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#### **MN Mamathashree**

College of Horticulture, Department of Biotechnology and Crop Improvement, UHS Campus, GKVK, Bengaluru, Karnataka, India

#### **BG** Prakash

Dean, College of Horticulture, Tamaka Kolar, Karnataka, India

#### **B** Fakrudin

Head of the Department, Department of Biotechnology and Crop Improvement, College of Horticulture, UHS Campus, GKVK, Bengaluru, Karnataka, India

Corresponding Author: MN Mamathashree College of Horticulture, Department of Biotechnology and Crop Improvement, UHS Campus, GKVK, Bengaluru, Karnataka, India

## Genetic variability for biochemical parameters among identified distinct genotypes of tamarind (*Tamarindus indica* L.) in niche areas of Karnataka

## MN Mamathashree, BG Prakash and B Fakrudin

#### Abstract

From root to shoot, every part of the tamarind tree is beneficial. Being the economic part, the pulp possesses useful nutrients. The present study aims at assessing the quantum of biochemical components present among 96 tamarind genotypes collected from thirty districts of Karnataka during the year 2018-19 at the College of Horticulture, Bengaluru. From the study of thirteen biochemical parameters, it was revealed that the significant variations among the mean values of genotypes for biochemical parameters viz., TSS (2.30 to 11.03), starch (0.36 to 1.99%), total sugars (40.35 to 49.18%), reducing sugars (31.41 to 40.48%), non-reducing sugars (6.43 to 11.78%), total phenols (36.32 to 70.39 mg/100g), total flavonoids (11.49 to 36.66 mg/100g), free amino acids (2.00 to 3.76 mg/100g), anthocyanin (2.68 to 7.21 mg/100g), crude fiber (6.66 to 11.23%), antioxidant activity (50.51 to 91.67%), tartaric acid (4.8 to 11.4 mg/100g) and tryptophan (2.03 to 3.93  $\mu$ g/g) contents indicated that the genotypes were highly diverse for all the biochemical parameters. The top-performing five genotypes in terms of fruit yield/plant did not possess good values for biochemical parameters except TAM\_KOL1 genotype, which had a fairly good amount of tartaric acid (11.40 mg/100g), free amino acid (3.58 mg/100g), total sugars (49.18%) and reducing sugars (39.78%). The genetic variation components viz., PCV ranged from 10.26 to 40.92% while GCV ranged from 8.93 to 38.51%. High heritability estimates coupled with high genetic advance as percent mean were observed in most characters. Hence, the selection based on such characters would be reliable for tamarind improvement programme.

Keywords: Tamarind, food value biochemical components, nutrition level, genetic variations

#### Introduction

Tamarind (*Tamarindus indica* L.) is a multipurpose fruit tree, belongs to a dicotyledonous family, *Leguminosae*. Tamarind has a wide geographical distribution in the subtropics and semiarid tropics and it is cultivated all over south India. The adaptation of the species to some of the geographies is deep and has become part of the culture and food system. Being a drought-tolerant tree, it is the source of income in dryland agriculture ecosystems besides serving diverse uses including industry, medicine and wood.

Tamarind is a rich source of nutrients and plays a vital role in human nutrition, particularly in developing countries (Rana and Sharma, 2018)<sup>[19]</sup>. Tamarind is rich in crude protein and proteins, with many essential amino acids required for the growth and development of the human body. It is high in carbohydrate, which is the source of energy and has high minerals such as potassium, phosphorus, calcium, and magnesium. Tamarind can provide a little amount of iron and vitamin-A. All the parts of tamarind are used abundantly for medicinal and industrial purpose mainly the pulp is highly valued (Zohrameena *et al.* 2017)<sup>[25]</sup>.

