

Genetic Variability Studies Based on Morphological and Physicochemical Characteristics Among Different Longan (*Dimocarpus longan* Lour.) Genotypes Under North Bihar Conditions

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Abstract

The present experiment was carried out in a randomized complete block design (RCBD) with three replications to study morphological variability, genetic variability, heritability, and genetic advance for different traits of twenty genotypes. The results indicated that the genotypes were diversified for all the quantitative and qualitative traits except a few qualitative traits. The phenotypic coefficient of variation (PCV) showed higher than the genotypic coefficient of variation (GCV) which indicates the meager effect of environment on the phenotypic expression of traits. The high heritability coupled with high genetic advance as percent of mean were recorded for the traits viz., plant height, trunk girth, crown diameter, tree volume, rachis and petiole length, duration of panicle immitation, number of days from panicle initiation to flowering, length and width of inflorescence, number of fruits per bunch, fruit, aril and seed weight, aril thickness, titratable acidity and TSS acid ratio. Therefore, these traits can be used as selection indices for indirect selection for the crop improvement programmes. On the basis of mean performance found best performing genotypes LGC-6 for yield attributing and fruit quality traits.

1. Introduction

Longan (*Dimocarpus longan* Lour.) is one of the most important tropical and subtropical evergreen fruit crops that is native to Southern China and was introduced into India in 1798 (Yang et al., 2009; Huang et al., 2021). It is primarily subtropical necessitating a seasonal change in order to flower, but it is also planted in the tropics (Mariana et al., 2011; Puri, 2001; Yang et al., 2009). It is grown in over 20 countries, ranging from Sri Lanka and India to East Malaysia and Australia (Huang et al., 2021). It is commonly cultivated in Asian countries and is grown throughout the South East Asia from tropical to subtropical regions. Longan was cultivated in Southern China from more than 2000 years ago and during this period about 300 cultivars have been selected (Li and Zhuang, 1983). Due to the long tradition of cultivation and being the center of origin, China has the richest germplasm diversity of litchi and longan. The leading producing countries in the world are China, Thailand, Vietnam, India and South Africa. These five countries produce 90% of the world's longan (Qiu, 2012; Huang et al., 2021). In India, longan is mainly cultivated in Assam, West Bengal, Bihar, Kerala and Karnataka. Even so, longan is less well-known in India than in other Asian nations, compared to the litchi. It is usually imported from Thailand to India (Kumar et al., 2022). In India, there is a lack of studies on the diversity and distribution of longan. There are numerous local cultivars of longan grown in India that are known by their regional names, most of which refer to their origins. Gandaki Longan-1 is the only cultivar developed by the ICAR-National Research Centre on Litchi at Muzaffarpur, Bihar.

The characterization of longan germplasms in India is very necessary for further crop improvement programme. Genetic improvement of any crop species is greatly depends upon the magnitude of existed variability among the different characters. A diverse gene pool is very essential for development of improved cultivars of any crop (Bailey-Serres et al., 2019). High heritability estimate coupled with high genetic advance as per cent of mean indicates that the breeding can be done by directly selecting these traits for further crop improvement

There have been several studies done on the genetic diversity analysis of longan through molecular markers such as ISSR markers (Mariana et al., 2011), SSR markers (Jia-xin et al., 2011), AFLP markers (Lin et al., 2005), and RAPD markers (Mei et al., 2014), but no study has been done on the genetic diversity of longan based on morphological traits. In India, studies have not been done on the diversity and distribution of longan. As a result, the current study was done to assess the genetic variability among different longan genotypes for morphological and biochemical traits. This is the first kind of study in India as it has a good bank of genetic variability, which might help in identifying the desirable genotypes.

2. Material and Methods

2.1. Experiment site

The experiment was conducted in the year 2019 at ICAR-National Research Centre on Litchi, Muzaffarpur (Bihar), located at an altitude of 210 meters above mean sea level, between 26.22° 564" North longitude and 85.11° 2664" East longitude. Muzaffarpur has a humid subtropical climate with hot, desiccating summers and an annual rainfall of roughly 1150 mm. The summer temperatures in this region range from 30°C to 43°C, while winter temperatures range from 5°C to 10°C. All agricultural activities are influenced by the three seasons, i.e., winter (November to February), summer (March to June), and the rainy season (mid-June to mid-October).

2.2. Plant material

The present study was conducted on 10 years old 20 longan genotypes collected from different sources and conserved in a field gene bank at ICAR- National Research Centre on Litchi, Muzaffarpur-Bihar. The genotypes were planted at a spacing of 8 m × 8 m and the uniform cultural practices were provided to all the trees.

S. No.	Genotypes	Experimental site	S. No.	Genotypes	Experimental site
1.	LGC-1	ICAR-NRC Litchi	11.	LGC-37	ICAR-NRC Litchi
2.	LGC-6	ICAR-NRC Litchi	12.	LGC-40	ICAR-NRC Litchi
3.	LGC-12	ICAR-NRC Litchi	13.	LGC-47	ICAR-NRC Litchi
4.	LGC-18	ICAR-NRC Litchi	14.	LGC-49	ICAR-NRC Litchi
5.	LGC-22	ICAR-NRC Litchi	15.	LGC-50	ICAR-NRC Litchi
6.	LGC-24	ICAR-NRC Litchi	16.	LGC-52	ICAR-NRC Litchi
7.	LGC-25	ICAR-NRC Litchi	17.	LGC-54	ICAR-NRC Litchi
8.	LGC-26	ICAR-NRC Litchi	18.	LGC-59	ICAR-NRC Litchi
9.	LGC-27	ICAR-NRC Litchi	19.	LGC-60	ICAR-NRC Litchi
10.	LGC-34	ICAR-NRC Litchi	20.	LGC-61	ICAR-NRC Litchi
Note: LGC is denoted as Longan Germplasm Collection while ICAR-NRC Litchi stands for ICAR- National Research Centre on Litchi, Muzaffarpur-Bihar					

