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 up to 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 *Microcylus 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 occurring 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 presumably 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 North-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. Hybridization 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 prerequisite 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.