

Assessment of Variability and Genetic Divergence of Longan Genotypes (*Dimocarpus longan* Lour.) based on Qualitative and Quantitative Traits

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Abstract

Longan (*Dimocarpus longan* Lour.) is an important underutilized fruit crop. There is currently limited information available on the genetic background of longans, which is a key bottleneck in longan improvement. Studies on the extent of genetic variability and genetic divergence are crucial and it can provide relevant information which can be very useful for crop improvement programmes. In the present study, a total of 54 qualitative and quantitative traits were investigated of 20 different longan genotypes to determine the morphological and physiochemical traits that. Results revealed that the significant variability is existed in the studied traits except few. Among the qualitative traits petiole colour, leaflet curvature, young leaf colour, mature leaf colour, branching density, leaflet midrib colour, abundance of flower, trunk surface, fruit maturity group, and tree vigour were showed more than the average value of Shannon's diversity index. Higher PCV and GCV were recorded for several traits *viz.*, 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, width of inflorescence, length of inflorescence, petiole length, fruit weight, plant height, crown diameter and rachis length. High heritability estimates coupled with high genetic advance as % of mean were recorded for the traits *viz.*, plant height, trunk girth, crown diameter, tree volume, rachis and petiole length, 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, fruit colour-a, titratable acidity and TSS acid ratio which is indicative of additive gene action and selection based on these traits would be more reliable. According to the Mahalanobis D² statistic, twenty diverse genotypes were grouped into eight groups. The presence of genetic divergence was also tested in cluster means by the significant amount of variability for various variables. Therefore, this study's findings imply that these genotypes have variability in terms of fruit quality traits, yield and traits that contribute to yield, and other agronomic traits that could be useful in future crop improvement initiatives.

Introduction

Longan (*Dimocarpus longan* Lour.) is a tropical and subtropical evergreen fruit crop that originated in Southern China and was brought into India in year 1798 (Leenhouts 1971). 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). China, Thailand, Vietnam, India, and South Africa are the world's leading producers. These five countries account for 90% of global longan production (Qiu, 2012; Huang et al., 2021). Although the longan production in India is still in its infancy and being grown only in few states *viz.*, Assam, West Bengal, Bihar, Kerala, and Karnataka, but it has the potential to be grown all over the country, from its southernmost regions to its northern limits. Most of the local cultivars are grown in India and they are known by their regional names, the majority of which refer to their origins.

Being rich in minerals and bioactive components including phenolics and flavonoids longan can be considered as suitable candidate in the fruit basket of India for combating nutritional insecurity. This fruit contains 458 kJ/100 g of energy. Fruits are high in sugar content, with 18.00 B of TSS and 0.18% of titratable acidity (Suiubon et al., 2017). It has higher amount of ascorbic acid (60.1 mg/100 g) than litchi and rambutan (Wall 2006). Longan fruit contains moisture (82.4 g), carbohydrates (15.8 g), fat (0.1 g), protein (1 g), ash (0.7 g), nicotinic acid (1.3 mg), thiamine (0.01 mg), fibre (0.4 g), calcium (10 mg), phosphorus (42 mg), and iron (1.2 mg) per 100g of fresh fruits Zn (Park et al., 2010; Wall 2006; Cheng 2014). Longan fruit contains 324.9 mg of K and 0.26 mg of Cu per 100 g of fresh fruits and provide 3 to 5% of the DRI for macro and micronutrients such as P, Mn, Mg, Fe, and Zn (Wall 2006).

Knowledge of germplasm genetic background is particularly useful for germplasm conservation and utilisation in longan improvement programmes. Genetic improvement of any crop species is greatly depending upon the magnitude of existed variability among the different characters (Alam et al., 2020). A diverse gene pool is very essential for development of improved cultivars of any crop (Bailey-Serres et al., 2019). Therefore, the characterization and evaluation of longan germplasms is a prerequisite for genetic enhancement of longan. In Indian context, longan is an underutilized fruit crops and the genetic information is not available for this crop. In addition, the available local cultivars and germplasm of longan has not been characterized yet. However, longan improvement program is being carried out in India at NRC, Litchi (Muzaffarpur). "Gandaki Longan-1" has been identified as potential genotype by the institute.

The component of genetic variability *viz.*, genotypic and phenotypic coefficient of variation, heritability and genetic advance are the essential biometric tools to assess the existed genetic variability among the genotypes which would help to selection of superior variety (Lal et al., 2022). Understanding the existing genetic variation and the origins of cultivated varieties will assist in choosing suitable parents for an efficient hybridization project. Therefore, multivariate analysis techniques like D² cluster and component analysis are highly valuable and efficient tools for selecting genotypes as parents. D² analysis has been used successfully in plant breeding to assess existing diversity in a crop. Molecular markers in assessing diversity in the germplasm has become routine and different marker system has been utilized to assess the genetic diversity of longan, such as Random Amplified Polymorphism DNA-RAPD (Mei et al., 2014); Simple Sequence Repeats-SSRs (Jia-xin et al., 2011 and Wen-shun et al., 2015); Inter Simple Sequence Repeats-SSRs (Zeng et al., 2009 and Mariana et al., 2011); Amplified Fragment Length Polymorphisms-AFLPs (Weiping et al., 2003 and Lin et al., 2005); and SCoT markers (Chen et al., 2010). Morphological traits being less in number pose a limitation to work out diversity but it is actual observable variability on which breeder relies during selection or hybridization. So,

in the present investigation, an attempt was made to understand the type and extent of genetic divergence of morphological and physiochemical traits for improvement of longan. This research is the first systematic documentation on genetic variability and genetic divergence across longan genotypes available in India, specifically focusing on morphological and physico-chemical characteristics. Prior to this, no information regarding these aspects was accessible. Hence, this report will aid in determining the criteria for selecting desired features and in accelerating the development of improved varieties.

Material and Methods

2.1. Plant material and experiment site

The current investigation was carried out on a sample of 20 longan genotypes which were surveyed and collected from different province of India. These genotypes were conserved in a Field Gene Bank located at ICAR- National Research Centre on Litchi in Muzaffarpur, Bihar. The ten year old genotypes were planted at 8 m × 8 m spacing, consistent and similar cultural practices provided for all the trees (Singh et al., 2011). The location of Field Gene Bank is situated at an elevation of 210 m above mean sea level, between 26.22° 564" North longitude and 85.11° 2664" East longitude. Bihar province is a humid subtropical climate with hot, dry summers and an annual rainfall of approximately 1150 mm. In this location, summer temperatures range from 08°C to 43°C. The present experiment was focused on to study the genetic variability of morphological and physiochemical traits during 2019-20.

Table 1
Details of genotypes used under the study

Genotypes	Experimental site	Genotypes	Experimental site
LGC*-1	ICAR-NRC on Litchi*	LGC-37	ICAR-NRC on Litchi
LGC-6	ICAR-NRC on Litchi	LGC-40	ICAR-NRC on Litchi
LGC-12	ICAR-NRC on Litchi	LGC-47	ICAR-NRC on Litchi
LGC-18	ICAR-NRC on Litchi	LGC-49	ICAR-NRC on Litchi
LGC-22	ICAR-NRC on Litchi	LGC-50	ICAR-NRC on Litchi
LGC-24	ICAR-NRC on Litchi	LGC-52	ICAR-NRC on Litchi
LGC-25	ICAR-NRC on Litchi	LGC-54	ICAR-NRC on Litchi
LGC-26	ICAR-NRC on Litchi	LGC-59	ICAR-NRC on Litchi
LGC-27	ICAR-NRC on Litchi	LGC-60	ICAR-NRC on Litchi
LGC-34	ICAR-NRC on Litchi	LGC-61	ICAR-NRC on Litchi
*LGC is denoted as Longan Germplasm Collection while ICAR-NRC on Litchi stands for ICAR- National Research Centre on Litchi, Muzaffarpur-Bihar			

2.2. 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 descriptor (IPGRI, 2002). The observations are as follows:

Qualitative traits

Twenty qualitative traits viz., trunk surface, tree growth habit, branching density, branching pattern, crown shape, young leaf colour, mature leaf colour, leaf arrangement, leaflet blade shape, leaflet apex shape, leaflet base shape, leaflet curvature, leaflet margin, petiole colour, leaflet midrib, leaflet midrib colour, leaflet venation, protuberance, abundance of flower, fruit maturity group, fruit intensity, and aril quality were recorded.

Quantitative traits

A total of 34 morpho-biochemical quantitative traits viz., plant height (PHT, m), trunk girth, (TG, cm), crown diameter (CD, m²), tree volume (TV, m³), number of leaflets (NFL), leaflet blade length (LLG, cm), leaflet blade width (LWD, cm), rachis length (RLG, cm), petiole length (PTLG, mm), duration of panicle initiation (DPI, days), number of days from panicle initiation to flowering (DPIF, days), duration of flowering (FRD, days), length of inflorescence (INLG, cm), width of inflorescence (INWD, cm), number of days from fruit set to maturity (DFSM, days), number of fruits per bunch (FTPb), fruit length (FTLG, mm), fruit width (FTWD, mm), fruit length width ratio (FLW, ratio), fruit weight (FTWT, g), fruit colour-I (FC-I), fruit colour-a (FC-a), fruit colour-b (FC-b), aril weight (AWT, g), aril thickness (AT, mm), peel weight (PLWT, g), seed length (SLG, mm), seed width

(SWD, mm), seed weight (SWT, g), Aril/seed weight ratio (ASWT, ratio), total soluble solids (TSS, °B), titratable acidity (TA, %), total soluble solids/acid ratio (TSS/TA) and ascorbic acid (AA, mg/100g) were observed.

