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Identification and divergence studies of genotypes of *Tamarindus indica* (Fabaceae) with superior pod traits

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ABSTRACT

Tamarind (*Tamarindus indica* L.) crop improvement depends on availability of diversity in the germplasm collection. An evaluation of 35 genotypes of tamarind was carried out to assess variability and character association and to identify diverse genotypes with superior pod traits. Variability studies for pod traits revealed that, genotype CPT–9 was desirable for eight traits and genotype CPT–26 exhibited the lowest values for six traits. A wide spread of variation was observed for pod weight (9.5 - 83.7 g), pulp weight (4.8 - 51.2 g), seed weight (2.4 - 12.2 g), shell weight (2.3 - 18.1 g), pod length (9.0 - 25.5 cm) and pod width (1.8 - 5.5 cm). Higher estimates of heritability for pod traits such as shell weight, pod weight, pulp weight, and vein weight coupled with higher genetic advance indicated possibility of progress by selection. Pulp weight per pod showed highest positive genotypic and phenotypic correlations with pod weight (rg = 0.99, rp = 0.98), vein weight (0.92, 0.91), shell weight (0.93, 0.91), pod length (0.89, 0.79), pod width (0.92, 0.86), and pulp: seed ratio (0.81, 0.77). The first three Principal Component (PCs) explained large portion (85.53 %) of the total variation. Clustering analysis resulted into two broad clusters. Genotypes in cluster-2 (CPT–1, CPT–2, CPT–3, CPT–9, CPT–10, CPT–11, CPT–17, CPT–22, and CPT–33) had combination of desirable traits and can be directly selected for further improvement by breeding.

Key words: *Tamarindus indica*, co-efficient of variation, heritability, correlation, diversity analysis, genetic advance.

INTRODUCTION

Tamarindus indica L. (ex *T. occidentalis* Gaertn., *T. officinalis* Hook. *T. indica*) (Fabaceae) is a multipurpose fruit tree grown pantropically and commonly known as Indian date, Madeira mahogany, tamarin, tamarind, tamarindier, tamarindo, tamarinier. The precise origin of tamarind is still under debate (Diallo et al., 2007). Yet, it has been extensively planted in Bangladesh, India, Myanmar, Malaysia, Sri Lanka, Thailand and several parts of the world viz. Australia, North

American and South American continents (El-Siddig et al., 2006). Tamarind is a slow-growing, long-lived, large, evergreen or semi-evergreen tree, 20-30 m tall with a thick trunk up to 1.5-2 m across and up to 8 m in circumference. It prefers mean annual rainfall of 500 to 1500 mm, tolerates water logging and grows well even with only 350 mm annual rainfall (El-Siddig et al., 2006). It adopts itself to a wide range of rainfall and shuns, alkaline, saline and waterlogged soils. It is a drought resistant tree and tolerates temperature up to 47°C (El-Siddig et al., 2006). Despite its preferred habitat of alluvial soils, it grows successfully in a wide range of soils varying from red loam, black clay loam, eroded hills, to sandy loam in India (Gunasena and Hughes, 2000).

Each and every part of the tree has specific use. It is an excellent multipurpose tree species which is used as minor timber, firewood fodder and drug (Fandohan et al., 2010), food and food preservative (Salazar-Montoya et al., 2002). The pulp is widely sold and used as a flavour in culinary preparations such as curries, chutneys, juice concentrate, and pulp powder juice. This is particularly so among communities of Asian and Arab origin (Jama et al., 2008). In Asia, the uses are greater, and include tamarind pickle and jam, syrup, candy, sauces, sweets, ice cream and sherbet (Gunasena and Hughes, 2000). Tamarind seeds yield amber colored oil, which could be used for making varnishes, paints and burning in oil lamps. Seeds are extensively used in jam, jelly and confectionery industries and for making condiments (El-Siddig et al., 2006). Tamarind has got tremendous export potential; currently tamarind products are exported to about 67 countries and the total export in 1995-96 was 16,000 metric tonnes worth of 4.5 million US$ and during 1996-97 it was 11,000 metric tonnes worth of 2.6 million US$ (see El-Siddig et al., 2006) .

Although tamarind has commercial potential as a species of wide adaptability and amplitude of uses, little attempt has been directed to improve it as a crop plant (Gunasena and Hughes, 2000; El-Siddig et al., 2006) and to reduce its reproductive age which would in turn make its cultivation economically feasible. As tamarind has a relatively long generation time and is believed to be primarily out-crossing, conventional breeding approaches would require considerable investment in time and money. Tree improvement research that combines developmental and operational phases is time consuming and large-scale cultivation of tamarind is still in early stages of development. Genetic improvement through selection of superior trees and their clonal development may be faster and may have speedy, greater impact than the conventional breeding. Hence it is necessary to understand the extent of variation before formulating any selection programme to identify superior genotypes and to apply them for increasing the pod and pulp production (Jamnadass et al., 2009). This will only emerge when the gene pool has been sampled from across its geographical range and analysed with a focused aim of characterization and evaluation for high-yielding lines. A recent work addressed genetic diversity among 10 populations of *T. indica* using RAPD with seeds collected from Asia (India and Thailand), Africa (Burkino Faso, Senegal, Kenya and Tanzania), from three islands (Madagascar, Reunion and Guadeloupe) and found high intra population variability in populations from Cameroon (Diallo et al., 2007). Unfortunately no such studies were taken-up to screen populations in south India. Added to this, information available in literature does not give a complete understanding of the geographical variations, which is of fundamental importance for the development of new varieties with good quality and higher yields (Lengkeek et al., 2006; Kyndt et al., 2009). As there exists paucity of information in areas of genetic improvement, the present study was designed

to exploit the resource base potentiality of thirty-five tamarind genotypes selected from various locations from south India with scope for further breeding program.

MATERIALS AND METHODS

Data collection

An extensive wild germplasm exploration survey was conducted to identify the high yielding CPTs (Candidate Plus Trees) of *T. indica* at fruiting stage from different predominant naturalized locations in South India. Since *T. indica* is grown as wild and has no definite geometry with neighboring trees for comparison hence, the selection was made by using single tree selection method based on phenotypic assessment of characters of economic interest *viz* yield potential, crown spread, total height, girth at breast height, age of the tree, free from pest and diseases etc. A total of thirty-five CPTs (phenotypically superior trees) were selected from three south Indian states viz. Tamil Nadu (14 CPTs), Karnataka (11 CPTs) and Andhra Pradesh (10 CPTs), including famous released varieties like Urigum, PKM – 1 (TN) and NT1 – 19 (Karnataka), covering a latitude and longitudinal range between 9° N to 16° 50' N and 73° 30' E to 80° E respectively (Figures 1 and 2, Table 1). Few Kg of pods were collected following a random sampling procedure from all the four directions of the crown of each selected tree during fruiting season. The total pods collected were randomly divided into three replications with each replication consisting of 50 pods was selected for recording observations at Forest college and Research Institute (FC and RI), Mettupalayam [11° 19' N and 76° 56' E, msl 1025 ft] during 2002. Average was computed for fourteen quantitative pod traits in all the genotypes as follows:

Pod length: Measured from the tip of the pod to the point of attachment of the pod by moving the thread from top to bottom of the pod. Thread length was measured using scale and expressed in cm.

