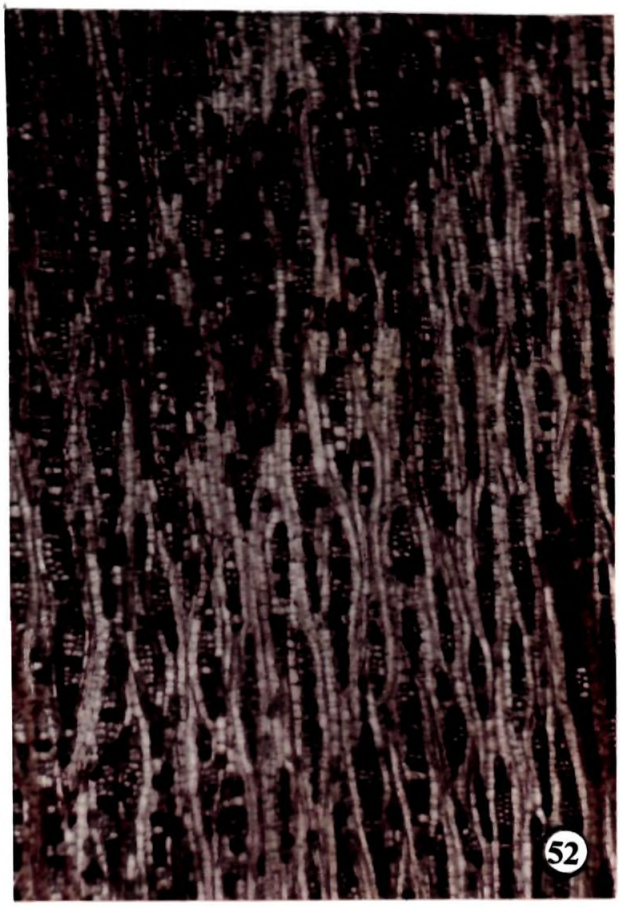
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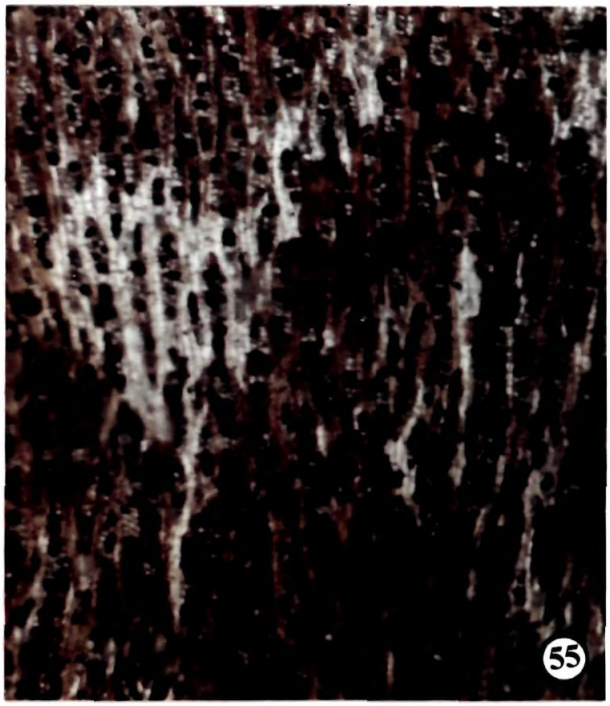
Fig 54 – 57. Tangential longitudinal sections of the bark of two Rondonian and two Mato Grosso genotypes

54. RO 399 with lesser number of laticifers x50.
55. RO 894 with more number of laticifers x50.
56. MT 1005 with lesser number of laticifers x50.
57. MT 1055 with more number of laticifers x50.


