The Pharma Innovation Journal 2023; 12(5): 1921-1926

www.ThePharmaJournal.com

The Pharma Innovation

ISSN (E): 2277-7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2023; 12(5): 1921-1926

www.thepharmajournal.com
Received: 01-02-2023
Accepted: 05-03-2023

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Genetic diversity in tamarind (*Tamarindus indica* L.)

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Abstract
An experiment on genetic diversity in tamarind (*Tamarindus indica* L.) was conducted at Horticultural College and Research Institute, Periyakulam, Tamil Nadu. The objective was to examine the genetic relatedness and genetic diversity among 31 tamarind genotypes. Significant differences were recorded among the 31 tamarind genotypes with regard to different morphological characters. Thirty one genotypes of tamarind were grouped into eight clusters by following the Tocher's method of clustering analysis utilizing data on a set of eleven traits related to yield, vegetative characters and quality characters. TI-23 (cluster VIII) and TI-12 (VII) formed individual clusters and had the maximum genetic divergence. Whereas Cluster II had the maximum of nine genotypes grouped together while cluster I had the seven genotypes and cluster IV had five genotypes. The intra and inter cluster genetic distance values ranged from 9.205 (cluster V) to 16.039 (cluster I). The maximum inter cluster distance was observed between cluster III (9.770) and cluster VIII (32.285). Cluster VII (550.33) showed the highest mean performance among 31 tamarind genotypes in five out of seven traits followed by cluster V and cluster II. Contribution of individual characters towards divergence recorded that maximum contribution to total divergence was recorded in acidity and number of fruits per tree; whereas the lowest contribution noticed in the traits such as tree circumference, fibre weight, pulp weight, pod width, pod length and tree height. The highest frequency was recorded on acidity, number of fruits per tree, fruit weight and shell weight. The lowest frequency exhibited in tree height, pod length, pod width, tree circumference, number of seeds per pod and fibre weight.

Keywords: Tamarind, genotypes, D^2 analysis, genetic divergence, yield per plant

Introduction
Tamarind (*Tamarindus indica* L) is a monotypic genus tree belonging to the family Leguminosae, sub family Leguminosae with somatic chromosome number of 2n=24 (Purseglove, 1997) [10]. It is indigenous to tropical Africa and Southern India (Nas, 1979) [8]. Tamarind also called as 'Indian date', a multipurpose tree known for drought tolerance and used primarily for its fruits, which are eaten fresh or processed, used as a seasoning or spice, or the fruits and seeds are processed for non-food uses. Tamarind fruit pulp is a main ingredient of many South Indian dishes preparations *viz.,* sambar, curries, chutney, jam, jelly and confectionary industries. It is widely distributed throughout tropic and sub tropics as stray plantation or avenue. In India, it is largely cultivated in Madhya Pradesh, Andhra Pradesh, Maharashtra, Tamil Nadu and Karnataka. In Tamil Nadu, tamarind is extensively cultivated in Theni, Madurai, Dindigul, Salem, Ramanathapuram, Sivagangai, Virudhunagar, Dharmapuri, Krishnagiri, Coimbatore, Tuticorin and Vellore districts. Tamarinds are highly suitable for wastelands, saline and alkaline soil and also act as a good wind break. The species has a wide geographical distribution in the subtropics and semi arid tropics and is cultivated in numerous regions. It is mostly self sown or sown with seeds of unknown parentage, which result in wide variation among seedling progenies. Owing to its wide geographical distribution and adaptability to different agro climatic zones, large genetic diversity is present in the seedling population. Due to cross pollination and predomination of seed propagation over large periods of time, it gives immense opportunity to locate elite trees having desirable horticultural traits. With the increasing population pressure, the demand for tamarind pulp has increased considerably. This has necessitated identifying superior elite trees like genotypes for monoculture plantations, without causing genetic erosion. Thus tree improvement through the application of genetic principles is basically directed towards modifying the heredity of tree populations to meet the needs of the farmers. Morphological characterization has been the major tool for classifying tamarind genotypes into different genomic groups. The use of Mahalanobis D^2 statistics is one of the tools for assessment of genetic diversity in tamarind as well as many crops.