The tamarind fruit pulp has a sweet-acidic taste due to a mixture of both high contents of tartaric acid and reducing sugars. The multiple purposes pulp is used in seasoning, in prepared foods, to flavour confections, curries and sauces, and as a major ingredient in juices and other beverages (Bhadoriya, *et al.* 2011) <sup>[3]</sup>. The fruit pulp of tamarind comprises 30-50% of the ripe fruit while its shell and fiber account for 11-30% and the seed about 25-40% (Shankaracharya, 1998) <sup>[22]</sup>. The dried tamarind pulp of commerce contains 8 to 18% tartaric acid (2, 3-dihydroxy butanedioic acid-C<sub>4</sub>H<sub>6</sub>O<sub>6</sub>, a dihydroxy carboxylic acid) and 25 to 45% reducing sugars, of which 70% is glucose and 30% fructose (Chandra and Samsher, 2006) <sup>[5]</sup>.

Pulp has low water content and a high level of protein, carbohydrates (60-72%), minerals (Potassium, Phosphorus, Calcium and Magnesium) and minerals. TSS content varies from 54-69.9 Brix. Variation in pulp quality characters among the genotypes depending on geographic isolation are well recognized (Divakara, 2009)<sup>[7]</sup>.

#### The Pharma Innovation Journal

Tamarind pulp was found to contain both essential and nonessential amino acids (Adeola, 2013)<sup>[1]</sup>. Anthocyanin is the vital polyphenolic compound present in red tamarind (Rampriya and Kumar, 2019)<sup>[18]</sup>.

The huge diversity of metabolites in tamarind influences the interest of the plant breeder to explore the various breeding options to combine desirable biochemical parameters with fruit yield components by executing careful selection of genotypes. Due to its diverse metabolite production among genotypes, various industrial sectors dependent would benefit. Fruit biochemical composition mostly depends on genetic factors but sometimes environmental conditions also influences. Hence, aim of the present study was to pin down the genetic variation for biochemical parameters present in the fruit pulp of tamarind genotypes of Karnataka for further selection and to adopt breeding strategies for improvement.

#### Material and Methods Plant Materials

The ninety-five tamarind genotypes which were distinct and popular were identified from niche areas of all the districts of Karnataka and one check variety *viz.*, GKVK17 was used in the study. The fruit samples were collected during 2017-2018 and studied for assessment of quantum of thirteen biochemical parameters at College of Horticulture, Bengaluru.

## **Total Soluble Solids (TSS)**

TSS is the refractive index of a soluble solid is an important index for consideration of quality. Sugars are the major soluble solids in fruit juice. Other soluble materials include organic acid and amino acids, soluble sugars, pectin etc. SSC Brix can be determined in a small sample of fruit juice using a handheld refractometer. This instrument measures the refractive Indices of how much a light beam is bent when it passes through the fruit juice. Sugar level varies within the fruit, being higher at the sugar levels often vary within the fruit. For assay of TSS, about 1 gram of tamarind pulp samples was extracted from the fruit and homogenized with 10 ml of distilled water. Place a drop twice on the refractometer prism lower cover plate and read. The instrument calibrated using a drop of distilled water and adjusts the reading to 0 °brix if required, with the small set screw on the back.

## Starch

One g of tamarind pulp was grounded with 80% ethanol. The supernatant were discarded and residues (starch) were collected by homogenizing the samples. 5ml of 2.5M HCL was added to the residue and heated to hydrolysis in a water bath at 100°C for 30 min. Diluted to 10ml with de-ionized water, later the solution was brought to neutral pH using  $Na_2CO^3$ .

## **Reducing sugars**

Reducing sugars were estimated by the following method of Karel and Labuza. Three replications were performed. One g of tamarind pulp was grounded and sugars are extracted by 80% ethanol by homogenizing the samples. Then it was centrifuged at 8000 rpm for 10 min. One ml of supernatant was taken in a test tube and 1 ml of DNS was added. Tubes were boiled for 10 min and cooled. Two ml of distilled water

was added and absorbance was read at a wavelength of  $550\,$  nm.