Methodology of observations

Plant height was measured with the help of measuring aluminium pole from the ground level to the highest tip of plant growth and the mean values were expressed in meter. Trunk girth was measured with the help of measuring tape at 15 cm above the ground level and the mean value presented in terms of centimeter. A mark indicating extend of spread of the plant was made on the ground with help of stick and then measuring aluminium pole was used to take measurement of canopy spread of the plant from North-South and East-West directions along the ground level and the mean value was expressed in meter. The tree volume of the plant was calculated according to the formula given by Westwood et al. (1963).

An average number of leaflets were randomly selected and visually counted from all the direction of the plant. The rachis length was measured from the base of shoot to the uppermost tip and mean value was expressed in centimeter. Leaflet length was measured from the base to the tip of leaflet while measurement of leaflet width was taken at widest part of the leaflet and mean value was expressed in centimeter. The petiole length was measured from rachis to the leaflet base and mean value was expressed in millimeter. The length of the inflorescence was recorded from the base to the uppermost tip portion of panicle, while the width of the inflorescence was measured at its widest point, and mean values were expressed in centimeter. Duration of flowering was calculated as the number of days between the first and last date of panicle initiation.

The number of fruits per panicle was recorded by selecting panicles randomly from all directions. The physical dimensions related to size of fruit and seed, as well as thickness of aril and peel were recorded with the help of a digital caliber vernier calipers (Aerospace, 150 mm) and mean value was presented in millimeter (mm). Fruit weight, aril weight and seed weight were measured on an electronic digital weighing balance (AFCOSET) and mean values were expressed in terms of gram (g). The length and width of fruit and seed were measured transversely and longitudinally at the widest point in a direction perpendicular to each other. Ten fruits were randomly taken for each replication to record observations of fruit and seed parameters *viz.*, fruit length, fruit width, fruit weight, aril weight, aril thickness, peel weight, seed length, seed width and seed weight.

The physico-chemical parameters like TSS (°Brix) determined by placing drops of pulp extract on prism-plate of the digital hand refractometer (ATAGO) at room temperature, titratable acidity (%) was estimated according to Ranganna (1997), and ascorbic acid (mg/100 g) 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

The experimental design employed in this study was Complete Randomized Block Design, and the data were subjected to ANOVA (Analysis of Variance) to assess the mean differences as per suggested by Panse and Sukhatme, 1984. The Tukey's post-hoc test is used to compare the mean differences, and the statistical significances was considered when the p-value was less than 0.05 ($p \leq 0.05$). The descriptive statistics of qualitative traits were analyzed using the Web Agri Stat Package-2 (WASP-2), developed by ICAR-Research Complex, Goa, India. The genotypic co-efficient of variation (G.C.V.) and phenotypic co-efficient of variation (P.C.V.) were calculated by the formula given by Burton (1952). For the estimates of heritability (broad sense) and genetic advance as percentage of mean, the method of Hanson et al. (1956) was followed. All of these analysis were performed with the help of software R studio (R.4.3.1). Mahalonobis D^2 statistic (1936) was used to determine the D^2 values in order to estimate the genetic divergence among the various genotypes used in the current experiment. The initial stage in clustering various genotypes is to arrange them in order of their relative distances (D^2 values) from one another. Tocher's method is employed for cluster construction after organizing the D^2 values in this sequence (Rao, 1952). The WINDOSTAT Version 9.3 application software was used to analyses it.

Results

3.1. Evaluation of qualitative traits

Table 2 shows the descriptive statistics of maximum, minimum, mean, SD, SEM, and CV for 20 qualitative characteristics among 20 longan genotypes. Except for a handful, including branching density, branching pattern, leaflet blade form, leaflet apex shape, and protuberance, all qualitative features were significantly diverse among the twenty longan genotypes. The variation of CV values were ranged from 0.00–60.54% for the studied qualitative traits. The higher CV value was observed in order for the traits *viz.*, young leaf colour (60.54%), trunk surface (53.04%), mature leaf colour (37.53%), branching density (35.51%), leaflet curvature, fruit maturity group, fruit intensity (34.20%), abundance of flower (32.44%), leaf arrangement (31.41%), and aril quality (30.96%). The lower CV value was recorded in order for the traits *viz.*, tree growth habit (29.77%), base shape (29.50%), tree vigour (24.69%), crown shape (16.76%), and leaflet venation (14.66%). The details of the qualitative characters and their characteristics of 20 studied longan genotypes are provided in supplementary Table S1.1 and Table S1.2. The variation in fruit bearing intensity and leaf characteristics have displayed in Fig. 2 and Fig. 4, respectively.

Table 2
Descriptive statistics of qualitative parameters of twenty longan genotypes.

Traits	Maximum	Minimum	Mean	Sd. deviation	Sd. Error of Mean	CV
Trunk Surface	3.00	1.00	1.65	0.88	0.20	53.04
Tree growth habit	4.00	1.00	2.80	0.83	0.19	29.77
Tree Vigour	7.00	3.00	4.90	1.21	0.27	24.69
Crown shape	7.00	3.00	4.85	0.81	0.18	16.76
Branching density	7.00	3.00	4.80	1.70	0.38	35.51
Branching pattern	5.00	5.00	5.00	0.00	0.00	0.00
Young leaf colour	7.00	1.00	4.50	2.72	0.61	60.54
Mature leaf colour	3.00	1.00	2.10	0.79	0.18	37.53
Leaf Arrangement	2.00	1.00	1.60	0.50	0.11	31.41
Leaflet blade shape	4.00	4.00	4.00	0.00	0.00	0.00
Leaflet apex shape	1.00	1.00	1.00	0.00	0.00	0.00
Base shape	3.00	1.00	2.05	0.61	0.14	29.50
Leaflet curvature	4.00	1.00	2.70	0.92	0.21	34.20
Leaflet midrib	3.00	3.00	3.00	0.00	0.00	0.00
Leaflet venation	3.00	2.00	2.80	0.41	0.09	14.66
Protuberance	1.00	1.00	1.00	0.00	0.00	0.00
Abundance of flower	3.00	1.00	2.00	0.65	0.15	32.44
Fruit maturity group	3.00	1.00	1.80	0.62	0.14	34.20
Fruit intensity	3.00	1.00	1.80	0.62	0.14	34.20
Aril Quality	4.00	1.00	3.55	1.10	0.25	30.96
Shannon's Diversity Index						

In current study, Shannon diversity index values were ranged from 0.432 to 1.333 (Table 3 and Fig. 1). The maximum diversity was recorded in petiole colour (1.333) among the studied qualitative traits. Traits such as tree vigour (0.886), fruit intensity and fruit maturity group (0.898), trunk surface (0.938), abundance of flower (0.950), leaflet midrib colour (1.033), branching density (1.081), mature leaf colour (1.089), young leaf colour (1.235), and leaflet curvature (1.278) have shown high value of Shannon diversity index. The overall mean value of the Shannon diversity index (H') was recorded as 0.898, which means the high level of diversity exists among the studied genotypes.

Table 3
Shannon's diversity indices for qualitative traits of 20 longan genotypes

Traits	Code	Variables	Frequency	Percentage (%)	H'	EH
Trunk Surface	1	Smooth	12	60	0.938	0.853
	2	Rough	3	15		
	3	Very rough	5	25		
Tree growth habit	1	Spreading	12	60	0.799	0.577
	2	Semi erect	3	15		
	3	Erect	2	10		
	4	Drooping	3	15		
Branching density	1	Dense	7	35	1.081	0.984
	2	Medium	8	40		
	3	Sparse	5	25		
Crown shape	1	Semicircular	16	80	0.708	0.511
	2	Spherical	2	10		
	3	Oblong	1	5		
	4	Irregular	1	5		
Young leaf colour	1	Reddish brown	9	45	1.235	0.891
	2	Light green	6	30		
	3	Pinkish green	2	10		
	4	Yellowish green	3	15		
Mature leaf colour	1	Green	8	40	1.089	0.991
	2	Dark green	6	30		
	3	Light green	6	30		
Leaf Arrangement	1	Opposite	12	60	0.673	0.971
	2	Alternate	8	40		
Leaflet Base shape	1	Ovate	16	80	0.500	0.722
	2	Lanceolate	4	20		
Leaflet curvature	1	Flat	11	55	1.278	0.794
	2	Upward	2	10		
	3	Downward along with margin	3	15		
	4	Slightly downward from the top	3	15		
	5	Upward from the midrib	1	5		
Leaflet margin	1	Entire	13	65	0.647	0.934
	2	Slightly wavy	7	35		
Petiole colour	1	Greenish brown	10	50	1.333	0.828
	2	Greenish	3	15		
	3	Greenish yellow	1	5		
	4	Pale green	2	10		
	5	Brown	4	20		
Leaflet Midrib colour	1	Pale green	2	10	1.033	0.745

Traits	Code	Variables	Frequency	Percentage (%)	H'	EH
	2	Greenish yellow	1	5		
	3	Pale yellow	5	25		
	4	Yellowish green	12	60		
Leaflet venation	1	Prominent	15	75	0.562	0.811
	2	Slightly prominent	5	25		
Abundance of flower	1	Profuse	4	20	0.950	0.865
	2	Moderate	12	60		
	3	Sparse	4	20		
Fruit maturity group	1	Early	6	30	0.898	0.817
	2	Medium	12	60		
	3	Late	2	10		
Fruit intensity	1	Heavy	2	10	0.898	0.817
	2	Medium	12	60		
	3	Poor	6	30		
Aril Quality	1	Sweet	17	85	0.423	0.610
	2	Insipid	3	15		
Tree Vigour	1	High	3	15	0.886	0.807
	2	Medium	13	65		
	3	Low	4	20		

3.2. Diversity in morphological and physiochemical traits

The analysis of variance (ANOVA) revealed that the mean sum of squares due to genotypes was observed significant for all the studied traits except fruit length/width ratio which indicating that the existence of considerable amount of variability in the studied genotypes (Table 4). The results indicated the presence of significant amount of variability among all the studied longan genotypes and the data subjected to mean performance is presented in the supplementary Table S2.1 and Table S2.2. A coefficient of variation (CV) was ranged from 3.46% (seed length) to 17.26% (TSS acidity ratio), and high CV was recorded for the traits *viz.*, TSS acidity ratio (17.26%), duration of panicle initiation (16.92%), duration of flowering (13.03%), fruit colour-I (12.10%), aril and seed weight ratio (11.91%), number of leaflets (10.88%), leaflet blade length and width (9.19%), fruit weight (8.43%), seed width (8.10%), trunk girth (8.07%), and petiole length (8.02%) (Table 4).