Pod width: Measured using vernier caliper and expressed in cm.

Pod thickness: Measured using vernier caliper and expressed in cm.

Pod weight: Weighed on electrical balance and average expressed in grams.

Seed weight per pod: Separated seeds were weighed and the average value was recorded as the seed weight per pod.

Pulp weight per pod: Pulp separated from the pod was weighed and the average value was recorded as pulp weight per pod.

Vein weight per pod: Vein separated from the pods was weighed and the average value was recorded as vein weight per pod.

Shell weight per pod: Shell separated from the pods was weighed and the average value was recorded as shell weight per pod.

Number of seeds per pod: Seeds were separated from pods and were recorded as number of seeds per pod.

From the observations made, the following parameters were derived:

Ratio of pulp/seed: The ratio is obtained by dividing pulp weight by seed weight.

Percent of pulp, seed, shell, and vein: The pulp, seed, skin and shell weight obtained from each pod was divided by respective pod weight and expressed as percentage.

i.e. $\text{Pulp \%} = \frac{\text{Pulp weight}}{\text{Pod weight}} \times 100$

$\text{Seed \%} = \frac{\text{Seed weight}}{\text{Pod weight}} \times 100$

$\text{Vein \%} = \frac{\text{Vein weight}}{\text{Pod weight}} \times 100$

$\text{Shell \%} = \frac{\text{Shell weight}}{\text{Pod weight}} \times 100$

Data analysis

Best Linear unbiased predictors (BLUPs) were obtained for each trait. BLUPs were subjected to significance test at 5% critical difference to know the differences between CPTs. Also pod traits of 35 genotypes of *T. indica* were analysed for Analysis of variance (ANOVA) to understand the significance among the genotypes for different pod traits (Gomez and Gomez, 1985). The phenotypic variation for each trait was partitioned into components due to genetic (hereditary) and non-genetic (environmental) factors and estimated using the following formula (Johanson et al., 1955):

$V_p = MSG/r$; $V_g = (MSG – MSE)/r$; $V_e = MSE$

Where, MSG, MSE and r are the mean squares of CPTs, mean squares of error and number of replications, respectively.

The phenotypic variance (V_p) is the total variance among phenotypes when grown over the range of environments of interest; the genotypic variance (V_g) is the part of the phenotypic variance that can be attributed to genotypic differences among the phenotypes, and the error variance (V_e) is part of the phenotypic variance due to environmental effects. To be able to compare the variation among traits, phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) were computed as follows (Burton, 1952):

$PCV = (\sqrt{V_p}/X) \times 100$; $GCV = (\sqrt{V_g}/X) \times 100$

V_p, V_g and X are the phenotypic variance, genotypic variance and grand mean for each pod and seed-related trait, respectively.

Broad sense heritability (h^2b) was calculated as the ratio of the genotypic variance (V_g) to the phenotypic variance (V_p) (Allard, 1999). Genetic advance (GA) expected and GA as per cent of the mean assuming selection of the superior 5% of the genotypes were estimated as below (Johanson et al., 1955):

$GA = K \cdot h^2b \cdot \sqrt{Vp}$; Genetic gain = $(GA/X) \times 100$

Where K is the selection differential (2.06 for selecting 5 % of the genotypes).

Phenotypic (r_p) and genotypic (r_g) correlations were further computed to examine inter-character relationships among seed and seedling traits as follows (Goulden, 1952):

$$r_p = Cov_p (x_1, x_2)/[V_p(x_1) \cdot V_p(x_2)]^{½}$$

$$r_g = Cov_g (x_1, x_2)/[V_g(x_1) \cdot V_g(x_2)]^{½}$$

Cov_p and Cov_g are phenotypic and genotypic covariances for any two traits x_1 and x_2, respectively, and Vp and Vg are the respective phenotypic and genotypic variances for those traits.

The mean observations for all traits for each season were standardized by subtracting from each observation the mean value of the character and subsequently dividing it by its respective standard deviation. These standardized values, with average 0 and standard deviation 1, were used for principal component analysis (PCA) on Genstat 10 to know the importance of different traits in explaining multivariate polymorphism. Cluster analysis was performed using the scores of first three PCs (Ward, 1963). Mean, range and variance were computed for each trait and cluster. Means of clusters were compared using Newman-Keuls procedure (Keuls, 1952; Newman, 1939). The homogeneity of variances among the clusters was tested using Levene's test (Levene, 1960).

RESULTS

In the present investigation, ANOVA and BLUPs obtained for all the pod traits (Pod length, Pod width, Pod thickness, Pod weight, Seed weight per pod, Pulp weight per pod, Vein weight per pod, Shell weight per pod, Number of seeds per pod, ratio of pulp: seed**,** Percent of pulp, seed, shell, and vein) showed significant variation among the selected 35 genotypes of *T. indica* indicating the presence of adequate variability (Table 2 and appendix 1, Figures 3 and 4). Variability studies for pod traits revealed that, genotype CPT–9 recorded maximum for eight traits viz. pod width (5.5

cm), pod thickness (2.4 cm), pulp weight (51.2 g), vein weight (4.2 g), shell weight (18.1 g), pod weight (83.7 g), pulp per cent (60.5) and pulp seed ratio (5.9) and minimum for trait seed per cent (12.5 %) (appendix 1). However maximum pod length (25.5 cm) was recorded by the genotype CPT–22. Genotype CPT–26 exhibited the lowest for six traits viz. pod length (9.0 cm), seed weight (2.4 g), vein weight (0.3 g), shell weight (2.3 g), pod weight (9.5 g) and pulp weight (4.8 g) (appendix 1). Though range is a crude measure of variability present in genotypes and does give an idea of spread of variation for a particular character, a wide spread of variation was observed for pod weight (9.5 - 83.7 g), pulp weight (4.8 - 51.2 g), seed weight (2.4 - 12.2 g), shell weight (2.3 - 18.1 g), pod length (9.0 - 25.5 cm) and pod width (1.8 - 5.5 cm) (Table 3).