The information about the extent of genetic divergence is critical for the improvement programme of any crop. Variability and genetic divergence studies on various crops already done by many researchers *viz.,* Algabal *et al.* (2011) [1], Divakara *et al.* (2012) [3], Gangaprasad *et al.* (2013) [4] in tamarind, Valsalakumari *et al.* (1985) [15], Rajamanickam and Rajmohan (2012) [13] in banana, Balasubramanian *et al.* (2008) [2] in mango, Rai and Mishra, (2005) [11] in bael. The present experiment on studies on genetic diversity in tamarind (*Tamarindus indica* L.) was conducted at Horticultural College and Research Institute, Periyakulam, Tamil Nadu.

Materials and methods

The field experiment was conducted at Horticultural College and Research Institute, Periyakulam. Thirty one tamarind genotypes were used for this study. This experiment was laid out in Randomized Block Design (RBD) as per the method was suggested by Panse and Sukhatme (1967) [9].

Data analysis

Statistically analysis for the morphological data was conducted using the software programme NTSYS pc version 2.02e (Rohlf, 1998). The data collected on various morphological traits varied with the unit of measurement; hence the means of morphological observations were standardized prior to cluster analysis by dividing these with standard deviation and subtracting the means from each trait. The matrix of average taxonomic distances (Σij) for individuals i and j and morphological traits was then computed using SIMINIT function and EUCLIDIAN distance coefficient.

Where

$\Sigma ij = (\Sigma k\ (n-1)\ (Xki - Xkj)2)$,

Where 'n' is number of genotypes (here n=12) Xki and Xkj are the mean values of ith and jth individual for the trait 'K'. This dissimilarity coefficient is based on interval measure data collected for the morphological traits. Cluster analysis was then conducted on the taxonomic distance matrix with the Un-Weighted Pair Group Method based on Arithmetic Average (UPGMA) and a dendrogram was generated based on the genetic distance matrix.

D^2 analysis

D^2 statistics, a measure for a group distance based on multiple characters as proposed by Mahalanobis (1936) [6]. Grouping of variance was done by Tocher's method (Rao, 1952) [14]. The relative contribution of characters to divergence at the cluster levels as well as the genotypes level was assessed the basis of the coefficients of variation of the individual traits. Average intraclones distances were calculated using the following formula

The D^2 is defined as

$$D^2 = di2 = \sum_{i=1}^{k} (Yi1 - Yim)2,\ (1 \pm m)$$

Where Yi1 and Yim are the uncorrelated means of the 1th and mth clones for the ith character. Σ Di2/n where Di2 is the sum of distance between possible combinations (n) of the populations included in the cluster.

Results and Discussion

Average inter-cluster distances were calculated by taking each cluster and their distances from the other cluster. The cluster diagram was drawn with the help of D values showing relationships within and between clusters. (Fig 1). Cluster analysis was conducted on average taxonomic distances with UPGMA (Un-weighted Pair Group Method Based on Arithmetic Average) as well as the dendrogram was constructed (Fig. 1). From the dendrogram, at a distance of 2.82 TI-23 and TI-13 have formed single cluster and there was no difference between two clusters at this distance. At a distance of 11.29, all the thirty one tamarind genotypes formed single group. At a distance of 8.0, thirty one tamarind genotypes formed two different groups. At a distance of 4.20, seven different groups were formed. At a distance of 6.0, there were five different groups were formed. At a distance of 9.5, all the tamarind genotypes came under single group and exception being TI-23 and TI-12 came under single stands and got the highest genetic divergence. This might be due to this genotype recorded the highest pod yield, fruit length, fruit weigh and tree spreading as well as collected from Lower Camp of cumbum. Another genotype TI-12 collected from near Endapuli and having a higher pulp weight to seed weight ratio collected through grafting technique.

