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Original Research Paper

Phenotypic characterization of *Garcinia* species: Implications for conservation and breeding

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ABSTRACT

The genus *Garcinia* (Clusiaceae) is renowned for its medicinal and nutritional value, yet its phenotypic diversity remains underexplored. In this study, 54 accessions from four species *viz*., *G. indica* (29), *G. xanthochymus* (13), *G. gummi-gutta* (10), and *G. mundro* (2), were evaluated for morphological and pomological traits. Significant variability was observed for various morphological traits. Leaf length ranged from 5.80 cm (*G. indica*) to 27.65 cm (*G. xanthochymus*), while, fruit weight varied from 15.10 g (*G. indica*) to 172.00 g (*G. xanthochymus*); total soluble solids (TSS) in rind and pulp showed wide ranges (7.8–26.6 and 1.8–26.0 °Brix, respectively), with a notable negative correlation between fruit length and TSS. Principal component analysis (PCA) revealed that tree spread (PC1: 41.18%), leaf traits (PC2: 33.92%), and tree height/ girth (PC3: 12.79%) were key discriminators, collectively explaining 87.89% of total variability. Cluster analysis segregated species into two groups namely, *G. indica* and *G. mundro* clustered together, while, *G. xanthochymus* formed a distinct group. Promising accessions were identified, including *G. xanthochymus* R2P4 with large fruit size (7.72 cm), weight (241.76 g), high TSS (15.26 °Brix), and *G. indica* KR4P9 with high TSS (20.11°Brix) and low acidity (0.29%). These findings highlight the potential for selecting elite genotypes for breeding programs and underscore the importance of conserving phenotypic diversity in *Garcinia* species.

Keywords: *Garcinia gummi-gutta*, *Garcinia indica*, *Garcinia mundro*, *Garcinia xanthochymus*, multivariate analysis, phenotypic diversity

INTRODUCTION

Garcinia is a genus of approximately 400 species of evergreen trees and shrubs belonging to the family Guttiferae (Clusiaceae). The genus is most diverse in the Malaysian region, with species distribution extending to India, the Micronesian islands, tropical Africa, and the Neotropics (Sarma et al., 2016). In India, *Garcinia* is represented by 43 species, of which 37 occur in the wild, while, the remaining are cultivated (Sabu et al., 2013; Sarma et al., 2016). Among these, 16 species are native to India. The Western Ghats are home to several commonly found *Garcinia* species, including *G. gummi-gutta* (syn. *G. cambogia*), *G. indica*, *G. morella*, *G. xanthochymus*, *G. spicata*, and *G. cowa*.

Garcinia species have diverse applications across the culinary, cosmetic, and pharmaceutical industries. *G. mangostana* is a well-known tropical fruit, consumed as a dessert and valued for its dried fruit rind, which contains tannins and xanthones. Paul, & Zaman (2022) reviewed comprehensively on ethnobotany, nutritional values, phytochemistry and pharmacolo-gical attributes of ten Garcinia species of South-east Asia. Singh et al. (2022) evaluated bioactive constituents of *Garcinia indica*. The sour fruit rind of *G. gummi-gutta* is widely utilized as a flavoring agent in fish curries and has ethnobotanical uses as a digestive aid and a traditional treatment for bowel complaints, intestinal parasites and rheumatism. Its fruit, resembling a small pumpkin, has gained popularity as a weight-loss supplement in recent years (Semwal et al., 2015). The young leaves of *G. cowa* are used as a food additive in various Thai dishes, while, the young shoots and mature fruit of *G. xanthochymus* are consumed as vegetables and edible fruits (Yapwattanaphun et al., 2002).

Effective morphological descriptors should be easily observable, highly discriminative, and stable across different environments. Statistically significant morphological traits, such as leaf and fruit characteristics, can aid in the taxonomic identification of *Garcinia* taxa (Shameer et al., 2016). Hazarika et al. (2024) revealed the genetic diversity of *Garcinia* *pedunculata* Roxb. with multivariate analysis. The present study assesses the phenotypic diversity of *Garcinia* germplasm from southern India, provides valuable insights for optimizing germplasm management and breeding programs. It highlights the potential to select elite and diverse parental accessions, maximizing genetic variability and improving productivity.

MATERIAL AND METHODS

Plant material

Fifty-four trees from four *Garcinia* species *viz.*, *G. indica* (29 accessions), *G. xanthochymus* (13 accessions), *G. gummi-gutta* (10 accessions), and *G. mundro* (2 accessions) referred to here on as GI, GX, GG and GM, were evaluated under Bangalore conditions between 2017 and 2019. The collections of *GI, GX,* and *GG* were obtained through extensive surveys conducted in the Western Ghats during 2001 to 2003. Additionally, an exotic species, *GM*, was procured from a local nursery. These accessions were planted in a field at a spacing of 6 × 6 meters at the ICAR-Indian Institute of Horticultural Research, Bangalore, during 2001 to 2003.