The genotype LGC-18 was found significantly 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). In leaf characteristics, three genotypes (LGC-47, LGC-54, and LGC-59) were found significantly superior for number of leaflets (10.00 leaflets), whereas, LGC-25 for leaflet length (17.13 cm), LGC-6 for leaflet width (5.28 cm) and LGC-47 for rachis length (21.98 cm), and LGC-24 for petiole length (10.33 mm). The presence of variability for leaf traits in the studied genotypes is illustrated in Fig. 3. In flowering characteristics, the genotype LGC-61 was significantly superior for duration of panicle initiation (13.00 days) and maximum inflorescence width (20.33 cm), whereas, maximum inflorescence length observed in LGC-49 and LGC-61 (39.33 cm); and LGC-6 had shortest duration of panicle initiation. The longest flowering duration was observed in LGC-18 (36 days); and maximum number of days from panicle initiation to flowering observed in LGC-18 (30 days) followed by LGC-1 and LGC-60 (29 days). However, the genotype LGC-37 was found significantly diverse for maximum number of days from fruit set to maturity (107days).

Furthermore, the yield and yield attributes traits were showing significant differences among all the studied genotypes. The genotype LGC-6 was found significantly superior for 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). This genotype 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%) while LGC-59 was statistically at par with LGC-6 for TSS (19.86 °B), TSS/acid ratio (198.60), and ascorbic acid (75.66 mg/100g). LGC-59 was found superior for fruit length (20.12 mm), while LGC-18 was superior for fruit color-I (28.70) and fruit color-b (12.48), but the genotype LGC-37 had the highest value for fruit color-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. The variation presence in size of fruit and seed; and thickness of peel, aril, and seed of studied longan genotypes is illustrated in Fig. 3.

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 20 genotypes was determined in terms of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) and data presented in Table 4. The PCV was slightly greater than the GCV for all traits under study. The PCV ranged from 5.87% (fruit length width ratio) to 43.51% (tree volume), whereas the GCV varies from 2.63% (fruit length width ratio) to 43.04% (tree volume). Higher PCV and GCV were recorded for the tree volume (43.51% and 43.04%, respectively), followed by aril weight (43.33% and 42.86%, respectively), number of fruits per branch (42.83% and 42.52%, respectively), aril/seed weight ratio (36.62% and 35.51%, respectively), trunk girth (34.28% and 33.68%, respectively), TSS acid ratio (32.55% and 32.04%, respectively), aril thickness (32.83% and 29.03%, respectively), number of days from panicle initiation to flowering (30.15% and 27.76%, respectively), titratable acidity (25.17% and 24.25%, respectively), width of inflorescence (24.27% and 20.74%, respectively), length of inflorescence (24.24% and 22.38%, respectively), petiole length (23.75% and 21.22%, respectively), fruit weight (22.65% and 22.15%, respectively), plant height (22.56% and 22.22%, respectively), crown diameter (22.42% and 22.14%, respectively) and rachis length (21.15% and 20.09%, respectively) demonstrating a higher level of genetic variability for these traits among diverse genotypes. However, the lowest PCV and GCV was observed for the traits *viz.*, fruit length/width ratio (5.87% and 2.63%, respectively), number of days from fruit set to maturity (6.19% and 5.75%, respectively), flowering duration (7.70% and 4.67%, respectively), fruit length (7.68% and 6.26%, respectively), fruit colour-I (8.00%), seed length (9.15% and 7.76%, respectively), and seed width (10.02% and 8.49%, respectively).

The proportion of GCV in PCV observed in this study was generally high ranged from 44.72% in fruit length width ratio to 99.99% in fruit colour (I, a, and b). The proportion of genetic contribution to the overall phenotypic expression of most of traits was very high. Therefore, their use as important discriminatory variable for longan classification studies seems relatively reliable.

3.4. Heritability and genetic advance

In the present experiment, heritability in broad sense was estimated for all the traits and expressed in percentage that is ranged from 20.00–99.12% (Table 4). The highest heritability in broad sense was observed for all the traits except for few *viz.*, fruit length-width ratio (20.00%), duration of panicle initiation (22.78%), number of leaflets (36.38%), and duration of flowering (36.70%). The maximum heritability was noticed for the traits *viz.*, tree volume (97.85%), crown diameter (97.57%), plant height (97.01%), trunk girth (96.51%), rachis length (90.18%), petiole length (79.81%), and leaflet blade length (77.38%) among vegetative traits; and for phenological, fruiting, and seed traits *viz.*, fruit colour I, a, and b (99.10%, 99.12%, 99.10%, respectively), number of fruits per branch (98.58%), aril weight (97.83%), number of days from panicle initiation to flowering (84.76%), aril/seed weight ratio (90.04%), aril thickness (78.20%), inflorescence width (92.30%), fruit weight (92.20%), duration of panicle initiation (72.99%), inflorescence length (85.23%), and peel weight (81.85%). Furthermore, the TSS (99.14%), TSS acid ratio (96.92%), ascorbic acid (96.07%), and titratable acidity (92.86%) had the highest heritability among the physiochemical characters.

The genetic advance as per cent mean of was ranged from 2.42–87.70% (Table 4). The highest genetic advance as per cent of mean was observed for the traits *viz.*, duration of flowering (87.70%), trunk girth (87.33%), length of inflorescence (86.97%), number of fruit per branch (70.94%), duration of panicle initiation (68.16%), fruit weight (65.11%), fruit colour-a (64.98%), TSS acidity ratio (52.89), aril thickness (52.65%), fruit colour-I (48.16%), fruit length width ratio (45.09%), number of leaflets (45.06%), titratable acidity (44.62%), petiole length (42.56%), seed length (39.29%), width of inflorescence (39.05%), peel weight (36.50%), tree volume (35.45%), ascorbic acid (29.30%), plant height (25.36%), seed width (24.19%), leaflet blade width (23.20%), and fruit colour-b (20.43%).

Table 4

ANOVA, descriptive statistics and genetic parameters for thirty-four morphological and physiochemical quantitative traits of 20 longan genotypes

Traits	Mean square (Genotypes)	Minimum Range	Maximum Range	Mean	C.V.*	Std. Errors	C.D.* 5%	GCV* (%)	PCV* (%)	GCV:PCV	h ² * (Broad Sense) (%)	GAM* 5%
PHT (m)	1.841***	2.00	6.00	3.51	6.96	0.88	2.51	22.22	22.56	98.50	97.01	45.09
TG (cm)	892.850***	18.35	100.00	50.92	8.07	0.96	2.76	33.68	34.28	98.24	96.51	68.16
CD (m ²)	3.237***	2.25	7.04	4.67	5.18	0.61	1.74	22.14	22.42	98.78	97.57	45.06
TV (m ³)	269.708***	9.61	88.20	35.56	5.37	1.10	3.16	43.04	43.51	98.92	97.85	87.70
NFL	1.308**	7.00	11.00	8.88	10.88	1.48	4.25	5.91	9.79	60.32	36.38	7.34
LLG (cm)	9.960***	9.40	19.70	13.59	9.19	1.03	2.94	12.80	14.55	87.97	77.38	23.20
LWD (cm)	1.143***	2.60	5.60	4.07	9.19	1.14	3.28	14.13	17.00	83.10	69.06	24.19
RLG (cm)	28.800***	9.70	22.45	15.15	5.10	0.68	1.96	20.09	21.15	94.97	90.18	39.29
PTLG (mm)	7.593***	4.00	11.00	7.20	8.02	1.04	2.99	21.22	23.75	89.34	79.81	39.05
DPI (days)	8.526*	4.00	16.00	10.00	16.92	1.82	5.22	11.55	24.20	47.72	22.78	11.36
DPIF (days)	107.020***	9.00	32.00	20.90	7.03	0.72	2.05	27.76	30.15	92.07	84.76	52.65
FRD (days)	10.697**	27.00	37.00	32.25	13.03	1.99	5.70	4.67	7.70	60.58	36.70	5.82
INLG (cm)	141.904***	18.00	40.00	29.88	7.07	0.79	2.26	22.38	24.24	92.32	85.23	42.56
INWD (cm)	33.488***	8.00	22.00	15.20	7.92	0.84	2.42	20.74	24.27	85.43	72.99	36.50
DFTSM (days)	95.034***	83.00	109.00	95.35	7.59	0.94	2.69	5.75	6.19	92.86	86.24	11.00
FTPb	695.880***	15.00	65.00	35.73	4.37	0.55	1.58	42.52	42.83	99.29	98.58	86.97
FTLG (mm)	4.584***	15.25	21.75	18.26	5.59	0.61	1.75	6.26	7.68	81.50	66.41	10.51
FTW (mm)	8.947***	16.25	25.18	19.65	5.44	0.50	1.44	8.43	9.46	89.11	79.41	15.48
FLW (ratio)	0.0042 NS	0.76	1.07	0.93	6.55	0.06	0.18	2.63	5.87	44.72	20.00	2.42
FTWT (g)	6.238***	4.86	12.25	6.46	8.43	0.90	2.58	22.15	22.65	97.79	95.64	44.62
FC-I	12.388***	21.63	28.71	25.41	12.10	1.98	5.69	8.00	8.00	99.99	99.10	16.47
FC-a	2.593***	1.42	4.28	2.94	4.31	0.45	1.30	31.61	31.61	99.99	99.12	65.11
FC-b	6.454***	7.38	12.51	10.31	6.96	0.82	2.36	14.22	14.22	99.99	99.10	29.30
AWT (g)	6.054***	1.92	9.80	3.30	5.49	0.77	2.20	42.86	43.33	98.91	97.83	87.33
AT (mm)	1.5718***	1.20	5.17	2.38	5.53	0.89	2.54	29.03	32.83	88.43	78.20	52.89
PLWT (g)	0.0830***	0.87	1.62	1.18	7.60	0.94	2.71	13.61	15.04	90.47	81.85	25.36
SLG (mm)	3.202***	10.10	15.20	12.52	3.46	0.37	1.05	7.76	9.15	84.88	72.04	13.58
SWD (mm)	3.923***	9.70	15.90	12.66	8.10	0.85	2.44	8.49	10.02	84.69	71.73	14.81
SWT (g)	0.190***	0.84	1.98	1.38	7.47	1.25	3.59	17.99	18.80	95.67	91.52	35.45
ASWT (ratio)	2.261***	1.60	5.94	2.42	11.91	0.12	0.34	35.51	36.62	96.97	94.04	70.94
TSS (°B)	8.434***	14.40	20.30	16.81	5.72	0.83	2.38	9.96	10.00	99.57	99.14	20.43
Note: *CV: Coefficient of variation; C.D.: Critical difference; h ² : Heritability; GAM: Genetic advance as per cent of mean. Significant level: *** <i>p</i> = 0.01 and ** <i>p</i> = 0.05												