In the principle component analysis (Fig. 2), 31 genotypes were grouped into four clusters of which five genotypes in cluster 1 and 7 genotypes comes under cluster II, 14 genotypes in cluster III and five genotypes in cluster IV. The results of clustering pattern showed that the clones collected from different locations were not necessarily grouped into different clusters. Grouping of genotypes in clustering is based on the qualitative and quantitative characters. The identified plus trees having a higher pulp weight to seed weight ratio can thus be suggested for clonal propagation. 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.

The analysis of variance showed highly significant differences among the genotypes. All the 31 genotypes grouped into eight clusters formed and presented in Table 2. The clusters based on the 11 qualitative and quantitative traits were studied. The clustering pattern not influenced by genomic constitution. In cluster 1 contains seven genotypes *viz.,* TI -1, TI-2, TI-3, TI-4, TI-5, TI-30, TI-31. In cluster 2 contains nine genotypes of which TI -6 TI-7, TI-8, TI-9, TI-10, TI-11, TI-24, TI-13, TI-29. Cluster 3 contains four genotypes such as TI -14, TI-15, TI-18, TI-22 and cluster 4 contains five genotypes (TI -16, TI-17, TI-19, TI-27, TI-28). The cluster 7 (TI – 23) and cluster 8 (TI – 12) were formed individual cluster, whereas cluster 5 (TI-25, TI-26) and cluster 6 (TI-20, TI-21) contains two genotypes respectively. Genotype TI-23 and TI-12 stands separate cluster and this may be due to the highest number of pod yield per plant, pod length and individual pod weight as well as tree height, tree vigour, tree spreading (both direction) also recorded the highest values in the morphological characters. These characters made it to occupy a separate cluster with single genotype. Algabal *et al.,* (2011) [1] stated that four tamarind genotypes (BT2, BT3, BT4, and PG1) of minor cluster showed orthotropic growth, semi-curved fruit shape and pulp

color was light to dark brown. However, five genotypes (H4, H5, PKM1, BT2 and BT1) of the 'A2b' cluster, showed plageotropic growth, curved fruits and dark green leaves, except for PKM-1 with orthotropic growth. Rajamanickam and Rajmohan, (2012) [13] reported that two genotypes formed individual clusters among 28 bananas. Similar results were also reported by Kumar *et al.,* (2015) [5] in tamarind.

Inter and intra cluster distances among the eight clusters of 31 tamarind genotypes are presented in Table 3. The intercluster D values expressed as the diversification among the groups of genotypes resembling each other based on eleven characters under this study, whereas, intracluster D values were expressed as the magnitude of divergence between genotypes within the cluster. The intra cluster genetic distance, D values ranged from 9.205 (cluster V) to 16.039 (cluster I) indicating wide divergence. The maximum inter cluster distance was observed between cluster VI and cluster VII (45.583), followed by cluster VII and cluster VIII (32.285) while minimum inter cluster distance D (9.770) was between cluster III and cluster VIII. Intercluster distances and their mutual relationship have been depicted in Fig. 3. The intercluster distance was higher than the intracluster distances in all the cases indicating more divergence of genotypes between the clusters. The similar relationships were also observed by Divakara *et al.,* (2012) [3], Kumar *et al.,* (2015) [5] in tamarind, Mercy and George, (1987) [7] and Rajamanickam and Rajmohan, (2010) [12] in banana, Balasubramanyan *et al.,* (2009) [2] in mango. Mean values for eleven characters in various clusters are depicted in Table. 4 and provided an interesting picture of the nature of diversity. Considerable differences in cluster mean values were evident for all the characters. Cluster VII showed the maximum mean performance among the 31 tamarind genotypes followed by cluster V and cluster II in five out of eleven characters studied *viz.,* tree height, pod length, fruit weight, number of fruits per plant and acidity.

