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Original Article

Clonal Variability and Divergence Studies in *Tamarindus indica* L.; A Multipurpose Fruit Tree

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Abstract

Exploration of clonal variability and divergence among thirty-five high yielding genotypes of Tamarindus indica L. selected from south India was carried out as a scope for further genetic improvement. Significant variation was expressed for all the growth characters under field condition. Maximum plant height (60.33 cm), number of branches (19.78) collar diameter (1.49 cm), and Volume index (245.78 cm3) was recorded by CPT-22, CPT-5, CPT-7 and CPT-7 respectively. Higher GCV (42.83 %), heritability (78.98 %) and genetic gain (78.40 %) were found to be high for trait volume index. All the morphometric traits registered positive and highly significant association with volume index at both phenotypic and genotypic level. Path analysis revealed that, collar diameter (0.594) followed by height (0.450) expressed maximum direct positive effect on volume index and number of branches contributed indirectly through height and collar diameter. Genetic diversity analysis resolved thirty-five genotypes under investigation into 6 clusters, indicating wide diversity. Cluster I contained eight genotypes and showed maximum intra cluster distance (2.74) closely followed by cluster-VI (2.73) because the genotypes used for breeding program were from different locations. The highest inter-cluster distance was found between cluster III and V (7.63) followed by II and V (7.45) suggesting wide diversity between these groups. Cluster V recorded maximum mean values for all traits, hence these genotypes can be directly selected and utilized for breeding program. The trait volume index contributed maximum for genetic diversity as per cent contribution and rank total, 34.96 and 208 respectively.

Keywords: *Tamarindus indica, variability, heritability, genetic advance, association, genetic divergence*

INTRODUCTION

Tamarindus indica L. [sub-family: Caesalpinioideae] a multipurpose fruit tree grown pantropically is commonly known as Indian date, Madeira mahogany, tamarin, tamarind, tamarindier, tamarindo, tamarinier. This tree is synonymously known as *T. occidentalis* Gaertn., *T. officinalis* Hook. *T. indica* originated in Madagascar [Hocking Drake 1993] and it has naturalized in the South Indian moist deciduous and tropical evergreen forests [Champion & Seth 1968]. It has been extensively planted in Bangladesh, India, Myanmar, Malaysia, Sri Lanka,
Thailand and several other parts of the world viz. Australia, African, North American and South American continents [Mishra 1997]. 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 [Singh 1982], tolerates water logging and grows well even with only 350 mm annual rainfall [Gupta 1993]. 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 [Parkash & Hocking Drake 1985]. 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 [Jambulingam *et al.* 1997].

Each and every part of the tree has specific use. It is an excellent multipurpose tree species which is used as minor timber, firewood [Mascarenhas *et al.* 1987], food, food preservative [Tsuda *et al.* 1995], fodder and drug [Mustapha *et al.* 1996]. Tamarind is valued mainly for its fruits. It's acidic pulp is a favourite ingredient in culinary preparations. Seeds are extensively used in jam, jelly and confectionery industries and for making condiments [Parkash & Hocking Drake 1985]. Tamarind has got tremendous export potential; currently tamarind products are exported to about 67 countries [Shinde *et al.* 1997] and the total export in 1995-96 was 16,000 metric tonnes worth of Rs.20 crores [Subba Rao 1997] and during 1996-97 it was 11,000 metric tonnes worth of Rs.12 crores [George & Rao 1997].

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 [Nicodemus *et al*. 1997; Gunasena & Hughes 2000] 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 outcrossing, 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 [Nicodemus *et al.* 1997]. This will only emerge when the genepool has been sampled from across its geographical range and analysed with a focused aim of characterization and evaluation for high-yielding lines. Added to this, no systematic germplasm collection and evaluation has been attempted to date although there is a wealth of tamarind germplasm across the regions. Hence the present study was designed to exploit the resource base potentiality of thirty-five tamarind genotypes selected from various locations from south India with on outlook for further breeding program.