TA (%)	0.004***	0.10	0.20	0.15	7.28	0.81	2.32	24.25	25.17	96.36	92.86	48.16
TSS/TA (ratio)	4596.300***	75.25	203.00	121.52	17.26	2.46	7.06	32.04	32.55	98.45	96.92	64.98
AA (mg/100g)	121.152***	55.18	79.85	66.85	4.93	0.69	1.97	9.44	9.63	98.02	96.07	19.07
Note: *CV: Coefficient of variation; C.D.: Critical difference; h ² : Heritability; GAM: Genetic advance as per cent of mean. Significant level: *** <i>p</i> = 0.01 and ** <i>p</i> = 0.05												

3.5. Cluster analysis

Twenty longan genotypes were grouped into eight clusters based on Tocher's method of D² statistic (Table 5 and Fig. 5). Maximum number of genotypes were contained by the Cluster II, III and VI (4 genotypes), followed by cluster I (3 genotypes) and cluster IV (2 genotypes), whereas, cluster V, VII and VIII were comprised only single genotype. The average intra-cluster and inter-cluster distance was ranged from 0.00 to 423.02 and 278.46 to 1861.31, respectively (Table 6). The maximum intra-cluster distance exhibited by cluster VI (423.02) followed by cluster III (358.31), cluster II (312.82), cluster I (207.97), and cluster IV (191.08), whereas cluster V, VII and VIII were obtained zero intra-cluster distance. Furthermore, the maximum inter-cluster distance was exhibited by cluster IV and VI (1861.31), followed by cluster VI and VIII (1787.33), cluster III and VI (1413.17), cluster II and IV (1300.74), cluster VII and VIII (1220.98), cluster V and VIII (1216.79), cluster II and VIII (1118.32), and cluster I and VI (1108.72), whereas, minimum inter-cluster distance was observed between cluster V and cluster VIII (278.46) followed by cluster II and V (405.87), cluster I and III (417.44), and cluster I and V (489.98).

The presence of diversity among genotypes was determined by the significant amount of variability in cluster means for various characters. The cluster mean value of different clusters for different traits is depicted in Table 7. Genotypes under Cluster-I characterized as highest in performance of fruit width (20.75 mm), aril/seed weight ratio (3.10), and TSS (18.15 °B) while cluster-II had highest cluster mean value for a single character i.e., number of leaflets (9.33).

Table 5
Clustering pattern of twenty longan genotypes on the basis of D² statistic

Clusters	Number of genotypes within cluster	Percentage (%)	Genotypes in cluster
Cluster I	3	15	LGC-47, LGC-59, LGC-27
Cluster II	4	20	LGC-1, LGC-26, LGC-60, LGC-52
Cluster III	4	20	LGC-22, LGC-24, LGC-6, LGC-54
Cluster IV	2	10	LGC-40, LGC-50
Cluster V	1	5	LGC-61
Cluster VI	4	20	LGC-25, LGC-34, LGC-49, LGC-12
Cluster VII	1	5	LGC-37
Cluster VIII	1	5	LGC-18

In cluster-III, the highest cluster mean value was obtained for the yield, yield attributing traits and fruit quality viz., number of fruits per bunch (49.83), fruit weight (7.21 g), aril weight (4.26 g), aril thickness (2.92 mm), and ascorbic acid (70.87 mg). Cluster IV had highest cluster mean value for rachis length (16.98 cm), peel weight (1.35 g), and TSS/acid ratio (152.37). The maximum cluster mean value was recorded in cluster-V for leaflet length (14.40 cm), duration of panicle initiation (13.00 days), length of inflorescence (39.33 cm), width of inflorescence (20.33 cm), fruit length (19.42 mm), and fruit length/width ratio (0.97), whereas cluster-VI had highest mean value for only a single traits i.e., petiole length (8.25 mm). However, cluster VII has obtained maximum mean value for number of days from fruit set to maturity (107.00 days), fruit colour-a (4.27), and titratable acidity (0.20%), whereas cluster-VIII was obtained maximum mean value for plant height (5.75 m), trunk girth (95.00 cm), crown diameter (6.81 m²), tree volume (81.69 m³), leaflet width (4.40 cm), number of days from panicle initiation to flowering (30.00 days), flowering duration (35.00 days), fruit colour-I (28.70), fruit colour-v (12.48), seed length (13.23 mm), seed width (14.20 mm), and seed weight (1.53 g).

Table 6
Mean intra and inter cluster distance (D^2 distance) among eight clusters in longan

Clusters	I	II	III	IV	V	VI	VII	VIII
I	207.97	526.84	417.44	829.44	530.89	1108.72	553.78	724.04
II		312.82	857.28	1300.74	405.87	784.15	580.02	1118.32
III			358.31	541.46	832.00	1413.17	788.31	550.98
IV				191.08	1269.62	1861.31	1199.67	489.98
V					0.00	639.82	278.46	1216.79
VI						423.02	736.99	1787.33
VII							0.00	1220.98
VIII								0.00

Cluster I exhibited lowest in performance of cluster mean value for seed length (12.20 mm) and seed width (12.17 mm) whereas, cluster II observed for leaflet blade length (12.95 cm), rachis length (13.37 cm), duration of flowering (32.75 days), number of fruit per bunch (26.17) and seed weight (1.28 g). Cluster IV had lowest cluster mean value for tree height (2.98 m), trunk girth (43.40 cm), crown diameter (4.30 m²), tree volume (10.76 m³), number of leaflets (8.67), number of days from fruit set to maturity (92.00), fruit length (16.58 mm), fruit diameter (17.67 mm), fruit weight (5.11 g), aril weight (2.63 g) and aril thickness (1.87 mm) while cluster V had for leaflet blade width (3.40 cm), petiole length (6.00 mm), length of inflorescence (21.00 cm), width of inflorescence (11.00 cm), peel weight (1.00 g) and TSS acidity ratio (105.71); cluster III had for fruit colour-I (23.04) and fruit colour-b (8.74); and cluster VI had observed for fruit colour-a (1.46), TSS (15.15) and ascorbic acid (58.32). However, number of leaflet (8.67) was observed lowest mean value in three clusters, cluster III, IV and VI whereas, titratable acidity (0.13) in two clusters, cluster IV and VI.

Table 7
Cluster mean performance of different clusters for 34 quantitative traits of 20 longan genotypes.