2.3. Characterization and evaluation

In current study, a total of 56 qualitative and quantitative traits were observed against twenty longan genotypes and all the morphological traits were recorded as per IPGRI Litchi descriptor. There are 22 qualitative traits which were recorded in studied genotypes *viz.*, trunk surface, tree growth habit, tree vigour, crown shape, branching density, young leaf colour, mature leaf colour, leaf arrangement, base shape, leaflet curvature, abundance of flower, fruit maturity group, fruit intensity, and aril quality. A total of 34 morpho-biochemical quantitative traits were observed *viz.*, plant height (PHT), trunk girth, (TG), crown diameter (CD), tree volume (TV), number of leaflets (NFL), leaflet blade length (LLG), leaflet blade width (LWD), rachis length (RLG), petiole length (PTLG), duration of panicle initiation (DPI), number of days from panicle initiation to flowering (DPIF), duration of flowering (FRD), length of inflorescence (INLG), width of inflorescence (INWD), number of days from fruit set to maturity (DFSM), number of fruits per bunch (FTPb), fruit length (FTLG), fruit diameter (FTWD), fruit length width ratio (FLW), weight (FTWT), fruit colour (FC I, a, b), aril weight (AWT), aril and seed weight ratio (ASWT), aril thickness (AT), peel weight (PLWT), seed length (SLG), seed width (SWD), seed weight (SWT), Aril/seed weight ratio (ASWT), total soluble solids (TSS°B), titratable acidity (TA), total soluble solids/acid ratio (TT) and ascorbic acid (AA).

Plant height and crown diameter were measured with the help of a pole. Trunk girth was measured with the help of measuring tape at 15 cm above the ground level. Leaf length, leaf width, rachis length, petiole length, inflorescence length and inflorescence width were measured with help of scale. Fruit length, fruit width, aril thickness, seed length and seed width were measured by digital Vernier caliper. Fruit weight, aril weight and seed weight were measured with the help of electric balance. The physico-chemical parameters like TSS determined by digital hand refractometer at room temperature, titratable acidity according to Ranganna (1997), and ascorbic acid determined by the indophenols method (Freed (1966). The TSS/Acidity ratio was calculated by dividing the total soluble solids by the titratable acidity.

2.4. Statistical analysis

Analysis of variance (ANOVA) was performed for testing the presence of significant differences among the genotypes. It was done according to procedure of complete randomized block design for each parameter as per methodology suggested by Burton (1952). Coefficient of variance (genotypic and phenotypic), heritability in broad sense and genetic advance as per cent of mean, were computed by standard statistical procedure and analyzed by software WINDOSTAT Version 9.3.

3. Results and Discussion

3.1. Evaluation of qualitative traits

In this experiment, the characterizations of qualitative traits have been done for twenty longan genotypes (Table 1). All the qualitative traits were highly diversified among the twenty longan genotypes except for a few *viz.*, branching density, branching pattern, leaflet blade shape, leaflet apex shape, and protuberance. The genotypes have shown three types of trunk surface (rough, very rough and smooth), and smooth trunk surface was predominant, noticed in 12 genotypes. The spreading growth habit of tree was noticed in 12 genotypes followed by semi erect in 3, erect in 2 and drooping in 3 genotypes. The medium branching density was predominant (8 genotypes), followed by dense (7 genotypes) and sparse (5 genotypes), with an irregular branching pattern in all the genotypes. Furthermore, four types of crown shape of tree (semicircular, spherical, oblong, and irregular) were noticed, and semicircular crown shape was predominant in 16 genotypes.

In this study, the predominant young leaf colour was observed as reddish brown (9 genotypes), followed by light green (6 genotypes), pinkish green (2 genotypes), and yellowish green (3 genotypes), while green colour was predominant in mature leaf in 8 genotypes, followed by dark green and light green. Opposite and alternate leaf arrangements were noticed in the studied genotypes, but opposite leaf arrangement was found to be predominant in 12 genotypes. Leaflet blade shape was observed as an elliptic and acute leaflet apex shape in all the studied genotypes, with a prominent ovate leaflet base shape in 16 genotypes. Furthermore, leaflet curvature (flat, upward, downward along with margin, slightly downward from the top and upward from the midrib) and petiole colour (greenish brown, greenish, greenish yellow, pale green, and brown) were found to be the most diversified traits among all the studied traits. Flat leaflet curvature along with the entire leaf margin was observed as a predominant trait in 11 and 13 genotypes, respectively. The greenish-brown

petiole colour was predominant in 10 genotypes. In all the studied genotypes, a prominent leaflet midrib and prominent leaflet venation were noticed in 15 genotypes, as well as a yellowish-green leaflet midrib colour in 12 genotypes. Protuberance was present in all the studied genotypes. The moderate type of abundance of flowers was observed as predominant in 12 genotypes. A medium fruit maturity group with medium fruit bearing intensity was observed in both 12 genotypes. The predominant aril quality was recorded as sweet over insipid with 17 genotypes.

3.2. Mean performance of quantitative traits

All the genotypes were observed most diversified for quantitative traits according their mean values (Table 2). On the basis of mean values of quantitative traits, the genotype LGC-18 was found superior for tree growth traits *viz.*, plant height (5.75 m), trunk girth (95 cm), crown diameter (6.81 m²), and tree volume (44.25 m³) while genotype LGC-47 was inferior for plant height (2.10 m), crown diameter (2.28 m²), and tree volume (1.82 m³); and LGC-26 for trunk girth (20.80 cm). In leaf characteristics, three genotypes (LGC-47, LGC-54, and LGC-59) were found superior for number of leaflets (10.00 leaflets). The genotypes were found superior for leaf size traits *viz.*, LGC-25 for leaflet length (17.13 cm), LGC-6 for leaflet width (5.28 cm), LGC-47 for rachis length (21.98 cm), and LGC-24 for petiole length (10.33 mm).