Morphological characterization

Since not all fifty-four trees were fruiting, vegetative traits were recorded for all trees, whereas pomological traits were recorded for thirty-three trees: *G. indica* (GI; 16 accessions), *G. xanthochymus* (GX; 12 accessions), *G. gummi-gutta* (GG; 3 accessions), and *G. mundro* (GM; 2 accessions). Fruit samples from each tree were randomly collected from various parts of the tree at full ripening and evaluated for fifteen morphological characters over two years. Eight tree growth and five leaf characters were recorded for individual trees. Quantitative traits, such as the length and width of leaves, fruits, and seeds, were measured using digital vernier calipers with an accuracy of 0.10 mm. Fruit weight and seed weight were determined using an analytical balance with a precision of 0.01 g. Fruit shape was characterized according to the morphological descriptors outlined by Parthasarathy & Nandakishore (2014), while fruit color was recorded using the Royal Horticultural Society Colour Chart. Total soluble solids (TSS) content was measured using an Erma Hand Refractometer (0-32 °Brix). For titratable acidity estimation, one gram of pulp was extracted with water, and the sample was homogenized using a pestle and mortar. The titratable acidity of the extract was determined by titration with 0.01 N NaOH in the presence of phenolphthalein as an indicator.

Statistical analysis

The data were analyzed for mean, variances, correlations, and genetic diversity to deduce the genetic similarity/dissimilarity. Coefficients of variation (CV) were determined as indicators of variability. Correlations between the traits were determined using the Pearson correlation coefficient, while, relationships among the accessions for tree and fruit traits were investigated with principal components analysis (PCA). The data analysis was performed using R software. Hierarchical clustering was carried out and the distance matrix required for hierarchical clustering was computed using the 'dist' function which is based on Euclidean distances. (R Core Team, 2019).

RESULTS AND DISCUSSION

Morphological diversity

A wide variation was detected among the studied species (Fig. 1) as confirmed by relatively high CV values obtained for most of the measured traits. Twelve out of seventeen characters measured (70.5% in total) showed CVs greater than 20%, which is an indication of presence of high variation among the accessions of different species (Table 1). Most of the accessions showed moderate variability for tree height, tree girth, tree spread (EW & NS) and number of main branches.

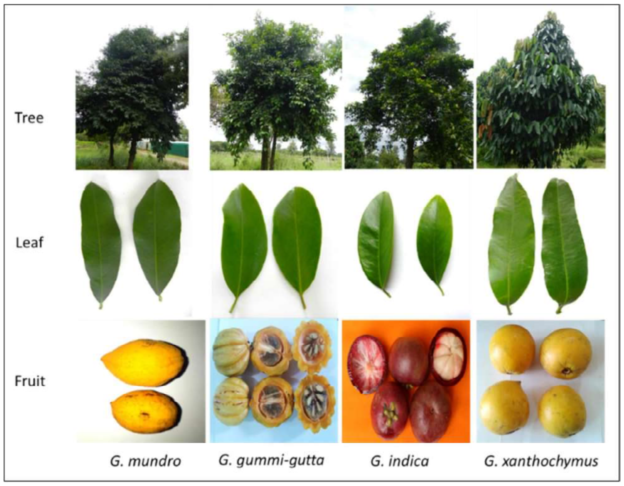

Fig. 1 : Morphological variability in four species of *Garcinia*

Table 1 : Descriptive statistics for morphological traits in *Garcinia* accessions