Variance due to genotype and other genetic estimates for pod traits in *T. indica* are presented in table 3. Genotypic coefficients of variations (GCV) and phenotypic coefficient of variation (PCV) were close to each other for all traits, however pulp weight, pod weight, and vein weight exhibited higher PCV and GCV than other traits. Estimates of individual heritabilities for pod traits were high and ranged from 50.7 to 95.4 % for number of seeds to pod width respectively. Pod traits viz. pulp weight, vein weight and pod weight expressed high genetic advance as percent of mean 139.4, 137.7 and 107.6 respectively. The correlation coefficient (r) among the pod traits which are greater than 0.71 or smaller than -0.71 are presented in table 4. Correlation studies showed that for most character pairs, genotypic and phenotypic association were in the same direction and that the genotypic estimates were higher than the phenotypic ones, indicating an inherent association between the characters. Of 182 correlations, 66 and 63 were significant at genotypic and phenotypic level respectively. Sixty three genotypic and fifty nine phenotypic combinations were significant at 1 % along with 3 genotypic and 4 phenotypic combinations at 5 % (data not given). The pod traits showing such high correlation were 53 (31 genotypic and 22 phenotypic). Forty-nine of these were positive while four (see per cent: pulp per cent and seed per cent: pulp/seed ratio, each genotypic and phenotypic level) were negative (Table 4). The trait of economic interest pulp weight was highly positively correlated with pod length (rg = 0.99, rp = 0.98), vein weight (0.92, 0.91), shell weight (0.93, 0.91), pod length (0.89, 0.79), pod width (0.92, 0.86), and pulp/seed ratio (0.81, 0.77) both at genotypic and phenotypic level.

The first three principal components (PCs) of the total ten explained are having large portion (85.53 %) of the total variation for pod traits in *T. indica*. The first PC alone accounted for 58.92 % of the variation followed by the second and third PCs, which explained 17.30 % and 9.31 % of the variation. Based on the loading for the first three PCs, traits such as pod weight, pulp weight, vein weight, pod width, shell weight, pod length, pulp/seed ratio, pod thickness, number of seeds, seed per cent and shell per cent are important and adequate descriptors for pod traits study in this material. Cluster analysis performed on the scores of the first three PCs resulted into two clusters (Figure 5). The first cluster comprised 26 genotypes (CPT–4, CPT–5, CPT–6, CPT–7, CPT–8, CPT–12, CPT–13, CPT–14, CPT–15, CPT–16, CPT–18, CPT–19, CPT–20, CPT–21, CPT–23, CPT–24, CPT–25, CPT–26, CPT–27, CPT–28, CPT–29, CPT–30, CPT–31, CPT–32, CPT–34 and CPT–35) and remaining 9 genotypes (CPT–1, CPT–2, CPT–3, CPT–9, CPT–10, CPT–11, CPT–17, CPT–22 and CPT–33) are grouped into second cluster. The range, mean and variance for the two clusters are provided in table 5. Cluster 2 was delineated from cluster 1, based on significantly higher means for all the pod traits under study except seed per cent.