#### Total sugars

Total sugars were estimated by the following method of Marshall, 1986<sup>[11]</sup>. Three replications were performed. One g of tamarind pulp grounded and sugars are extracted by 80% ethanol by homogenizing the samples. Then it was centrifuged at 8000 rpm for 10 min. One ml of supernatant was taken in a test tube and 4ml of Anthrone reagent was added and heated under a boiling water bath for about 8-10 min. After heating, it was rapidly cooled down and absorption was recorded at 630nm. Glucose was used as standard in the concentration of 100 mic g/ml.

#### Non-reducing sugars

The non-reducing sugar is calculated by subtracting the total sugar value and the reducing sugar value.

## Preparation of tamarind fruit pulp for phenolic extract

Approximately 1 g of pulp was grounded and homogenated by adding 10 times the volume of 80% ethanol. Then it was centrifuged at 10,000 rpm for 20 min. The resultant extract was filtered through filter papers followed by evaporation of alcohol. The residue was extracted with alcohol three times as described by Owen *et al.* (2003) <sup>[16]</sup>.

This extract was used to determine total phenolic, total flavonoid, free amino acids, and anthocyanin.

## **Total phenolic content**

The total phenolic content of the tamarind pulp extract was determined by the Folin Ciocalteu assay according to the method of Anyasi *et al.* (2015) <sup>[2]</sup>, using GA as the standard. The total phenolic content was expressed as gallic acid equivalents (mg of GAE/100 g sample).

#### Total flavonoid content

Total flavonoid content was determined using the colorimetric method as described in Meyers *et al.*  $(2003)^{[15]}$  using rutin as the standard. The results were expressed grams of rutin equivalents g-1 using the calibration curve.

#### Free amino acids

The spectrophotometric analysis of free amino acids content determined by the Ninhydrin reagent assay according to the method of Adeola (2013)<sup>[1]</sup> using leucine as the standard. The values were expressed in grams of leucine equivalent g-1.

#### Total anthocyanin

The spectrophotometric analysis of anthocyanin content determined by the anthocyanin reagent assay according to the method of Rubinskiene *et al.* (2007) <sup>[21]</sup> using the cyaninhydrochloride as the standard. The values were expressed as milligrams per 100 g of fresh weight.

#### **Crude fiber**

The crude fiber is determined using the muffle furnace in accordance with the method of Maynad (1970) <sup>[14]</sup>. The percentage of crude fiber determined using the following equation,

## (Weight of crucibles before ash (W2) – Pre weighed dish weight (W1)) – (Weight of crucibles after ash (W3) - Pre weighed dish weight (W1) X 100

Crude fiber (%) = 
$$\cdot$$

Weight of the sample (2g)

## DPPH radical scavenging activity

Antioxidant capacity per cent inhibition of tamarind pulp extract was determined using the stable radical DPPH according to Anyasi *et al.* (2015) <sup>[2]</sup>. The reaction mixture containing 1.5 ml of a DPPH methanolic solution (0.2 mg/ml) and 0.75 mL of the crude extract (methanol for the control)

was incubated at 37°C for 20 min, and the absorbance was measured spectrophotometrically at 520 nm. The per cent of DPPH discolouration of the sample was then calculated. GA (10 $\mu$ g/ml) was used as a positive control. The percentage of DPPH free radical quenching activity determined using the following equation.

## DPPH Scavenging activity (%) = $\frac{\text{Absorption (DPPH)} - \text{Absorption of extracted sau}}{\text{Absorption DPPH}} X 100$

#### Tartaric acid

Tartaric acids were estimated by the following method of Roopa and Kasiviswanatham, 2013 <sup>[20]</sup>. Three replications were performed. The tartaric acid extracted from tamarind fruit pulp by hot and cold extraction followed by cooling. Tartaric acid was used as standard in the concentration of 100 mic g/ml.