Characters	I	II	III	IV	V	VI	VII	VIII
PHT (m)	3.00	3.16	3.85	3.45	4.15	3.50	2.30	5.75
TG (cm)	40.43	43.85	60.85	45.45	60.00	50.60	30.00	95.00
CD (m2)	3.65	4.09	5.41	4.84	4.98	4.82	3.75	6.81
TV (m3)	24.10	27.16	43.62	34.89	43.22	35.74	18.03	81.89
NFL	8.78	9.33	9.08	8.50	8.00	8.75	9.00	8.67
LLG (cm)	14.24	12.95	13.42	13.60	14.40	14.02	12.03	13.77
LWD (cm)	4.21	4.22	4.09	3.85	4.28	4.09	2.88	4.40
RLG (cm)	16.42	13.37	14.60	16.98	13.93	16.41	13.00	15.40
PTLG (mm)	7.00	6.92	7.42	6.33	7.33	8.25	6.33	6.33
DPI (days)	9.33	10.00	9.75	11.00	13.00	9.50	9.00	11.00
DPIF (days)	15.33	25.50	18.25	18.00	26.00	22.00	17.00	30.00
FRD (days)	31.00	32.50	32.25	33.50	33.00	32.25	29.00	35.00
INLG (cm)	34.00	28.83	25.92	23.00	39.33	34.42	18.67	35.00
INWD (cm)	17.11	14.75	13.58	11.50	20.33	17.17	9.33	18.00
DFTSM (days)	93.78	96.75	94.92	93.83	86.00	97.08	107.00	90.00
FTPb	48.11	26.17	49.83	36.50	23.33	29.67	24.33	27.00
FTLG (mm)	19.13	18.19	18.15	17.85	19.42	18.06	17.16	18.00
FTW (mm)	20.75	19.12	19.86	19.16	20.12	19.26	19.37	19.91
FLW (ratio)	0.92	0.95	0.92	0.93	0.97	0.94	0.89	0.91
FTWT (g)	6.84	5.78	7.21	6.09	6.86	6.45	5.36	6.54
FC-I	25.97	24.94	26.86	28.08	23.69	22.47	24.70	28.70
FC-a	2.55	1.88	3.02	3.64	3.67	3.73	4.27	1.46
FC-b	10.61	10.16	11.12	12.17	10.23	8.38	8.71	12.48
AWT (g)	3.82	2.69	4.26	3.02	2.30	3.16	2.74	3.06
AT (mm)	2.74	2.01	2.92	2.18	2.77	2.05	2.17	2.23
PLWT (g)	1.26	1.17	1.09	1.35	1.16	1.15	1.15	1.13
SLG (mm)	12.74	12.51	12.06	12.82	12.50	12.65	11.90	13.23
SWD (mm)	12.71	12.66	12.07	12.93	12.82	12.75	12.37	14.20
SWT (g)	1.36	1.28	1.43	1.50	1.30	1.40	1.24	1.53
ASWT (ratio)	3.10	2.14	2.84	2.02	1.77	2.28	2.22	2.01
TSS (°B)	18.15	16.51	17.55	17.14	17.83	15.79	15.06	15.15
TA (%)	0.16	0.15	0.15	0.12	0.17	0.14	0.20	0.13
TSS/TA (ratio)	130.09	113.60	127.65	152.37	107.08	118.56	75.28	113.76
AA (mg)	70.76	65.92	70.87	68.47	70.77	63.51	57.40	58.32

Discussion

Morphological Diversity

In the present study, a total of 54 qualitative and quantitative traits were investigated in a set of 20 longan genotypes to determine the morphological and physiochemical traits that might be helpful for identification of longan genotype. The characterization and assessment of genotypes is necessary for crop improvement programmes before choosing the genotypes for breeding programme. Most of the studied quantitative traits had potential economic value, particularly yield, yield attributing and fruit quality traits.

The results from this study revealed that all the qualitative characteristics were highly diversified within the twenty longan genotypes except for a few *viz.*, branching pattern, leaflet blade shape, leaflet apex shape, and presence of protuberance. The results of this study follow the findings of earlier researchers, showing the morphological qualitative traits of leaf and stem are essential for identification and evaluation of litchi cultivars (Wu et al., 2016; Khurshid et al., 2004). Furthermore, Singh et al. (1999) has reported that the genetic characteristics of leaf is an essential parameter which will help in identification and classification of litchi cultivars. Similarly, the findings of this study are in accordance with Lal et al. (2022) and Lal et al. (2023) for qualitative traits in litchi. However, above studied these qualitative traits can be utilized efficiently for identification and discrimination of longan genotypes.

Shannon's diversity indices were computed to assess the phenotypic diversity among the qualitative traits, and the mean diversity index was 0.78 (Table 3). Petiole colour, leaflet curvature, young leaf colour, mature leaf colour, branching density, leaflet midrib colour, abundance of flower, trunk surface, fruit maturity group, and tree vigour were recorded more than average value of Shannon's diversity index. The results were consistent with the finding of Qiying et al. (2023) for qualitative traits of leaf in litchi. Alcasid et al. (2015) have also reported the similar results in mango for fruit quality. Overall, Shannon's diversity indices indicated there was a high level of diversity among the studied longan genotypes for qualitative traits.

Mean square was highly significant for all the studied morphological and physiochemical quantitative traits due to their genotypes except for fruit length width ratio, which may be due to their different genetic make-up, plant type, and genotypic and environmental interactions. The presence of variability among these traits can be directly exploited through selection. These results were in accordance with the findings of Wu et al. (2016) and Saikia and Kotoky (2018) in litchi for vegetative, flowering, fruit and seed characteristics. Arora et al. (1996) have also reported significant variability in litchi genotypes with regard to fruit, aril, and seed characters at different locations. The variation observed among the litchi genotypes might be due to the genetic make-up of plant (Lal et al., 2022); nutrition and climatic conditions (Cronje et al., 2009). 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.

Genetic variability

The significant level of the coefficient of variations (genotypic and phenotypic) resulted in variation for most of the studied traits among longan genotypes, which can be improved through further breeding programmes. The estimates of phenotypic coefficient of variation (PCV) was slightly greater than the genotypic coefficient of variation (GCV) but in rare cases the PCV and GCV were the same. The difference between PCV and GCV indicating that environment has a minor effect on the phenotypic manifestation of characteristics. Hence, this variation is occurred due to both the environment and genotype (Marboh et al. 2018). High PCV and GCV of traits such as 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 and width of inflorescence, petiole length, fruit weight, plant height, crown diameter and rachis length indicated that the genotypes had a broad genetic base for these traits, so based on these traits, the scope of selection would be reliable and could easily adapt to environmental changes. These findings were consistent with the similar findings of other researchers with the several similar outcomes in litchi (Marboh et al. 2018; Kumari et al., 2017; Lal et al., 2022; and Lal et al., 2023). Patel et al. (2015) and Singh et al. (2015) have also reported the similar findings in guava. Furthermore, the similar findings were reported in different crops such as in mango (Gill and Navprem, 2015; Majumder et al., 2012); pomegranate (Perveen et al., 2018); and in pummelo (Wangchu et al., 2017). Unfortunately, leaflet length and leaflet width were not in accordance with the findings of Kumari et al. (2017) in litchi.

Hence, 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. GCV alone does not provide a complete package of estimation of variability that is heritable in nature; therefore, heritability estimation becomes more important.

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 (Lal et al., 2022). 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 (Dabholkar, 1992). This suggests that selection will be successful in identifying genotypes with highly heritable traits that are helpful in projecting the expected rate of advancement and long term genetic improvement (Singh 2000). The high magnitude of broad-sense heritability was recorded for most of the studied traits under this study except for number of leaflets, width of leaflets, duration of panicle initiation, flowering

duration, and fruit length /width ratio. The high heritability strongly suggests that the traits under this study have great scope for genetic improvement through breeding programmes because these characters are less influenced by the environment (Supriya et al., 2016). Moderate to low heritability indicates a limited scope for crop improvement through selection. These results were consistent with the findings of Marboh *et al.* (2017); Lal et al. (2022); Lal et al. (2023); and Kumari et al. (2017) in litchi.

Therefore, estimation of heritability alone will not be an effective selection criteria because it express effect of both additive and non-additive gene actions (Lipi et al., 2020). 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). Hence, for predicting the impact of selection, estimated heritability linked with genetic advance is more reliable than heritability alone (Marboh *et al.*, 2017). The most effective selection criteria is high broad-sense heritability combined with high genetic advance (Johnson et al. 1955). Results revealed high heritability coupled with high genetic advance was estimated for plant height, trunk girth, crown diameter, tree volume, rachis and petiole length, 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, fruit colour-a, titratable acidity and TSS acid ratio, indicating that these traits exhibit additive gene action and that phenotypic selection based on these traits would be more effective (Table 3). These results were in accordance with the findings of several researchers on various crops such as in litchi (Marboh *et al.*, 2017; Lal et al., 2022; and Lal et al., 2023; Kumari et al., 2017); guava (Singh et al., 2015 and Patel et al., 2015); strawberry (Mishra et al., 2015); and mango (Majumder et al., 2012; Das et al., 2021). High broad-sense heritability associated with a low genetic advance indicates non-additive gene action; low broad-sense heritability with a high genetic advance suggests additive gene effect; and low broad-sense heritability followed by low genetic advance indicates that the traits are extremely influenced by environmental factors and leading to unsuccessful selection (Mishra et al., 2015). Hence, the traits with high heritability and high genetic advance are not influenced by environment in expression of those traits and these traits can be directly improved through natural selection (Rasheed et al., 2023).

Cluster analysis

It is crucial to any crop improvement to choose desirable parent material, but it is a quite challenging task for crop breeders. The genetic divergence of any crop is regarded as a key component in achieving heterotic response in the F1 generation, and a large range of diversity exists in segregating generations (Arunachalam, 1981; Benbrahim et al., 2019). The estimation of genetic diversity is critical for identifying genetically different genotypes (Mukhopadhyay and Bhattacharjee, 2016). D² statistics developed by Mahalanobis is a one-of-a-kind approach to identifying genetically distinct genotypes that can be exploited in hybridization programmes.

In present study, the studied genotypes were grouped into eight groups based on the 34 quantitative traits. The results revealed that cluster VI exhibited maximum intra-cluster distance and the genotypes that come under this cluster are more diverse from the other clusters, which have lower intra-cluster distance, except for clusters V, VII, and VIII, which have exhibited null genetic diversity due to their monogenic properties. However, intra-cluster distance is indicating that the genotypes within the cluster will be more closely related to each other. The higher and lower intra-cluster distance was also indicated that the genotypes were heterogamous between and homogenous within the clusters (Sankaran *et al.*, 2020). Clusters IV and VI had the greatest inter-cluster distance indicating that there is presence of wide genetic diversity between the genotypes of these clusters. Therefore, the genotypes grouped into cluster IV and VI are expected to express high heterosis in hybridization programme. The clusters with the minimum inter-cluster distance have significantly lower genetic differences among their genotypes and were not reliable for hybridization programme. These results are in accordance with the findings of previous researcher *viz.*, Indian et al. (2019) in mango, Singh et al. (2015) in guava, Sharma et al. (2015a) in pear, Sinha et al. (2016) in pomegranate, and Mir et al. (2017) in apple.