Character	Abbrev.	*Garcinia indica*					*Garcinia gummigutta*					*Garcinia xanthochymus*					*Garcinia mundro*				
		Mean	Max	Min	SD	CV (%)	Mean	Max	Min	SD	CV (%)	Mean	Max	Min	SD	CV (%)	Mean	Max	Min	SD	CV (%)
Tree height (cm)	Tr_height	442.4	922.5	135	196.87	44.5	587.35	995	350	192.62	32.79	430.46	462.5	345	33.14	7.7	468.75	620	317.5	213.9	45.63
Tree girth (cm)	Tr_girth	48.62	86	21	19.92	40.98	52	78.5	35	13.18	25.35	46.15	57.5	32.5	6.78	14.7	69.75	88.5	51	26.52	38.02
Tree spread EW (cm)	Sp_EW	324.38	685	110	138.65	42.74	249.1	390	80	119.64	48.03	283.27	415	177.5	82.15	29	415	477.5	352.5	88.39	21.3
Tree spread NS (cm)	Sp_NS	318.19	550	120	117.12	36.81	252.3	385	97	113.16	44.85	278.31	365	195	62.63	22.5	356.25	385	327.5	40.66	11.41
No. of main branch	Main_bra	4.59	11	2	2.57	56.05	3.7	6	2	1.49	40.39	5	6.5	2	1.32	26.46	1	1	1	0	0
Leaf length (cm)	L_len	6.42	7.25	5.8	0.37	5.77	12.75	13.45	11.85	0.59	4.6	23.68	27.65	21.8	1.73	7.32	9.43	9.6	9.25	0.25	2.63
Leaf width (cm)	L_wid	3.41	4	3	0.23	6.63	5.3	5.65	5.05	0.15	2.92	7.22	7.55	6.9	0.18	2.52	3.4	3.45	3.35	0.07	2.08
Petiole length (cm)	P_len	1.13	1.3	0.95	0.1	8.42	1.37	1.55	1.25	0.1	7.13	1.65	1.75	1.5	0.09	5.53	1.2	1.25	1.15	0.07	5.89
No. of fruit/ tree	Fr/tree	139.94	653	8	155.94	111.44	58.67	114.5	12	51.86	88.4	33.13	77.5	16	18.39	55.51	17.75	24	11.5	8.84	49.8
Fruit yield (kg/tree)	F_yield	2.98	16.98	0.2	4.05	135.74	3.91	8.45	0.61	4.06	104.02	3.87	10.26	1.43	2.94	75.84	0.37	0.46	0.28	0.13	35.6
fruit length (cm)	F_len	2.94	3.86	2.21	0.44	14.83	4.39	4.86	4.15	0.4	9.21	3.45	4.19	2.9	0.46	13.46	4	4.25	3.75	0.35	8.84
Fruit width (cm)	F_wid	4.85	3.91	2.61	0.41	13.19	5.35	5.72	5.17	0.32	5.93	6	7.21	4.74	0.66	11.05	2.8	2.85	2.75	0.07	2.53
Fruit weight (g)	F_wt	22.48	31.8	15.1	5.06	22.51	61.13	77.34	50.95	14.19	23.21	103.94	172	72	29.57	28.45	19.75	22	17.5	3.18	16.11
Pulp (%)	Pulp_wt	47.62	65	26	9.7	20.37	33.47	35.42	30.29	2.78	8.31	42.04	48.2	40.1	2.32	5.52	95.95	96.75	95.15	1.13	1.18
Rind (%)	Rind_wt	44.79	64	33.1	8.62	19.25	52.8	56.6	50.36	3.33	6.31	88.88	55.2	48.2	2	3.91	-	-	-	-	-
No. of seed/fruit	S/fr	5.21	7.4	2	1.62	31.05	7.82	8.3	7.45	0.44	5.59	2.54	4	1.5	0.72	28.39	1	1	1	0	0

Leaf length (cm) ranged from 5.80 to 7.25 in *G. indica* (GI), 11.85 to 13.45 in *G. gummi-gutta* (GG), 21.80 to 27.65 in *G. xanthochymus* (GX), and 9.25 to 9.60 in *G. mundro* (GM). Leaf width (cm) ranged from 3.00 to 4.00 in GI, 5.05 to 5.65 in GG, 6.90 to 7.55 in GX, and 3.35 to 3.45 in GM. Petiole length (cm) ranged from 0.95 to 1.30 in GI, 1.25 to 1.55 in GG, 1.50 to 1.75 in GX, and 1.15 to 1.25 in GM. Thatte et al. (2012) reported that leaf length and width in GI from the Maharashtra region ranged from 9.23 cm to 16.3 cm and 3.8 cm to 5.73 cm, respectively. Additionally, Gupta et al. (2018) reported that leaf length and leaf width in GX from the Assam region ranged from 20 cm to 28 cm long and 5 cm to 7 cm wide, with petiole lengths ranging from 1.5 cm to 2.5 cm. Leaf color and shape were recorded for all accessions. Leaf color ranged from light green (41 accessions) to dark green (13 accessions), while leaf shape ranged from oval (41 accessions) to linear (13 accessions). Thatte et al. (2012) and Shmeer et al. (2016) reported similar leaf shapes for GI and GG.

