

Genetic diversity analysis of guava (*Psidium guajava* L) genotypes in West Bengal, India

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Abstract

A total of 28 traits enabled an assessment of the genetic variability of twenty-four guava genotypes. Many of these traits have significantly important and use for improvement programme in terms of fruit quality and yield. The TSS of fruit ranged from 8.57 °B (China genotype) to 12.19 °B (Arka Kiran) and seed number/fruit from 109.58 (Taiwan) to 303.67 (China genotype). Correlation studies revealed a strong positive correlation among quantitative traits related to fruit yield and quality, whereas some negative correlation between qualitative traits. Principal component analysis showed that the first three components with Eigen values were able to explain more than 76.99% of the total variation. PC1, PC2 and PC3 accounted for 41.15%, 24.74% and 11.10%, respectively. Cluster analysis distinguished all the genotypes into three clusters/groups. The PCA and clustering analysis indicated a higher level of diversity in guava genotypes. The local cultivars, viz., Baruipur Local, Khaja and Mohammad Khaja genotypes and improved cultivars like Arka Kiran and Philippines were identified with desirable fruit quality traits useful for commercialization and crop improvement programme.

Key words: Correlation studies, dendrogram, germplasms, morphological variation, PCA

Introduction

Guava (*Psidium guajava* L.) belongs to the family Myrtaceae and is native to Tropical America, stretching from Mexico to Peru (Singh, 2011). The Spanish and Portuguese colonizers brought it into the New World, the East Indies and Guam. Portuguese introduced the guava crop in India during the 17th century (Menzel and Paxton, 1985). Among the tropical and subtropical fruit species, guava is one of the more tolerant to environmental stress, which makes it relatively easy to grow all over the tropical and subtropical regions of the world (Shigeura and Bullock, 1983). The genus *Psidium* (2n=22) has approximately 150 species; about 20 species produce edible fruits; the rest are primarily wild with inferior quality fruits, and the important species with edible fruits is *Psidium guajava* L. (Common guava). The other *Psidium* species are utilized to fulfil breeding objectives like vigour, high yielding, fruit quality and resistance to pests and diseases. (Dinesh and Vasugi, 2010).

Its cultivation is well distributed in almost all states of India and commercially cultivated in Uttar Pradesh, Bihar, Karnataka, Punjab, West Bengal, Madhya Pradesh, Tamil Nadu and Andhra Pradesh. The total guava production in the country is about 4107 metric tonnes, covering 270 thousand hectares of area with a productivity of 15.61 metric tonnes per hectare (NHB, 2019). The crop has gained commercial importance in most parts of the country and the state of West Bengal for its high nutritional value and comparatively low cost of production. In West Bengal, guava is commercially cultivated mainly in Nadia, North and South 24 Parganas, Howrah, Hooghly and Murshidabad. The total guava production in West Bengal is about 202.95 metric tonnes from an area of 15.67 thousand hectares (NHB, 2019).

Its being a cross-pollinated species, significant variation in the seedling population is observed in different growing regions. The new guava genotypes are being developed through a hybridization programme and commercial exploitation of seedling selection from hybrid population. The new genotype varies in several characters from their parent (Saxena *et al.*, 2007). High heterozygosity and frequent cross-pollination resulted in variability in promising genotypes when propagated through seed (Dinesh and Vasugi, 2010). In a Crop improvement program aiming to develop a model plant ideotype in guava, a proper understanding of interactions between plant growth processes and yield is essential. The varietal specification is the most important aspect for commercializing of any crop under specific agro-climatic conditions. However, some long-standing problems, such as the lack of dwarf and prolific fruit-bearing genotypes and, lack of soft-seeded and coloured fruit genotypes, require urgent research.

A diverse gene pool is highly essential for crop improvement programmes. The origin of cultivars and knowledge about genetic diversity would help select better parents for the hybridization programme. Selection of parents based on morphological characters is the first step towards conserving and maintaining of the existing diversity. A careful study of the existing germplasm would help eliminate the duplicate germplasm collection (Prakash *et al.*, 2002). Knowledge of genetic variation and relationships between germplasms is important to understand genetic variability and its potential use in the breeding programme. Quantitative traits provide an estimate of phenotypic diversity among germplasm collections. Therefore, this study analyzes the genetic diversity of guava germplasm based on quantitative and qualitative traits to improve guava fruit yield and quality.