The longest duration of panicle initiation (13 days) and maximum inflorescence width (20.33 cm) were recorded in the genotype LGC-61, while the longest flowering duration was exhibited by LGC-18 (36 days). The maximum number of days from panicle initiation to flowering was noticed in the genotypes LGC-18 (30 days), followed by LGC-1 and LGC-60 (29 days). However, the genotype LGC-6 had shortest duration of panicle initiation and minimum number of days taken from panicle initiation to flowering was recorded in LGC-27 (11 days). The maximum inflorescence length (39.33 cm) was recorded for LGC-49 while minimum inflorescence length (18.67 cm) and width (9.33 cm) were observed in LGC-37. The genotypes LGC-37 and LGC-25 took the maximum number of days from fruit set to maturity, 107 and 106 days, respectively.

Furthermore, the genotype LGC-6 was found superior for yield attribute traits *viz.*, numbers of fruits per bunch (64 fruits), fruit width (24.38 mm), fruit weight (11.71 g), aril weight (8.78 g), and aril thickness (4.64 mm), along with the highest aril/seed weight ratio (5.06). It was also superior for physiochemical traits *viz.*, TSS (20.09 °B), TSS/acid ratio (200.87), and ascorbic acid (76.26 mg) along with the lowest titratable acidity (0.10%). LGC-59 was found superior for fruit length (20.12 mm) followed by LGC-6 (19.93 mm).

The maximum fruit length/width ratio was observed in the genotype LGC-60 (0.99) while minimum was observed in LGC-6 (0.82). The lowest fruit length was recorded in LGC-24 (17.26 mm), fruit weight in LGC-22 (5.24 g), and aril/seed weight ratio in LGC-47 (1.67). LGC-18 was found superior for fruit colour-I (28.70) and fruit colour-b (12.48) while LGC-37 had highest value for fruit colour-a (4.27). LGC-47 had significantly maximum seed length (14.60 mm), seed width (14.90 mm), and seed weight (1.90 g), while LGC-27 had minimum seed length (10.57 mm) and seed width (10.27 mm). The lowest peel weight (0.91 g) and seed weight (0.89 g) were recorded for LGC-1.

Table 1: Summary of morphological qualitative traits observed according to IPGRI descriptor (now Bioversity International) in twenty Longan genotypes.

Sr. No.	Traits	Phenotypic classes				
1	Trunk Surface	Rough (3)	Smooth (12)	Very rough (5)		
2	Tree growth habit	Spreading (12)	Semi erect (3)	Erect (2)	Drooping (3)	
3	Branching density	Dense (7)	Medium (8)	Sparse (5)		
4	Branching pattern	All Irregular				
5	Crown shape	Semicircular (16)	Spherical (2)	Oblong (1)	Irregular (1)	
6	Young leaf colour	Reddish brown (9)	Light green (6)	Pinkish green (2)	Yellowish green (3)	
7	Mature leaf colour	Green (8)	Dark green (6)	Light green (6)		
8	Leaf Arrangement	Opposite (12)	Alternate (8)			
9	Leaflet blade shape	All Elliptic				
10	Leaflet apex shape	All Acute				
11	Leaflet Base shape	Ovate (16)	Lanceolate (4)			
12	Leaflet curvature	Flat (11)	Upward (2)	Downward along with margin (3)	Slightly downward from the top (3)	Upward from the midrib (1)
13	Leaflet margin	Entire (13)	Slightly wavy (7)			
14	Petiole colour	Greenish brown (10)	Greenish (3)	Greenish yellow (1)	Pale green (2)	brown (4)
15	Leaflet midrib	All Prominent				
16	Leaflet Midrib colour	Pale green (2)	Greenish yellow (1)	Pale yellow (5)	Yellowish green (12)	
17	Leaflet venation	Prominent (15)	Slightly prominent (5)			
18	Protuberance	All Present				
19	Abundance of flower	Profuse (4)	Sparse (4)	Moderate (12)		
20	Fruit maturity group	Early (6)	Medium (12)	Late (2)		
21	Fruit intensity	Heavy (2)	Medium (12)	Poor (6)		
22	Aril Quality	Sweet (17)	Insipid (3)			

Note: Numbers in brackets indicate the number of genotypes per class

Table 2: Mean performance of quantitative characters of different longan genotypes