54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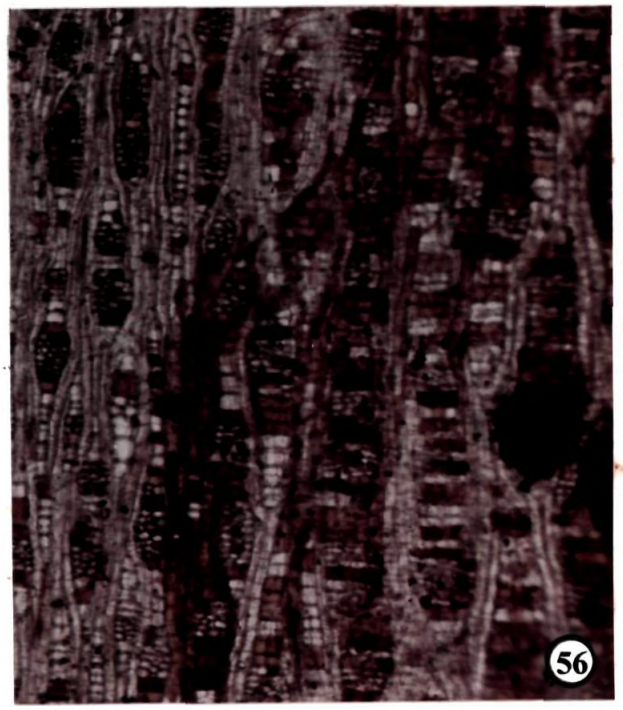
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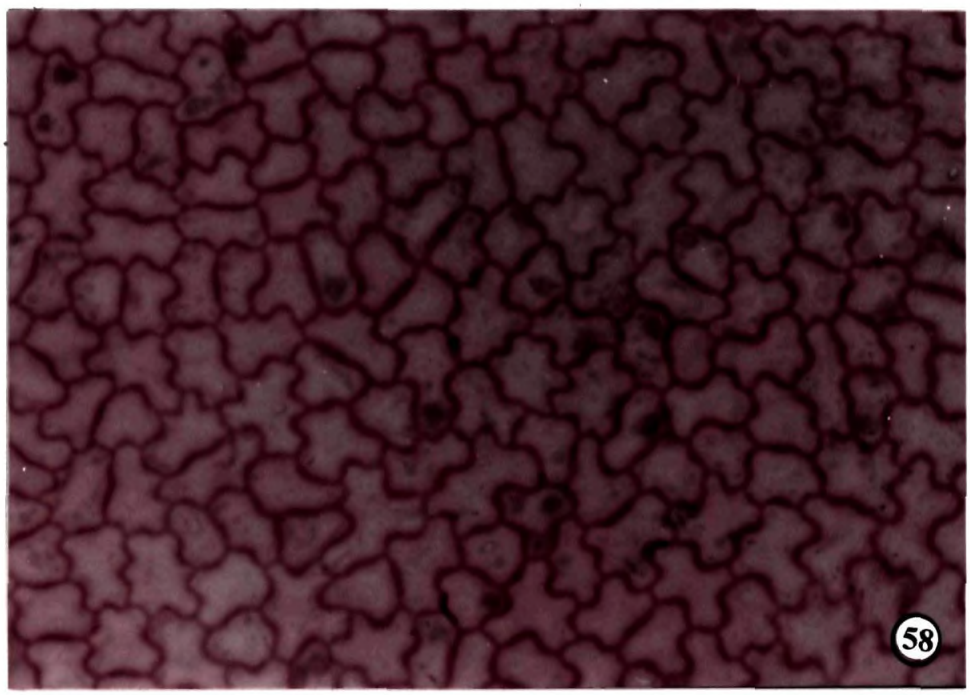
Fig. 58. Epidermal peeling of the adaxial surface of the lamina showing absence of stomata x50.

Fig. 59. Epidermal peeling of the abaxial surface of the lamina showing stomata x50.



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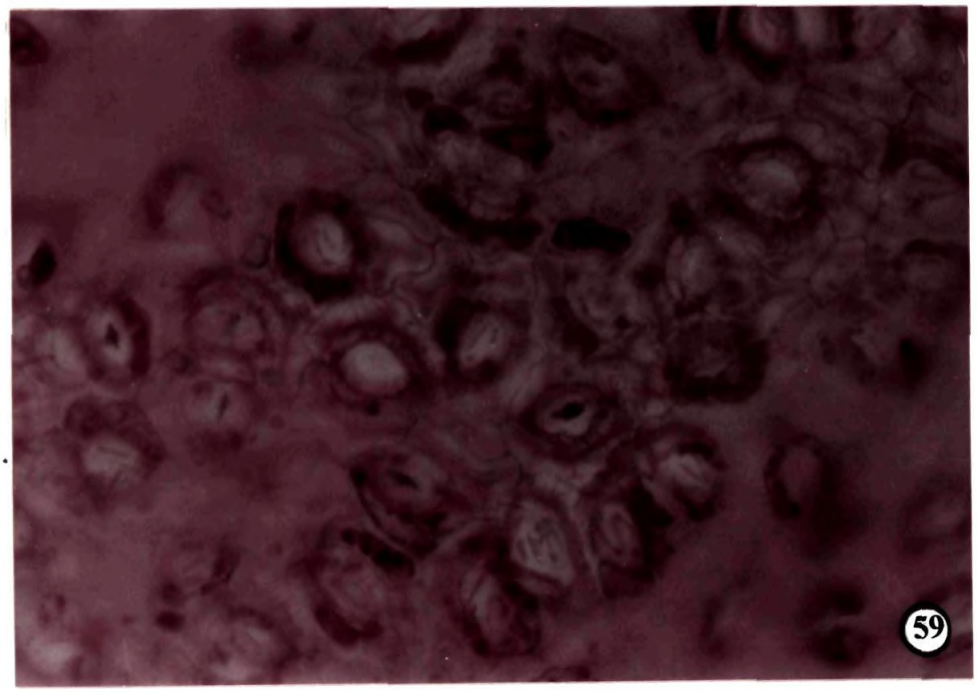