Fruit length (cm) ranged from 2.21 to 3.86 in *G. indica* (GI), 4.15 to 4.86 in *G. gummi-gutta* (GG), 2.90 to 4.19 in *G. xanthochymus* (GX), and 3.75 to 4.25 in *G. mundro* (GM). Fruit width (cm) varied from 2.61 to 3.91 in GI, 5.17 to 5.72 in GG, 4.74 to 7.21 in GX, and 2.75 to 2.85 in GM. Fruit weight (g) ranged from 15.10 to 31.80 in GI, 50.95 to 77.34 in GG, 72.00 to 172.00 in GX, and 17.50 to 22.00 in GM. Fruit yield (kg/tree) ranged from 0.02 to 16.98 in GI, 0.61 to 8.45 in GG, 1.43 to 10.26 in GX, and 0.28 to 0.46 in GM (Table 2). Fruit skin color exhibited variation across accessions, with dark red (6) and deep pink (10) found in GI, while other species displayed yellow-colored fruits. Fruit shape ranged from globose (4) to flat round (12) in GI, round (3) in GG, globose in GX, and ovoid in GM. Accessions with higher yields and larger fruits may be considered for commercial cultivation. Priya Devi et al. (2013) reported that fruit weight in GI accessions from Goa ranged from 6.80 to 47.60 g, with fruit diameter varying from 1.79 to 5.51 cm. In GG, fruit color was reported as yellow, and in GI, it was purple (Shameer et al., 2016). Patil et al. (2005) noted that GI fruits are typically globose or spherical, dark red when ripe, and contain 5 to 8 large seeds. Kadam et al. (2012) observed that fruit shape in GI ranged from round, oblong to oval with pointed tips. Babu et al. (2021) reported variation in fruit weight, fruit length and fruit width in GG. Consistent findings in other perennial crops such as *Phoenix dactylifera* (Ennouri et al., 2017) and *Ziziphus mauritiana* (Norouzi et al., 2017) have been reported.

Table 2 : Frequency distribution of qualitative morphological traits observed among the accessions of various *Garcinia* species

Character	Abbrev.	*Garcinia indica*	*Garcinia gummigutta*	*Garcinia xanthochymus*	*Garcinia mundro*
Tree nature	Tr_nature	Upright (23), semi spreading (2), spreading (4)	Upright (9), spreading (1)	Upright (13)	Spreading (2)
Shoot colour	Shoot_col	Brown (29)	Brown (9), cream (1)	Cream (13)	Brown (2)
Foliage density	Fol_density	Dense (2), semi dense (13), sparse (14)	Dense (4), semi dense (5), Sparse (1)	Highly dense (13)	Dense (2)
Leaf colour	L_col	Light green (29)	light green (10)	Light green (2), Dark green (11)	Dark green (2)
Leaf shape	L_shap	Oval (29)	Oval (10)	Linear (13)	Oval (2)
Fruit shape	F_shp	Globose (4), flat round (12)	Round (3)	Globose (13)	Ovoid (2)
Fruit tip	F_tip	Normal (4), pointed (2), depreseed (10)	Pointed (3)	Pointed (13)	Pointed (2)
Fruit colour	Fr_col	Dark red (6), deep pink (10)	Green yellow (3)	Deep yellow (13)	Deep yellow (13)
Pulp colour	Pulp_col	White (16)	White (3)	Yellow (13)	Yellow (2)
Pulp taste	Pulp_taste	Sweet (16)	Very sour (3)	Sour (13)	Sour (2)

The range of pulp weight in *G. indica* (GI) was from 26% to 65%, while, it ranged from 30.29% to 35.42% in *G. gummi-gutta* (GG), 40.10% to 48.20% in *G. xanthochymus* (GX), and 95.15% to 96.75% in *G. mundro* (GM). The rind weight varied from 33.14% to 64% of the fruit in GI, 50.36% to 56.60% in GG, and 48.20% to 55.2% in GX. Since, the rind is attached to the pulp in GM, rind weight was not recorded for this species. The number of seeds per fruit ranged from 8.3 to 7.45 in GG and 1.00 in GM. Total soluble solids are a key component of fruit sweetness and are used to estimate sugar content (Hirsch et al.,

Table 3 : Morphological characterization of *G. xanthochymus* accessions

Collector ID	Fruit length (cm)	fruit breadth (cm)	breadth xweight (g)	Pulp weight (g)	weight seed weight (g)	Pulp recovery (%)	Number of seeds	TSS (°Brix)	Acidity (%)
R1P4	6.34	6.83	147.44	123.84	22.73	84.00	2.70	12.54	4.74
R1P5	7.17	7.31	181.44	156.31	22.33	86.15	2.70	14.42	3.54
R2P4*	7.72	8.09	241.76	205.08	33.34	84.83	3.40	15.26	4.16
R5P4	7.36	7.88	216.08	185.68	33.09	85.93	2.90	16.29	3.07
R5P5	7.50	7.47	191.62	163.70	25.89	85.43	2.40	14.34	3.89
R6P4	7.03	7.82	212.81	180.46	36.59	84.80	2.90	14.82	4.48
R6P5*	7.53	7.86	222.32	190.86	31.04	85.85	3.10	15.32	3.28
R7P4	7.04	7.10	169.76	148.58	19.67	87.52	2.30	13.27	4.00
R7P5	7.09	7.46	189.84	161.68	28.51	85.17	3.20	13.05	3.97
R8P4	7.08	7.45	191.98	164.74	25.77	85.81	2.50	14.44	4.84
R9P5	7.13	7.18	173.32	150.32	21.99	86.73	2.40	13.84	3.94
R10P4	6.46	6.46	132.26	114.16	21.15	86.31	2.40	13.18	3.56
R10P5	6.64	6.37	139.70	121.72	22.00	87.13	2.10	14.36	3.49