Materials and methods

Experimental Site: The present investigation was conducted at the Horticultural Research Station, Mondouri and Department of Fruit Science, Bidhan Chandra Krishi Viswavidyalaya, Mohanpur, Nadia, West Bengal. The Horticulture Research Station, Mondouri, is located at 22.9452° N latitude, 88.5336° E longitudes, having an average altitude of 9.75 m from the mean sea level.

Planting materials: Twenty-four guava genotypes were used for study from the germplasm collection at the Horticultural Research Station, Bidhan Chandra Krishi Viswavidyalaya, West Bengal, India (Table 1) with a randomized block design with three replications over seven years. The genotypes came from different sources, like exotic genotypes and plant prospected from other research stations throughout the country.

Quantitative and qualitative traits evaluation: The 28 quantitative and qualitative traits investigated included plant girth (PG), plant height (PH), plant width (East-West), plant width (North-South), leaf Length (LL), leaf breadth (LB), leaf length (cm): breath ratio (LLB), petiole length (PL), leaf area (LA), fruit weight (FW), fruit length (FL), fruit width (FW), fruit length: width ratio (FWLR), outer flesh thickness (OFT), core thickness (CT), pulp weight (PW), fruit volume (FV), total soluble solids (TSS), titrable acidity (TA), ascorbic acid (AA), total sugar (TS), reducing sugar (RS), non-reducing sugar (NRS), sugar: acid ratio (S:A), seed number/fruit (SN), total seed weight/fruit (SW), 100 seed weight and yield.

Total soluble solids content of fruits was determined with the help of a digital hand refractometer and expressed in ⁰Brix (RX 5000, ATAGO, Japan). The total titrable acidity was estimated by Sadasivam and Manickam (1996) method, and the ascorbic acid was estimated using the Ruck (1969) method. The total sugar content of fruit was calculated as the sum of non-reducing

Table 1. List of twenty-four guava genotypes

Genotype	Parentage	Source of collection	Pulp colour
Pant Prabhat	Selection from Allahabad Safeda	GBPAU&T, Pantnagar	White
Lalit	Half sib progeny of Apple Guav	CISH, Lucknow	Pink
Allahabad Safeda	Selection from local population	CISH, Lucknow	White
Lucknow-49	Open pollinated seedling of Allahabad Safeda	CISH, Lucknow	White
Shweta	Half sib progeny of Apple Guava	CISH, Lucknow	Pink
Philippines	Unknown	Private nursery	White
China	Unknown	Private nursery	White
Arka Mridula	Selection from Allahabad Safeda	IIHR, Bangalore	White
Arka Kiran	Kamsari x Purple Local	IIHR, Bangalore	Pink
Arka Amulya	Allahabad Safeda x Triploid	IIHR, Bangalore	White
Kohir Safeda	Kohir x Allahabad Safeda	FRS, Sangareddy, Telengana	White
Kohir Red	Selection from Kohir Village	FRS, Sangareddy, Telengana	Pink
Kohir Long	Selection from Kohir Village	FRS, Sangareddy, Telengana	Pink
Kohir Round	Selection from Kohir Village	FRS, Sangareddy, Telengana	White
Safed Jam	Allahabad Safeda x Kohir	FRS, Sangareddy, Telengana	White
Hissar Surkha	Apple Color x Banarasi Surkha	CCSHAU, Hissar	Pink
Hissar Safeda	Allahabad Safeda x Seedless	CCSHAU, Hissar	White
SRD-1	Safed Jam x Red Fleshed 1/6	FRS, Sangareddy, Telengana	Pink
Kafri	Selection in Baruipur	Baruipur Nursery, West Bengal	White
Khaja	Selection in Baruipur	Baruipur Nursery, West Bengal	White
Dudh Khaja	Selection in Baruipur	Baruipur Nursery, West Bengal	White
Mohammad Khaja	Selection in Baruipur	Baruipur Nursery, West Bengal	White
Baruipur Local	Selection in Baruipur	Baruipur Nursery, West Bengal	White
Taiwan	Unknown	Private Nursery	Deep red

and reducing sugars using the method described by Dubois *et al.* (1951).

Statistical analysis: Data from the 24 guava genotypes of involving 28 traits were analyzed by XLSTAT (2013), XLSTAT software (version 2013.1). The correlation analyses used parametric Pearson correlations to analyze the quantitative and qualitative traits. The combined data from quantitative and qualitative traits were used for dendrogram construction. Euclidean distance was used to analyze the genetic dissimilarity component and Ward's method was used for the agglomerative hierarchical clustering (AHC).