Therefore, the D² distance of clusters alone is not reliable for choosing the genotypes for an effective hybridization programme. Hence, the cluster distance along with the average cluster mean value will provide a more accurate result for selection of a parent for the hybridization programme. In this study, the average cluster mean value revealed that the genotypes under cluster III had highest mean value for yield, yield attributing traits and fruit quality with the lower value of seed characters. This cluster also had a medium duration for fruit ripening. Cluster I had the highest mean value for fruit width, aril/seed weight ratio, and TSS, but the genotypes under this cluster have also shown a parity mean value with Cluster III for the number of fruit per bunch, fruit length, and ascorbic acid. Cluster VII was observed for highest mean value of tree, leaf, flower and seed characters. Cluster V had the highest mean value for duration of panicle initiation, length and width of inflorescence, fruit length, and fruit length/width ratio, it also obtained a parity mean value of ascorbic acid with cluster III. This study has shown that the Cluster II, VI and VII are not significantly important as they exhibited the lowest cluster mean value for almost all the studied traits. Hence, it is clear from this study that in order to introduce desired quality genes into the high producing varieties, it may be advantageous to use the genotypes of these clusters in the breeding programme. The results of this study are in support view of previous findings of researcher *viz.*, Sharma et al. (2015b) in apple, Raina et al. (2015) in pomegranate, Sankaran *et al.* (2020) in mango, Garg et al. (2015) in strawberry, Gupta et al. (2017) in grapes, and Sundharaiya et al. (2022) in avocado.

Conclusion

Longan genotypes demonstrated significantly immense variability in qualitative and quantitative studied characteristics. High PCV and GCV were found for economic importance traits, indicate that selection based on these characteristics can result in greater improvement. In this study, we could identify the most important traits based on high heritability coupled with genetic advance that will be useful in improvement of longan genotypes like plant height, trunk girth, crown diameter, tree volume, number of days from panicle initiation to flowering, width of inflorescence, number of fruits per bunch, fruit weight, fruit colour-a, aril weight, aril thickness, seed weight, aril weight and seed weight ratio, titratable acidity, and TSS acidity ratio. It is indicative of additive gene action, and selection based on these traits would be more reliable. The 20 diverse longan genotypes could be grouped into eight clusters and the greatest inter-cluster distance was found between Cluster IV and VI. Furthermore, the most important traits were identified in clusters I, III, and V, which can be useful for the genetic improvement of longan. Thus, it is concluded that the longan genotypes from the most distantly related clusters that also have valuable traits could be advantageously utilised in inter-cluster hybridization with the hope that this would lead to improvement in one or more horticultural traits of longan. We could identify two most promising genotypes based on *per se* performance along with the cluster mean value, LGC-6 and LGC-59, with respect to yield and fruit quality traits. Understanding and structuring the genetic diversity of longan genotypes will be a significant step towards linkage analysis, association mapping, and cross breeding programmes, which will aid in the design of strategies for germplasm characterization, conservation, and genetic improvement of this fruit crop.

Future prospects

Longan is an important fruit crop with a high market value in both the Indian and global markets. In India, it is a fruit crop that is underutilised. Researchers must conduct genetic diversity research on this species, which could lead to future crop enhancing efforts. Gandaki Longan-1 is India's sole recently developed variant. Research institutes are required to explore and advocate for the cultivation of this fruit crop, while also undertaking enhancement initiatives to develop high-yield cultivars with superior fruit quality.

Declarations

Author Contribution

Ajay Kumar conducted the experiment and authored the main manuscript text. Dr. Alok Kumar Gupta provided significant guidance and provided necessary facilities in his lab for the smooth conduct of research. He also assisted in preparing the manuscript draft. Dr. Neeharika Kanth provided guidance for the experiment and contributed to the preparation of the manuscript draft. Sudheer Kumar Yadav prepared Figure 1 and assisted in the data analysis. Dr. ES Marboh provided facilities in his lab for conducting the experiment. All authors reviewed the manuscript.

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References

1. Alam K, Singh MK, Kumar M, Singh A, Kumar V, Ahmad M, and Keshari D (2020) Estimation of genetic variability, correlation and path coefficient in okra (*Abelmoschus esculentus* (L.) Moench). J. pharmacogn. Phytochem 9(5), pp.1484-1487.
2. Alcasid CE, Gueco LS, Valencia LD (2015) Diversity analysis based on morphological traits of different mango accessions collected from selected areas in the Philippines. Asian J. Agri. F. Sci 11:3(6).
3. Arora RK, Rao VR, and Rao AN (1996) Status Report on Genetic Resources of Litchi in China. IGPRI Regional Office for Asia, the Pacific and Oceanic, Singapur, pp1-18.
4. Arunachalam V (1981) Genetic distance in plant breeding. Indian J Genet Plant Breed 41, pp.226-236.
5. Bailey-Serres J, Parker JE, Ainsworth EA, Oldroyd GE and Schroeder JI (2019) Genetic strategies for improving crop yields. Nature 575:109-118. <http://dx.doi.org/10.1038/s41586-019-1679-0>
6. Benbrahim N, Mentag R, Elghzaoui Y, Triqui AZ, Gmouh S, ES-Safi N, Taghouti M (2019) Fruits morphological qualitative traits, biochemical components and pungency strength of spicy pepper from Maleh Valley in Morocco. J. Plant Sci.7:29-43. <https://doi.org/10.13189/ujs.2019.070301>
7. Burton GW (1952) Quantitative inheritance in grasses. Pro VI Int Grassl Cong, 277-283.
8. Chen H, He X, Luo C, Zhu J, Li F (2010) Analysis on the genetic diversity of 24 longan (*Dimocarpus longan*) accessions by SCoT markers. Acta Hortic. Sin. 37(10):1651-4. <https://www.ahs.ac.cn/EN/Y2010/V37/I10/1651>

9. Cheng A, Yan H, Han C, Wang W, Tian Y, Chen X (2014) Polyphenols from blueberries modulate inflammation cytokines in LPS-induced RAW264. 7 macrophages. *Int. J. Biol. Macromol.* 1;69:382-7. <https://doi.org/10.1016/j.ijbiomac.2014.05.071>
10. Cronje RB, Sivakumar D, Mostert PG and Korsten L (2009) Effect of different preharvest treatment regimes on fruit quality of litchi cultivar 'Maritius'. *J. Plant Nutri.* 32:19-29. <https://doi.org/10.1080/01904160802530987>
11. Dabholkar AR (1992). *Elements of biometrical genetics*. Concept Publishing Company, (Eds.), New Dehli. p. 431.
12. Das SS, Kishore K, Lenka D, Dash DK, Samant D, Panda CM, Samal KC, Sahoo SC, Dash SN (2021) Studies on genetic variability, heritability and character association of yield and quality traits in mango germplasm in eastern tropical region of India. *Agril. Res. J.* 58(6), pp.998-1005. <https://doi.org/10.5958/2395-146X.2021.00141.1>
13. Freed M (1966) *Methods of Vitamin Assay*. 3rd edn, The Association of Vitamin Chemists, Inc., J. Wiley, Interscience Publishers, New York, pp. 287-344
14. Garg S, Sharma G, Lata S, Devi I (2015) Genetic divergence analysis for vegetative, flowering, fruit quality and yield characters in strawberry, *Fragaria x ananassa* Duch. *Int. J. Farm Sci.* 5(4):145-9.
15. Gill MS and Navprem S (2015) Genetic parameters, character association and path analysis for fruit yield and its component characters in mango (*Mangifera indica* L.). *Indian J. Plant Genet. Resources* 28(3), pp.292-295. <https://doi.org/10.5958/0976-1926.2015.00037.6>
16. Gupta N, Gill MI, Arora NK (2017) Cluster analysis for fruit yield components in grapes. *Electron. J. Plant Breed.* 8(1):306-10. <https://doi.org/10.5958/0975-928X.2017.00044.8>
17. Hanson CH, Robinson HF, and Comstock RE (1956) Biometrical studies of yield in segregating populations of Korean lespedeza 1. *J. Agron.* 48(6), pp.268-272.
18. Huang S, Han D, Wang J, Guo D and Li J (2021) Floral induction of longan (*Dimocarpus longan*) by potassium chlorate: application, mechanism, and future perspectives. *Front. Plant Sci.* 12:670587 (Art.). <https://doi.org/10.3389/fpls.2021.670587>
19. Indian G, Sankaranarayanan R, Murugesan S, Rajangam J (2019) Assessment of genetic divergence using Mahalanobis D2 analysis in mango. *J. agric. ecol.* 7:38-46.
20. IPGRI (2002) *Descriptors for Litchi (Litchi chinensis)*. International Plant Genetic Resources Institute, Rome, Italy.
21. Jia-xin F, Ying W, Jia Z, Hai-yan Z, Sui-sheng H, You-li H, Gui-bing H and Cheng-ming L (2011) Genetic diversity of germplasm resources of Litchi and Longan using SSR analysis. *Acta Hort.* 918:363. <https://doi.org/10.17660/ActaHortic.2011.918.47>
22. Johnson HW, Robinson HF and Comstock RE (1955) Estimates of genetic and environmental variability in soybeans. *Agronomy Journal* 47:314-318.
23. Khurshid S, Ahmad I, and Anjum MA (2004) Genetic diversity in different morphological characteristics of litchi (*Litchi chinensis* Sonn.). *Int J Agric Biol* 6:1062-1065. <https://doi.org/1560-8530/2004/06-6-1062-1065>
24. Kumari A, Mankar A and Mir H (2017) Genetic Variability and Heritability among the different Traits in Litchi (*Litchi chinensis* Sonn.) Hybrids. *Indian J. Ecol.* 44:484-487.
25. Lal N, Pandey SK, Pandey SD and Nath V (2023) Genetic Diversity and Grouping of Litchi Genotypes Based on 83 Qualitative and Quantitative Traits. *Erwerbs-Obstbau* 65:1003-1012. <https://doi.org/10.1007/s10341-022-00747-x>
26. Lal N, Singh A, Kumar A, Marboh ES, Gupta AK, Pandey SD and Nath V (2022) Genetic variability, correlation and path-coefficient studies in litchi (*Litchi chinensis* Sonn.) for plant growth, panicle and yield attributes. *Int. j. bio-resour. stress manag.* 13:29-36. <https://doi.org/10.23910/1.2022.2640>
27. Leenhouts PW (1971) A revision of *Dimocarpus* (Sapindaceae). *Blumea-Biod, Evol Biogeo of Plants.* 19(1): 113-131.
28. Lin T, Lina Y, and Ishikib K (2005) Genetic diversity of *Dimocarpus longan* in China revealed by AFLP markers and partial rbcL gene sequences. *Sci Hortic* 103:489–498. <https://doi.org/10.1016/j.scienta.2004.08.005>
29. Lipi LF, Hasan MJ, Akter A, Quddus MR, Biswas PL, Ansari A and Akter S (2020) Genetic variation, heritability and genetic advance in some promising rice hybrids. *SAARC J. Agri.* 18:39-49. <https://doi.org/10.3329/sja.v18i2.51107>
30. Majumder DA, Hassan L, Rahim MA, Kabir MA (2012) Correlation and path coefficient analysis of mango (*Mangifera indica* L.). *Bangladesh J. Agric. Res.* 37(3):493-503.
31. Marboh ES, Gupta AK, Gyanesh K, Singh M, Singh A and Nath V (2018) Genetic variability, heritability and genetic advance in litchi (*Litchi chinensis*). *Indian J. Agric. Sci.* 88:1510-1514.
32. Mariana BD, Sugiyatno A and Supriyanto A (2011) Genetic diversity of local accessions of *Dimocarpus longan* revealed by ISSR markers. *Buletin Plasma Nutfah* Vol.17 No.1 Th.
33. Mei Z Q, Fu SY, Yu HQ, Yang LQ, Duan CG, Liu XY, Gong S, and Fu JJ (2014) Genetic characterization and authentication of *Dimocarpus longan* Lour. using an improved RAPD technique. *Genet. Mole Res.* 13:1447– 1455. <http://dx.doi.org/10.4238/2014.March.6.3>
34. Mir JI, Ahmed N, Singh DB, Padder BA, Shafi W, Zaffer S, Hamid A, Bhat HA (2017) Diversity evaluation of fruit quality of apple (*Malus domestica* Borkh.) germplasm through cluster and principal component analysis. *Indian J. Plant Physiol.* 221-6.