Contributions of individual character towards divergence are depicted in Table 5. The present study revealed that the maximum contribution to total differences was recorded in acidity (231 %), number of fruits per tree (173 %), fruit weight (34 %) and shell weight (14 %) whereas, the lowest frequency was noticed in tree height, pod length, pod width, tree circumference, number of seeds per pod and fibre weight. The contribution recorded the highest in acidity (15.48) and number of fruits per tree (13.69). The lowest contribution exhibited in tree circumference, fibre weight, pulp weight, pod width, pod length and tree height. This result might be due to genotypes having desirable characters such as yield, pod length, pod weight, salinity tolerance and high intercluster distance would result in highly segregating generation in breeding programmes. Hence, it was concluded from the present study that TI-23 and TI-12 recorded the highest yield per plant, pod length and pod weight and formed separate cluster and stand single in the cluster diagram.

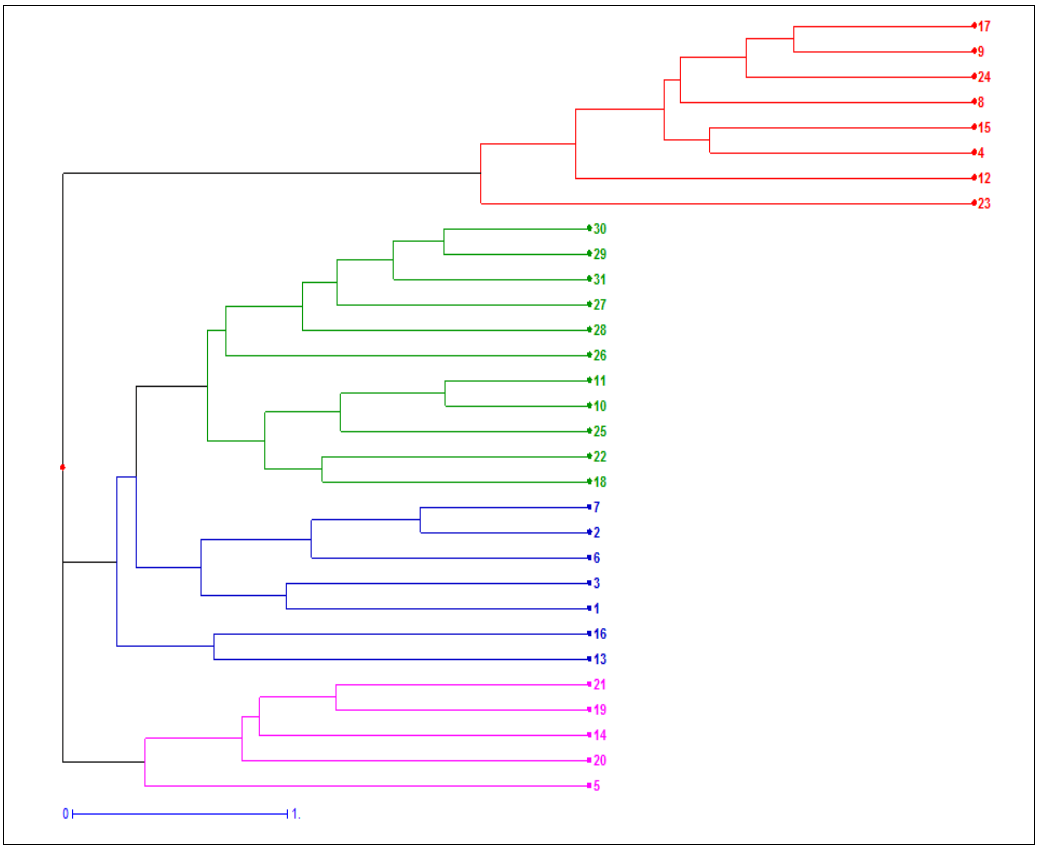

Fig 1: Dendrogram clustering based on similarity co-efficient among 31 tamarind genotypes using morphological markers