MATERIAL & METHODS

An extensive wild germplasm exploration survey was conducted to identify the high yielding CPTs [Candidate Plus Trees] of *Tamarindus indica* at fruiting stage from different predominant naturalized locations in South India [Table 1]. The selection was made 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 [morphologically superior trees] were selected from three south Indian states viz. Tamil Nadu [14 CPTs], Karnataka [11 CPTs] and Andhra Pradesh [10 CPTs] covering a latitude and longitudinal range between 9° N to 16° 50' N and 73° 30' E to 80° E respectively. Ramets of thirty-five candidate plus trees [CPTs] formed the basic material for the evaluation. Samples of nine grafts in three replications were planted in randomized completely block design [spacing of 6 m x 6 m] at Forest College and Research Institute, Mettupalayam [11° 19`N, 76° 56`E, 300 msl] after 12 months in nursery for field evaluation. Growth measurements like total height [measured from ground level to tip], diameter at the collar region [measured at the base of the stem], number of branches [all live primary branches] and volume index {Volume index = [Diameter [cm]]^2 x Height [cm] [Hatchell 1985; Manavalan 1990]} at juvenile stage were recorded during planting and at quarterly intervals viz., 3 months after planting [MAP], 6 MAP and 9 MAP. The data recorded at 9 MAP {21 months after grafting} alone was considered for variability and divergence studies.

Data analysis

The ramets growth measurements of thirty-five CPTs were analysed for Analysis of variance [ANOVA] and Duncan Multiple Range Test [DMRT] to understand the significance of differences between CPTs [Gomez and Gomez 1984]. 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 [PCV] and genotypic [GCV] coefficients of variation were computed according to the method suggested by 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 according to Allard [1999] as the ratio of the genotypic variance [V_g] to the phenotypic variance [V_p]. Genetic advance [GA] expected and GA as per cent of the mean assuming selection of the superior 5% of the genotypes were estimated in accordance with Johanson *et al*. [1955] as:

$$GA = K \cdot h^2B \cdot \sqrt{Vp}; \; GA \text{ [as \% of the mean]} = [GA/X] \times 100$$

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 following Varghese *et al*. [1976] as:

$$r_p = Cov_p [x_1, x_2]/[V_p[x_1] \cdot V_p[x_2]]^{½}$$
$$r_g = Cov_g [x_1, x_2]/[V_g[x_1] \cdot V_g[x_2]]^{½}$$

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.

Path coefficient analysis was done using genotypic correlation coefficients following Dewey and Lu [1959]. The genetic diversity was estimated using the Mahalanobis D2 statistics [Mahalanobis 1936]. Tracing D^2 as a generalized distance, the criterion used by Tocher as described by Rao [1952] was applied for determining the clustration group. Average intra and inter cluster distances were determined using GENRES version 3.11, 1994 Pascal Intl. Software and suggested by Singh and Chaudhary [1977].

RESULTS & DISCUSSION

Clonal variation

The genetic variation of tamarind has been based on the phenotypic variation observed [Gunasena & Hughes 2000]. A wider variation is fundamental for the development of new varieties with good quality and higher yields [Frankel & Hawkes 1975; Holden & Williams 1984]. Although all the ramets of all thirty-five clones were planted under uniform conditions, there was highly significant difference in the growth behaviour of the clones [Table 2]. For instance, the plant height, ranged from 60.33 [CPT-22] to 115.00 cm [CPT-9] shows a variation of 91 per cent. Maximum collar diameter [1.49 cm] and volume index [245.78 cm^3] was recorded by CPT-7. CPT-5 recorded maximum for number of branches [19.78]. CPT-16 [0.91 cm] and CPT-22 [9.78, 53.36cm^3] recorded lowest for collar diameter, number of branches and volume index respectively. This indicates that, the trend of growth is not uniform for all the clones.

Genetic estimates

Though the selection of superior trees was carried out intensively and clonal superiority over seed raised plants was established [Ashok kumar 1995], genetic superiority *per se* needs to be determined. The genetic estimates can be very useful tools in predicting the amount of gain expected from clonal material in short period. The variation among clones is commonly used as an estimate of total genetic variation and to calculate the degree of genetic control for a particular trait [Foster & Shaw 1988].