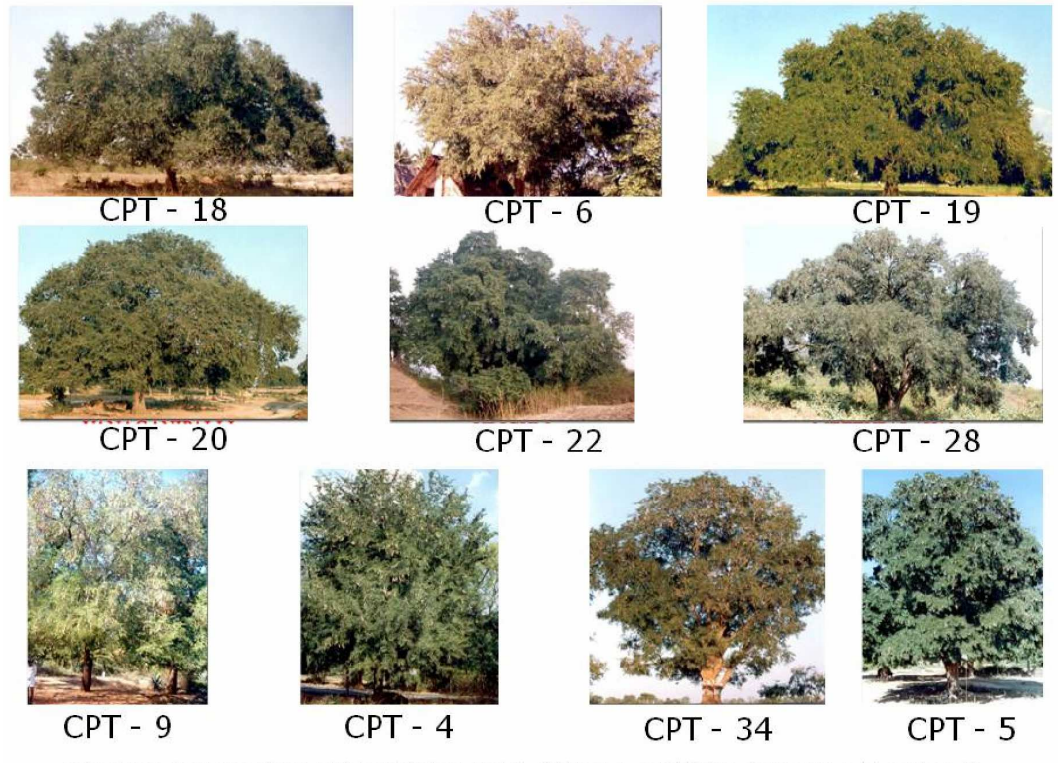

Figure 1: Selected Candidate Plus Trees (CTP) of *Tamarindus indica*

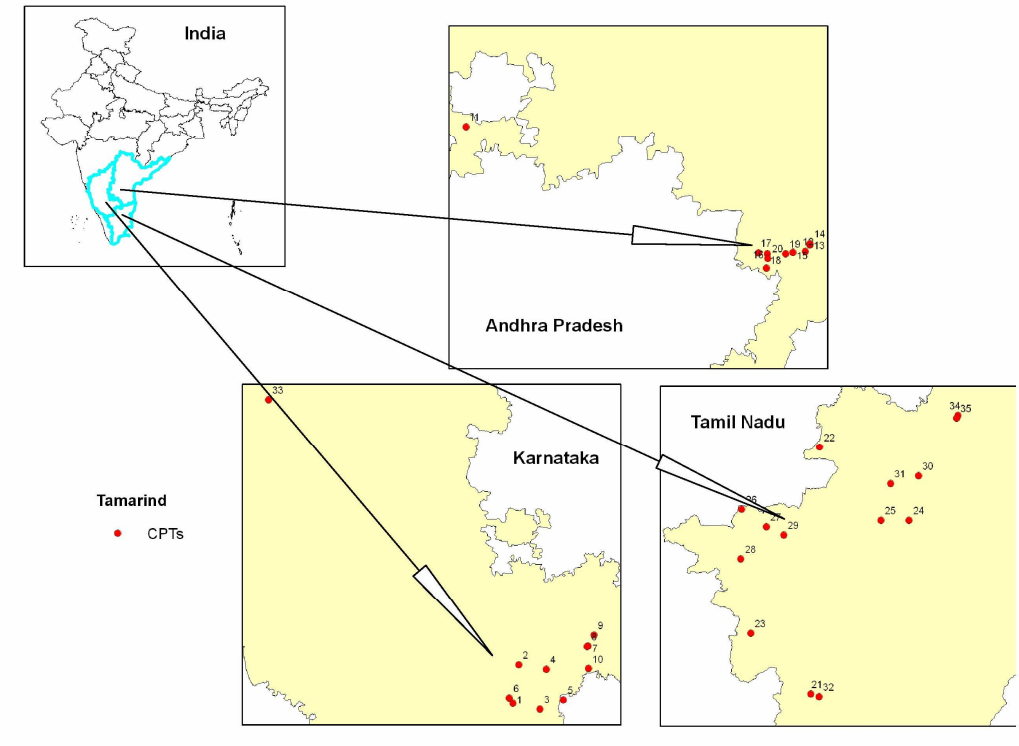

Figure 2: Distribution map of candidate plus tree of *Tamarindus indic*a

Note: Details of number representation is in table 1.

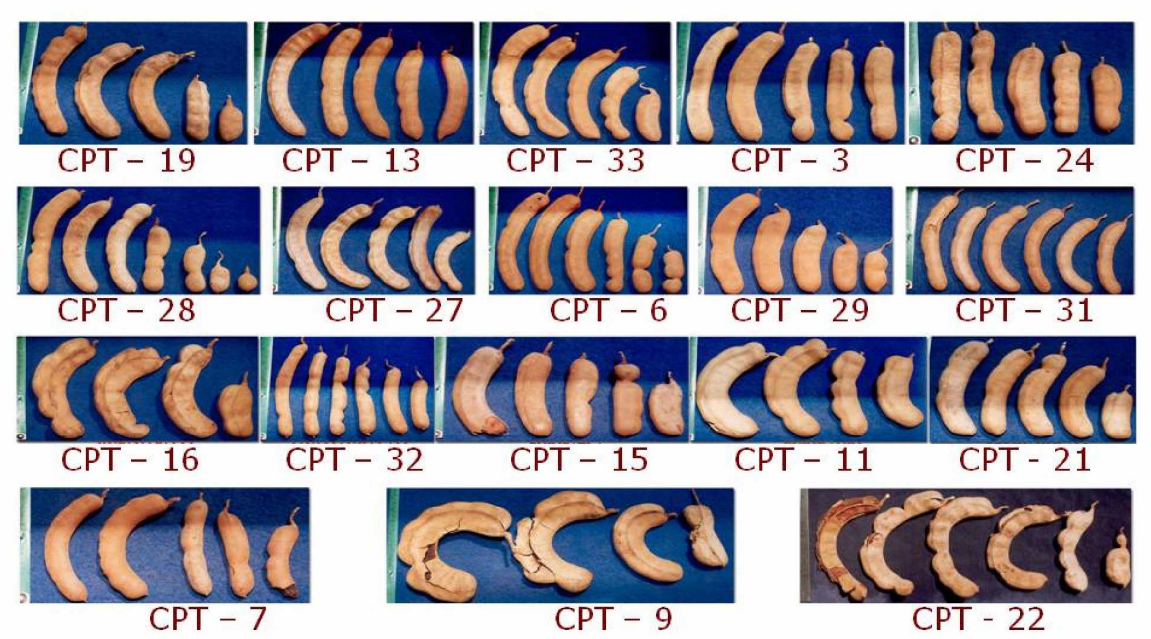

Figure 3: Morphological variations in pods of selected Candidate Plus Trees (CTP) of *Tamarindus indica*

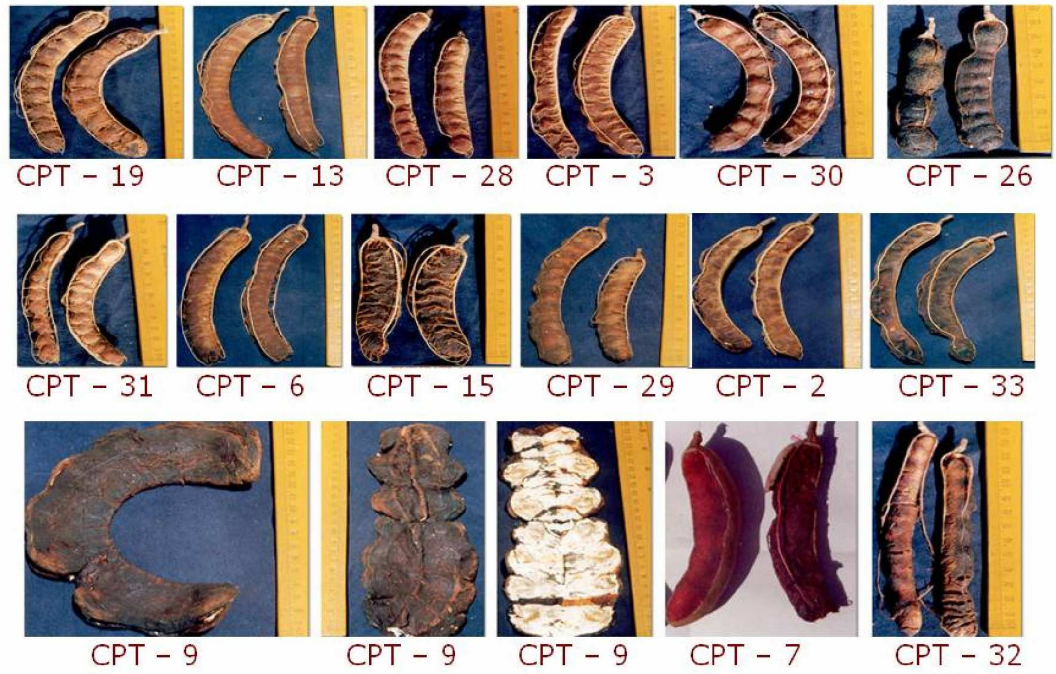

Figure 4: Morphological variations in pulp of selected Candidate Plus Trees (CTP) of *Tamarindus indica*