## Tryptophan

The ethanol extracted samples were used to determine the tryptophan content using HPLC (Shimadzu Analysis India Pvt. Ltd) system was equipped with C-18 RP Column (4.6 x 150 mm), PDA detector, sample loop of 20  $\mu$ l and Lab solutions software for data acquisition and analysis. The analytes were detected by absorbance and quantified with external calibration graphs at  $\lambda$ =254 nm. The extracted amino acids samples were kept for derivatization for 24 hours before HPLC analysis. The standard tryptophan of 1mg amino acid dissolved in 1ml HPLC grade water and kept for derivatization along with the samples (Figure 2). The Ammonium acetate buffer and Acetonitrile were used as solvent A and solvent B respectively. The total run of HPLC for each sample was 30min.

## **Statistical Analysis**

The data of all the parameters were subjected to Fischer's method of analysis of variance and the level of significance used in 'F' was at p=0.01. Critical differences were worked

out when the 'F' test was significant. The within and between biochemical variability was evaluated using variance component analysis (Wildt and Ahtola, 1978)<sup>[24]</sup>. The various components of genetic variation such as the Genotypic coefficient of variation (GCV%), Phenotypic coefficient of variation (PCV%) and Environmental coefficient of variation (ECV%) were analyzed. Heritability in a broad sense (h2  $_{bs}$ ) is the ratio of genotypic variance to phenotypic variance was calculated (Burton and DeVane, 1953; Johnson et al., 1955) [4, <sup>9]</sup>. The expected genetic advance (GA) resulting from the selection of 5% superior individuals was calculated following Burton and DeVane (1953)<sup>[4]</sup> and Johnson et al. (1955)<sup>[9]</sup>. Cluster analysis was conducted on SPSS software to grouping the genotypes based on the biochemical parameters variations. The main parameter that guided the joining (tree clustering) process linkage rule was UPGMA and the distance was computed from raw data using Euclidean distance. The HPLC data were analyzed using standard retention time and area by Indo stat statistical software to depict the tryptophan variations in genotypes.

## Results

The study indicated that the various biochemical parameters from each of 96 tamarind genotypes showed a significant amount of variation for all the traits. For the sake of discussion only top twenty top performing genotypes (Table 1) in terms of fruit yield were considered to compare the biochemical parameters.