Genotypes	PHT	TG	CD	TV	NFL	LLG	LWD	RLG	PTLG	DPI	DPIF	FRD	INLG	INWD	DFTSM	FT
	(m)	(cm)	(m ²)	(m ³)		(cm)	(cm)	(cm)	(mm)	(days)	(days)	(days)	(cm)	(cm)	(days)	
LGC- 1	3.60	64.00	4.48	12.10	9.33	12.37	4.00	11.23	6.00	8.00	29.00	34.00	20.00	11.00	96.00	24
LGC-6	3.70	72.00	6.68	27.53	8.33	16.43	5.28	21.17	8.00	6.00	28.00	32.00	30.67	16.33	88.00	64
LGC-12	4.10	70.00	6.08	25.27	8.67	14.73	4.47	15.93	8.67	10.00	21.00	29.00	37.67	18.00	97.67	15
LGC-18	5.75	95.00	6.81	44.24	8.67	13.77	4.40	15.40	6.33	11.00	30.00	35.00	35.00	18.00	90.00	27
LGC-22	4.35	50.70	5.18	19.41	9.33	13.37	3.70	11.90	5.33	10.00	19.00	33.00	27.00	14.00	97.00	44
LGC-24	4.15	50.70	5.33	19.53	8.67	10.87	3.97	10.33	10.33	11.00	12.00	32.00	25.00	13.00	98.00	41
LGC-25	3.00	40.00	4.23	8.99	8.33	17.13	4.80	19.73	9.33	8.00	25.00	34.00	30.67	15.67	105.67	19
LGC-26	2.90	20.80	3.53	5.99	9.33	14.57	4.37	14.03	5.67	11.00	21.00	29.00	36.67	18.33	96.00	16
LGC-27	3.30	40.60	4.40	10.65	8.33	13.53	3.70	13.07	4.67	8.00	11.00	33.00	36.33	18.33	95.67	32
LGC-34	3.30	50.70	4.65	11.93	9.67	10.50	3.17	15.10	6.00	10.00	23.00	33.00	30.00	15.33	97.00	24
LGC-37	2.30	30.00	3.75	5.36	9.00	12.03	2.88	13.00	6.33	9.00	17.00	29.00	18.67	9.33	107.00	24
LGC-40	3.30	40.30	4.84	12.90	8.67	15.20	4.25	18.25	6.67	12.00	23.00	34.00	24.67	12.33	98.00	42
LGC-47	2.10	30.70	2.28	1.82	10.00	16.53	5.15	21.98	9.67	10.00	21.00	31.00	34.00	17.00	98.00	50
LGC-49	3.60	41.70	4.30	11.08	8.33	13.70	3.92	14.88	9.00	10.00	19.00	33.00	39.33	19.67	88.00	59
LGC-50	3.60	50.60	4.83	14.06	8.33	12.00	3.45	15.70	6.00	10.00	13.00	33.00	21.33	10.67	89.67	31
LGC-52	3.15	40.60	4.10	8.80	10.00	11.75	4.03	15.50	8.33	9.00	23.00	34.00	22.67	11.67	97.00	38
LGC-54	3.20	70.00	4.43	10.42	10.00	13.03	3.40	15.02	6.00	12.00	14.00	32.00	21.00	11.00	96.67	49
LGC-59	3.60	50.00	4.25	10.79	8.00	12.67	3.78	14.20	6.67	10.00	14.00	29.00	31.67	16.00	87.67	61
LGC- 60	3.00	50.00	4.25	8.98	8.67	13.13	4.48	12.70	7.67	12.00	29.00	33.00	36.00	18.00	98.00	25
LGC-61	4.15	60.00	4.98	17.12	8.00	14.40	4.28	13.93	7.33	13.00	26.00	33.00	39.33	20.33	86.00	23
Mean	3.51	50.92	4.67	14.35	8.88	13.59	4.07	15.15	7.20	10.00	20.90	32.25	29.88	15.20	95.35	35
C.V.	5.15	6.58	5.25	5.42	8.22	6.79	9.50	6.48	10.61	6.51	7.05	6.68	9.32	6.26	6.08	5.0
S.E.	0.10	1.94	0.14	0.45	0.42	0.53	0.22	0.57	0.44	0.38	0.85	1.24	1.61	0.55	3.35	1.0
C.D. 5%	0.30	5.53	0.40	1.28	1.21	1.52	0.64	1.62	1.26	1.07	2.43	3.55	4.59	1.57	9.56	2.9
Range Lowest	2.10	20.80	2.28	1.82	8.00	10.50	2.88	10.33	4.67	6.00	11.00	29.00	18.67	9.33	86.00	15
Range Highest	5.75	95.00	6.81	44.24	10.00	17.13	5.28	21.98	10.33	13.00	30.00	35.00	39.33	20.33	107.00	64
LGC- 1	17.52	0.96	5.31	25.10	1.63	10.67	2.01	1.55	0.91	11.27	11.55	0.89	2.26	14.98	0.13	11
LGC-6	24.38	0.82	11.71	26.84	2.59	9.81	8.78	4.64	1.09	10.74	11.26	1.74	5.09	20.09	0.10	20
LGC-12	17.59	0.94	6.24	23.45	3.37	9.43	2.61	1.40	1.27	12.57	13.53	1.49	1.76	14.43	0.14	10
LGC-18	19.91	0.90	6.54	28.70	1.46	12.48	3.06	2.23	1.13	13.23	14.20	1.53	2.01	15.15	0.13	11
LGC-22	17.97	0.95	5.24	27.40	2.92	12.25	2.40	2.20	1.20	12.87	12.33	1.29	1.86	16.30	0.20	81
LGC-24	17.26	0.96	5.29	27.09	2.50	12.09	2.56	2.63	1.04	10.80	10.83	1.09	2.36	16.20	0.13	12
LGC-25	18.20	0.95	5.75	21.63	3.38	7.39	2.76	2.12	1.09	12.18	12.30	1.16	2.38	16.01	0.13	12
LGC-26	20.04	0.94	5.07	25.90	1.42	10.04	2.89	1.70	1.18	13.30	13.90	1.60	1.81	15.38	0.13	11
LGC-27	20.03	0.92	6.38	26.31	2.71	9.65	3.98	3.43	1.32	10.57	10.27	1.03	3.89	18.60	0.17	11
LGC-34	20.50	0.90	6.54	21.95	4.03	8.46	3.20	1.83	1.11	12.77	13.03	1.52	2.11	15.53	0.20	77
LGC-37	19.37	0.89	5.36	24.70	4.27	8.71	2.74	2.17	1.15	11.90	12.37	1.24	2.22	15.06	0.20	75
LGC-40	17.67	0.94	5.11	28.06	4.17	12.20	2.63	1.87	1.35	12.87	13.23	1.51	1.74	15.69	0.13	11
LGC-47	20.08	0.94	6.72	26.14	2.54	10.99	3.18	2.07	0.96	14.60	14.90	1.90	1.67	16.00	0.20	80
LGC-49	20.75	0.97	7.26	22.83	4.12	8.22	4.07	2.83	1.13	13.10	12.12	1.42	2.87	17.20	0.10	17
LGC-50	20.66	0.93	7.06	28.10	3.12	12.14	3.41	2.50	1.35	12.77	12.63	1.48	2.30	18.60	0.10	18

