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Multivariate Diversity Analysis of Tamarind (*Tamarindus indica* L.) Genotypes Arid Condition of Western Maharashtra

Rajender Kumar, P.D. Dalve, A.L. Palande and S.M. Choudhary

Department of Horticulture, Post Graduate Institute, Mahatma Phule Krishi Vidyapeeth, Rahuri-413 722, India
E-mail: rajender.horti@gmail.com

Abstract: To estimate the variability among tamarind genotypes for different tree growth, flowering and fruiting parameters and to identify the potential genotypes with promising attributes, the present investigation was carried out under the arid conditions of Nashik Division of Western Maharashtra. All the reddish-brown pulp genotypes indicated reddish-brown flush colour and most of the brown pulp genotypes for the green colour flush. Most precocious flowering was in the genotype RHRTG 1 and RHRTG 9 and the most late in RHRTG 7. Minimum numbers of days taken to ripening were noted in RHRTG 13 (240 days) and RHRTG 16 (245 days), while the genotype RHRTG 1 (258 days), RHRTG 5 (258 days) and RHRTG 4 (260 days) obtained the maximum days. The major contributing trait for the diversity in the principal component one (PC1) was pulp per cent (0.333) followed by pulp weight (0.302) and pod breadth (0.251) while, in the PC2, the highest positive loading was obtained from seed weight (0.355), pod weight (0.319) and shell weight (0.315). Genotypes identified as promising in the investigation may prove to be potential genetic resource in tamarind improvement programme.

Keywords: *Tamarindus indica*, Variability, Genetic divergence

Tamarind (*Tamarindus indica* L.) is a hardy tropical tree that belongs to the Fabaceae family. It is an excellent agroforestry tree as it grows well alongside both annual and perennial crops and is deliberately retained on-farm (Okello et al 2018). Due to its capacity to withstand droughts, salinity and high temperatures, it holds greater significance in waste land development and dry land horticulture (Karale 2002). In India, tamarind is grown in an area of 44.99 thousand hectares (ha) with an annual production of 162.03 thousand MT. Tamil Nadu is the leading producer with more than 27.20% share to the total production followed by Karnataka (22.75%), and Kerala (19.94%) (NHB 2022).

Tamarind being a cross pollinated specie and predominance of propagation *via* seed provides ample opportunities for the selection of outstanding types with desirable horticultural characteristics (Pooja 2018). Thus, identifying and describing genetic variability within genotypes is a preliminary step before formulating any selection programme (Verma et al 2014). Genetic variability can be examined using a variety of methods, of which two are commonly used in the divergence studies such as principal component analysis (PCA) and hierarchical cluster analysis (HCA). The principal component analysis (PCA) is a statistical technique used to analyze data sets in order to emphasize variation and draw out strong patterns (Ayala-Silva et al 2016). It was conducted to provide a better understanding of the genetics and environmental interactions that have contributed to the genetic diversity. A hierarchical cluster analysis is also used to explain the dissimilarities among genotypes based on Euclidean distance and to investigate the relationship between them based on their potential characteristics. The multivariate analysis is an effective means of understanding genetic similarities and dissimilarities among the genotypes, where the several different traits are examined simultaneously to understand the clustering mechanism for their utility breeding, commercialization and conservation of plant genetic resources. This study aims to determine the morphological differences among the tamarind genotypes and to establish a relationship between them for their further utility in tamarind crop improvement programme.

MATERIAL AND METHODS

The field experiment was conducted at Instructional-cum-Research Farm, Department of Horticulture, Mahatma Phule Krishi Vidyapeeth, Rahuri, Dist. Ahmednagar (MS), India. It is situated at 19º20′36″ North latitude and 74º39′38″ East longitudes at an altitude of 519 meters above mean sea level in the Nashik Division of Western Maharashtra. The climate of the experimental site is arid to semi-arid with dry and hot summer and receives an annual rainfall of 479.7 mm on an average. The highest average temperature ranges from 32ºC to 45ºC in summer and the lowest temperature from 8.5ºC to 10ºC in winter. The experimental material consisted of 25 years old tamarind genotypes maintained under uniform cultural practices throughout the investigation. A detailed

analysis of genotypes for various tree growth, flowering and fruiting attributes was performed from the flowering month of May 2018 through the harvesting month of March 2019. The PPV&FRA (Protection of Plant Varieties & Farmer's Right Authority) test guidelines were followed to evaluate the tamarind genotypes for qualitative growth attributes (Anonymous, 2017). The observations on quantitative pod attributes were recorded as per standard procedures. The biochemical parameters *viz*. TSS, titratable acidity (%) and ascorbic acid (mg/100g) were assessed following standard methodology (AOAC 2000).

