

Original Research Article

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## Genetic Variability Studies in Tamarind (*Tamarindus indica* L.)

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### ABSTRACT

#### Keywords

Tamarind,  
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L., GCV, PCV,  
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#### Article Info

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Genetic variability, heritability, genetic advance and genetic advance as a per cent over mean for twenty characters were assessed by field evaluation (part of survey) of two thirty one tamarind genotypes in six districts (*viz.*, Belagavi, Dharwad, Gadag, Bellary, Chitradurga and Gulbarga) with different location during 2018. High degree of variation was observed for all characters. In all cases, phenotypic variances were higher than the genotypic variance. The difference between phenotypic coefficient of variation and genotypic coefficient of variation were found to be narrow for most of the traits except trunk diameter, spread of the east to west and spread of the tree north to south, crown size, pod thickness, pulp per cent, seed per cent and shell per cent. The high estimates of heritability as well as genetic advance over per cent mean were found for tree height, trunk diameter, spread of the tree east to west, spread of the tree north to south, crown size, pod length, pod thickness, pod weight, pulp weight, number of seeds per pod, seed weight per pod, shell weight per pod, vein weight per pod, pulp per cent, seed per cent, shell per cent, vein per cent, tamarind pod yield and tartaric acid content.

### Introduction

Tamarind (*Tamarindus indica* L.) is a monotypic genus tree belonging to the family Leguminosae, sub-family caesalpiniaceae with somatic chromosome number of  $2n=24$  (Purseglove *et al.*, 1987). It is indigenous to tropical Africa and southern India (Nas, 1979). It is estimated that India produces an annual production of pulp over 1.99 lakh

tones and exported the tamarind products worth of rupees 57 crores per annum during 2017-18 (Anon., 2017). The sticky pulp is often eaten fresh but has many other culinary uses *viz.*, in pickles, jam, candy, juices, curries, sauces, chutneys and certain drinks (Archana *et al.*, 2013). Tamarind is a highly cross pollinated and seed propagated crop; hence wide variability is common in this species. The individual variation between the

trees within a population is of paramount importance and it may be worthwhile concentrating only on best trees with respect to neighbouring ones and plus trees may be selected within ecological zones for increasing their frequencies. The magnitude of variability and its quantitative estimation for each character would indicate the potential of each tree and scope for improving the desirable and economic characters through selection (Feungchan *et al.*, 1996a). Therefore, a field investigation was carried out with a view to study the genetic variability, heritability and genetic advance in tamarind by assessing the tamarind genotypes at K. R. C. College of Horticulture, Arabhavi (Karnataka).

### Materials and Methods

The experimental material comprised of 231 randomly selected elite tamarind genotypes from six districts with different locations (*viz.*, Belagavi, Dharwad, Gadag, Bellary, Chitradurga and Gulbarga) which is away from K. R. C. College of Horticulture, Arabhavi, Karnataka, India. The observation on twenty quantitative and qualitative parameters like tree height (m), trunk diameter (m), spread of the tree east to west (m), spread of the tree north to south (m), crown size (m), pod length (cm), pod width (cm), pod thickness (cm), pod weight (g), pulp weight (g), number of seeds per pod, seed weight per pod (g), shell weight per pod (g), vein weight per pod (g), pulp per cent (%), seed per cent (%), shell per cent (%), vein per cent (%), tamarind pod yield (kg/tree) and tartaric acid content (%) were recorded 10 representative samples of ripe pods (fruits) from all the directions of the tree and were analysed statistically (Sundarraaj *et al.*, 1972). The biometrical analyses were carried out according to estimation of genotypic and phenotypic coefficients of variation (Burton and Devane, 1953),

heritability in broad sense (Hanson *et al.*, 1956), genetic advance and genetic advance over per cent mean (Johnson *et al.*, 1955).

### Results and Discussion

The analysis of variance was conducted to test significance difference among genotype studied. The mean sums of squares due to various sources for different characters are presented in table 1. The genotypic and phenotypic coefficient of variability, heritability, and genetic advance as per cent over mean for each of the characters are presented in table 2 and 3. A range of variation was observed for all the characters. It was maximum in case of tamarind pod yield (280-1200) and minimum for the vein weight per pod (0.25-2.76). The difference between the genotypic (GCV) and phenotypic coefficient of variation (PCV) were found to be narrow for trunk diameter, spread of the east to west and spread of the tree north to south, crown size, pod thickness, pulp per cent, seed per cent and shell per cent. The results suggest that these traits are least affected by environment and selection for these traits on phenotypic would be rewarding. For the rest of the character the estimates of PCV were greater than GCV. This indicates that the variation for these traits is not only by genotypes but also due to environment. Selection based on phenotypes may miss lead as their expression depends more on genetical factors. Similar observations were reported in tamarind by Hanamashetti (1996), Mastan *et al.*, (1997), Biradar (2001), Patil (2004), Ganachary (2005), Divakara (2008), Divakara (2009) and Singh and Nandini (2014).