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Summary

Eighty wild genotypes representing the three provenances of Acre (AC), Rondonia (RO) and Mato Grosso (MT) of Brazil, chosen from the 1981 International Rubber Research and Development Board (IRRDB) wild germplasm accessions of *Hevea brasiliensis* (Willd. Ex Adr.de Juss.) Muell.Arg., maintained at the Central Experiment Station, Chethackal of the Rubber Research Institute of India (RRII), were studied in the immature phase. The main objectives of the studies were (1) to characterize the wild genotypes for morphological characters at the juvenile phase; (2) to assess the nature and extend of variability present in the wild germplasm; (3) to estimate the genetic parameters - heritability and genetic advance; (4) to study the degree of associations between the different characters with test tap yield and their inter-correlations and (5) to study the extend of genetic divergence available in the wild population and to identify highly divergent wild clones. The study also aimed at identification of certain marker traits, so as to reduce the number of characters for recording, in future biometrical investigations. Genotypes were also ranked based on their superiority for the pooled performance of a set of selected characters. The popular high yielding clone RRII 105 was taken as the control.

Data were recorded over a period of three years, immediately following planting. Impor-

tant characters recorded were girth, height, number of leaf flushes, total number of leaves, petiole length, inter-flush distance, total leaf area, leaf area index, test tap yield, number of stomata and number of epidermal cells per mm^2 of leaf surface, stomatal index, thickness of the lamina, mid-rib, palisade layer and spongy layer, number of cells per mm of the palisade and spongy layer, thickness of the cuticle and single leaflet area, total bark thickness, soft bark and hard bark thicknesses, number of latex vessel rows in soft bark and hard bark regions, total number of latex vessel rows, average distance between the latex vessel rows in the soft bark region, density of latex vessels per row per mm circumference of the plant, diameter of the latex vessels, total cross sectional area of the latex vessels and frequency, height, width and height / width ratio of phloic rays. The wild genotypes at the end of first year, were characterised for their morphological characters using standard descriptors.

The data generated over the three years were subjected to detailed statistical analysis like analysis of variance, variability estimates like phenotypic and genotypic coefficients of variation and genetic parameters - heritability and genetic advance. Correlation coefficients between yield and other characters, D^2 analysis to estimate genetic divergence and factor analysis for reduction of characters to be studied and finally a performance index on the population of wild germplasm was worked out and the individual genotypes were ranked accordingly based on their superiority.

The morphological characterization of the wild genotypes revealed wide variability for the various plant characters like height, leaf orientation, petiolar architecture, arrangement of leaflets in the flushes, and other leaf characters. This will help the breeder in identification of genotypes as per his requirement for even minor characters of importance. Analysis of variance revealed significant differences among the genotypes for all the characters studied, thus revealing good scope for their appropriate utilization in genetic improvement. High range of variation was noted for the growth characters girth (4.72-10.41 cm), height (100.89-322.99 cm), number of leaf flushes per plant (4.89-9.12), total number of leaves per plant (41.20-119.80), inter-flush distance (13.86-28.46 cm), petiole length (13.03-32.47 cm), total leaf area of the plant (4583.39 –28683.45 cm^2) and leaf area index (0.08- 0.46). The average test tap yield in the first three

years had a range of 0.0027 to 0.2327 g $t^{-1}t^{-1}$, 0.0212 to 0.6369 g $t^{-1}t^{-1}$ and 0.0481 to 4.2711 g $t^{-1}t^{-1}$ respectively. The test tap yield in the wild genotypes was much lower than the control clones, except for one genotype MT 1057, which recorded double the yield of the control clone.

Range of variation for the number of stomata per mm^2 leaf area was 281.16 - 612.67, for the number of epidermal cells per mm^2 leaf area, 1132.84 -2741.23 and 10.81 - 27.43 for the stomatal index. Single leaflet area had a range of 59.94 - 189.58cm^2. Range for other structural characters were - thickness of lamina (0.1107 - 0.1760 μm), thickness of leaf midrib (0.6300 - 1.3220 mm), thickness of palisade layer (42.57 - 81.01 μm), thickness of spongy layer (45.00 - 93.50 μm), number of cells per mm distance of palisade layer (100.62 - 134.34), number of cells per mm length of spongy layer (189.24 - 417.06) and the thickness of cuticle (1.22 - 4.27 μm).