The phenotypic and genotypic coefficients of variations were also close to each other for all traits, but volume index exhibited higher PCV [48.19] and GCV [42.83] than the other traits [Table 3]. The magnitude of the error variance was relatively lower than the genotypic variance for all traits except number of branches. Estimates of broad sense heritability ranged from 30.67 [number of branches] to 78.98 [volume index], genetic gain [%] ranged between 13.47 % and 78.40 % with number of branches giving the lowest value and volume index giving the highest value. The magnitude of genotypic variance was higher than the error variance in the one hand, while the phenotypic and genotypic variances were close to each other on the other hand except number of branches. It indicates that the genotypic component was the major contributor to the total

variance for these traits; i.e., most of the variability observed in the phenotype for these traits has more of a genetic than a non-genetic basis. This variability due to genotypic variance further indicates considerable scope for selection. In the present study the genotypic coefficient of variation and the genetic gain were found to be high for volume index. Higher GCV indicates that worthwhile improvement could be achieved for this trait through simple selection while higher genetic advance value suggests that population means for volume index may be changed considerably by selecting the superior 5 % of the genotypes.

Association

The ultimate goal of the tree improvement is to improve tree species for growth and yield. Since it is a complex and the end product depends on the interplay of many characters, improvement based on per se performance alone might prove to be less effective as this trait is highly complex and is dependent on many physiological and morphological attributes. This can be over come through the selection of superior genotypes for which an indirect selection is often performed. Knowledge of the association between different traits is very useful in indirect selection. Correlation and path analysis establish the extent and cause of association between growth and its attributes so that these growth components may form additional criteria for selection in breeding programme. In the present study, investigation on association of morphometric characters and volume index is elucidated.

Correlation

Correlation coefficient analysis helps to determine the nature and degree of relationship between any two measurable characters. It resolves the complex relations between important characters, which is of immense help in the selection of suitable clones. As variation among clones used for estimation of genetic variation and genetic gain, co-variance estimates between traits can be used to estimate genetic correlations between the traits [Foster 1986]. *Inter se* phenotypic and genotypic correlation coefficients were worked out for morphometric traits to determine the nature of association existing between the characters. All the morphometric traits registered positive and highly significant association with volume index at both phenotypic and genotypic level [Table 4]. Plant height expressed positively significant correlation with collar diameter [0.672] and number of branches [0.649] only at genotypic level. Collar diameter recorded positively significant correlation with number of branches [0.830] only at genotypic level. Similarly positive and significant correlation between volume and growth parameters was registered in *Acacia nilotica* [Jayaprakash 2000], Dalbergia *sissoo* [Dhillon *et al*. 1992] and *Leucaena leucocephala* [Chandrasekaran *et al*. 1985]. The present study revealed that plant height and collar diameter expressed high positive association with volume index and could serve as selection criteria.

Path analysis

The direct contribution of each component to the yield and the indirect effect it has through its association with other components cannot be differentiated from mere correlation studies. A statistical device called the path coefficient analysis developed by Wright [1921] fulfills this lacuna. Path coefficient analysis is further helpful in knowing the relative contribution of different traits to the trait of major interests. The genotypic correlation coefficients of morphometric traits with volume index were partitioned into direct and indirect effects by path coefficient analysis. Path analysis using morphometric traits revealed that, collar diameter [0.594] followed by height [0.450] expressed maximum direct positive effect on volume index and number of branches contributed indirectly through height and collar diameter [Table 5]. Diameter was relatively more reliable component as in mathematical terms, as a 10 percent increase in diameter will give approximately 20 percent increase in basal area and hence in volume [Lauridsen *et al*. 1987; Goel *et al*. 1997]. Collar diameter had a maximum direct effect indicating a better scope for improvement of volume by selecting this trait. Positive direct effects of collar diameter on volume was also reported by Rathinam *et al*. [1982] in *Eucalyptus tereticornis*, Patil *et al*. [1997], Venkataramanan [1996], Arun Prasad [1996] in teak and Jayaprakash [2000] in *Acacia nilotica* reported same findings. Morphometric trait like plant height expressed maximum positive indirect effect through number of branches and number of branches via collar diameter. The results are in conformation with the studies in kapok [Rajendran 2001].