Results

Descriptive statistics and correlations for the quantitative traits: The quantitative characteristics were measured, and the descriptive statistics of minimum, maximum, means and standard deviation are shown in Table 2. Some traits had high standard deviation. These included total seed number (49.61 %), ascorbic acid (25.92 %), fruit volume (14.52 %), fruit weight (14.24 %) and pulp weight (10.09 %). The remaining traits showed comparatively low standard deviations <10 %. Fruit length: width ratio and acidity had a minimum standard deviation of 0.7% each.

The exotic genotype Philippines had the highest fruit weight (168.40 g), followed by Arka Kiran (150.30 g), Shweta (144.61 g) and Allahabad Safeda (144.19%). The lowest fruit weight (97.68 g) was recorded in the Taiwan genotype, followed by Pant Prabhat (109.79 g), SRD-1 (118.56 g) and Kohir Long (120.73 g). Arka Kiran recorded the China genotype's maximum TSS (12.19 0B) and the minimum TSS (8.57 0B). The highest acidity (0.52 %) was recorded in the Philippines genotype, followed by China (0.45 %) and Kafri (0.41 %) and the lowest acidity (0.22 %) was recorded in Arka Kiran, followed by Lalit (0.24 %) and Shweta (0.27 %). The minimum seed number/fruit was recorded

Table 2. Descriptive statistics for quantitative traits of 24 guava genotypes

Variable	Minimum	Maximum	Mean	SD
Fruit weight	97.68	168.40	133.17	14.24
Fruit length	4.16	6.58	5.87	0.47
Fruit diameter	5.20	6.60	5.95	0.40
Fruit length: width ratio	0.68	1.09	0.99	0.07
Outer flesh thickness	9.55	16.64	12.20	1.36
Core thickness	29.09	40.79	33.47	2.88
Pulp weight	93.46	130.71	110.19	10.09
Fruit volume	105.93	173.25	144.50	14.52
TSS	8.57	12.19	10.06	0.89
Acidity	0.22	0.52	0.34	0.07
Ascorbic acid mg/100g	138.56	260.78	177.34	25.92
Total sugar	4.52	6.96	6.16	0.65
Reducing sugar	2.51	3.71	3.29	0.37
Non reducing sugar	2.28	3.54	3.00	0.33
Sugar: acid ratio	8.88	31.65	19.43	5.21
Total seed number	109.58	303.67	179.06	49.61
Total seed weight/fruit	0.94	2.65	1.62	0.44
100 Seed weight	0.78	1.06	0.93	0.08
Yield	6.14	27.54	21.70	5.14

SD: Standard deviation

in Taiwan (109.58) followed by Kohir red (112.67 %) and SRD-1 (122.33 %), whereas the maximum seed number/fruit (303.67) was recorded in China genotype. The maximum yield (27.34 kg/plant) was recorded in the Baruipur Local genotype, whereas the minimum (6.14 kg/plant) was recorded in Taiwan genotype.

A strong positive correlation was observed between all the quantitative traits of guava genotypes (Table 3). The maximum positive correlation (0.976) was observed between fruit weight and fruit volume. A Positive correlation was also observed between fruit volume and fruit length (0.914), fruit length and fruit weight (0.905), yield and fruit length (0.833), pulp weight

and fruit diameter (0.814), total seed weight and pulp weight (0.824), total seed number and pulp weight (0.807), core thickness and fruit diameter (0.728). By contrast, some quantitative traits were negatively correlated (Table 3). These included between fruit weight and TSS (-0.076), fruit weight and total sugar (-0.148), yield and fruit acidity (-0.088), outer flesh thickness and TSS (-0.155), fruit volume and TSS (-0.067).

Principal component analysis (PCA) of quantitative variables:

PCA put the total quantitative traits into six components that explained 92.35 % of the total variation (Table 4). The first component, which accounted for 41.15 % of the total variation, included fruit weight, pulp weight, fruit volume, total seed number/fruit and total seed weight/ fruit. The second component, explaining 24.74 % of the total variation, included TSS, acidity, total sugar, reducing sugar, non-reducing sugar and sugar: acid ratio. The third component, accounting for 11.20 %, included fruit diameter, length, and 100 seed weight. The fourth component, which accounted for 7.69 % of total variation, included ascorbic acid and 100 seed weight. The fifth component accounted for 4.03 % of total variation, including outer flesh thickness, ascorbic acid and 100 seed weight. The six components accounted for 3.54 % of total variation, including TSS, core thickness and 100 seed weight.