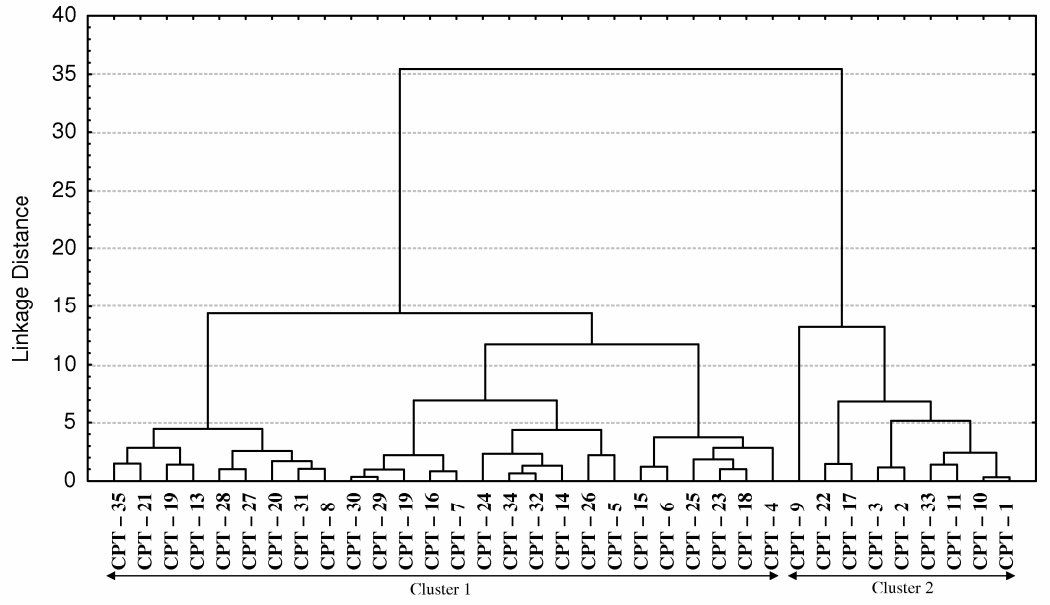

Figure 5: Grouping of 35 *Tamarindus indica* genotypes based on scores of first three principal components

Table 1: Locational and morphological details of *Tamarindus indica* candidate plus trees (CPTs)

Genotypes	State	District	Village	Longitude	Latitude	Altitude	Age in years	Height (m)	GBH (m)	Pod yield (kgs)	Crown area (m^2)	Pod size
CPT–1	Karnataka	Bangalore	Mallarpatna	77.18	12.60	647	90	10.0	4.71	750	527.07	Big
CPT–2	“	“	Dabguli	77.24	12.94	863	50	14.0	2.73	300	132.79	Big
CPT–3	“	“	Anahosali	77.42	12.54	645	100	9.0	5.25	400	555.94	Big
CPT–4	“	“	Sulikera	77.48	12.90	793	60	12.0	2.57	450	250.35	Big
CPT–5	“	“	Siddhadavarbetta	77.63	12.62	925	90	17.0	2.34	500	328.59	Medium
CPT–6	“	“	Mathikare	77.15	12.64	672	30	9.5	2.05	600	169.79	Big
CPT–7	“	“	Guttipura	77.85	13.11	891	20	4.5	1.15	35	30.69	Medium
CPT–8	“	“	Guttipura	77.84	13.10	891	22	4.0	1.65	50	15.91	Medium
CPT–9	“	“	Nandhgudi	77.90	13.20	912	19	9.5	2.13	100	103.91	Very big

CPT–10	“	“	Tathnur	77.85	12.91	870	60	19.0	3.75	150	135.87	Big
CPT–11	Andhra Pradesh	Anantpur	Gudibanda	77.09	13.99	677	80	20.0	3.41	900	346.5	Big
CPT–12	“	Chitroor	Charala	78.71	13.40	717	60	15.0	2.40	700	154.00	Medium
CPT–13	“	“	Chukkavaripalli	78.73	13.43	757	200	9.5	5.50	600	366.58	Big
CPT–14	“	“	Thuppireddypalli	78.73	13.43	757	150	34.0	4.80	1000	463.96	Medium
CPT–15	“	“	Pudipatla	78.65	13.39	720	100	32.0	5.10	600	320.60	Medium
CPT–16	“	“	Kuppanapalli	78.52	13.39	758	150	15.0	3.70	850	602.87	Medium
CPT–17	“	“	Kurapalli	78.48	13.39	794	60	17.0	2.10	750	152.90	Very Big
CPT–18	“	“	Mirjepalli	78.52	13.32	761	130	23.0	3.30	1200	344.85	Medium
CPT–19	“	“	Gollapalli	78.61	13.39	729	150	30.0	3.60	1000	361.51	Big
CPT–20	“	“	Vanaganipalli	78.53	13.36	753	100	20.0	2.40	800	113.14	Big
CPT–21	Tamil Nadu	Thani	Periakulam (Endapalli)	77.54	10.12	300	150	19.0	5.57	236	180.34	Big
CPT–22	“	Dharmapuri	Urigum	77.62	12.30	691	150	19.0	5.57	400	616.00	Very Big
CPT–23	“	Coimbatore	Pollachi	77.01	10.66	300	60	8.0	2.70	350	148.55	Big
CPT–24	“	Salem	Kavarkalpatti	78.40	11.66	321	65	21.0	2.95	250	388.98	Medium
CPT–25	“	Salem	Salem	78.16	11.66	281	35	12.0	2.27	200	133.81	Big
CPT–26	“	Erode	Mallankuli	76.93	11.75	824	70	15.0	2.10	300	103.91	Medium
CPT–27	“	Erode	Hassanur	77.15	11.60	684	65	13.0	2.30	400	105.73	Big
CPT–28	“	Coimbatore	Mettupalayam	76.92	11.32	317	45	13.0	3.73	700	103.01	Big
CPT–29	“	Erode	Pulinjur	77.30	11.53	274	62	23.5	2.40	400	330.20	Medium
CPT–30	“	Dharmapuri	Harur	78.49	12.05	355	40	18.0	3.32	400	127.73	Big