Divergence studies

Genetic diversity in plant species is a gift to mankind as it forms the basis for selection and further improvement. Determining the level of genetic diversity among the collected germplasm would indicate the potentiality for maximising the

yield. In the present investigation, attempts were made to assess the genetic diversity among the thirty-five candidate plus trees using Mahalanobis D^2 analysis. Morphometric traits had been utilized to assess the relationship among germplasm and cultivars before [Sorvells 1991; Cross 1994]. The information on the genetic structure and relationship of these populations provide a basis for planning and conducting future collections and efficient utilization of them as genetic resources [Tsegaye *et al*. 1996].

Application of MAHALANOBIS D^2 analysis and TOCHER's clustering methods resolved thirty-five genotypes under investigation into 6 clusters, indicating wide diversity [Table 6]. The maximum number of genotypes [17] was included in cluster-VI followed by cluster-I with 8 genotypes. The cluster-V contained four genotypes. Cluster II, III, and IV had two genotypes each. The clustering pattern proved that geographical diversity need not necessarily be related to genetic diversity. This kind of genetic diversity might be due to differential adoption, selection criteria, selection pressure and environment [Vivekananda & Subramanian 1993]. This indicated that genetic drift produce greater diversity than the geographic diversity [Singh et al. 1996]. Absence of any relationship between genetic diversity and geographical distribution is in accordance with the findings of Kaushik *et al*. 2007 and Gohil & Pandya 2008 in *Jatropha curcas*; *Madhuca latifolia* [Divakara & Krishnamurthy 2009]. Similar results had earlier been reported by Hanamashetti [1996] in tamarind pod characters by using Mahalanobis D^2 technique. The divergence within the cluster indicates the divergence among the genotypes in the same cluster. On the other hand, inter-cluster divergence suggests the distance [divergence] between the genotypes of different clusters [Table 7]. The tendency of genotypes from diverse eco-geographic regions to group together in the same cluster or scattered distributions of genotypes of same geographic origin in different clusters have been observed in the present study. Cluster I contained eight genotypes and showed maximum intra cluster distance [2.74] closely followed by cluster-VI [2.73, Table 7] because the genotypes used for breeding program were from different locations. Thus these genotypes in cluster I and VI were most heterogeneous and can be best used for within group hybridization. The highest inter-cluster distance [Table 7] was found between cluster III and V [7.63] followed by II and V [7.45] suggesting wide diversity between these groups. Cluster means indicated a wide range of variation for all the morphometric traits [Table 8]. Cluster V recorded maximum for all traits, hence these genotypes can be directly selected and utilized for breeding program. The contribution of individual characters to the diversity has been worked. The trait volume index contributed maximally genetic diversity as per cent contribution and rank total, 34.96 and 208 respectively. The character contributing maximum diversity can be given more emphasis for the purpose of fixing priority of parents in hybridization program. It is also suggested that for creating variability and developing the best selection a large number of divergent lines, instead of few should be used in the hybridization.

CONCLUSION

All thirty-five clones expressed significant variation for all the growth characters under field condition. Genetic estimates revealed the presence of variability in the phenotype for all growth traits except number of branches has more of genetic contribution than non-genetic contribution. Trait volume index having higher GCV, heritability and genetic gain could be worthwhile improving through selecting 5 % of the genotypes. Since height and collar diameter is having maximum direct positive effect on volume index, improvement in these traits will automatically take care of improvement in volume index. Genetic diversity studies indicated the presence of high diversity among the selected genotypes by resolving the whole genotypes into 6 clusters. Cluster I and cluster-VI showed maximum intra cluster distance can be best used for within group hybridization. Since cluster V is having maximum mean values for all morphometric traits, can be directly selected and utilized for breeding program to cope up the fore coming food crisis.