In the present study, most of the characters exhibited high estimates of heritability except for pod width. The high estimates of heritability for tree height (65.26 %), trunk diameter (76.74 %), spread of the tree east to

west (75.04 %), spread of the tree north to south (71.74 %), crown size (86.46 %), pod length (96.01 %), pod thickness (68.79 %), pod weight (89.13 %), pulp weight (92.49 %), number of seeds per pod (87.61 %), seed weight per pod (89.21 %), shell weight per pod (75.78 %), vein weight per pod (67.06 %), pulp per cent (99.09 %), seed per cent (99.93 %), shell per cent (99.85 %), vein per cent (99.32 %), tamarind pod yield (99.80 %) and tartaric acid content (98.64 %). Suggest that selection will be effective for these

characters. These results are in accordance with Keskar *et al.*, (1989), Jambulingam *et al.*, (1997), Karale *et al.*, (1999), Biradar (2001), Patil (2004), Singh *et al.*, (2008), Prasad *et al.*, (2009) in tamarind crop.

High heritability along with high genetic advance as a per cent over mean is an important factor for predicting the resultant effect for selecting the best individuals.

**Table.1** Analysis of variance (ANOVA) for growth, yield and quality attributes in tamarind genotypes

Sl. No.	Source of variance	Replication	Treatment (Genotypes)	Error	CD @ 5%	CD @ 1%
Degrees of freedom		1	230	230		
1	Tree height (m)	730.52	36.26**	7.62	5.44	7.17
2	Trunk diameter (m)	2099.96	4.91**	0.64	1.58	2.08
3	Spread of the tree EW (m)	1920.41	4.01**	0.57	1.49	1.96
4	Spread of the tree NS (m)	2048.73	4.36**	0.71	1.67	2.20
5	Crown size (m)	51.87	3.90**	0.28	1.05	1.38
6	Pod length (cm)	1140.16	30.71**	0.62	1.56	2.05
7	Pod width (cm)	2533.05	2.34**	1.64	2.53	3.32
8	Pod thickness (cm)	1710.65	10.98**	2.03	0.28	0.63
9	Pod weight (g)	1377.96	89.44**	5.14	4.47	5.89
10	Pulp weight (g)	1970.65	17.82**	0.69	1.64	2.16
11	Number of seeds per pod	1390.75	10.66**	0.70	1.65	2.17
12	Seed weight per pod (g)	1424.06	11.69**	0.66	1.61	2.12
13	Shell weight per pod (g)	1246.73	5.44**	0.74	1.71	2.24
14	Fiber or Vein weight per pod (g)	30.46	0.58**	0.11	0.67	0.88
15	Pulp per cent	7.63	56.29**	0.25	1.00	1.31
16	Seed per cent	8.80	56.01**	0.02	0.27	0.35
17	Shell per cent	7.24	24.77**	0.01	0.26	0.34
18	Vein per cent	7.89	5.19**	0.01	0.26	0.39
19	Tamarind pod yield (tree/kg)	1575.62	7.24**	0.02	0.24	0.37
20	Tartaric acid content (%)	1045.93	81.81**	0.56	1.47	1.94

**Table.2** Estimates of mean, range, co-efficient of variability, heritability and genetic advance for growth parameters of tamarind genotypes

Sl. No.	Characters	Mean	Range	Variance			Co-efficient of variability		h <sup>2</sup>	GA	GAM
				PV	GV	EV	PCV	GCV			
1	Tree height (m)	21.36	13.22-36.95	21.94	14.32	7.62	21.92	17.71	65.26	6.29	29.48
2	Trunk diameter (m)	8.84	4.46-11.87	2.78	2.13	0.64	18.85	16.51	76.74	2.63	29.81
3	Spread of the tree EW (m)	9.50	5.12-12.07	2.29	1.72	0.57	15.94	13.81	75.04	2.34	24.64
4	Spread of the tree NS (m)	8.83	4.41-11.48	2.54	1.82	0.71	18.05	15.29	71.74	2.35	26.68
5	Crown Size (m)	9.16	5.14-11.65	2.09	1.81	0.28	15.79	14.68	86.46	2.57	28.12

GV- Genotypic variance  
h<sup>2</sup>- Broad sense heritability

GA- Genetic advance  
GAM- Genetic advance as per cent of mean

PV- Phenotypic variance  
EV- Environmental variance  
GCV- Genotypic co-efficient of variation  
PCV- Phenotypic co-efficient of variation