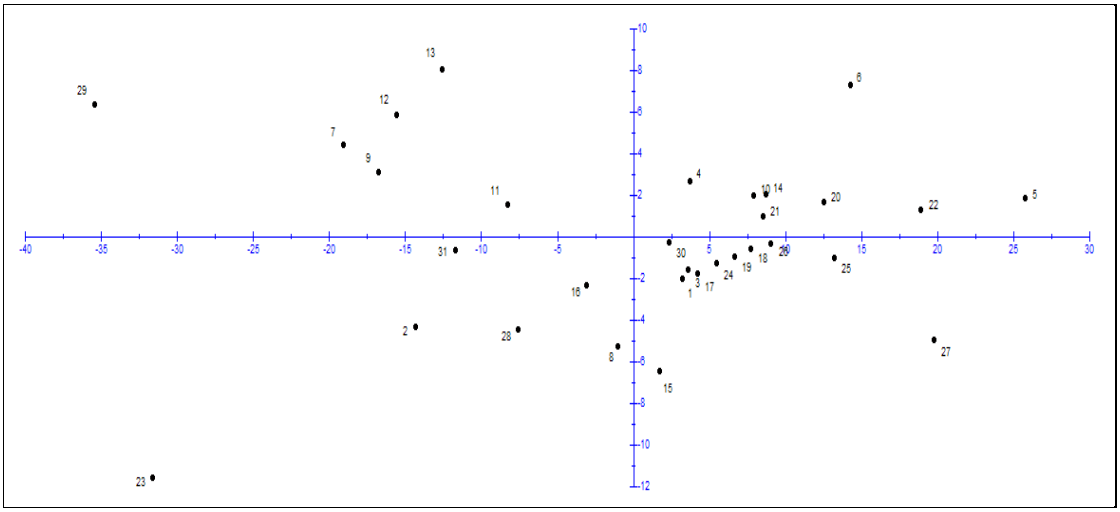

Fig 2: Principle component analysis of grouping of 31 tamarind genotypes

Table 1: Tamarind collections from Tamil Nadu

Treatments	Place of collection
TI-1	Jayamangalam, Periyakulam
TI -2	Kullapuram, Periyakulam
TI -3	Vaigaidam, Aundipatti
TI -4	Vettaikaranputhur, Pollachi
TI -5	Sethumadai, Pollachi
TI -6	Rajapalayam
TI -7	Vemparpatti, Natham
TI -8	Kanniyapuram, Natham
TI -9	Parali, Natham
TI -10	Velampatti, Natham
TI -11	Ganesapuram, Kandamanur
TI -12	Endapuli, Periyakulam
TI -13	Puthupatti, Periyakulam
TI -14	Kumbakarai, Periyakulam
TI -15	Genguvarpatti
TI -16	Senthurai, Dindigul
TI -17	Tamaraipadi, Dindigul
TI -18	Kottampatti, Madurai
TI -19	Podinayakkanur
TI -20	Chinnamanur
TI -21	Chothuparai dam, Periyakulam
TI -22	Gudalur
TI -23	Lowercamp, Cumbum
TI -24	Tamaraikulam, Gudalur
TI -25	Kombai, Theni
TI -26	Cumbum mettu
TI -27	Vettikadu, Cumbum
TI -28	Puthukulam, Cumbum
TI -29	Ekaluthu road, Cumbum Reserve Forest
TI -30	Kailasapatti, Periyakulam
TI -31	Eriyodu, Dindigul

Table 2: Group constellations of 31 tamarind genotypes on similarity index for morphological traits