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Table 1. Locational and morphological details of *T. indica* candidate plus trees (CPTs)

CPTs	State	Division	Location	Age in years	Height (m)	GBH (cm)	Pod yield (kgs)	Crown area (m^2)	Pod size
CPT - 1	Karnataka	Bangalore	Mallarpatna	90	10.0	4.71	750	527.07	Big
CPT - 2	"	"	Dabguli	50	14.0	2.73	300	132.79	Big
CPT - 3	"	"	Anahosalli	100	9.0	5.25	400	555.94	Big
CPT - 4	"	"	Sulikera	60	12.0	2.57	450	250.35	Big
CPT - 5	"	"	Siddhadavarbetta	90	17.0	2.34	500	328.59	Medium
CPT - 6	"	"	Mathikare	30	9.5	2.05	600	169.79	Big
CPT - 7	"	"	Guttipura	10	4.5	1.15	35	30.69	Medium
CPT - 8	"	"	Guttipura	12	4.0	1.65	50	15.91	Medium
CPT - 9	"	"	Nandhgudi	09	9.5	2.13	100	103.91	Very big
CPT - 10	"	"	Tathnur	60	19.0	3.75	150	135.87	Big
CPT - 11	Andhra Pradesh	Ananthpur	Gudibanda	80	20.0	3.41	900	346.5	Big
CPT - 12	"	Chitroor west	Charala	60	15.0	2.40	700	154.00	Medium
CPT - 13	"	"	Chukkavaripalli	200	9.5	5.50	600	366.58	Big
CPT - 14	"	"	Thuppireddypalli	150	34.0	4.80	1000	463.96	Medium
CPT - 15	"	"	Pudipatla	100	32.0	5.10	600	320.60	Medium
CPT - 16	"	"	Kuppanapalli	150	15.0	3.70	850	602.87	Medium
CPT - 17	"	"	Kurapalli	60	17.0	2.10	750	152.90	Very Big
CPT - 18	"	"	Mirjepalli	130	23.0	3.30	1200	344.85	Medium
CPT - 19	"	"	Gollapalli	150	30.0	3.60	1000	361.51	Big
CPT - 20	"	"	Vanaganipalli	100	20.0	2.40	800	113.14	Big
CPT - 21	Tamil Nadu	Thani	Periakulam (Endapalli)	150	19.0	5.57	236	180.34	Big
CPT - 22	"	Dharmapuri	Urigum	150	19.0	5.57	400	616.00	Very Big
CPT - 23	"	Coimbatore	Pollachi	60	8.0	2.70	350	148.55	Big
CPT - 24	"	Salem	Kavarkalpatti	65	21.0	2.95	250	388.98	Medium
CPT - 25	"	Salem	Salem	35	12.0	2.27	200	133.81	Big
CPT - 26	"	Erode	Mallankuli	70	15.0	2.10	300	103.91	Medium
CPT - 27	"	Erode	Hassanur	65	13.0	2.30	400	105.73	Big
CPT - 28	"	Coimbatore	Mettupalayam	45	13.0	3.73	700	103.01	Big
CPT - 29	"	Erode	Pulinjur	62	23.5	2.40	400	330.20	Medium
CPT - 30	"	Dharmapuri	Harur	40	18.0	3.32	400	127.73	Big
CPT - 31	"	Dharmapuri	Bommidi	45	13.0	4.52	350	132.79	Big
CPT - 32	"	Thani	Jayamangalam	25	15.0	1.78	200	117.91	Medium
CPT - 33	Karnataka	Dharwad	Yellapur	30	12.0	3.45	200	167.48	Big
CPT - 34	Tamil Nadu	North Arcot	Vellore	70	10.0	2.60	600	86.63	Medium
CPT - 35	"	North Arcot	Reddiyur	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)