**Table.3** Estimates of mean, range, co-efficient of variability, heritability and genetic advance for yield and quality parameters of tamarind genotypes

Sl. No.	Characters	Mean	Range	Variance			Co-efficient of variability		h <sup>2</sup>	GA	GAM
				PV	GV	EV	PCV	GCV			
1	Pod length (cm)	16.00	9.34-27.72	15.67	15.04	0.62	24.74	24.24	96.01	7.82	48.93
2	Pod width (cm)	6.31	3.99-9.38	1.99	0.34	1.64	22.38	9.38	17.57	0.51	8.10
3	Pod thickness (cm)	1.72	1.17-2.34	6.50	4.47	2.03	14.83	12.30	68.79	3.61	21.02
4	Pod weight (g)	22.02	9.11-45.84	47.29	42.15	5.14	31.23	29.48	89.13	12.62	57.34
5	Pulp weight (g)	8.68	3.11-18.86	9.26	8.56	0.69	35.05	33.71	92.49	5.79	66.79
6	Number of seeds per pod	8.09	3.90-14.91	5.68	4.98	0.70	29.46	27.57	87.61	4.30	53.17
7	Seed weight per pod (g)	6.99	2.52-14.89	6.18	5.51	0.66	35.58	33.60	89.21	4.56	65.39
8	Shell weight per pod (g)	5.57	1.82-10.22	3.09	2.34	0.75	31.58	27.49	75.78	2.74	49.30
9	Fiber or Vein weight per pod (g)	0.85	0.25-2.76	0.34	0.23	0.11	69.14	56.62	67.06	0.81	95.52
10	Pulp per cent	39.49	25.52-51.39	28.27	28.01	0.25	13.46	13.40	99.09	10.85	27.48
11	Seed per cent	31.84	17.96-46.69	28.01	27.99	0.02	16.63	16.62	99.93	10.89	34.22
12	Shell per cent	25.66	16.80-37.68	12.39	12.37	0.01	13.72	13.71	99.85	7.24	28.22
13	Vein per cent	3.90	0.97-9.83	2.60	2.58	0.01	41.38	41.24	99.32	3.30	84.68
14	Tamarind pod yield (tree/kg)	643.38	280-1200	36200.24	36198.22	0.01	29.44	29.41	99.80	391.94	60.64
15	Tartaric acid content (%)	16.39	3.82-33.92	41.18	40.62	0.56	39.14	38.88	98.64	13.04	79.55

GV- Genotypic variance  
h<sup>2</sup>- Broad sense heritability  
GA- Genetic advance  
GAM- Genetic advance as per cent of mean

PV- Phenotypic variance  
EV- Environmental variance  
GCV- Genotypic co-efficient of variation  
PCV- Phenotypic co-efficient of variation

**Table.4** Top 20 ranking genotypes of tamarind with respect to yield and quality characters

SI No.	Characters	Top ranking genotypes
1	Pod length	BGK-12, CLK-10, BGK-18, GRG-10, KDL-10
2	Pod weight	GRG-10, UDP-08, KDL-18, KOL-08, UDP-10
3	Pulp weight	BGK-13, GRG-15, UDP-08, KNU-06, GRG-16
4	Number of seeds per pod	GRG-10, UDP-08, BCM-06, GRG-07, UDP-04
5	Seed weight per pod	GRG-10, UDP-08, CLK-10, GRG-07, GRG-11
6	Shell weight per pod	GRG-11, GRT-14, UDP-18, CLK-10, BGK-13
7	Pulp per cent	KOL-08, GRG-10, GRG-11, BGK-12, BGK-13
8	Seed per cent	UDP-10, GRT-14, BGK-08, BCM-06, KDL-10
9	Tartaric acid content	BGK-12, KNU-06, TKD-12, KNU-15, GRG-11
10	Pod yield per tree	GRG-11, BGK-11, UDP-15, CLK-10, UDP-08

In the present study, high heritability was accompanied with high values of genetic advance as a per cent over mean for tree height, trunk diameter, spread of the tree east to west, spread of the tree north to south, crown size, pod length, pod thickness, pod weight, pulp weight, number of seeds per pod, seed weight per pod, shell weight per pod, vein weight per pod, pulp per cent, seed per cent, shell per cent, vein per cent, tamarind pod yield and tartaric acid content indicating predominance of additive gene component. Thus, there is ample scope for improving these characters based on direct selection.

The present study revealed the identification of top 20 genotypes based on the different characters as given in the table 4. These genotypes may be further utilized for selecting superior genotype having major plus characters and also further crop improvement programmes.

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