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 mm² 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, D² 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 cm²) 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 mm² leaf area was 281.16 - 612.67, for the number of epidermal cells per mm² leaf area, 1132.84 - 2741.23 and 10.81 - 27.43 for the stomatal index. Single leaflet area had a range of 59.94 - 189.58 cm². 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 mm²), average distance between latex vessel rows (0.12 - 0.75 mm), frequency of phloic rays per mm² 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.