A two-dimensional PCA plot was constructed based on the first two components (Fig. 1). The plot distributed the genotypes according to their morphological characteristics and phenotypic resemblance. For example, China and Philippines genotypes with the highest total seed number, total seed weight/fruit, and outer flesh thickness were placed closely in the lower right plane, where SRD-1, Taiwan and Kohir Long with the lowest fruit weight, core thickness, total seed weight/fruit were placed close together in

Table 3. Correlation coefficients among 19 quantitative traits in 24 guava genotypes

Variables	FL	FD	FL:W	OFT	CT	PW	FV	TSS	FA	AA	TS	RS	NRS	S:A	TSN	TSW	100SW
Fruit weight																	
Fruit length	1																
Fruit diameter (cm)	0.492	1															
Fruit length:width ratio	0.610	-0.389	1														
Outer flesh thickness	0.548	0.652	-0.015	1													
Core thickness (mm)	0.648	0.728	0.022	0.709	1												
Pulp weight (gm)	0.758	0.814	0.055	0.767	0.871	1											
Fruit volume (ml)	0.914	0.711	0.317	0.720	0.788	0.893	1										
TSS	-0.007	-0.154	0.126	-0.155	-0.034	0.033	-0.067	1									
Acidity	0.099	-0.105	0.207	0.317	0.169	-0.016	0.128	-0.624	1								
Ascorbic acid mg/100g	0.101	-0.033	0.141	0.041	-0.128	0.018	0.076	0.391	-0.227	1							
Total sugar	-0.062	-0.101	0.011	-0.268	-0.193	-0.067	-0.081	0.582	-0.640	-0.001	1						
Reducing sugar	-0.042	-0.081	0.011	-0.182	-0.168	-0.034	-0.066	0.575	-0.594	-0.014	0.967	1					
Non reducing sugar	-0.106	-0.182	0.032	-0.253	-0.130	-0.062	-0.157	0.629	-0.587	-0.010	0.894	0.884	1				
Sugar:acid ratio	0.018	0.192	-0.164	-0.143	-0.047	0.145	0.018	0.704	-0.936	0.212	0.765	0.739	0.698	1			
Total seed number	0.632	0.748	-0.012	0.693	0.752	0.807	0.752	-0.219	0.260	0.065	-0.370	-0.326	-0.324	-0.163	1		
Total seed weight/fruit	0.653	0.693	0.057	0.721	0.739	0.824	0.749	-0.222	0.283	0.023	-0.312	-0.254	-0.258	-0.161	0.959	1	
100 Seed weight	0.288	-0.023	0.318	0.287	0.140	0.160	0.251	-0.197	0.251	-0.168	0.108	0.106	0.032	-0.141	0.003	0.233	1
Yield	0.833	0.397	0.516	0.277	0.373	0.570	0.770	0.085	-0.088	0.182	0.295	0.288	0.126	0.200	0.390	0.416	0.284

Table 4. First 6 components from the PCA analysis of quantitative traits of 24 guava genotypes

Variable	F1	F2	F3	F4	F5	F6
Fruit weight	0.342	0.096	0.058	0.053	-0.048	-0.042
Fruit length	0.299	0.125	0.267	0.107	-0.209	0.029
Fruit diameter	0.272	0.086	-0.367	-0.084	-0.141	-0.270
Fruit length:width ratio	0.069	0.047	0.616	0.200	-0.100	0.269
Outer flesh thickness	0.291	-0.009	-0.096	-0.098	0.451	0.037
Core thickness	0.303	0.050	-0.134	-0.110	0.034	0.376
Pulp weight	0.324	0.138	-0.124	-0.033	0.023	0.101
Fruit volume	0.335	0.113	0.087	0.025	-0.109	-0.043
TSS	-0.086	0.338	-0.023	0.290	0.280	0.445
Acidity	0.110	-0.355	0.224	-0.147	0.171	0.202
Ascorbic acid mg/100g	0.008	0.097	0.025	0.678	0.452	-0.340
Total sugar	-0.119	0.401	0.065	-0.226	-0.004	-0.064
Reducing sugar	-0.104	0.396	0.057	-0.244	0.051	-0.016
Non reducing sugar	-0.125	0.373	0.034	-0.202	0.115	0.270
Sugar:Acid ratio	-0.065	0.414	-0.193	0.062	-0.033	-0.126
Total Seed number/fruit	0.318	-0.027	-0.169	0.070	0.007	0.106
Total Seed weight/fruit	0.320	-0.011	-0.087	-0.039	0.160	0.055
100 Seed weight	0.089	0.015	0.367	-0.429	0.502	-0.377
Yield	0.213	0.228	0.304	0.065	-0.317	-0.306
Variability (%)	41.15	24.74	11.20	7.69	4.03	3.54