LGC-52	20.12	0.92	6.52	24.22	1.83	9.56	3.12	2.73	1.08	12.63	13.00	1.43	2.18	17.03	0.20	85
LGC-54	19.83	0.97	6.62	26.10	4.06	10.35	3.30	2.22	1.00	13.83	13.83	1.60	2.07	17.60	0.17	10
LGC-59	22.12	0.91	7.42	25.46	2.41	11.18	4.31	2.73	1.51	13.07	12.97	1.15	3.74	19.86	0.10	19
LGC-60	18.78	0.99	6.24	24.56	2.63	10.39	2.73	2.07	1.53	12.83	12.20	1.19	2.30	18.65	0.13	14
LGC-61	20.12	0.97	6.86	23.69	3.67	10.23	2.30	2.77	1.16	12.50	12.82	1.30	1.77	17.83	0.17	10
Mean	19.65	0.93	6.46	25.41	2.94	10.31	3.30	2.38	1.18	12.52	12.66	1.38	2.42	16.81	0.15	12
C.V.	6.27	5.27	6.40	6.43	6.53	6.63	6.44	8.42	6.31	6.65	5.21	5.73	9.40	6.63	5.42	6.0
S.E.	0.71	0.03	0.24	0.94	0.11	0.39	0.12	0.12	0.04	0.48	0.38	0.05	0.13	0.64	0.00	4.2
C.D. 5%	2.03	NS	0.68	2.70	0.32	1.13	0.35	0.33	0.12	1.37	1.09	0.13	0.38	1.84	0.01	12
Range Lowest	17.26	0.82	5.07	21.63	1.42	7.39	2.01	1.40	0.91	10.57	10.27	0.89	1.67	14.43	0.10	75
Range Highest	24.38	0.99	11.71	28.70	4.27	12.48	8.78	4.64	1.53	14.60	14.90	1.90	5.09	20.09	0.20	20

3.3. Genotypic and phenotypic coefficients of variation

In the present study, the genotypes have shown a considerable amount of variation for morphological and physiochemical parameters. The extent of variability among the twenty genotypes was determined in terms of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) (Table 3 and Figure 4). The PCV was slightly greater than the GCV for all of the traits. The PCV ranged from 5.88% to 66.23%, whereas the GCV varies from 2.62% to 66.01% for all the characters. The highest PCV and GCV were recorded as for the tree volume (66.23% and 66.01%), followed by aril weight (43.34% and 42.86%), number of fruits per branch (42.82% and 42.52%), aril/seed weight ratio (36.70% and 35.47%), trunk girth (34.30% and 33.67%), TSS acid ratio (32.58% and 32.02%), aril thickness (31.12% and 29.96%), number of days from panicle initiation to flowering (29.15% and 28.28%), titratable acidity (24.96% and 24.37%), length of inflorescence (24.24% and 22.38%), petiole length (23.73% and 21.23%), fruit weight (22.92% and 22.01%), plant height (22.73% and 22.14%), crown diameter (22.64% and 22.03%), width of inflorescence (22.57% and 21.68%), and rachis length (21.12% and 20.10%) demonstrating a higher level of genetic variability for these traits among diverse genotypes. However, the lowest PCV was observed for the traits *viz.*, fruit length/width ratio (5.88%), number of days from fruit set to maturity (7.71%), flowering duration (8.00%), fruit length (8.51%), fruit colour-I (9.57%), and 9.88% for both seed length and seed width. While, the lowest GCV was recorded for the traits, *viz.*, fruit length/width ratio (2.62%), flowering duration (4.40%), number of days from fruit set to maturity (4.75%), fruit length (5.70%), number of leaflets (5.72%), fruit colour-I (7.08%), seed length (7.31%), ascorbic acid (7.62%), fruit width (8.01%), seed width (8.51%), and TSS (9.21%). These traits have low PCV and GCV, indicating a lower level of genetic variability.

3.4. Heritability and genetic advance

Heritability is a measure of the genetic link between parent and progeny that has been frequently used to determine the degree to which a character can be transferred from parents to offspring (Singh *et al.*, 2015). In the present experiment, heritability in broad sense was estimated for all the traits and expressed in percentage that is ranged from 19.80% to 99.30% (Table 3 and Figure 5). The highest heritability in broad sense was observed for vegetative traits *viz.*, tree volume (99.30%), trunk girth (96.30%), plant height (94.90%), crown diameter (94.60%), rachis length (90.60%), and petiole length (80.00%); and for phonological, fruiting, and seed traits *viz.*, number of fruits per branch (98.60%), aril weight (97.80%), fruit colour-a (95.80%), number of days from panicle initiation to flowering (94.20%), aril/seed weight ratio (93.40%), aril thickness (92.70%), inflorescence width (92.30%), fruit weight (92.20%), duration of panicle initiation (86.50%), inflorescence length (85.20%), peel weight (82.40%), and fruit colour-b (81.00%). Furthermore, the TSS acid ratio (96.60%) and titratable acidity (95.30%) had the highest heritability among the physiochemical characters. The traits with the lowest heritability among all the traits studied were fruit length to width ratio (19.80%), flowering duration (30.30%), number of leaflets (32.60%), ascorbic acid (37.40%), and number of days from fruit set maturity (37.90%).

Genetic advance is determined by the heritability of the trait under selection, the genetic variability of the genotypes, and the degree of selection. A high heritability combined with a high genetic advance results in efficient selection criteria. The genetic advance as percent of mean observed highest for the traits *viz.*, tree volume (135.52%), aril weight (87.31%), number of fruits/ bunch (86.99%), pulp to seed weight ratio (70.64%), trunk girth (68.06%), TSS/ titratable acidity ratio (64.83%), fruit colour-a (63.30%), aril thickness (59.41%), number of days from panicle initiation to flowering (56.54%), titratable acidity (48.99%), plant height (44.41%), crown diameter (44.14%), fruit weight (43.54%), width of inflorescence (42.91%), length of inflorescence (42.56%), rachis length (39.41%), petiole length (mm) (39.12%), and duration of panicle initiation (31.49%) (Table 3 and Figure 5).