CPT–31	“	Dharmapuri	Bommidi	78.24	11.98	425	45	13.0	4.52	350	132.79	Big
CPT–32	“	Thani	Jayamangalam	77.61	10.09	271	25	15.0	1.78	200	117.91	Medium
CPT–33	Karnataka	Dharwad	Yellapur	75.01	15.31	621	30	12.0	3.45	200	167.48	Big
CPT–34	Tamil Nadu	North Arcot	Vellore	78.83	12.59	609	70	10.0	2.60	600	86.63	Medium
CPT–35	“	North Arcot	Reddiyur	78.82	12.56	660	56	20.0	2.20	720	616.00	Medium

Pod size: Medium (7 to 13cm), Big (13 to 19 cm) and Very Big (>19 cm)

DISCUSSION

T. indica is being explored for its sour pulp yield potentiality throughout the world. Under improvement programmes, attempts are therefore aimed at screening out *T. indica* sources, which can produce higher pulp yield. In the present study, pods collected from 35 CPTs selected from different parts of south India reveled wide spread variation for pod, pulp, seed and shell weight. These observations are congruent with previous investigations that reported extreme variation of metric traits among tamarind provenances (Nandini et al., 2011). The variations in the pulp, seed, shell, and vein weight is due to their genotypic differences. The difference in the length, width and thickness of pod may be partly attributed to either genetic differences among the CPTs as for other species' morphotypes such as *Vitellaria paradoxa* C.F. Gaertn (Sanou et al., 2005) and *Adansonia digitata* L. (Assogbadjo et al., 2006) or differences in climatic conditions as for *Manilkara zapota* L. (Heaton et al., 1999). In the same way, the difference in shell weight can be attributed to the difference in size of the fruit whereas the difference in fibre weight among the genotypes may be due to the differences in the rate of development of vascular tissue in fruits (Hanamashetti, 1997). Likewise, the difference in seed weight may be attributed to the difference in the number and size of seeds while the difference in seed number may be attributed to the difference in length of pod and ovule fertility. Variation in pod size and in number of seeds per fruit among *T. indica* trees and /or provenances were previously reported to be strongly affected by cross pollination, fruit abortion and resource availability (Diallo et al., 2008; Fandohan et al., 2011). The pod data of individual CPTs have clearly indicated that, the genotype CPT-9 is superior to other genotypes for eight traits. Hence clones of genotypes CPT-9 may be encouraged as superior material for immediate needs of afforestation activities.

Apart from significant difference in pod traits of *T. indica*, genotypes also expressed considerable amount of genetic variability indicating a scope of genetic improvement among the collected CPTs. The decision on tree breeding/improvement strategy is largely dependent upon the extent of variability in the collected genotypes which is measured by different population parameters including genotypic and phenotypic variance, and genotypic and phenotypic co-efficient of variation (Assogbadjo et al., 2010).

Table 2: Mean squares from analysis of variance for pod traits in *Tamarindus indica*,

Source	df	Pod length (cm)	Pod width (cm)	Pod thickness (cm)	Seed weight (g)	Vein weight (g)	Shell weight (g)	Pod weight (g)	Seed per cent	Pulp per cent	Vein per cent	Shell per cent	Pulp: Seed	Number of seeds	Pulp weight (g)
Replication	2	47.44	0.22	0.03	17.47	0.65	26.76	350.20	2.88	11.04	0.63	14.35	0.01	14.54	78.31
Genotypes	34	47.70**	1.68**	0.23**	20.50**	2.80**	29.10**	708.54**	99.68**	142.52**	5.53**	58.36**	2.68**	8.22**	278.44**
Error	68	5.07	0.03	0.01	1.85	0.20	1.89	43.10	5.25	8.96	0.35	5.30	0.13	2.01	18.91

**significantly different at 1 per cent level of probability

Table 3: Estimates of variance components and other parameters for pod traits in *Tamarindus indica*

Characters	Mean ±SD	Range	Variance due to genotypes	Heritability	Coefficient of variation (%)		Genetic advance (%) of mean
					Genotypic	Phenotypic	
Pod length (cm)	14.7±3.5	9.0 - 25.5	14.2	73.7	25.6	29.8	45.3
Pod width (cm)	3.0±0.7	1.8 - 5.5	0.5	95.4	24.9	25.4	50.1
Pod thickness (cm)	1.8±0.2	1.4 - 2.4	0.1	83.3	14.8	16.2	27.9
Seed weight (g)	6.8±2.3	2.4 - 12.2	6.2	77.1	36.6	41.7	66.2
Vein weight (g)	1.3±0.9	0.3 - 4.2	0.8	81.6	74.0	81.9	137.7
Shell weight (g)	5.7±2.9	2.3 - 18.1	9.1	82.8	53.1	58.3	99.5
Pod weight (g)	26.1±14.4	9.5 - 83.7	221.8	83.7	57.1	62.3	107.6
Seed per cent	27.9±5.4	12.5 - 36.2	31.4	85.7	20.1	21.7	38.4
Pulp per cent	45.4±6.4	33.3 - 60.5	44.5	83.2	14.7	16.1	27.6
Vein per cent	4.0±1.2	1.8 - 6.9	1.7	83.1	33.2	36.4	62.4
Shell per cent	22.8±4.0	13.3 - 31.0	17.6	76.9	18.5	21.0	33.3
Pulp: Seed	1.9±0.9	1.0 - 5.9	0.8	86.5	49.8	53.6	95.5
Number of seeds	7.2±1.2	3.7 - 9.5	2.0	50.7	19.9	27.9	29.3
Pulp weight (g)	12.5±8.9	4.8 - 51.2	86.5	82.1	74.7	82.5	139.4

Table 4: Pairs of pod traits in *Tamarindus indica* showing more than 0.71 or less than -0.71 correlation coefficients

Pair of pod traits	Genotypic correlation coefficient	Phenotypic correlation coefficient
Pod length: Pod width	0.73	-
Pod length: Seed weight	0.82	0.79
Pod length: Vein weight	0.89	0.82
Pod length: Shell weight	0.84	0.77
Pod length: Pod weight	0.92	0.85
Pod length: Pulp weight	0.89	0.79
Pod width: Pod thickness	0.74	-
Pod width: Seed weight	0.71	-
Pod width: Vein weight	0.90	0.83
Pod width: Shell weight	0.87	0.82
Pod width: Pod weight	0.93	0.87
Pod width: Pulp: Seed	0.73	-
Pod width: Pulp weight	0.92	0.86
Pod thickness: Vein weight	0.74	-
Pod thickness: Shell weight	0.72	-
Pod thickness: Pod weight	0.72	-
Seed weight: Vein weight	0.79	0.73
Seed weight: Pod weight	0.79	0.74
Vein weight: Shell weight	0.89	0.87
Vein weight: Pod weight	0.95	0.94
Vein weight: Vein per cent	0.73	0.72
Vein weight: Pulp weight	0.92	0.91
Shell weight: Pod weight	0.95	0.94
Shell weight: Pulp: Seed	0.71	-
Shell weight: Pulp weight	0.93	0.91