Cluster	No. of genotypes	Genotypes
C_1	7	TI -1, TI-2, TI-3, TI-4, TI-5, TI-30, TI-31
C_2	9	TI -6 TI-7, TI-8, TI-9, TI-10, TI-11, TI-24, TI-13, TI-29
C_3	4	TI -14, TI-15, TI-18, TI-22
C_4	5	TI -16, TI-17, TI-19, TI-27, TI-28
C_5	2	TI-25, TI-26
C_6	2	TI-20, TI-21
C7	1	TI-23
C8	1	TI-12

Table 3: Estimation of average intra and inter cluster distance for eight clusters constructed from 31 tamarind genotypes

	Cluster Number							
	C_1	**C_2**	**C_3**	**C_4**	**C_5**	**C_6**	**C_7**	**C_8**
C_1	16.039	20.028	14.714	17.362	20.517	19.982	31.697	12.198
C_2		14.715	23.155	13.416	12.563	31.044	20.983	20.817
C_3			12.992	20.237	24.481	15.131	15.666	9.770
C_4				12.799	11.837	27.600	23.600	17.859
C_5					9.205	31.703	20.927	22.205
C_6						13.976	45.583	15.775
C_7							0.000	32.285
C_8								0.000

Bold figures in diagonals are the intra-cluster distances

Table 4: Character means in different clusters of tamarind genotypes

S.No.	Characters	I	II	III	IV	V	VI	VII	VIII
1.	Tree height (m)	16.239	14.896	14.127	13.086	12.915	13.030	19.230	12.430
2.	Pod length (cm)	14.016	14.199	13.927	14.312	14.565	13.880	18.230	16.800
3.	Pod width (cm)	3.467	3.862	3.740	3.714	3.035	3.215	4.670	4.400
4.	Tree circumference (cm)	7.029	7.638	7.610	7.248	6.715	6.520	9.230	7.870
5.	Shell weight (g)	5.107	4.498	4.698	3.938	4.900	4.305	7.340	6.410
6.	Fibre weight (g)	0.911	1.003	0.591	1.112	1.280	0.325	1.670	0.840
7.	Pulp weight (g)	7.521	7.761	6.310	9.306	7.245	4.200	11.180	9.270
8.	No. of seeds per pod	7.281	8.206	8.329	7.822	8.330	6.170	10.670	7.330
9.	Fruit weight (g)	23.223	29.957	24.833	25.434	23.850	12.620	50.880	23.800
10.	No. of fruits per tree	279.333	411.59	222.00	369.93	422.50	134.165	550.33	258.67
11.	Acidity (%)	10.329	12.334	11.890	11.534	13.740	12.045	14.880	10.580

Table 5: Contribution of various characteristics to divergence

Sl. No.	Characters	Frequency %	Contribution
1.	Tree height (m)	0	2.98
2.	Pod length (cm)	1	1.19
3.	Pod width (cm)	0	1.19
4.	Tree circumference (cm)	0	0.60
5.	Shell weight (g)	14	2.38
6.	Fibre weight (g)	9	1.19
7.	Pulp weight (g)	2	1.79
8.	No. of seeds per pod	1	6.55
9.	Fruit weight (g)	34	7.74
10.	No. of fruits per tree	173	13.69
11.	Acidity (%)	231	15.48