Table 3: Genetic parameters for quantitative traits of twenty longan genotypes

Traits	GCV	PCV	h ² (Broad Sense)	GA 5%	GAM 5%
PHT (m)	22.14	22.73	94.90	1.56	44.41
TG (cm)	33.67	34.30	96.30	34.66	68.06
CD (m ²)	22.03	22.64	94.60	2.06	44.14
TV (m ³)	66.01	66.23	99.30	19.45	135.52
NFL	5.72	10.02	32.60	0.60	6.73
LLG (cm)	12.83	14.51	78.10	3.17	23.35
LWD (cm)	14.12	17.02	68.80	0.98	24.14
RLG (cm)	20.10	21.12	90.60	5.97	39.41
PTL (mm)	21.23	23.73	80.00	2.82	39.12
DPI (days)	16.44	17.68	86.50	3.15	31.49
DPIF (days)	28.28	29.15	94.20	11.82	56.54
FRD (Days)	4.40	8.00	30.30	1.61	4.99
INLG (cm)	22.38	24.24	85.20	12.72	42.56
INWD (cm)	21.68	22.57	92.30	6.52	42.91
DFTSM (days)	4.75	7.71	37.90	5.74	6.02
FTPb	42.52	42.82	98.60	31.08	86.99
FTLG (mm)	5.70	8.51	44.90	1.44	7.87
FTWD (mm)	8.01	10.17	62.00	2.55	12.98
FLW (ratio)	2.62	5.88	19.80	0.02	2.40
FTWT (g)	22.01	22.92	92.20	2.81	43.54
FC-I	7.08	9.57	54.80	2.74	10.80
FC-a	31.39	32.06	95.80	1.86	63.30
FC –b	13.70	15.22	81.00	2.62	25.40
AWT (g)	42.86	43.34	97.80	2.88	87.31
AT (mm)	29.96	31.12	92.70	1.42	59.41
PWT (g)	13.64	15.03	82.40	0.30	25.50
SLG (mm)	7.31	9.88	54.70	1.39	11.13
SWD (mm)	8.51	9.98	72.70	1.89	14.95
SWT (g)	17.97	18.86	90.80	0.49	35.26
ASWT	35.47	36.70	93.40	1.71	70.64
TSS (°B)	9.21	11.35	65.90	2.59	15.40
TA (%)	24.37	24.96	95.30	0.07	48.99
TSS/TA	32.02	32.58	96.60	78.78	64.83
AA (mg/100 g)	7.62	12.45	37.40	6.42	9.60

4. Discussions

4.1. Morphological variability

All the qualitative characteristics were highly diversified within the twenty longan genotypes except a few *viz.*, branching pattern, leaflet blade shape, leaflet apex shape, and presence of protuberance. Wu et al. (2016) have reported the morphological diversity of leaf and stem qualitative characteristics in litchi. The greenish brown colour of the petiole was predominant over the other colors, and the opposite leaflet arrangement was observed in all the accessions studied. The narrowly elliptic leaflet shape was dominant. The predominant leaflet apex shape was acuminate, while the broadly cuneate leaflet base shape was dominant. The predominant leaflets were slightly curved upward, and the entire leaflet margin was dominant over the others. They have also reported light green midrib of leaflets.

The different crown shapes of plant were identified in litchi such as symmetrical, non-symmetrical, dense, and round shaped (Khurshid *et al.*, 2004). According to Singh *et al.* (1999) the genetic characteristic of leaf shape aids in identifying cultivars of a crop plant. The variation in morphological qualitative traits was observed among the twenty genotypes could be due to genetic factors interacting with the local climatic conditions.

The morphological and physiochemical quantitative traits were significantly diverse among all the genotypes except one trait fruit length width ratio. The plant height, trunk girth, canopy diameter and tree volume among the cultivars were found to differ significantly from one another, which may be due to their different genetic make-up, plant type, and due to genotypic and environmental interactions. Wu *et al.* (2016) have also reported that the vegetative characteristics were highly diversified in litchi. Saikia and Kotoky (2018) have reported maximum plant height (1.64 m), canopy diameter (3.11 m²), fruit weight (25.40 g), aril weight (16.62 g), and aril thickness (0.70 mm) with longest flowering duration for the variety Bilati of litchi. Saikia and Kotoky (2018) also have reported similar findings in terms of vegetative, flowering, fruit and seed characteristics. The variation observed among the litchi genotypes were might be due to the genetic make-up of plant (Lal *et al.*, 2022); nutrition and climatic conditions (Cronje *et al.*, 2009). The variation in aril thickness among the longan genotypes that might be due to their fruit size and seed size. Arora *et al.* (1996) have also reported variability in litchi genotypes with regard to fruit, aril, and seed characters in various diverse regions. Wall (2006) has reported that the same cultivar of longan may differ in ascorbic acid and TSS at different locations. It's clear from the above study that the climatic condition also plays an important role for physiochemical traits.

4.2. Genetic variability

The significant level of the coefficient of variations (genotypic and phenotypic) resulted in variation for all traits studied among longan genotypes, which can be improved through further breeding programmes. According to the genetic parameters, the PCV was slightly greater than the GCV for all of the traits, which indicates that the phenotypic expression of characters has less environmental influence. A significant amount of PCV and GCV were found higher for many quantitative traits studied among the longan genotypes, *viz.*, tree volume, aril weight, number of fruits per branch, aril/seed weight ratio, trunk girth, TSS acid ratio, aril thickness, number of days from panicle initiation to flowering, titratable acidity, length of inflorescence, petiole length, fruit weight, plant height, crown diameter, width of inflorescence, and rachis length. Many researchers have found similar results in their findings for different traits, *viz.*, fruit weight in strawberry (Mishra *et al.*, 2015); length and width of inflorescence, leaf length, seed weight, peel thickness, pulp thickness and fruit weight in litchi (Marboh *et al.* 2018; Kumari *et al.*, 2017); plant height, flowering duration, fruit yield, number of fruit per plant, pulp seed ratio, and fruit weight in guava (Patel *et al.*, 2015), in mango (Gill and Navprem, 2015; Majumder *et al.*, 2012); number of seeds per fruit, seed weight per fruit, fruit weight, and petiole length in guava (Singh *et al.*, 2015); fruit weight, aril weight and titratable acidity in pomegranate (Perveen *et al.*, 2018); and in pummelo (Wangchu *et al.*, 2017). These findings unfortunately were not similar with the earlier report for leaf length and leaf width in litchi (Kumari *et al.*, 2017). However, it is implied that the material used for the investigation contained enough variability to allow for the selection of elite and superior genotypes for further crop improvement.