Table 5: Range, mean, and variance for different pod traits in two clusters of selected genotypes of *Tamarindus indica*

	Range		**Mean[1]**		**Variance[2]**		**F value**	**Prob > F**
Pod traits	**Cluster 1**	**Cluster 2**	**Cluster 1**	**Cluster 2**	**Cluster 1**	**Cluster 2**		
Pod length (cm)	9.0 - 17.3	16.3 - 25.5	13.1[b]	19.2[a]	3.5	12.4	6.9	0.01
Pod width (cm)	1.8 - 3.5	2.9 - 5.5	2.7[b]	3.8[a]	0.2	0.6	4.8	0.04
Pod weight: Pulp: Seed			0.72				-	
Pod weight: Pulp weight			0.99				0.98	
Seed per cent: Pulp per cent			-0.79				-0.77	
Seed per cent: Pulp: Seed			-0.89				-0.88	
Pulp per cent: Pulp: Seed			0.81				0.80	
Pulp:Seed: Pulp weight			0.81				0.77	
Pod thickness (cm)	1.4 - 2.2	1.7 - 2.4	1.7[b]	2.0[a]	0.1	0.1	2.3	0.14
Seed weight (g)	2.4 - 8.8	6.0 - 12.2	5.9[b]	9.5[a]	3.3	2.8	0.2	0.68
Vein weight (g)	0.3 - 1.6	1.6 - 4.2	0.7[b]	2.4[a]	0.1	0.7	7.1	0.01
Shell weight (g)	2.3 - 7.0	6.2 - 18.1	4.5[b]	9.1[a]	1.8	12.7	3.6	0.07
Pod weight (g)	9.5 - 30.2	30.8 - 83.7	19.8[b]	44.4[a]	29.2	288.9	6.0	0.02
Seed per cent	19.5 - 36.2	12.5 - 33.2	29.4[a]	23.5[b]	19.7	36.2	1.3	0.27
Pulp per cent	33.3 - 55.3	41.0 - 60.5	43.7[b]	50.2[a]	33.5	37.7	0.01	0.93
Vein per cent	1.8 - 6.0	4.0 - 6.9	3.5[b]	5.3[a]	1.1	0.6	0.8	0.38
Shell per cent	13.3 - 31.0	18.3 - 23.3	23.4[a]	21.0[a]	19.6	2.2	3.8	0.06
Pulp: Seed	1.0 - 3.2	1.3 - 5.9	1.6[b]	2.6[a]	0.2	1.9	4.1	0.05
Number of seeds	3.7 - 8.9	6.6 - 9.5	6.9[b]	8.1[a]	1.5	0.8	1.1	0.31
Pulp weight (g)	4.8 - 15.2	13.2 - 51.2	8.7[b]	23.2[a]	7.7	144.7	6.5	0.02

Appendix 1 Mean performance of selected *Tamarindus indica* genotypes for pod traits

Genotypes	Pod length (cm)	Pod width (cm)	Pod thickness (cm)	Seed weight (g)	Vein weight (g)	Shell weight (g)	Pod weight (g)	Seed per cent	Pulp per cent	Vein per cent	Shell per cent	Pulp: Seed	Number of seeds	Pulp weight (g)
CPT – 1	16.5	3.5	2.2	9.1	1.9	7.6	36.3	25.3	48.6	5.2	21.0	2.0	8.2	17.6
CPT – 2	16.8	2.9	1.8	10.3	1.7	6.2	31.5	33.2	41.4	5.4	20.1	1.3	8.9	13.2
CPT – 3	16.5	3.4	1.9	10.0	2.3	7.2	33.3	30.5	41.0	6.9	21.7	1.4	8.4	13.7
CPT – 4	17.3	3.2	1.6	8.0	1.0	3.9	28.3	29.2	54.3	3.5	13.3	1.9	7.1	15.3
CPT – 5	9.9	2.9	1.6	3.0	0.7	2.8	14.2	19.5	55.3	4.7	20.5	3.2	3.7	7.9
CPT – 6	14.8	2.8	2.0	8.3	0.8	6.0	30.2	27.2	50.0	2.5	20.4	1.9	8.1	15.0
CPT – 7	12.4	2.1	1.6	5.2	0.5	3.3	16.4	31.9	44.9	2.8	20.5	1.5	8.0	7.4
CPT – 8	13.1	2.2	1.5	4.5	0.7	3.8	15.4	28.4	41.8	4.7	25.0	1.5	7.9	6.6
CPT – 9	23.8	5.5	2.4	9.7	4.2	18.1	83.7	12.5	60.5	4.9	22.0	5.9	6.6	51.2
CPT – 10	17.6	3.8	1.7	9.5	1.6	8.7	39.3	24.7	49.1	4.0	22.2	2.0	9.5	19.3
CPT – 11	16.3	4.1	2.1	8.4	2.4	7.6	37.9	21.9	51.4	6.1	20.6	2.4	7.1	19.4
CPT – 12	11.8	2.8	1.8	6.0	0.7	4.0	19.3	31.1	44.8	3.6	20.7	1.5	6.6	8.8
CPT – 13	16.4	2.6	1.7	8.3	0.7	6.7	25.4	32.7	38.0	2.8	26.5	1.2	8.3	9.6
CPT – 14	11.9	2.3	1.5	4.2	0.4	3.5	13.4	30.6	40.4	2.6	26.3	1.4	5.4	5.5
CPT – 15	12.8	3.5	2.1	6.9	1.1	6.0	27.4	25.2	48.3	3.9	22.6	2.0	6.6	13.5
CPT – 16	11.7	2.3	1.6	5.1	0.5	3.1	14.3	35.8	39.2	3.4	21.7	1.1	7.1	5.7
CPT – 17	21.4	4.6	2.4	12.2	3.2	9.6	55.2	22.2	54.1	5.4	18.3	2.5	7.6	29.8
CPT – 18	13.0	3.0	2.1	7.0	0.7	3.4	21.7	32.2	46.9	3.1	18.0	1.5	7.1	10.6
CPT – 19	14.5	3.1	2.2	8.4	1.6	7.0	27.0	31.2	37.4	5.6	25.8	1.2	6.6	10.0
CPT – 20	13.4	2.4	1.7	5.7	0.6	4.2	15.9	36.2	33.3	3.8	26.7	1.0	8.8	5.6
CPT – 21	13.4	3.0	1.9	6.4	0.9	6.6	23.3	27.9	39.6	3.9	28.4	1.4	7.4	9.4
CPT – 22	25.5	3.4	1.7	10.4	2.6	9.7	51.2	21.2	53.9	5.0	20.0	2.6	8.3	28.2