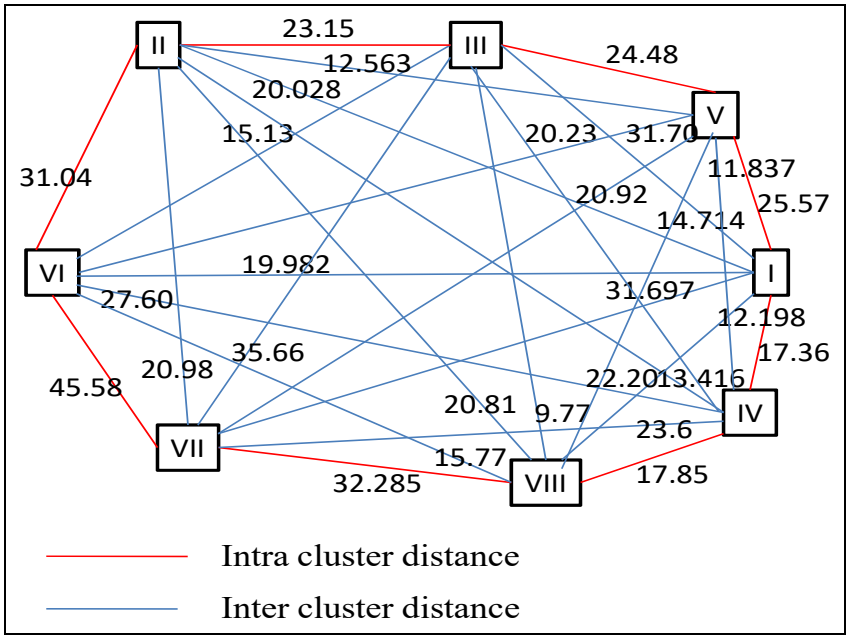

Fig 3: D^2 diagram of grouping of tamarind genotypes

Acknowledgements
The authors gratefully acknowledge Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu for providing funds and facilities to carry out the research work.

References

1. Algabal AQAY, Papanna N, Simon L. Amplified Fragment Length Polymorphism marker based genetic diversity in tamarind (*Tamarindus indica* L.). International Journal of Fruit Science. 2011;11:1-16.
2. Balasubramanyan S, Manivannan MI, Vani V, Saraswathy S, Rajamanickam C. Genetic divergence in mango. Research paper presented in National Seminar on Production, postharvest technology and marketing of mango organized by Department of Fruit Science, Horticultural College and Research Institute, TNAU, Periyakulam, Tamil Nadu, India; c2009.
3. Divakara BN. Variation and character association for various pod traits in *Tamarindus indica* L. Indian Forester. 2008;15(2):687-695.
4. Gangaprasad S, Rajkumar R, Ravikumar L, Savitha MH, Krishnamurthy K, Hittalamani S. Genetic diversity analysis in tamarind (*Tamarindus indica* L.). Journal of Spices and Aromatic Crops. 2013;22(1):55-61.
5. Kumar M, Ponnuswami V, Rajamanickam C, Preethi TL. Assessment of genetic diversity in tamarind (*Tamarindus indica* L.) using random amplified polymorphic DNA markers. SAARC J. Agriculture. 2015;13(1):27-36.
6. Mahalanobis PC. On the generalized distance in statistics. Proc. Nat. Acad. Sci. India, 1936;2:49-55.
7. Mercy KA, George KC. Genetic divergence in culinary varieties of banana. Agric. Res. J Kerala. 1987;25:11-16.
8. Nas S. In: Tropical Legumes: Resources for the future, Washington DC, 1979, 117-121.
9. Panse VG, Sukhatme PV. Statistical Methods for Agricultural Workers. 2nd Edition. Indian Council of Agricultural Research, New Delhi; c1967.
10. Purseglove JW. Tropical Crops. Dicotyledons. Longman Science and Technology; c1997. p. 204-206.
11. Rai D, Mishra KK. Studies on genetic divergence in bael (*Aegle marmelos* Correa.). Ind. J Horticulture. 2005;62:152-154.
12. Rajamanickam C, Rajmohan K. Genetic diversity in banana (*Musa* spp.). Madras Agric J. 2010;97(4-6):106-109.
13. Rajamanickam C, Rajmohan K. Diversity studies in ecotypes of banana (*Musa* spp.) using molecular markers and D^2 analysis. J Hort. Sci. 2012;7(1):34-40.
14. Rao CR. Advanced statistical methods in biometrical research. John Wiley and Sons, New York; c1952.
15. Valsalakumari PK, Nair PCS, Prabhakaran PV. Genetic divergence in banana. Agril. Res. J Kerala. 1985;22:146-149.