Table 2. Mean performance of tamarind clones under field conditions

Genotypes	Height (cm)	Collar Diameter (cm)	Number of branches	Volume index (cm^3)
CPT - 1	$74.89^{fghijkl}$	1.38^{ab}	11.89^{cd}	143.11^{b}
CPT - 2	69.89^{ijkl}	1.14^{cdefgh}	12.22^{cd}	$91.70^{cdefghi}$
CPT - 3	66.67^{ijkl}	1.38^{ab}	12.67^{bcd}	128.19^{bcd}
CPT - 4	73.00^{ghijkl}	1.18^{cde}	11.55^{cd}	$104.30^{bcdefgh}$
CPT - 5	79.44^{defghi}	1.29^{bc}	19.78^{a}	131.66^{bc}
CPT - 6	89.61^{cdef}	1.24^{bcd}	14.56^{bc}	137.33^{bc}
CPT - 7	107.00^{ab}	1.49^{a}	17.00^{ab}	245.78^{a}
CPT - 8	107.66^{ab}	1.43^{ab}	15.22^{bc}	220.16^{a}
CPT - 9	115.00^{a}	1.39^{ab}	15.45^{bc}	221.98^{a}
CPT - 10	110.44^{ab}	1.39^{ab}	14.78^{bc}	213.39^{a}
CPT - 11	86.00^{cdefg}	$1.11^{cdefghi}$	12.00^{cd}	107.61^{bcdefg}
CPT - 12	$76.56^{efghijk}$	0.95^{ghi}	11.78^{cd}	73.64^{efghi}
CPT - 13	73.11^{ghijkl}	$1.12^{cdefghi}$	13.34^{bcd}	$92.99^{cdefghi}$
CPT - 14	$76.45^{efghijk}$	1.07^{defghi}	13.11^{bcd}	$103.47^{bcdefgh}$
CPT - 15	77.11^{efghij}	$1.09^{cdefghi}$	11.00^{cd}	$93.61^{cdefghi}$
CPT - 16	73.33^{ghijkl}	0.91^{i}	12.78^{bcd}	61.33^{ghi}
CPT - 17	66.55^{ijkl}	1.08^{defghi}	13.33^{bcd}	80.37^{defghi}
CPT - 18	75.33^{fghijk}	1.00^{efghi}	13.33^{bcd}	76.21^{efghi}
CPT - 19	70.56^{hijkl}	0.92^{i}	13.00^{bcd}	60.01^{ghi}
CPT - 20	85.00^{cdefgh}	0.94^{ghi}	11.11^{cd}	75.24^{efghi}
CPT - 21	92.67^{cd}	$1.10^{cdefghi}$	11.67^{cd}	114.52^{bcde}
CPT - 22	60.33^{l}	0.93^{hi}	9.78^{d}	53.36^{i}
CPT - 23	70.22^{ijkl}	0.96^{fghi}	10.89^{cd}	65.97^{fghi}
CPT - 24	89.67^{cdef}	1.17^{cdef}	11.55^{cd}	125.01^{bcd}
CPT - 25	87.33^{cdefg}	1.14^{cdefgh}	13.33^{bcd}	114.91^{bcde}
CPT - 26	90.56^{cde}	1.05^{defghi}	13.67^{bcd}	$100.00^{bcdefghi}$
CPT - 27	99.11^{bc}	1.06^{defghi}	11.11^{cd}	113.53^{bcdef}
CPT - 28	89.11^{cdef}	1.02^{efghi}	12.33^{cd}	$93.67^{cdefghi}$
CPT - 29	68.00^{ijkl}	1.15^{cdefg}	11.33^{cd}	$90.90^{cdefghi}$
CPT - 30	65.11^{ijkl}	1.04^{defghi}	12.78^{bcd}	72.97^{efghi}
CPT - 31	86.00^{cdefg}	1.17^{cdef}	14.00^{bcd}	120.51^{bcde}
CPT - 32	68.78^{ijkl}	1.01^{efghi}	9.78^{d}	72.46^{efghi}
CPT - 33	62.11^{kl}	0.92^{i}	11.56^{cd}	57.03^{hi}
CPT - 34	63.66^{jkl}	0.96^{fghi}	10.89^{cd}	59.16^{hi}
CPT - 35	87.78^{cdefg}	1.14^{cdefgh}	13.89^{bcd}	113.40^{bcdef}
MEAN	**80.97**	**1.12**	**12.81**	**109.42**
SEM	**6.14**	**0.09**	**1.86**	**19.74**
CD (0.05)	**12.26**	**0.17**	**3.71**	**39.39**

Trait means not followed by the same superscript letter and significantly different at p = 0.05.