CPT – 23	14.4	3.0	1.5	8.5	0.9	4.6	24.7	34.5	43.0	3.6	19.1	1.3	7.5	10.7
CPT – 24	12.6	3.0	1.9	4.5	0.6	4.9	19.3	22.6	49.0	2.9	25.4	2.4	5.7	9.4
CPT – 25	16.4	2.6	1.7	8.8	1.5	3.6	24.9	35.7	43.6	6.0	15.0	1.3	7.2	10.9
CPT – 26	9.0	2.3	1.5	2.4	0.3	2.3	9.5	22.1	50.5	2.4	24.9	2.5	5.0	4.8
CPT – 27	14.3	2.2	1.5	5.1	0.6	5.1	16.6	30.7	34.8	3.4	31.0	1.2	8.2	6.0
CPT – 28	13.9	2.6	1.8	6.4	0.8	6.4	21.1	30.3	35.0	3.8	30.7	1.2	7.5	7.5
CPT – 29	11.3	2.8	1.5	5.1	0.5	3.5	16.7	30.0	46.3	2.6	21.2	1.6	6.5	7.8
CPT – 30	13.1	3.1	1.4	6.6	0.4	4.5	20.9	31.6	45.0	1.8	21.6	1.5	6.0	9.5
CPT – 31	13.8	2.1	1.6	5.4	0.5	4.0	16.3	33.0	39.4	2.9	24.7	1.2	8.9	6.5
CPT – 32	12.2	1.8	1.6	3.3	0.3	3.2	13.2	24.7	47.8	2.5	25.0	2.1	7.5	6.5
CPT – 33	18.5	3.4	1.8	6.0	1.7	7.1	30.8	20.1	51.4	5.2	23.3	2.9	8.1	16.0
CPT – 34	11.7	2.8	1.7	4.7	0.5	4.2	17.4	26.8	46.2	2.7	24.3	1.8	5.8	8.1
CPT – 35	12.9	3.1	1.9	4.9	1.1	6.3	21.3	23.6	41.3	5.1	29.8	1.9	5.7	9.0
Mean	**14.7**	**3.0**	**1.8**	**6.8**	**1.3**	**5.7**	**26.1**	**27.9**	**45.4**	**4.0**	**22.8**	**1.9**	**7.2**	**12.5**
SEM	**1.2**	**0.1**	**0.1**	**0.8**	**0.3**	**0.8**	**3.7**	**1.3**	**1.7**	**0.3**	**1.3**	**0.2**	**0.7**	**2.4**
CD (5%)	**3.6**	**0.3**	**0.2**	**2.2**	**0.7**	**2.2**	**10.7**	**3.8**	**4.9**	**1.0**	**3.7**	**0.6**	**2.1**	**7.1**
C.V. (%)	**15.3**	**5.4**	**6.6**	**20.0**	**38.1**	**24.2**	**25.2**	**8.2**	**6.6**	**15.0**	**10.1**	**19.7**	**19.6**	**34.9**

Trait means not followed by the same superscript letter are significantly different at $P = 0.05$.

In the present study, the magnitude of error variance was relatively lower than the genotypic variance for all traits (data not given), indicating that the variability observed in the phenotype for these traits has more of a genetic than a non-genetic basis. Results are in similar lines with previous findings that reported an extensive variability in tamarind populations from West Africa (Diallo et al., 2007; Fandohan et al., 2011). Further, the higher estimates of heritability coupled with higher genetic advance for shell weight, pod weight, pulp weight and vein weight, indicated that heritability of the trait is mainly due to additive effects and selection is effective for such traits (Table 3). A maximum heritability of 0.5 and the highest genetic advance percentage were recorded over a mean of 42.5 for pulp weight (Shanthi, 2003) and this may be because of considering only 10 populations for study. High heritability accompanied by medium to low genetic advance for pod width, pod thickness and pulp percent is indicative of non-additive gene action and the high heritability is being exhibited due to favourable influence of environment rather than genotype.

Only those correlation coefficients which are greater than 0.71 or smaller than -0.71 are biologically meaningful so that 50 % of the variation in one trait is predicted by the other (Skinner et al., 1999). Hence correlation coefficients greater than 0.71 or smaller than -0.71 are presented in table 4 and discussed. Pulp weight is highly significant with pod length, Vein weight, shell weight, pod length, pod width, and pulp: seed ratio both at genotypic and phenotypic level. However, seed percent is negatively correlated with pulp percent and pulp: seed ratio. Thus, suggested that these characters may be used to the advantage of the breeder for bringing improvement in these traits simultaneously. Similar trend was previously observed (Fandohan et al., 2011) where the fruit weight is positively and significantly associated with pulp, fibre, seed weight, fruit length and breadth.

Genetic diversity in plant species is a gift to mankind as it forms the basis for selection and further improvement. Variability is a backbone, in order to exercise selection of superior genotypes from natural population. Morphometric traits had been utilized to assess the relationship among the germplasm/cultivars in trees (Abasse et al., 2010; Diallo et al., 2010; Fandohan et al., 2011). The study of relationships based on assumption that the difference in the characters reveals their genetic divergence. The information on the genetic structure and relationship of these populations provide a basis for planning and conducting future collections and their efficient utilization as genetic resources (Kyndt et al., 2009). In the present study, 35 genotypes were grouped into 2 clusters with 26 genotypes in cluster one and 9 genotypes in cluster two based on the first three principal components of principal component analysis. The results of clustering pattern showed that the clones collected from different locations were not necessarily grouped into different clusters. Geographic diversity though important may not be the only one factor in determining genetic divergence (e.g. *V. paradoxa*, Bouvet et al., 2008; *A. digitata*, Kyndt et al., 2009). The clustering pattern revealed that the tendency of clones from diverse geographic region to be grouped together in one cluster might be due to the similarity of the nature of selection pressure operating under the respective domestic conditions. Outputs from this study indicated that factors other than geographical divergence might be responsible for the differential grouping of the seed sources. The clustering pattern thus highlighted no direct relationship between the genetic divergence and geographical distribution. Since seed percent and pulp weight are negatively correlated and improvement is targeted for increasing pod and pulp yield, cluster 1 is ideal for getting higher yields. Hence genotypes (CPT–1, CPT–2, CPT–3, CPT–9, CPT–10, CPT–11, CPT–17, CPT–22, and CPT–33) can be directly selected and utilized

for breeding program. Inter-mating of divergent groups may lead to greater opportunity for crossing over which would release latent variation by breaking up predominantly repulsion linkage.

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