*Promising accessions

Table 4 : Morphological characterization of *G. indica* accessions

Collector ID	Fruit length (cm)	Fruit breadth (cm)	Fresh weight (g)	Rind weight (g)	Rind thickness (cm)	Aril weight (g)	Rind: Aril	Aril TSS (°Brix)	Rind TSS (°Brix)	Acidity (%)	Total anthocyanins (mg C3G/100 g FW)	Total fruits/ tree	Yield (kg)
KR2P7	3.36	4.34	33.80	18.60	0.31	9.94	1.10	16.66	17.97	0.35	843.7808	3330	376.126
KR4P7*	3.07	3.74	26.42	11.56	0.25	10.47	2.19	16.87	15.89	0.26	732.6758	4100	205.006
KR4P8	2.65	3.31	16.50	9.80	0.27	4.47	1.43	20.25	20.80	0.35	657.6799	11070	210.886
KR4P9*	2.75	3.22	21.38	10.88	0.25	7.62	1.72	20.46	20.11	0.29	748.107	7560	178.18
KR5P7	3.52	3.94	28.96	15.98	0.32	9.31	2.19	16.50	16.19	0.61	883.2848	3875	211.441
KR6P7	3.26	3.38	19.89	13.00	0.42	5.93	1.34	16.87	13.43	0.96	923.406	15	4.041
KR6P9	3.60	3.53	23.42	11.54	0.30	8.60	1.48	22.11	21.76	1.79	907.9748	1040	84.063
KR7P7	3.09	3.98	28.72	14.30	0.26	9.68	1.75	17.74	17.69	0.74	908.2834	1100	100.551
KR8P7*	3.65	4.07	35.48	20.02	0.30	11.43	1.42	17.31	18.16	0.83	873.4088	4004	255.755
KR8P8	3.07	3.67	25.60	13.48	0.27	9.49	1.59	19.89	20.68	0.54	815.0786	5850	264.689
KR9P8	3.47	3.54	24.46	14.16	0.31	8.90	1.69	16.66	16.42	0.61	826.4978	850	102.785
KR10P7	2.78	2.92	14.06	7.82	0.25	4.64	1.69	18.42	18.06	0.54	860.1379	550	47.198

*Promising accessions

2012). Significant differences were observed among the accessions for this biochemical property. The range of rind TSS in GI was from 12.5 to 26.60 °Brix, while in GG it ranged from 12.10 to 12.7 °Brix, in GX from 12.00 to 13.40 °Brix, and in GM from 7.8 to 8.1 °Brix. Pulp TSS (°Brix) ranged from 12 to 26 in GI, 14.05 to 15.10 in GG, 1.8 to 16.10 in GX, and 7 in GM. Patil et al. (2005) reported that 9.08% TSS in GI var. *Kokum Amruta*. This may be due to the fact that fruits growing in arid regions with limited water tend to accumulate more dry matter and have lower moisture content, which may lead to higher TSS (Meghwal & Azam, 2014). When selecting superior genotypes, breeders should prioritize the TSS content of the fruits (Hazarika & Lalnunsangi, 2019). Korikanthimath & Desai (2006) also reported similar variation in TSS across various *Garcinia* species. Based on morphological analysis, the following accessions were identified as promising namely, R2P4 (fruit size, fruit weight, high TSS) and R6P5 (fruit size, fruit weight, TSS) in *Garcinia xanthochymus*; and KR4P7 (fruit size and weight, low acidity Table 3), KR8P7 (fruit size, rind weight), and KR4P9 (high TSS, low acidity, more number of fruits per plant) in *Garcinia indica* (Table 4).

Correlation analysis

The strength of the correlation between traits reflects the potential of the studied germplasm in breeding programs, assisting breeders in selecting suitable parental partners and setting breeding goals (Khadivi-Khub & Anjam, 2014). Additionally, correlation analysis aids in developing selection strategies for traits that are difficult to assess directly, by examining the response of correlated traits when one is under selection pressure (Fereidoonfar et al., 2018). The bivariate correlations among ten parameters (Table 5), revealed a negative correlation between fruit length and both rind TSS and pulp TSS. A positive correlation was found between fruit length and fruit weight, and between fruit weight and fruit yield. These findings suggest that fruit length to be considered in selection criteria for fruit quality traits. De Salvador et al. (2006) observed negative correlation between fruit size and TSS content, and a strong positive correlation between fruit size and fruit weight in apples.