4.3. Heritability and genetic advance

Heritability can be an effective tool for determining the potential for improvement through selection because the majority of desired traits, like yield, are quantitative in nature, complex in their inheritance, and significantly influenced by environmental factors. This suggests that selection will be successful in identifying genotypes with highly heritable traits that are helpful in projecting the expected rate of advancement. The genotypes and phenotypes would be closely related due to the smaller environmental effects. According to Singh (2000), variation due to heritability is very helpful for long-term genetic improvement. The most important role of heritability in the genetic study of quantitative traits is to predict the validity of the phenotypic value as a guide to breeding value. The highest heritability in broad sense above 80% was observed for traits such as, tree volume, number of fruits per branch, aril weight, TSS acid ratio, titratable acidity, trunk girth, plant height, fruit colour-a, crown diameter, number of days from panicle initiation to flowering, aril/seed weight ratio, aril thickness, inflorescence width, fruit weight, duration of panicle initiation rachis length, inflorescence length, peel weight, fruit colour-b and petiole length among the studied traits. Similar results were also reported by some researchers for different traits in other fruit crops, such as in litchi for fruit yield, length and weight of fruit, aril weight, aril thickness, seed weight and TSS (Marboh *et al.*, 2017; Lal *et al.*, 2022(b); and Kumari *et al.*, 2017); in mango for sex ratio, fruit and peel weight, thickness of peel, stone weight, pulp to stone ratio, TSS, and titratable acidity (Das *et al.*, 2021), in strawberry for fruit length, fruit yield and leaf area index (Mishra *et al.*, 2015); in pear for fruit weight and yield (Bhat and Dhillon, 2015); in cashew for plant height, trunk girth, canopy diameter, flowering duration, nuts per panicle, kernel weight, nut weight and nut yield (Chandrasekhar *et al.*, 2018); in jackfruit for leaf blade width, core weight of fruit, seed weight, flake to seed ratio and yield per tree (Debnath and Deb, 2022); and in guava for fruit length to width ratio, seed weight, ascorbic acid, petiole length, and fruit weight (Singh *et al.*, 2015) leaf length, diameter of flower bud and fruit yield (Patel *et al.*, 2015). Unfortunately, the ascorbic acid trait was not similar to the findings by Singh *et al.* (2015). The high heritability strongly suggests that the traits under this study have great scope for genetic improvement through breeding programmes (Supriya *et al.*, 2016). Moderate to low heritability indicates a limited scope for crop improvement through selection. Therefore, calculating heritability alone won't be enough to effectively improve fruit traits unless there is a higher genetic gain involving additive gene action, which can be attained through selection (Lipi *et al.*, 2020).

The highest genetic advance as percent of mean was observed for the tree volume, aril weight, number of fruits/ bunch, pulp to seed weight ratio, trunk girth, TSS/ titratable acidity ratio, fruit colour-a, aril thickness, number of days from panicle initiation to flowering, titratable acidity, plant height, crown diameter, fruit weight, width of inflorescence, length of inflorescence, rachis length, petiole length, and duration of panicle initiation. There are several researchers have been reported the similar findings in other fruit crops such as in litchi for yields, and length of rachis and panicle (Lal *et al.*, 2022b), in mango for fruit weight, number of branches per inflorescence, percentage of flowering shoot, fruit set, and number of fruits per plant (Majumder *et al.*, 2012), in strawberry for dry fruit weight, fruit volumes and fresh fruit weight (Mishra *et al.*, 2015), in guava for seed weight, ascorbic acid, fruit weight and pedicel length (Singh *et al.*, 2015) canopy spread and duration of flowering (Patel *et al.*, 2015). Unfortunately, few traits were not similar to the earlier findings, such as seed width in litchi (Marboh *et al.*, 2017); duration of flowering in guava (Patel *et al.*, 2015)

For predicting the impact of selection, estimated heritability linked with genetic advance is more reliable than heritability alone (Marboh *et al.*, 2017). The effects of both additive and non-additive genes are included in the heritability estimates alone, but this information is incomplete and of limited practical value

unless it is combined with genetic advancement. Estimates of genetic advance can be used to better understand the type of gene action underlying various polygenic traits (Lipi et al., 2020). The most effective selection criteria are high heritability combined with high genetic advance (Johnson et al. 1955). As per results, high heritability along with genetic advance estimated for plant height, trunk girth, crown diameter, tree volume, rachis and petiole length, duration of panicle imatation, number of days from panicle initiation to flowering, length and width of inflorescence, number of fruits per bunch, fruit, aril and seed weight, aril thickness, titratable acidity and TSS acid ratio (Table 3 and Fig. 5). These findings are similar to the earlier reports in other fruit crops such as in litchi for fruit weight, length and width of fruit, pulp weight, pulp thickness, peel thickness, peel weight, seed width, seed weight, and fruit yield per plant (Marboh *et al.*, 2017), in guava for seed weight, fruit weight and thickness of outer flesh (Singh et al., 2015), fruits yield per plant in strawberry (Mishra et al., 2015), and guava (Patel et al., 2015), days to maturity in mango (Majumder et al., 2012). As a result, it suggests that the breeder can perform direct selection by utilising these traits for future crop improvement. High heritability along with great genetic advance suggested additive gene action, whereas a low genetic advance value indicates non-additive gene action was responsible for the variation in traits (Mishra et al., 2015).

5. Conclusion

It was possible to conclude that the genotypes studied demonstrated morphological variability and genetic diversity in terms of qualitative and quantitative characteristics. On the basis of mean performance we found best performing genotypes LGC-6 followed by LGC-59 for yield attributing and fruit quality traits. The highest PCV and GCV were found higher for tree volume, followed by aril weight, number of fruits per branch, aril/seed weight ratio, trunk girth, TSS acid ratio, aril thickness, number of days from panicle initiation to flowering, titratable acidity, length of inflorescence, petiole length, fruit weight, plant height, crown diameter, width of inflorescence, and rachis length indicate that selection based on these characteristics can result in greater improvement. The traits are having high heritability coupled with high genetic advance were indicative of additive gene action, and selection based on these traits would be more reliable and suggested that selections could be made in earlier generations.

6. Future prospects

Longan is an important fruit crop, and it has a very good market value in Indian markets as well as the world market. It is an underexploited fruit crop in India. Researchers have to conduct studies on the genetic diversity present in this species which can be lead to the further crop improvement programmes. In India, Gandaki Longan-1 is the only variety that has recently been developed. The research institutes need to explore and promote this fruit crop and also conduct crop improvement programmes to develop high-yield varieties coupled with quality fruits.