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<b>Table 1.</b> The mean values for biochemical	narameters among ton	hest nerforming i	tamarind geno	tvnes in terms (	at truit vi	eld/nlant
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Sl. No	Genotypes	TSS	Starch (%)	Reducing sugars (%)	Total sugars (%)	Non-reducing sugars (%)	Total phenols (mg/100g)	Total flavonoids (mg/100g)	Free amino acids (mg/100g)	Total anthocyanin (mg/100g)	Fiber (%)	Antioxidant (% inhibition)	Tartaric acid (mg/100g)	Tryptophan (µg/g)	Fruit yield/Plant (kg)
1	TAM_KOL4	3.80	1.07	38.85	47.83	8.98	53.68	26.03	3.61	4.87	6.95	55.68	5.90	3.78	298.50
2	TAM_BEN(U)4	4.70	1.99	37.31	44.42	7.11	36.32	13.66	3.53	6.00	10.17	50.51	5.05	2.15	286.00
3	GKVK17	5.60	0.78	38.83	47.41	8.58	52.75	31.21	3.65	4.00	7.06	52.64	8.95	2.90	284.50
4	TAM_KOL1	4.60	0.97	39.78	49.18	9.40	48.91	27.89	3.58	5.18	7.65	51.55	11.40	3.71	277.00
5	TAM_CHK1	6.10	0.90	39.60	47.91	8.31	52.12	32.69	3.50	4.71	7.58	55.54	6.17	2.91	270.00
6	TAM_KOL2	4.30	1.03	38.57	47.59	9.02	54.80	28.39	3.58	4.59	7.73	51.56	7.76	3.72	268.50
7	TAM_BEN(U)2	4.40	1.94	37.89	45.17	7.28	39.36	16.17	3.60	4.50	10.12	52.94	4.80	2.54	260.50
8	TAM_CHK4	5.90	0.80	39.60	48.02	8.42	53.65	30.00	3.58	4.75	7.35	56.07	7.49	2.93	216.50
9	TAM_RAM1	4.70	1.26	35.70	44.34	8.64	48.50	20.33	3.32	5.75	9.93	53.72	8.07	3.21	216.50
10	TAM_HAV1	9.90	0.67	39.30	48.53	9.23	53.40	20.14	2.88	5.53	7.39	58.76	8.10	3.89	215.50
11	TAM_MYS4	9.50	1.02	37.13	45.94	8.81	49.22	18.56	3.47	4.28	8.02	57.11	7.35	3.83	211.50
12	TAM_MAN5	4.30	0.78	40.48	47.26	6.78	46.12	20.08	3.58	4.50	9.75	54.80	6.67	3.17	203.00
13	TAM_KOL3	3.90	1.09	39.88	48.51	8.63	43.02	28.98	3.71	7.21	7.51	54.95	7.07	3.62	201.00
14	TAM_UDP2	3.50	1.17	35.12	45.92	10.80	59.63	33.84	2.12	6.87	8.04	77.59	9.90	3.86	97.00
15	TAM_UDP1	5.50	1.39	35.47	46.66	11.19	60.44	33.87	2.36	7.12	7.04	79.06	7.00	3.41	91.50
16	TAM_UK3	4.40	1.86	33.33	44.14	10.81	65.09	36.42	2.05	6.06	8.49	76.73	4.80	3.76	67.00
17	TAM_CHM3	3.70	1.31	38.39	49.17	10.78	63.26	36.57	2.36	5.21	6.66	79.56	11.05	3.00	62.00
18	TAM_UK1	2.90	1.89	34.05	45.83	11.78	63.17	36.66	2.23	6.37	8.36	91.67	8.80	3.41	58.00
19	TAM_DK2	4.00	1.17	35.91	46.33	10.42	70.39	35.48	2.05	5.12	8.25	87.60	10.97	3.10	51.50
20	TAM_UK2	3.90	1.75	34.35	46.04	11.69	60.32	36.63	2.03	6.28	8.55	78.85	10.52	3.67	49.50
	Grand Mean	5.06	1.17	37.31	46.34	9.02	53.93	26.28	2.96	4.64	7.83	65.01	7.94	3.22	191.85
	CV	3.49	6.19	3.95	2.74	3.40	4.64	4.03	2.65	3.17	5.04	4.15	5.25	6.65	16.05
	CD @ 5%	0.28	0.21	1.17	1.30	0.49	0.63	1.70	0.12	0.23	1.63	0.35	1.67	1.34	19.59
	S.Em±	0.10	0.07	0.42	0.46	0.17	1.44	0.61	0.04	0.08	0.22	1.56	0.24	0.12	17.77

Table 2:	Genetic	variations	for various	biochemical	parameters among	g the 96	genotypes of tamarin	d
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Traits	Minimum	Maximum	Mean	PCV (%)	GCV (%)	Heritability (%)	GA	GAM (%)
TSS	2.30	11.03	5.06	36.79	34.62	99.00	3.80	75.11
Starch (%)	0.36	1.99	1.17	33.83	31.92	89.00	0.72	62.05
Reducing sugars (%)	31.41	40.48	37.31	40.92	38.51	84.00	3.18	80.54
Total sugars (%)	40.35	49.18	46.34	30.69	29.26	77.00	2.74	50.92
Non-reducing sugars (%)	6.43	11.78	9.02	12.76	11.30	92.00	2.20	24.42
Total phenols (mg/100g)	36.32	70.39	53.93	12.92	11.05	87.00	12.50	23.18
Total flavonoids (mg/100g)	11.49	36.66	26.28	25.75	22.43	97.00	13.60	51.74
Free amino acids (mg/100g)	2.00	3.76	2.96	17.03	16.82	97.00	1.01	34.23
Total anthocyanin (mg/100g)	2.68	7.21	4.64	25.64	23.45	98.00	2.41	52.02
Crude fiber (%)	6.66	11.23	7.83	10.26	8.93	75.00	1.25	16.02
Antioxidant activity (per cent inhibition)	50.51	91.67	65.01	18.13	17.65	94.00	23.01	35.38
Tartaric acid (mg/100g)	4.8	11.4	7.94	19.01	18.27	92.00	2.87	36.18
Tryptophan (µg/g)	2.03	3.93	3.22	14.97	13.41	80.00	0.79	24.74
Fruit yield/plant (Kg)	49.50	298.50	191.85	34.55	30.60	78.00	17.11	55.83