Principal component and cluster analysis

Principal Component Analysis (PCA), a multivariate statistical technique, was employed to identify the most significant traits in the dataset. This analysis helps clarify the primary differences between the accessions while reducing the volume of data (Ringner, 2008). The relative variance of each component, expressed as percentages, indicates its importance in explaining the variance of the studied traits. PCA has been widely used in germplasm evaluation for various fruit species, including *Carissa* (Kanupriya et al., 2019) and *Mangifera* (Jena et al., 2021). The main goal of PCA is to determine the principal factors that reduce the number of parameters necessary for genotype discrimination. In general, the high correlation between the original variables and the extracted principal components (PCs) highlighted by this method simplifies the evaluation indices.

Table 5 : Correlation coefficients among fruit morphological traits observed in the accessions of various *Garcinia* species

Trait	F/tree	F_yield	F_len	F_wid	F_wt	P_wt	R_wt	S/fr	R_TSS	P_TSS
F/tree	1									
F_yield	0.73	1								
F_len	-0.29	0.05	1							
F_wid	0.11	0.08	-0.1	1						
F_wt	-0.28	0.3	0.43	0.14	1					
P_wt	-0.13	-0.3	0.08	-0.05	-0.34	1				
R_wt	-0.07	-0.01	-0.07	0.02	0.18	-0.23	1			
S/fr	0.35	0.14	-0.13	0.17	-0.37	-0.37	-0.05	1		
R_TSS	0.56	0.16	-0.64	0.21	-0.44	-0.18	-0.1	0.49	1	
P_TSS	0.46	0.15	-0.49	0.24	-0.37	-0.23	-0.09	0.59	0.81	1

F_yield: fruit yield (kg/tree), F_len: fruit length (cm), F_wid: fruit width (cm), F_wt: fruit weight (g), P_wt: pulp weight (%), R_wt: rind weight (%), S/fr: seeds per fruit, R_TSS: rind TSS (%), P_TSS: pulp TSS (%)

Table 6 : Eigen values and cumulative variance for the three principal components derived from PCA in *Garcinia* species accessions

Character	Component		
	1	2	3
T_height	-0.3053	-0.3027	0.4802**
T_girth	-0.3738	-0.2871	0.4307**
Sp_EW	-0.4363**	-0.2406	-0.1688
Sp_NS	-0.4489**	-0.2581	-0.2187
Main_br	-0.1658	-0.2737	-0.7112**
L_len	0.3360	-0.4613**	-0.0005
L_wid	0.3347	-0.4726**	0.0097
P_len	0.3503	-0.4362**	0.0421
% of variance	41.18	33.92	12.79
Cumulative %	41.18	75.1	87.89

**Eigen values > 0.40 are significant

The results of the PCA (Table 6) revealed that three PCs with Eigen values greater than 1 were extracted, explaining 87.89% of the total variance. Traits with a PC loading greater than 0.400 were considered significant. The results indicated that tree growth parameters, including tree spread, were prominent in PC1; leaf morphological variables (leaf length, leaf width, and petiole length) were significant in PC2; and PC3 represented primarily variables related to tree height, tree girth, and the number of main branches. A bi-plot based on the first two main PCs, accounting for 75.10% of the variance, depicted the relationship among the four *Garcinia* species. The bi-plot visualizes the two-dimensional distribution of the accessions, with accumulation in specific regions reflecting their similarity. According to the bi-plot (Fig. 2), the populations were divided into two groups: GI and GM were grouped together, GX formed a second group, and GG was placed in between. The scatter plot showed the genetic distances between the species, reflecting their relationships.

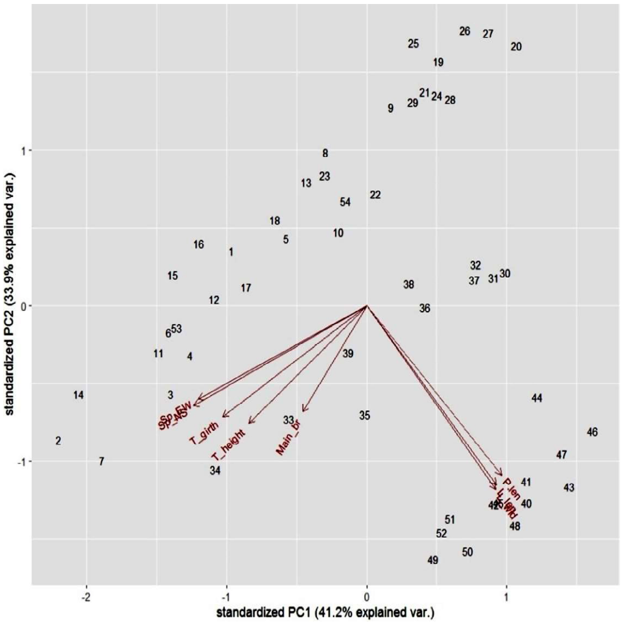

Fig. 2 : A scatter plot revealed by PC1 and PC2 using tree morphological characters of the *Garcinia* accessions