Statistical analysis: The statistical analysis for mean, standard deviation and coefficient of variation was done using IBM SPSS Statistics 19 statistical software (IBM, NY, USA). The genetic divergence among 20 tamarind genotypes was estimated using the Principal Component Analysis and Hierarchical Cluster Analysis (HCA) where the data was subjected to multivariate statistical analysis (PCA and HCA) using the R Statistical Software (2021).

RESULTS AND DISCUSSION

Out of 20 genotypes, 6 genotypes exhibited upright growth habit, 4 spreading, 10 semi-spreading (Table 1). The tree foliage density of varied from dense type (14 genotypes) to sparse (6 genotypes). For new flush colour, genotypes namely; RHRTG 1, RHRTG 3 and RHRTG 16 showed reddish brown flush and rest all displayed reddish-green flush colour (Plate 1). The differences in tree growth habit and tree morphological attributes might be due to the genotypic characteristics of the tree. Earlier workers had also reported variability in morphological attributes of different tamarind genotypes under Bangalore conditions (Nandini et al 2011, Algabal et al 2012).

Date of inflorescence emergence was early in genotype RHRTG 1 (17-05-2018) and late on 29th May, 2018 in the genotype RHRTG 7 (Fig. 1). The date of harvesting spanned from 26-02-2019 to 02-03-2019. The minimum number of days taken to maturity was estimated in RHRTG 13 (240 days) and maximum in RHRTG 4 (260 days) followed by RHRTG 5 (258 days) and RHRTG 1 (258 days) (Table 2). Previous study on tamarind also reported a high variability among genotypes for these parameters (Bhogave et al 2018). Genotype RHRTG 20 (6.60 m), RHRTG 2 (6.30 m) and RHRTG 17 (6.10 m) recorded highest tree height and the

Table 1. Variability among tamarind genotypes for tree growth habit, foliage type and new flush colour

Genotype	Growth habit	Tree foliage type	New flush colour
RHRTG 1	Semi-spreading	Dense	Reddish brown
RHRTG 2	Upright	Dense	Reddish green
RHRTG 3	Semi-spreading	Dense	Reddish brown
RHRTG 4	Spreading	Dense	Reddish green
RHRTG 5	Semi-spreading	Dense	Reddish green
RHRTG 6	Upright	Sparse	Reddish green
RHRTG 7	Semi-spreading	Sparse	Reddish green
RHRTG 8	Semi-spreading	Sparse	Reddish brown
RHRTG 9	Upright	Dense	Reddish green
RHRTG 10	Upright	Sparse	Reddish green
RHRTG 11	Semi-spreading	Dense	Reddish green
RHRTG 12	Spreading	Sparse	Reddish green
RHRTG 13	Upright	Dense	Reddish brown
RHRTG 14	Spreading	Dense	Reddish green
RHRTG 15	Semi-spreading	Sparse	Reddish green
RHRTG 16	Semi-spreading	Sparse	Reddish brown
RHRTG 17	Semi-spreading	Dense	Reddish green
RHRTG 18	Spreading	Dense	Reddish green
RHRTG 19	Upright	Dense	Reddish green
RHRTG 20	Semi-spreading	Dense	Reddish green

Reddish-green flush colour **Reddish-brown flush colour**

Plate 1. Variability among the genotypes for new flush colour

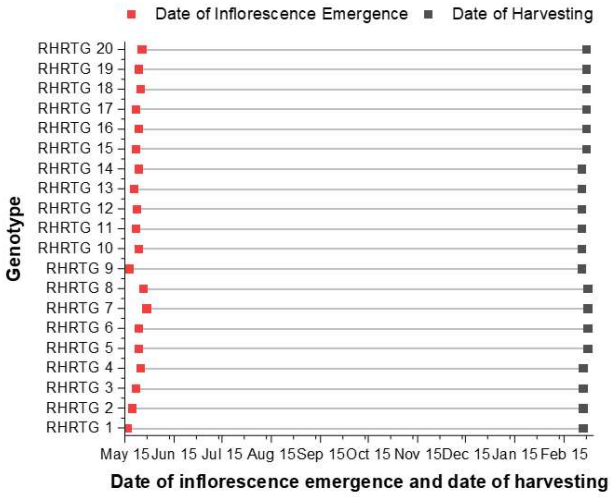

Fig. 1. Variability among tamarind genotypes for date of inflorescence emergence and harvesting