PCV (%) = Phenotypic Co-efficient of Variability, GCV (%) = Genotypic Co-efficient of Variability, GA = Genetic Advance, GAM = GA as % mean



Fig 1: Clustering of 96 tamarind genotypes based on major food value biochemical traits relationship (Tocher'smethod)



Fig 2: Chromatogram of HPLC analyses for standard tryptophan indicated by arrow

#### Total soluble solids (TSS)

The TSS content ranged from 2.30 to 11.03 with an average mean of 5.06. Maximum TSS content was recorded in the genotype TAM\_MYS3 with 11.03 followed by the genotype TAM\_HAV1 with 9.90 of TSS content (Table 1). The high PCV (36.79%) and high GCV (34.62%) along with high heritability (99.00%) and expected genetic advance as % mean (75.11%) were observed (Table 2).

#### Starch content

The starch content ranged from 0.36 to 1.99% with an average mean of 1.17%. Maximum starch content was recorded in the genotype TAM\_BEN(U)4 with 1.99% followed by the genotype TAM\_BEN(R)2 with 1.98% (Table 1). The high PCV (33.83%) and high GCV (31.92%) along with high heritability (89.00%) and expected genetic advance as% mean (62.05%) were observed (Table 2).

#### **Reducing sugars**

The reducing sugars content ranged from 31.41 to 40.48% with an average mean of 37.31%. Maximum reducing sugars content was recorded in the genotype TAM\_MAN5 with 40.48% followed by the genotype TAM\_MAN1 with 40.00% (Table 1). The high PCV (40.92%) and high GCV (38.51%) along with high heritability (84.00%) and expected genetic advance as% mean (80.54%) were observed (Table 2).

#### **Total sugars**

The total sugars content ranged from 40.35 to 49.18% with an average mean of 46.34%. Maximum total sugars content was recorded in the genotype TAM\_KOL1 with 49.18% followed by the genotype TAM\_CHM3 with 49.17% (Table 1). The high PCV (30.69%) and high GCV (29.26%) along with high heritability (77.00%) and expected genetic advance as% mean (50.92%) were observed (Table 2).

#### Non-reducing sugars

The non-reducing sugars content ranged from 6.43 to 11.78% with an average mean of 9.02%. Maximum non-reducing sugars content was recorded in the genotype TAM\_UK1 with 11.78% followed by the genotype TAM\_UK2 with 11.69%

(Table 1). The high PCV (12.76%) and high GCV (11.30%) along with high heritability (92.00%) and expected genetic advance as% mean (24.42%) were observed (Table 2).

#### **Total phenols content**

The total phenols content ranged from 36.32 to 70.39 mg/100g with an average mean of 53.93 mg/100g. Maximum total phenols content was recorded in the genotype TAM\_DK2 with 70.39 mg/100g followed by the genotype TAM\_DK1 with 66.05 mg/100g (Table 1). The high PCV (12.92%) and high GCV (11.05%) along with high heritability (87.00%) and expected genetic advance as% mean (23.18%) were observed (Table 2).