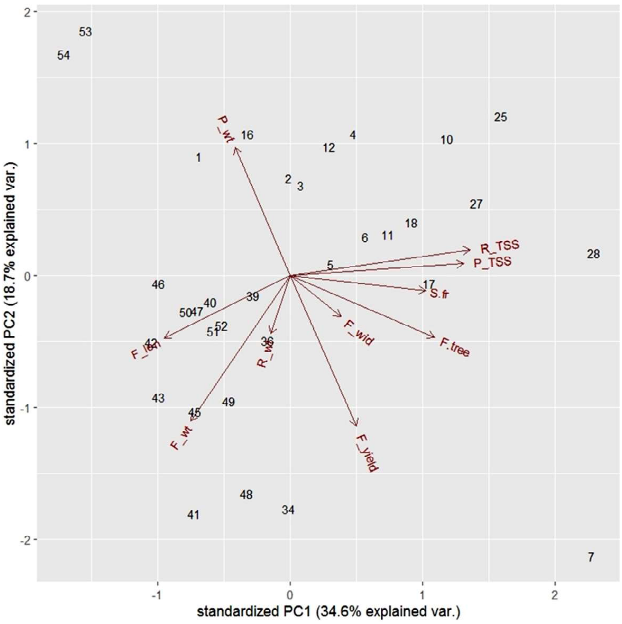

Fig. 3: A scatter plot revealed by PC1 and PC2 using fruit morphological characters of the *Garcinia* accessions

The PCA for fruit traits across thirty-three accessions is presented in Table 7. PCA explained 75.88% of the total variance with four main components having eigen values greater than 1. PC1, which accounted for 34.63% of the variance, was associated with rind TSS and pulp TSS. PC2, which explained 18.66% of the variance, included traits such as fruit yield, fruit weight, and pulp weight. Traits such as number of fruits per tree and fruit yield were represented in PC3, explaining 12.47% of the variance. PC4, which explained 10.13% of the variance, included fruit width and rind weight. These components played a major role in distinguishing the accessions. A biplot analysis of PC1 and PC2, which together accounted for

Table 7 : Eigen values and cumulative variance for three principal components derived from PCA in *Garcinia* species accessions

Character	Component			
	1	2	3	4
Fruit/tree	0.3899	-0.2266	0.4277**	-0.1888
F_yield	0.1794	-0.5536**	0.4377**	-0.1338
F_ len	-0.3377	-0.2295	0.2364	0.2502
F_ wid	0.1369	-0.1507	-0.2093	0.7765**
F_wt	-0.2672	-0.5339**	-0.1123	0.1718
P_wt	-0.1485	0.4709**	0.3944	0.1262
R_wt	-0.0510	-0.2133	-0.5666**	-0.4394
S.fr	0.3650	-0.0567	-0.1290	0.1668
R_TSS	0.4853**	0.0964	-0.0647	0.0021
P_TSS	0.4671**	0.0450	-0.1256	0.1203
% of variance	34.63	18.66	12.47	10.13
Cumulative %	34.63	53.29	65.76	75.88