lowest was noted in RHRTG 15 (3.80 m) (Table 2). For East-West tree spread, the genotypes RHRTG 14 (7.10 m) followed by RHRTG 1, RHRTG 20 and RHRTG 11 were superior when compared with rest of genotypes and the lowest was in the genotype RHRTG 9 (3.25 m). Similarly for North-South spread genotype RHRTG 20 (6.95 m) followed by RHRTG 14 and RHRTG 12 were found superior and the lowest spread was in RHRTG 9 (3.00 m). The canopy volume ranged between 5.11 m^3 to 36.17 m^3 and the genotypes RHRTG 20, RHRTG 14 and RHRTG 1 were superior and RHRTG 9 showed the minimum (5.11 m^3). With respect to trunk girth, the genotypes RHRTG 14 (91.3 cm) followed by RHRTG 2, RHRTG 1 and RHRTG 12 estimated maximum and RHRTG 15 (45.2 cm) the minimum. Individual genotypes may have different genetic constitutions, which could explain the diversity in different metric traits of tree growth. Similar variability for plant growth attributes were reported by Tania et al (2018). Reddy et al (2022) determined the genotype NZB(S) to be best performing accessions in terms of growth, yield and quality characters.

Principal Component Analysis (PCA)

The principal component analysis of 20 tamarind genotypes based on correlation matrix of tree growth and physico-chemical traits reduced the original data set of 24 metric attributes to 18 vector or principal components. The first six components in the PCA analysis with Eigen values more than one contributed 87.48% of the total variability among the different genotypes evaluated (Table 3). The PC1 accounts for the maximum variability (30.64%) in the data, while PC2 with Eigen value of 5.03 accounted for 20.98% of the total variability observed. PC3 had Eigen value of 3.20 and contributed 13.33% to the observed variability. Meanwhile, PC4, PC5 and PC6 had Eigen value 2.745, 1.525 and 1.136 which contributed 11.44%, 6.35% and 4.74% of total variability, respectively.

In the present study, only the first 6 principal components with eigen values >1 explaining 87.48% of variation among 20 tamarind genotypes are being discussed and interpreted. For each principal component, there are several characters contributing to the total variation. Major contributing characters for the diversity in the principal component one (PC1) was pulp per cent (0.333) followed by pulp weight (0.302), pod breadth (0.251) while, seed per cent (-0.304), shell per cent (-0.303), ascorbic acid content (-0.235) had the highest negative loading (Table 3). In PCA, characteristics are analyzed in terms of their association and direction of variation. As a result of these findings, genotypes with high pulp percent and pulp weight will tend to have a greater pod breadth and lower seed/shell percents and ascorbic acid content. If the ascorbic acid content is high, then the positively correlated traits for PCI will tend to have lower values. The second PC accounted for 20.98% of the additional variability not explained by PCI. Seed weight (0.355), pod weight (0.319), shell weight (0.315) was positively correlated with PC2. Vein per cent (-0.175), pulp per cent (-0.116) and shell per cent (-0.030) decreased in PC2. Moreover in 3rd, 4th, 5th and 6th principal component, trait such as canopy volume (0.373), yield per tree (0.363), vein per cent (0.412) and days to maturity (0.588) had the highest positive loading, respectively. A positive and a negative loading of factors was observed in the above 2 major principal components, which indicate that the components and variables had both positive and negative correlations. Pulp per cent and seed weight was examined to be best choice which had the highest loading from the principal component one (PC1) and two (PC2), respectively. In principal component analysis (PCA) the amount of variation among the genotypes can be attributed to every axis of differentiation by the largest contributor. To aid the

Table 2. Days to maturity (days), tree growth and pod attributes of tamarind genotypes under the arid conditions of Western Maharashtra