35. Mishra PK, Ram RB, Kumar N (2015) Genetic variability, heritability, and genetic advance in strawberry (*Fragaria × ananassa* Duch.). Turk J Agric For. 39(3):451-8. <https://doi.org/10.3906/tar-1408-99>
36. Mukhopadhyay T, Bhattacharjee S (2016) Genetic Diversity: Importance and Measurements. Conserving Biological Diversity: A Multiscaled Approach. Research India Publications, New Delhi. 2016:251-95.
37. Panse VG, Sukhatme PV (1954) Statistical methods for agricultural workers. Statistical methods for agricultural workers
38. Park SJ, Park DH, Kim DH, Lee S, Yoon BH, Jung WY, Lee KT, Cheong JH, Ryu JH (2010) The memory-enhancing effects of Euphoria longan fruit extract in mice. J. Ethnopharmacol. 128(1):160-5. <https://doi.org/10.1016/j.jep.2010.01.001>
39. Patel RK, Maiti CS, Deka BC, Vermav VK, Deshmukh NA, Verma MR (2015) Genetic variability, character association and path coefficient study in guava (*Psidium guajava* L.) for plant growth, floral and yield attributes. Int. J. Bio-Resour. Stress Manag. 4:457-66. <https://doi.org/10.5958/0976-4038.2015.00068.8>
40. Perveen N, Cholin SS, Hipparagi K, Murthy BN, Peerjade D (2018) Genetic variability studies in pomegranate. Indian J. Hortic. 75(3):355-61. <https://doi.org/10.5958/0974-0112.2018.00062.2>
41. Puri RK (2001) Local knowledge and manipulation of the fruit 'mata kucing' (*Dimocarpus longan*) in East Kalimantan. In: Victor M, Barash A (eds) Cultivating forests: alternative forest management practices and techniques for community forestry. RECOFTC, Bangkok, pp 98–110.
42. Qiu DL (2012) Longan production and research in China. *IV International Symposium on Lychee, Longan and Other Sapindaceae Fruits*. 1029: 39-46.
43. Qiying LI, Fang LI, Rupeng CA, Lei ZH, Yao LI, Huanling LI, Jiabao WA (2023) Diversity analysis of leaf traits of litchi genetic resources in Hainan. J. Tropic. Bio. 14(6), pp.628-635. <https://doi.org/10.15886/j.cnki.rdswwb.20220126>
44. Raina D, Dhillon WS, Gill PP, Singh NP (2015) Assessment of genetic divergence using Mahalanobis D^2 and principal component analysis of qualitative and quantitative characters in pomegranate genotypes under sub-tropics. Indian J. Horti. 72(4):451-6.
45. Ranganna S (1997) Handbook of analysis and quality control for fruits and vegetable products (2nd Ed.). Tata Mc Grow Hill Publishing Pvt. Ltd., New Delhi, pp. 3-621.
46. Rao CR (1952) Advanced statistical methods in biometric research. John Wiley and Sons, New York.
47. Rasheed A, Ilyas M, Khan TN, Mahmood A, Riaz U, Chattha MB, Al Kashgry NA, Binothman N, Hassan MU, Wu Z, Qari SH (2023) Study of genetic variability, heritability, and genetic advance for yield-related traits in tomato (*Solanum lycopersicon* MILL.). Front. Genet. 13:1030309. <https://doi.org/10.3389/fgene.2022.1030309>
48. Saikia P and Kotoky U (2022) A Study on the morphological characters of elite Litchi (*Litchi chinensis*) cultivars in Jorhat, Assam. J. Pharm. Innov. 11:1934-1938.
49. Sankaran M, Dinesh MR, Gowda DC, Venugopalan R. Genetic Analysis in mango (*Mangifera indica* L.) based on fruit characteristics of 400 genotypes. J. Hortic. Sci. 15(2):161-72. <https://doi.org/10.24154/jhs.v15i2.944>
50. Sharma A, Kumar R, Mankotia MS, Mahajan PK, Belwal OK, Sharma SK (2015) Genetic divergence evaluation of apple germplasm by D^2 multivariate analysis. J. Appl. Nat. Sci. 7(2):889-92. <https://doi.org/10.31018/jans.v7i2.702>
51. Sharma G, Lata S, Yadav A, Sharma OC, Sharma N (2015) Assessment of variation in pear genotypes through genetic divergence and cluster analysis using D^2 statistics. Afr. J. Agric. Res. 10(10):1063-6. <https://doi.org/10.5897/AJAR2014.9063>
52. Singh BD (2000) Plant Breeding: Interrelationships between yield and yield components in mung bean. Indian J Genet Plant Breed 30:244-250
53. Singh D, Gill MIS, Boora RS and Arora NK, (2015) Estimates of genetic variability, heritability, genetic advance, correlation coefficients and their prospects for crop improvement in guava (*Psidium guajava* L.). J. Appl. Hortic. 17:76-78. <https://doi.org/10.37855/jah.2015.v17i01.15>
54. Singh G, Nath V, Pandey SD and Ray PK (2011) Good Management Practices in litchi. Ministry of Agriculture, Govt. of India and National Research Centre on Litchi, Mushahari, Muzaffarpur.
55. Singh K, Choudhary BM, Shanker R, Jain BP (1999) Studies on the physical changes in Litchi fruits during growth and development under Ranchi condition. Prog. Hortic. 3:151-5.
56. Sinha S, Thakur DS, Mishra PK and Sinha R (2016) D^2 -analysis suggests wider genetic divergence in ysis suggests wider genetic divergence in pomegrana pomegranate genotypes TE genotypes. The Bioscan, 11(2), pp.1011-1015.
57. Suiubon S, Supapvanich S, Promyou S (2017) Postharvest quality maintenance of longan fruit by ultra violet-C incorporated with salicylic acid application. Emir J Food Agric. 2017 Feb 3:179-87. <https://doi.org/10.9755/ejfa.2016-09-1269>
58. Sundharaiya K, Thangaselvabai T, Sathish G, Mohanalakshmi M, Sivakumar V (2022) D^2 analysis in avocado (*Persea americana* Mill). J. Pharm. Innov. 11(1): 1916-1919