## **Total flavonoids content**

The total flavonoids content ranged from 11.49-36.66 mg/100g with an average mean of 26.28 mg/100g. Maximum total flavonoids content was recorded in the genotype TAM\_UK1 with 36.66 mg/100g followed by the genotype TAM\_UK2 with 36.63 mg/100g (Table 1). The high PCV (25.75%) and high GCV (22.43%) along with high heritability (97.00%) and expected genetic advance as% mean (51.74%) were observed (Table 2).

#### Free amino acids content

The free amino acids content ranged from 2.00 to 3.76 mg/100g with an average mean of 2.96 mg/100g. Maximum free amino acids content was recorded in the genotype TAM\_KOL5 with 3.76 mg/100g followed by the genotype TAM\_KOL3 with 3.71 mg/100g (Table 1). The low PCV (17.03%) and low GCV (16.82%) along with high heritability (97.00%) and moderate expected genetic advance as% mean (34.23%) were observed (Table 2).

## Total anthocyanin content

The anthocyanin content ranged from 2.68 to 7.21 mg/100g with an average mean of 4.64 mg/100g. Maximum anthocyanin content was recorded in the genotype TAM\_KOL3with 7.21 mg/100g followed by the genotypes TAM\_UDP1 and TAM\_UDP3 with 7.12 mg/100g (Table 1). The high PCV (25.64%) and high GCV (23.45%) along with

high heritability (98.00%) and expected genetic advance as% mean (52.02%) were observed (Table 2).

## Crude Fiber content

The crude fiber content ranged from 6.66 to 11.23% with an average mean of 7.83%. Maximum fiber content was recorded in the genotype TAM\_BAG2 with 11.23% followed by the genotype TAM\_BEN(U)4 with 10.17% (Table 1). The high PCV (10.26%) and high GCV (8.93%) along with high heritability (75.00%) and expected genetic advance as% mean (16.02%) were observed (Table 2).

## Antioxidant activity (per cent inhibition)

The antioxidant activity ranged from 50.51 to 91.67% with an average mean of 65.01%. Maximum antioxidant activity was recorded in the genotype TAM\_UK1 with 91.67% followed by the genotype TAM\_BAG2 with 90.13% (Table 1). The high PCV (18.13%) and high GCV (17.65%) along with high heritability (94.00%) and expected genetic advance as% mean (35.38%) were observed (Table 2).

## Tartaric acid content

The tartaric acid content ranged from 4.80 to 11.4 mg/100g with an average mean of 7.94 mg/100g. Maximum tartaric acid content was recorded in the genotype TAM\_HAV1 with 11.40 mg/100g followed by the genotype TAM\_DK1 with 11.15 mg/100g (Table 1). The variation for high per cent PCV (19.01 per cent) and high per cent GCV (18.27 per cent) along with high heritability (92.00 per cent) and expected genetic advance as% mean (36.18 per cent) were observed (Table 2).

## **Tryptophan content**

The tryptophan content ranged from 2.03 to 3.93  $\mu$ g/g with an average mean of 3.22  $\mu$ g/g. Maximum tryptophan content was recorded in the genotype TAM\_GUL2 with 3.93  $\mu$ g/g followed by the genotype TAM\_HAS1 with 3.90  $\mu$ g/g (Table 1). The high PCV (14.97%) and high GCV (13.41%) along with high heritability (80.00%) and expected genetic advance as% mean (24.74%) were observed for this trait (Table 2).

## Discussion

The table 1 indicated that the top performing five genotypes in terms of fruit yield did not possess good values for biochemical parameters except TAM\_KOL1 genotype which had fairly good amount of tartaric acid (11.40 mg/100g), free amino acid (3.58 mg/100g), total sugars (49.18%) and reducing sugars (39.78%). The study also indicated that generally fruit yield and biochemical parameters do not go together and show inverse relationship. However, tamarind genotypes TAM\_BEN(U)2, TAM\_UK1, TAM\_UK2,TAM\_KOL3, TAM\_MAN5, TAM\_UK2 and TAM\_CHM3 were the best genotypes possessing desirable biochemical parameters in good proportions over the check GKVK17.