**Eigen values > 0.40 are significant

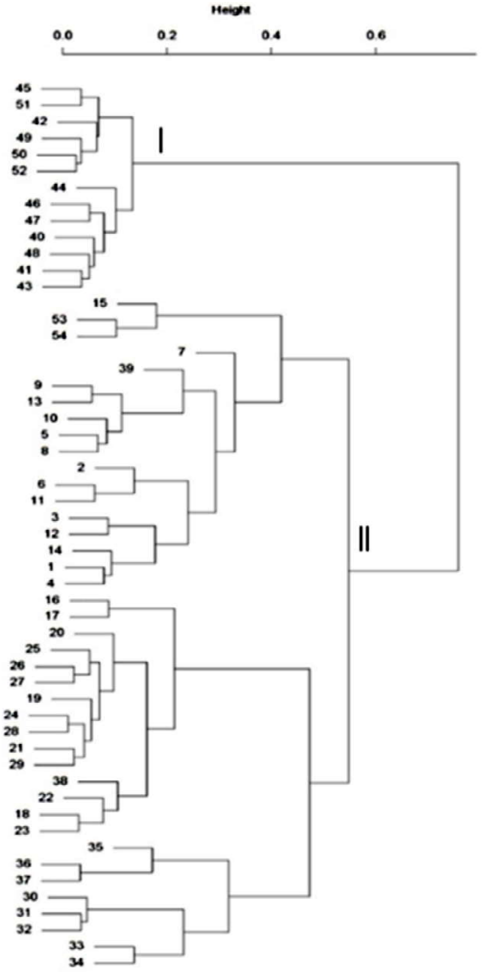

Fig. 4 : Dendrogram A generated based on tree morphological traits

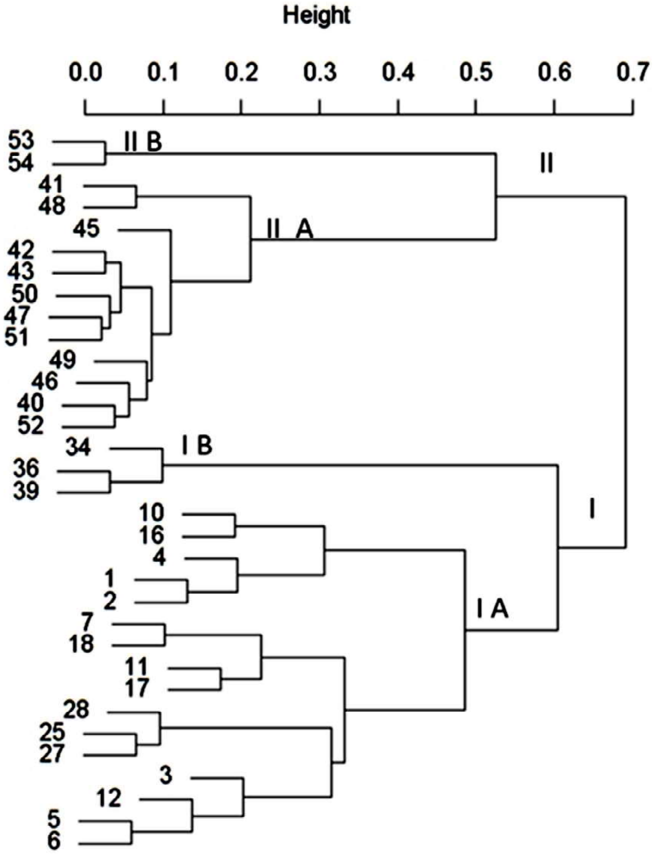

Fig. 5 : Dendrogram B generated based on fruit morphological traits

53.29% of the variance (Fig. 3), grouped accessions that were similar in terms of the effective traits. The GG and GX accessions were clustered closely, indicating high similarity, while the GM accessions were separated from the others.

Cluster analysis was performed on standardized data for hierarchical associations using Ward's method for agglomeration and the squared Euclidean distance as a dissimilarity measure. Two dendrograms were constructed: one based on tree and leaf traits, and the other based on pomological traits. Dendrogram A (Fig. 4) included 54 accessions and formed two main clusters. Cluster I consisted of accessions from three species (GI, GG, and GM), characterized by brown shoot color and oval leaf shape. Cluster II included all the accessions of GX, distinguished by their upright tree structure, cream-colored shoots, dense foliage, and linear leaf shape. Dendrogram B (Fig. 5) represented 33 accessions of *Garcinia* species that had started fruiting under Bangalore conditions. The pomological data revealed two primary clusters. The first major cluster (I) was split into two sub-clusters: Sub-cluster I-A, consisting entirely of GI accessions, and sub-cluster I-B, which contained GG accessions. The second cluster (II) included accessions of GX (sub-cluster II-A) and GM (sub-cluster II-B).

Hierarchical cluster analysis (HCA) provided insights into the similarity and dissimilarity of the accessions, offering a clearer understanding of the relationships among the four species. This approach, which incorporates all the variance in the dataset, contrasts with PCA, which typically highlights only the first few principal components. The dendrograms from morphological traits clearly separated the four *Garcinia* species, aligning with the results from the PCA bi-plot. This consistency verifies the reliability of present findings and demonstrates that both methods are valuable for evaluating the diversity within *Garcinia* species. Mohan et al. (2012) reported species-specific differences in seed germination and plant development patterns within *Garcinia*. Moreover, GI, GG, and GX have been identified as genetically and chemically distinct among the nine *Garcinia* species (Anerao et al., 2021).

CONCLUSION

This study characterized 54 accessions of four *Garcinia* species, revealing significant phenotypic diversity in fruit traits and vegetative features, with distinct clustering separating *G. xanthochymus* from other species. The negative correlation between fruit length and TSS highlights important breeding trade-offs. Promising accessions such as *G. xanthochymus* R2P4 and R6P5 and *G. indica* KR4P9, KR4P7 and KR8P7should be prioritized for commercial cultivation, while, underrepresented species (e.g., *G. mundro*) warrant expanded germplasm collection. Future work should integrate molecular markers with these phenotypic data to identify QTLs for superior traits and explore postharvest applications of high-TSS varieties. These findings provide a robust foundation for both conservation strategies and breeding programs aimed at unlocking the economic potential of *Garcinia* species through scientifically-informed selection of elite genotypes.

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