the lower left plane. These results revealed that the fruit weight, diameter, total seed number/fruit, and total seed weight/fruit are positively correlated and the highest loading factors in this PCA analysis.

Descriptive statistics and correlations for the qualitative traits:

The descriptive statistics presented in Table 5 had wider variability among variables. Some traits had high standard deviation; for example, the highest standard deviations (10.05 %) was recorded in leaf area followed by plant girth (6.94 %) and leaf length (1.19 %). Some traits have very low standard deviation <1%, viz., plant width (E-W) (0.67 %), plant width (N-S) (0.60 %), leaf breadth (0.41 %) and plant height (0.33 %).

Table 5. Descriptive statistics for quantitative traits of 24 guava genotypes

Variable	Minimum	Maximum	Mean	SD
Plant girth	26.42	50.14	39.63	6.94
Plant height	1.72	3.08	2.69	0.33
Plant width (E-W)	2.48	5.22	4.39	0.67
Plant width (N-S)	2.47	4.96	4.42	0.60
Leaf length (cm)	9.87	15.18	11.89	1.19
Leaf breadth (cm)	4.41	6.11	5.37	0.41
Petiole length (cm)	0.59	1.63	0.82	0.20
Leaf area (cm ²)	45.02	92.79	64.08	10.05
Leaf length: width ratio	1.80	2.48	2.22	0.18

The qualitative characters of popular and exotic genotypes performed better in new environments than local genotypes. The highest plant girth (50.14 cm) was recorded in Hissar Surkha followed by Shweta (49.78 cm), Hissar Safeda (49.08 cm), Philippines (48.19 cm) and Allahabad Safeda (45.31 %) whereas,

the lowest plant girth (26.42 cm) recorded in Taiwan genotype followed by Pant Prabhat (26.75 cm) and Kohir Long (32.29 cm). The maximum plant height (3.08 m) was observed in Lalit, followed by Arka Kiran (3.03 m) and Shweta (2.97 m), whereas the minimum plant height (1.72 m) in the Taiwan genotype was followed by Pant Prabhat (1.78 m) and Kohir Long (2.52 m). The maximum leaf length (15.18 cm) was recorded in Lalit, followed by Kohir Round (13.09 cm), Shweta (12.93 cm) and Kohir Safeda (12.90 cm). In contrast, the minimum leaf length (9.87 cm) was recorded in the Philippines genotype, followed by China (10.22 cm) and Dudh Khaja (10.64 cm). The shortest petiole (0.59 cm) was recorded in the Kohir Round, whereas the longest petiole (1.63 cm) was recorded in the Philippines genotype.

The correlation studies for qualitative traits showed a strong positive correlation among the variables (Table 6). A higher significantly positive correlation (0.92) was found between leaf area and length. There were also positive correlations between plant width (N-S) and plant width (E-W) (0.89), plant width (N-S) and plant height (0.85), leaf area and leaf breadth (0.83). Negative correlation included between leaf length: width ratio and petiole length (-0.39), Leaf length: width ratio and leaf breadth (-0.28), petiole length and leaf length (-0.20), leaf breadth and plant width (N-S) (-0.15).