Table 3. Genetic estimates of morphometric traits in *T. indica*

Characters	Variation (%)			Coefficient of variation (%)					
	Genotypic	Phenotypic	Environmental	Genotypic	Phenotypic	Environmental	Heritability (%)	Genetic advance	Genetic gain (%)
Height	188.86	245.46	56.60	16.97	19.35	9.29	76.94	24.84	30.67
Collar Diameter	0.02	0.03	0.01	13.38	16.40	9.48	66.57	0.25	22.50
Number of branches	2.29	7.47	5.18	11.81	21.32	17.76	30.67	1.72	13.47
Volume	2195.64	2780.09	584.45	42.83	48.19	22.10	78.98	85.86	78.40

Table 4. Genotypic and phenotypic correlation coefficient matrix of morphometric traits

Characters		Collar Diameter	Number of branches	Volume index
Height	G	0.672**	0.649**	0.874**
	P	0.496	0.391	0.775**
Collar Diameter	G	1.000	0.830**	0.928**
	P	1.000	0.451	0.905**
Number of branches	G		1.000	0.822**
	P		1.000	0.504**

*significant at p = 0.05, **significant at p = 0.01

Table 5. Path analysis of *T. indica* for morphometric traits with volume index

Characters	Height	Collar Diameter	Number of branches	r-value
Height	0.450	0.399	0.025	0.874
Collar Diameter	0.303	0.594	0.031	0.928
Number of branches	0.292	0.493	0.038	0.822

Residual = 0.1584606

Table 6. Clustering of *T. indica* genotypes using Tocher's method.

Clusters	Number of accessions	Accessions (CPTs)
I	8	CPT-1, CPT-2, CPT-3, CPT-4, CPT-5, CPT-6, CPT-25, CPT-35.
II	2	CPT-19, CPT-16.
III	2	CPT-17, CPT-30.
IV	2	CPT-26, CPT-28.
V	4	CPT-7, CPT-8, CPT-9, CPT-10
VI	17	CPT-11, CPT-12, CPT-13, CPT-14, CPT-15, CPT-18, CPT-20, CPT-21, CPT-22, CPT-23, CPT-24, CPT-27, CPT-29, CPT-31, CPT-32, CPT-33, CPT-34.

Table 7. Average intra and inter-cluster distance and D^2 values*

Clusters	I	II	III	IV	V	VI
I	**2.74**	3.87	3.05	3.14	6.54	3.43
	(7.52)	(14.94)	(9.27)	(9.86)	(42.73)	(11.79)
II		**0.42**	1.81	2.86	7.45	2.48
		(0.18)	(3.26)	(8.18)	(55.57)	(6.15)
III			**0.64**	3.33	7.63	2.61
			(0.41)	(11.08)	(58.161)	(6.83)
IV				**0.68**	6.04	2.68
				(0.47)	(36.48)	(7.21)
V					**1.88**	6.74
					(3.52)	(45.44)
VI						**2.73**
						(7.45)

*Figures given in the parenthesis are D^2 values.

Table 8. Cluster wise mean values of four morphological traits in *T. indica*

Traits\Clusters	I	II	III	IV	V	VI	Percent contribution
Height	78.58	71.95	65.83	89.83	110.03	77.07	26.89
Collar Diameter	1.24	0.92	1.06	1.03	1.43	1.04	25.38
Number of branches	13.74	12.89	13.06	13.00	15.61	11.66	12.77
Volume	120.58	60.67	76.67	96.84	225.33	87.96	34.96