SUMMARY

The success of genetic improvement in a multipurpose tree species like *Tamarindus indica* L. depends to a large extent on the assessment of variability for quantitative characters, diversity and identification of plus trees. No concerted efforts have been made so far to study systematically the genetic variation for yield bearing habit and other quality parameters except for few reports (Gangaprasad, 1993; Hanumashetty, 1996). The present inquiry, characterization using morphological and molecular traits help in the diversity analysis and identification of elite genotypes for further tree improvement programme. The silent features of the findings are as follows:

Appreciable range of variations was observed for characters like pod length, trunk diameter, pod weight, seed weight, pod yield, pulp yield and percentage of tartaric acid.

Pod yield per tree is the most important character contributed for divergence of all genotypes, followed by pulp yield per tree, seed yield per tree. Germplasm I showed the association of pulp yield per tree was positive and significant with pod length, thickness of pod, breadth of pod, pod weight, pulp weight per pod, number of seeds per pod and seed weight per pod.

Germplasm II showed that, Pulp yield was associated positively and significantly with pod weight. This showed further association with pod length; breadth of pod and thickness of pod was positive and significant.
Appreciable range of variability was noticed for sugar content. PKM 1 showed highest total sugar content, 434.2 milligrams per gram of fruit. Lowest content was shown by NTI 14, 179.61 mg/g. Reducing sugars was found to be high in SMG 4, 376.2mg/g. NTI 14 showed lowest reducing sugar content, 179.42mg/g.

Appreciable variability was observed for phenol content among the genotypes studied. NTI 75 showed highest phenol content 2.25 mg/g. Ortho-dihydroxy phenols was high in NTI 5 of 0.23mg/g. NTI 15 showed lowest value for both phenols and ortho-dihydroxy phenols among the genotypes studied.

*Tamarindus indica* L. exhibited heterogeneous in venation pattern, which can be used to classify genotypes in the vegetative condition.

D² analysis of morphological characters of germplasm I were grouped into V clusters, among them two clusters namely NTI – 32 and SMG – 2 are most diversified genotypes. Germplasm II was grouped into four clusters, NTI – 32 of cluster I & NTI 79 of cluster III were left with distinct solitary clusters and most diversified genotypes.

Dice similarity coefficient observed for genotypes of germplasm I ranged fairly high. The greatest similarity was observed between the genotypes SMG 2 and NTI 31.
Dice similarity coefficient for elite genotypes of germplasm II ranged very high. Even though genotypes NTI 32 and PKM 1 are from distant locations they exhibited greatest similarity.

Among the 53 accessions of germplasm I for molecular analysis NTI – 78 was identified as the most divergent genotype.

With 13 accessions of germplasm II for molecular analysis, SMG – 13 stood as the most divergent genotype.

The greatest genetic similarity was observed between the genotypes NTI 7 and NTI 77 based on molecular analysis of 53 accessions of germplasm I based on molecular analysis.

NTI82 and NTI84 showed greatest genetic similarity among the 13 accessions of germplasm II based on molecular analysis.

NTI 19, PKM 6, NTI 14 and SMG 13 are identified as the most productive (pod yielding) genotypes of germplasm I for the trait pod yield per tree.

The most productive (pod yielding) genotypes of germplasm II are NTI 79, SMG 4, NTI 84 and NTI 19.
NTI 19, NTI 80, BADAM 15 and NTI 56 are identified as the most seed productive genotypes of germplasm I.

The most seed yielding genotypes of germplasm II are PKM 1, SMG 4, NTI 14 and NTI 75.