59. Supriya SM, Kulkarni VV, Lokesha R and Govindappa MR (2016) Genetic variability studies for yield and yield components in sunflower (*Helianthus annuus* L.). Electron. J. Plant Breed. 7:737-741. <https://doi.org/10.5958/0975-928X.2016.00096.X>
60. Wall MM (2006) Ascorbic acid and mineral composition of longan (*Dimocarpus longan*), lychee (*Litchi chinensis*) and rambutan (*Nephelium lappaceum*) cultivars grown in Hawaii. J Food Compost Anal. 19(6-7):655-63. <https://doi.org/10.1016/j.jfca.2005.12.001>
61. Wangchu L, Tamut G, Singh B, Singh SR, Singh S (2017) Studies on genetic variability of pummelo (*Citrus grandis* L.) in East Siang District of Arunachal Pradesh, India. Int J Basic Appl Biol. 4(2):64-73.
62. Weiping T, Heqiang H, Qiuming Z, Jianguang L, Birong Z (2003) Studies on the genetic diversity and relationship of longan cultivars by AFLP analysis. Acta Hortic Sin 30(03):272. <https://www.ahs.ac.cn/EN/Y2003/V30/I03/272>
63. Wen-shun HU, Ai-ping H, Fan J, Ji-mou J, Xiu-ping CH, Shao-quan Z. Identification and genetic diversity of reciprocal hybrids in longan (*Dimocarpus longan*) by SSR. Acta Hortic. Sin. 42(10):1899. <https://www.ahs.ac.cn/EN/Y2015/V42/I10/1899>
64. Westwood MN, Reimer FC and Quackenbush VL (1963) Long term yield as related to ultimate tree size of three pear varieties grown on rootstocks of five *Pyrus species*. In Proc. American Society for Horticultural Science 82:103-113.
65. Wu J, Zhang C, Chen J, Cai C, Wang L, Fu D and Ou L (2016) Morphological diversity within litchi (*Litchi chinensis* Sonn.) based on leaf and branch traits. Sci. Hortic. 207:21-27. <https://doi.org/10.1016/j.scienta.2016.05.004>
66. Yang WH, Zhu XC, Bu JH, Hu GB, Wang HC and Huang XM (2009) Effects of bagging on fruit development and quality in cross-winter off-season longan. Sci. Hortic. 120:194-200. <https://doi.org/10.1016/j.scienta.2008.10.009>
67. Zeng L, Hong Z, Lin W, Zheng J, Wu S (2009) ISSR analysis of germplasm in longan. J. Fujian Agric.For. Uni. (Natural Science Edition), 38(3), pp.238-242.

Figures

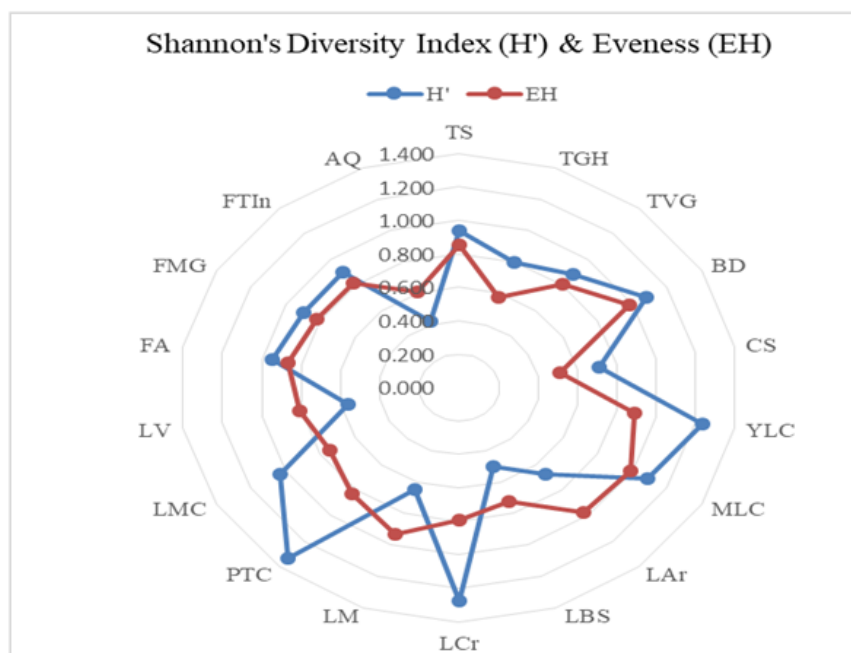


Figure 1

Graphical representation of Shannon's diversity indices. H': Shannon's diversity index and EH: Shannon's diversity evenness or diversity equitability



Figure 2

Variation in fruit bearing intensity in longan genotypes.

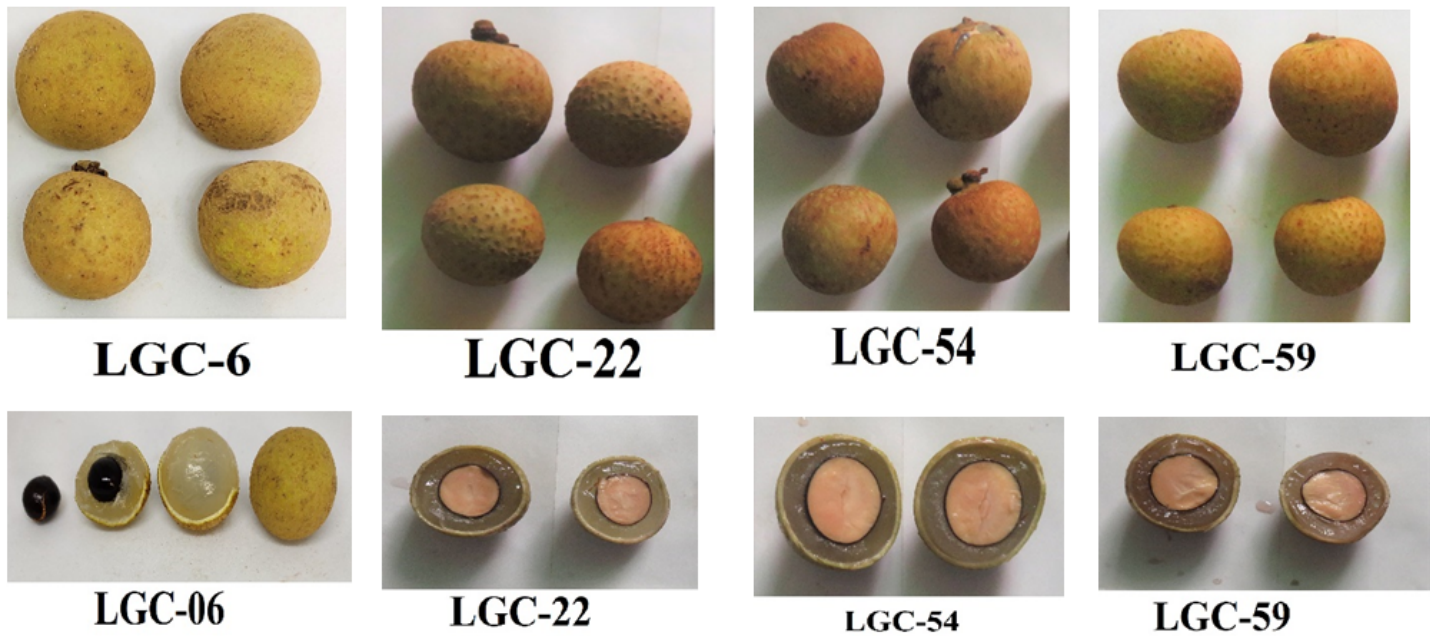


Figure 3

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



Figure 4

Variation in leaf shape, size and types of leaflet arrangement

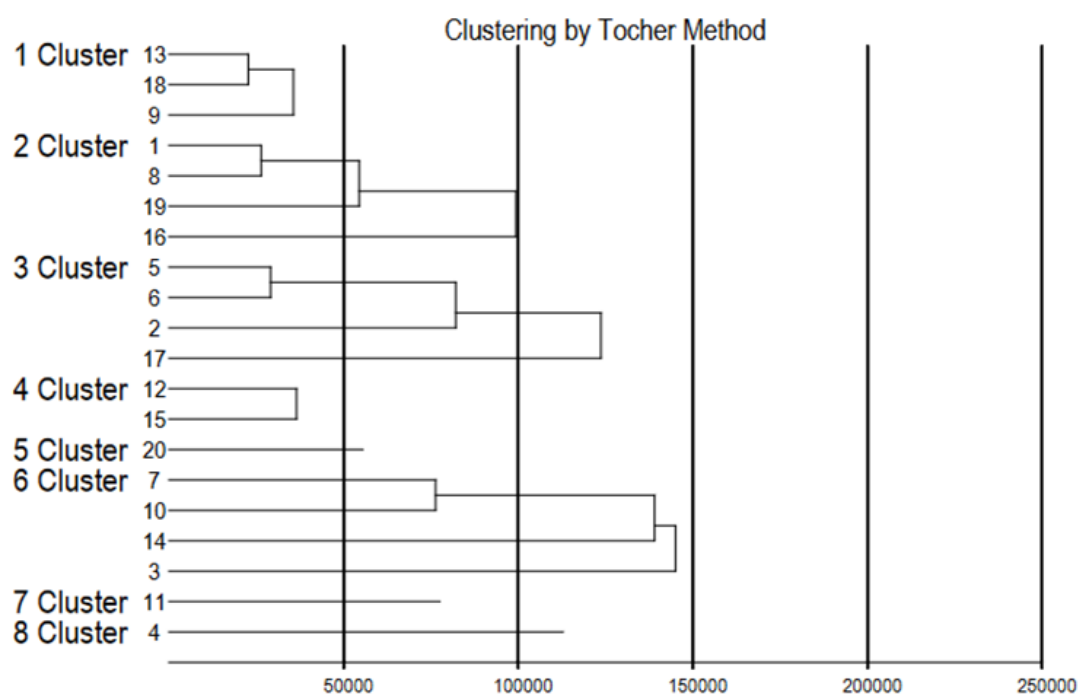


Figure 5

Dendrogram showing the clustering groups based on quantitative traits among 20 longan genotypes using hierarchal clustering analysis (Tocher's method).

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