The biochemical parameter grouped into 7 major clusters recorded in the dendrogram and presented in Figure 1. Ninety six tamarind genotypes were presented in 7 clusters of which the maximum number of genotypes is included in cluster II having 34 numbers of genotypes and the minimum number in cluster VII having only one genotype and this implied that good the biochemical parameters variations existed among genotypes although variations scattered among genotypes irrespective of locations. The analysis of variance for biochemical parameters showed a highly significant difference among the tamarind genotypes. The GCV and PCV are needed to quantifying the extent of variability in different characters. The estimates of the phenotypic coefficient of variation were higher than the genotypic coefficient of variation for most of the biochemical parameters in tamarind. The results indicated the influence of the environment on the expression of the characters. The PCV ranged from 10.26% (fiber) to 40.92% (reducing sugars) (Table 2). The GCV ranged from 8.93 (fiber) to 38.51% (reducing sugars) among the biochemical parameters of tamarind studied. GCV does not give the entire variation present in the genotypes because the variation in the genotypes is the total of heritable and non-heritable components. Higher heritability also plays an important role which indicates that the phenotype of the traits is strongly influenced by genotype. The heritability value ranged from 75.00% (fiber) to 99.00% (TSS). In the present investigation, high heritability was recorded in most of the biochemical parameters of tamarind genotypes. The genetic advance as% of mean ranged from 16.02% (fiber) to 80.54% (reducing sugars) and the higher value of genetic advance as% a mean recorded in most of the characters expect non-reducing sugars, total phenols, tryptophan and fiber (low) (Table 2). It might be due to the high range of variation among the genotypes. High heritability estimates coupled with high genetic advance as% of mean were observed in all the character except fiber content. It is indicative of additive gene action and selection based on these characters would be more reliable. Moderate/low heritability with low genetic advance as% of the mean value attribute to the presence of nonadditive gene action which indicates the presence of dominance/epistasis and their response to selection would be poor. Environment plays an important role in the expression of the characters. The present finding is in accordance with the finding of Patilshekar and Hanamashetti, (2009)<sup>[17]</sup> and Divakara, (2009)<sup>[7]</sup>, Hamacek et al., 2012<sup>[8]</sup>, Singh and Nandini, (2014)<sup>[23]</sup>, Mayavel et al., 2018<sup>[12]</sup>.

An increase in total soluble solids content reflects the hydrolysis of starch into sugars as fruits ripen, whereas the decrease in TSS content is due to the utilization of carbohydrates as metabolites (Dadzie, 1998)<sup>[6]</sup>. The starch content reflects in the sugar content, that how much starch is undergoing conversion of sugar. The total phenol and total flavonoid content implied that the sensory and nutritional qualities of foods are closely associated with phenolic and contributing directly or indirectly to the desirable or undesirable aroma and taste of the fruit. The free amino acids are very important as a taste substance in fruits development and maturation; they also contribute to stress tolerance as indicated by Kato, et al. (1989) [10]. The% inhibition of antioxidants radical scavenging activity towards DPPH free radical assay allows comparison of relativities of powerful oxidants such as BHT with those present in the extract obtained from fruit residue. Free radical scavenging ability by hydrogen donation is a known mechanism for antioxidation.

The present study revealed the high variations among the tamarind genotypes for biochemical parameters. We conclude that tamarind is rich source of carbohydrates, free amino acids, total phenols, crude fibers and high antioxidant activity in the selected genotypes. Hence, tamarind can be used to supplement cereals and legume crops. The genotypes with high variations for biochemical parameters such as TAM\_BEN(U)2, TAM\_UK1, TAM\_DK2, TAM\_KOL3, TAM\_MAN5, TAM\_UK2 and TAM\_CHM3 could be further exploited in tamarind tree improvement program for selecting the elite genotypes for desirable high biochemical parameters.

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## **Conflict of interest**

The authors declare that there are no conflicts of interest in the reported research.

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