Parameters	Range	Mean	CV (%)
Days to maturity (days)	240-260	248.25	2.33
Tree height (m)	3.80-6.60	5.25	13.79
Tree spread EW (m)	3.25-7.10	5.37	16.84
Tree spread NS (m)	3.00-6.95	5.29	20.21
Canopy volume (m^3)	5.11-36.17	19.06	42.04
Trunk girth (cm)	45.20-91.30	65.54	20.94
Pod weight (g)	16.85-28.07	21.55	16.79
Pod length (cm)	9.81-17.27	12.69	16.2
Pod breadth (cm)	2.05-2.95	2.48	8.71
Shell weight (g)	3.65-6.80	4.75	16.37
Pulp weight (g)	7.29-17.45	11.17	24.94
Seed weight (g)	2.37-6.67	4.44	26.5
Vein weight (g)	0.57-1.58	1.01	28.19
No. of seeds per pod	4.33-10.00	6.28	23.05
Weight of 100 seeds (g)	46.40-98.60	77.85	19.3
Shell per cent (%)	16.13-26.88	22.20	12.89
Pulp per cent (%)	37.12-62.16	51.42	13.24
Seed per cent (%)	12.32-31.34	20.75	24.56
Vein per cent (%)	2.57-6.65	4.66	22.66
Yield per tree (kg)	9.00-85	44.05	54.19
Yield efficiency (kg/m^3 CV)	0.53-5.81	2.48	58.93
TSS (°Brix)	28.68-34.80	31.20	4.58
Acidity (%)	8.08-11.18	8.76	9.2
Ascorbic acid (mg/100g)	1.35-3.54	2.06	22.86

visualization of variations among the genotypes, the score of first two principal component were represented graphically in the form of principal component biplot (Fig. 2 and Fig. 3). Biplot data revealed that the attributes displaying acute angles are positively correlated, whereas those exhibiting obtuse or parallel angles are negatively correlated and those showing right angles have no correlation at all. The graphical representation of data also reveals that the shell weight and pod length; pod weight and weight of 100 seeds are positively correlated. However, the seed per cent and pulp per cent were found to be negatively correlated. Further, PCA also helped to identify RHRTG 14, RHRTG 9 and RHRTG 12 as superior tamarind genotypes which performed well with respect to the PC1 and PC2 (Fig. 3). Using PCA, Kidaha et al (2019) assessed morphological diversity of tamarind germplasm from Eastern parts of Kenya. Trunk diameter pod weight, number of seeds per pod, height to the first branch and pod breadth showed highest variation in principal component analysis.

Hierarchical cluster analysis (HCA): Hierarchical cluster analysis also showed the dissimilarity among the tamarind genotypes and further revealed the relationship between them. The highest dissimilarity matrix was determined between the genotypes RHRTG 14 & RHRTG 9 (93.05) followed by RHRTG 7 & RHRTG 4, RHRTG 14 & RHRTG 7, however it was lowest for RHRTG 12 & RHRTG 11 (9.73) and RHRTG 14 & RHRTG 12 (Table 4). The hierarchical cluster analysis classified 20 tamarind genotypes into two major groups at 186.20 Euclidean distance and further in clusters according to their different morphological characteristics

Table 3. Eigenvalue, percentage of variance (%) and cumulative variations (%) for six major principal components among the tamarind genotypes

Character	Component					
	PC1	PC2	PC3	PC4	PC5	PC6
Days to maturity (days)	-0.122	0.128	0.107	0.200	-0.312	0.588
Tree height (m)	0.080	0.077	0.368	-0.230	0.345	-0.054
Tree spread EW (m)	0.216	0.173	0.288	0.231	-0.111	0.045
Tree spread NS (m)	0.242	0.168	0.280	0.201	0.034	0.084
Canopy volume (m^3)	0.212	0.172	0.373	0.075	0.126	0.035
Trunk girth (cm)	0.192	0.149	0.254	-0.137	0.215	0.047
Pod weight (g)	0.175	0.319	-0.214	-0.177	-0.018	-0.094
Pod length (cm)	-0.083	0.290	0.005	-0.338	-0.212	-0.005
Pod breadth (cm)	0.251	0.193	-0.058	-0.100	-0.143	0.251
Shell weight (g)	-0.093	0.315	-0.205	-0.186	-0.127	0.166
Pulp weight (g)	0.302	0.156	-0.177	-0.140	-0.091	-0.122
Seed weight (g)	-0.180	0.355	-0.042	-0.080	0.164	-0.132
Vein weight (g)	0.234	0.082	-0.315	0.018	0.308	0.188
No. of seeds per pod	-0.205	0.290	-0.034	-0.232	0.137	-0.114
Weight of 100 seeds (g)	0.148	0.260	-0.052	0.196	-0.342	-0.254
Shell per cent (%)	-0.303	-0.030	0.073	-0.028	-0.158	0.263
Pulp per cent (%)	0.333	-0.116	-0.092	-0.066	-0.165	-0.061
Seed per cent (%)	-0.304	0.168	0.110	0.070	0.194	-0.142
Vein per cent (%)	0.184	-0.175	-0.214	0.071	0.412	0.267
Yield per tree (kg)	0.117	0.267	-0.111	0.363	0.145	0.063
Yield efficiency (kg/m^3 CV)	-0.082	0.184	-0.357	0.290	0.131	0.101
TSS (°Brix)	-0.020	0.033	0.096	-0.380	0.093	0.460
Acidity (%)	-0.187	0.198	0.175	0.274	0.030	-0.055
Ascorbic acid (mg/100g)	-0.235	0.136	-0.100	0.174	0.229	0.046
Eigenvalue	7.353	5.035	3.200	2.745	1.525	1.136
Percentage of variance (%)	30.64	20.98	13.33	11.44	6.35	4.74
Cumulative variations (%)	30.64	51.62	64.95	76.39	82.74	87.48