Declarations

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Figures



Figure 1

Variation in fruit bearing intensity in longan genotypes.



Figure 2

Variation in fruit size, seed size, thickness of peel and aril in longan genotypes



Figure 3

Variation in leaf shape, size and types of leaflet arrangement

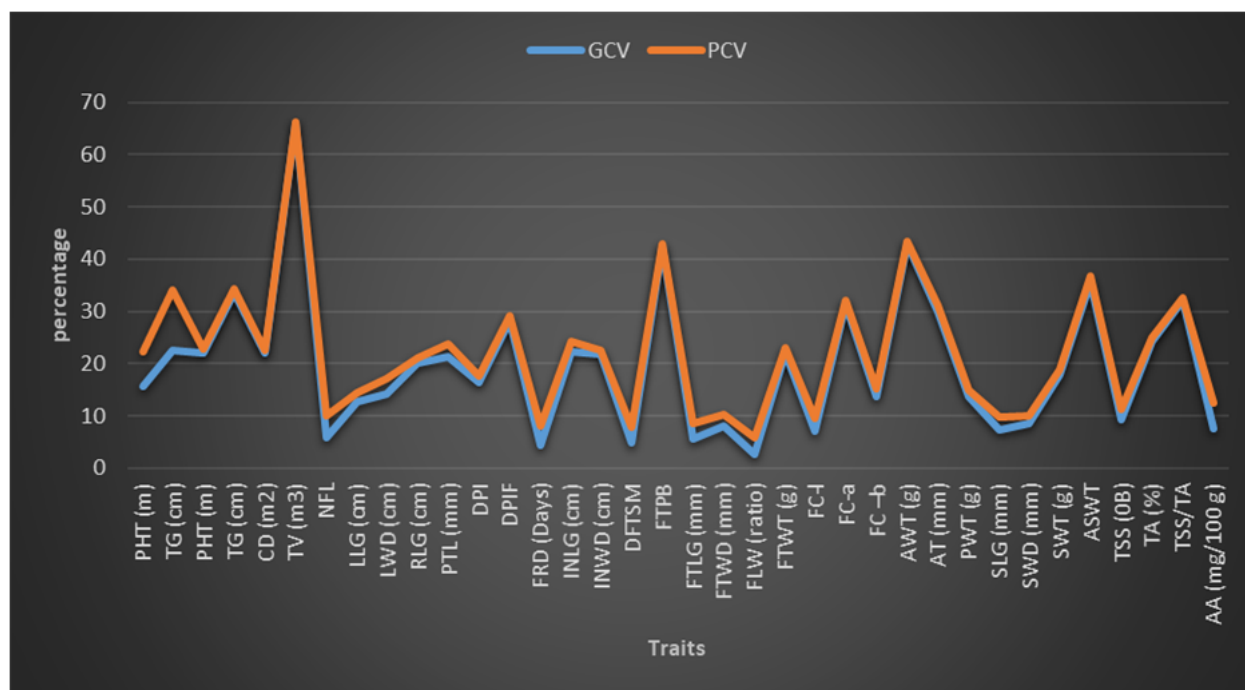


Figure 4

Graphical representation of GCV and PCV for different traits

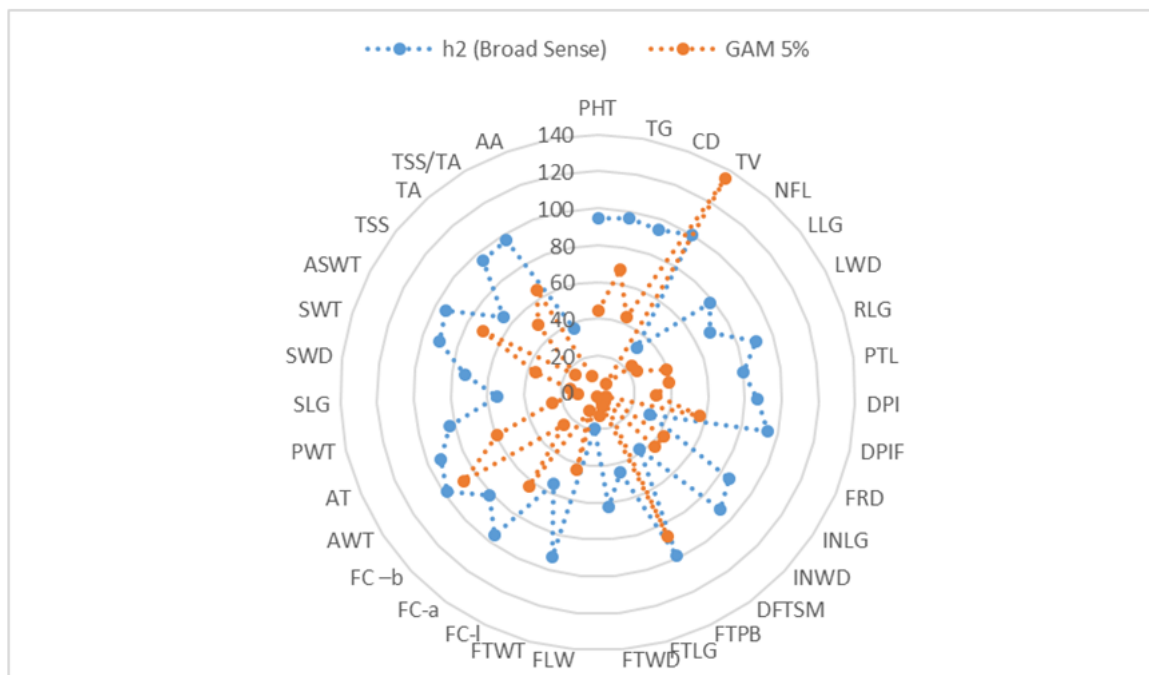


Figure 5

Graphical representation of heritability (h^2) and genetic advance as percent of mean (GAM 5%) for different traits.