A wide range in the mean values were noted for the bark structural characters also, as follows: total bark thickness (2.00 - 4.00 mm), soft bark thickness (0.87 - 1.75 mm), hard bark thickness (0.84 - 2.53 mm), soft bark thickness in percentage (31.26 - 64.88), hard bark thickness in percentage (35.12 - 68.74), number of latex vessels rows in the soft bark (1.74 -8.01), number of latex vessels rows in the hard bark (1.00 - 5.01), total number of latex vessel rows (2.99 - 11.01), average distance between latex vessel rows in soft bark (0.12 - 0.75 mm), density of latex vessels per mm circumference of the plant (11.50 - 25.00), diameter of latex vessels (13.44 - 34.00 μm), total cross sectional area of the latex vessels (1.33 - 17.77 mm^2), average distance between latex vessel rows (0.12 - 0.75 mm), frequency of phloic rays per mm^2 area (2.50 - 7.75), height of phloic rays (0.18 - 0.41 mm), width of phloic rays (0.03 -0.08 mm) and height / width ratio (3.48 - 11.35).

Phenotypic coefficient of variation was found to be higher than the genotypic coefficient of variation, as expected, for all the characters. Higher values of GCV and PCV were found for the characters total leaf area of the plants (35.63 and 50.82 respectively) and leaf area index (35.34 and 50.48 respectively), test tap yield in the first (74.15 and 80.35 respectively), second (72.15 and 106.91 respectively) and third year (95.54 and 117.01 respectively) and total cross sectional area of latex vessels (55.62 and 58.53 respectively). Medium estimates of GCV and PCV were recorded for most of the remaining characters. Medium to high estimates of the coefficients

of variation at the genotypic and phenotypic levels, identified the nature of variation as being contributed mainly by the genetic make up of the clones.

High estimates of heritability along with higher estimates of genetic advance were observed for the test tap yield in the first (85.17 and 140.98 respectively), second (45.5 and 100.30 respectively) and third year (66.67 and 160.7 respectively), while medium to high heritability estimates along with medium to high genetic advance, were recorded for most of the remaining characters. This indicates the advantage of additive gene action and the significant genetic contribution in the expression of these characters, thus making them highly heritable.

Phenotypic, genotypic and environmental correlation coefficients revealed that the correlation of majority of the major characters with the yield was weak or negligible at this very early stage of growth. The weak association of most of the structural characters with the test tap yield, might be due to the early growth stage for these characters to have any contribution to the test tap yield, which would have been contributed by other factors like growth factors as evidenced by the strong correlation of girth with other growth characters.

Factor analysis carried out in 33 selected morphological and structural characters identified 12 factors as controlling these characters, contributing 82.3 % of the total variation. Out of the twelve factors identified three factors controlled the morphological characters, five factors controlled bark structural characters and four factors controlled the leaf anatomical characters. Thus each factor could be identified with a particular character, which is expected to control the set of related traits. Such traits identified were girth, total number of leaves per plant, petiole length, number of stomata and number of epidermal cells per unit area, thickness of leaf blade, number of cells per unit length of spongy layer, total bark thickness, total number of latex vessel rows, height of phloic rays, diameter and density of latex vessels.

. Genetic divergence studies assigned the wild genotypes into 9 divergent clusters, revealing the very high amount of genetic divergence existing in this particular set of wild genotypes. Among the divergent clusters, maximum genetic divergence based on the magnitude of the genetic distance was observed between the genotypes in the clusters 3 and 4 (2005.33). Geno-

types in such clusters can serve as potential parents in hybridization programmes.

The 80 wild genotypes studied were ranked for their superiority, based on an index prepared by pooling the performance of these genotypes for 16 selected variables. It was seen that 64 of the 80 wild genotypes studied, had an index above that of the popular clone RRII 105, in the immature phase and hence, were ranked above it. Thirty eight wild genotypes were ranked high as per their higher performance index, than the average index value of 247.10. To make an efficient selection, the best 10 per cent of the population was identified based on their top rankings. Those eight genotypes ranked from one to eight were RO 395, AC 953, AC 1043, RO 876, AC 654, MT 944, RO 399 and RO 894. These genotypes can be considered as one of the potential parents in future hybridization programmes with popular cultivars.

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