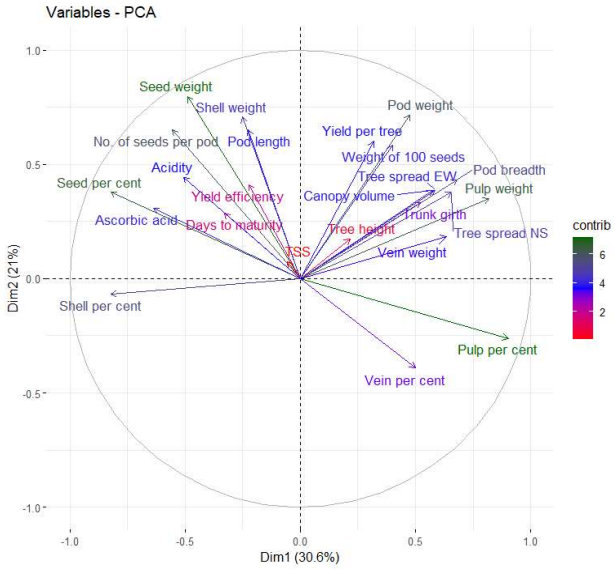

Fig. 2. Traits contribution toward genetic divergence based on PC1 and PC2

(Fig. 4). The first cluster included 14 genotypes which contributes 70.00% of the total genotypes in this population while the second group consisted 6 genotypes contributing 30% of the total genotypes. The 1st major cluster is further divided in to two sub-clusters at 90.97 Euclidean distance in

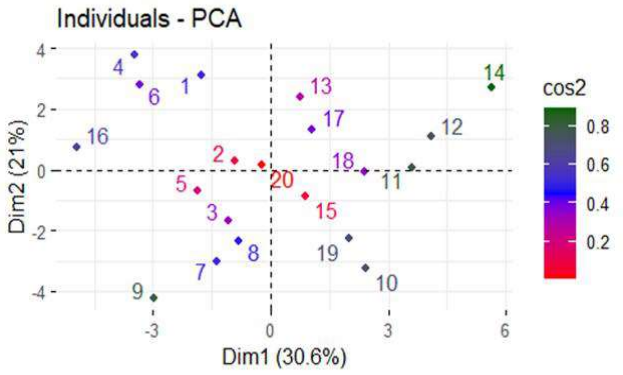

Fig. 3. Distribution of genotypes in the scatter plot along with PC 1 and PC 2

Table 4. Dissimilarity matrix among the tamarind genotypes based on Euclidean distance

Genotypes*	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
1	0.00	23.79	40.88	44.21	53.14	44.75	59.46	51.26	64.48	39.73	31.01	34.08	38.96	38.67	46.56	39.46	27.48	37.39	33.31	31.17
2		0.00	40.45	60.85	51.58	36.19	40.41	40.69	47.78	26.15	43.58	48.42	33.91	51.05	54.49	45.72	36.31	37.62	26.97	22.48
3			0.00	53.14	39.22	22.70	48.65	38.04	41.81	32.81	51.14	57.20	51.29	66.97	33.78	31.93	32.30	27.28	25.08	36.48
4				0.00	73.58	63.18	91.73	78.36	88.57	69.69	39.73	38.41	69.47	52.52	35.72	29.76	37.82	48.72	57.12	67.52
5					0.00	41.53	56.62	20.75	50.07	44.09	65.30	70.89	37.87	77.03	56.21	58.55	52.75	48.73	40.51	49.49
6						0.00	38.19	34.19	30.31	30.42	59.43	65.28	47.34	72.75	47.12	41.21	42.20	34.43	29.91	37.59
7							0.00	39.37	22.33	32.59	77.93	84.65	57.55	87.60	76.34	69.74	65.43	58.02	45.70	35.58
8								0.00	34.89	31.48	64.96	71.28	33.01	75.99	59.21	58.47	51.85	44.96	32.71	39.80
9									0.00	36.77	80.65	87.18	59.42	93.05	70.39	63.99	64.88	55.56	45.08	44.80
10										0.00	49.17	56.80	39.51	60.48	50.75	51.52	40.77	32.03	20.20	30.00
11											0.00	9.73	48.74	19.74	35.75	42.12	24.45	33.05	38.54	53.46
12												0.00	52.41	15.73	40.17	44.57	28.12	39.56	44.97	58.34
13													0.00	53.21	58.06	57.58	43.60	43.57	34.29	43.58
14														0.00	53.39	57.82	38.21	48.17	51.17	61.32
15															0.00	25.67	24.48	22.92	36.10	58.56
16																0.00	25.79	31.17	37.42	50.63
17																	0.00	17.84	23.82	40.55
18																		0.00	17.32	42.35
19																			0.00	30.21
20																				0.00

Genotypes*

1.	RHRTG 1	5.	RHRTG 5	9.	RHRTG 9	13.	RHRTG 13	17.	RHRTG 17
2.	RHRTG 2	6.	RHRTG 6	10.	RHRTG 10	14.	RHRTG 14	18.	RHRTG 18
3.	RHRTG 3	7.	RHRTG 7	11.	RHRTG 11	15.	RHRTG 15	19.	RHRTG 19
4.	RHRTG 4	8.	RHRTG 8	12.	RHRTG 12	16	RHRTG 16	20.	RHRTG 20

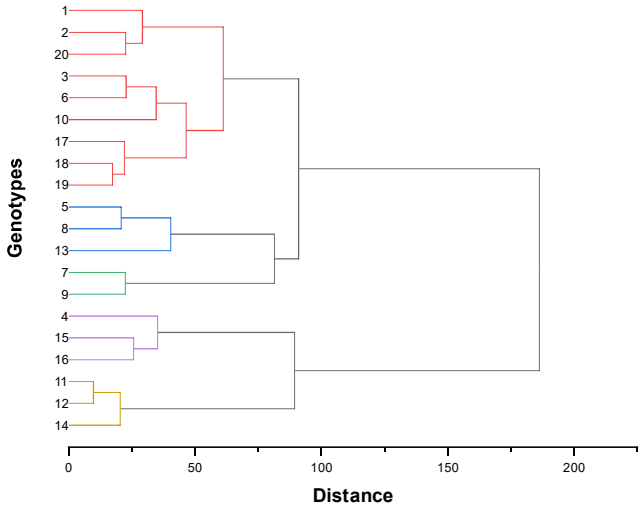

Fig. 4. Dendrogram grouping of 20 tamarind genotypes

which first sub cluster comprised 9 genotype and second sub-cluster consisted 5 genotypes. The 1st sub cluster is again divided into the two- cluster further at 61.10 Euclidean distance and 2nd at Euclidean distance of 81.33 and consisted of three and six genotypes, respectively. The 2nd major cluster is further divided in to two sub-clusters at 89.38 and consisted of RHRTG 4, RHRTG 15, RHRTG 16 in 1st sub cluster and RHRTG 11, RHRTG 12 and RHRTG 14 in 2nd sub cluster. Based on 18 qualitative and quantitative traits, Ayala-Silva et al (2016) analyzed pomological diversity of 13 tamarind genotypes at Miami, Florida. Cluster analysis grouped all tamarind genotypes into three major clusters where the semi-sour genotypes were grouped in cluster 'A' and the sour genotype in cluster 'C'. Cluster 'B' contained genotypes predominantly characterized by sweet, dark pulp, and smaller fruit size.

CONCLUSIONS

Tamarind germplasm maintained at Instructional-cum-Research farm of Department of Horticulture, MPKV., Rahuri exhibits considerable variations in terms of different metric and non-metric parameters. In conclusion, the PCA was able to capture 87.48% of the variations present in the 20 genotypes of tamarind taken into consideration. PCA study revealed the RHRTG 14, RHRTG 9 and RHRTG 12 to be superior tamarind genotypes that outperformed PC1 and PC2 based on the quality of representation of these genotypes on the factor map. The genotypes that have demonstrated superiority in a number of key attributes can be exploited more efficiently in the tamarind crop improvement programme..

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