Table 6. Correlation coefficients of qualitative traits of 24 guava genotypes

Variable	Plant height	Plant width (E-W)	Plant width (N-S)	Leaf length	Leaf breadth	Petiole length	Leaf area
Plant girth							
Plant height	1.00						
Plant width (E-W)	0.82	1.00					
Plant width (N-S)	0.85	0.89	1.00				
Leaf length	0.20	0.04	-0.01	1.00			
Leaf breadth	-0.09	-0.06	-0.15	0.56	1.00		
Petiole length	0.23	0.29	0.18	-0.20	0.16	1.00	
Leaf area	0.11	0.01	-0.07	0.92	0.83	-0.04	1.00
Leaf length:width ratio	0.31	0.09	0.12	0.64	-0.28	-0.39	0.30

Principal component analysis (PCA) of qualitative variables:

Principal component analysis put the total qualitative traits into five components that explained 97.45 % of the total variation (Table 7). The first component, which accounted for 37.12 % of the total variation, included plant girth (E-W and N-S), plant height and plant girth. The second component, explaining 30.08 % of the total variation, included leaf length, breadth, area and length: width ratio. The third component, accounting for 18.57 %, included leaf breadth, petiole length and leaf length: width ratio. The fourth component, which accounted for 7.16% of the total variation, included petiole length, plant girth and leaf length: width ratio. The fifth component accounted for 4.53 % of the total variation, including plant girth and petiole length.

A two-dimensional PCA plot based on the first two components grouped genotypes according to morphological and phenotypic

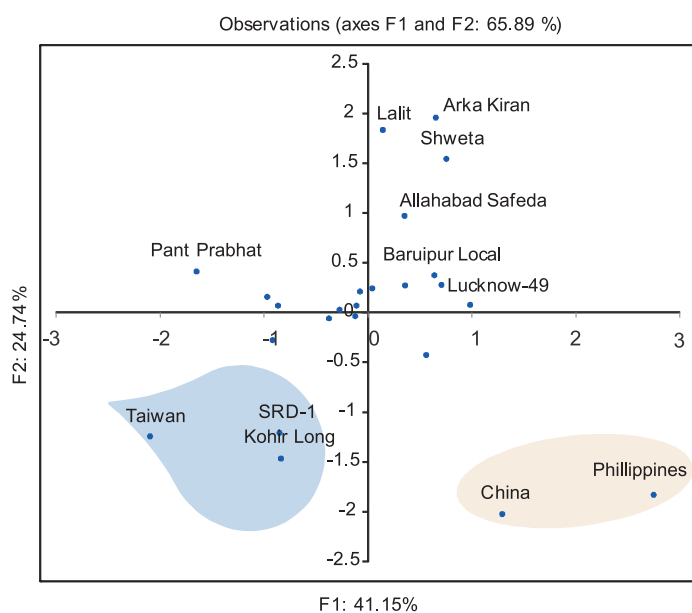


Fig. 1. Two dimensional PCA plot based on the first 2 components for 19 quantitative traits of 24 guava genotypes.

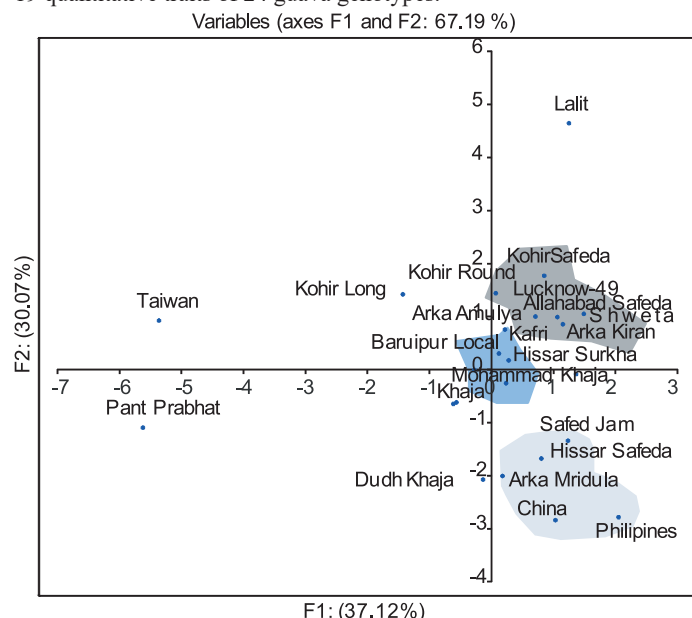


Fig. 2. Two-dimensional PCA plot based on the first 2 components for 9 qualitative traits of 24 guava genotypes.

resembles (Fig. 2). For example, five genotypes with a long petiole length and medium leaf area were placed as a distinct group (Hissar Safeda, Safed Jam, Arka Mridula, China and Philippines) on the lower left plane. The local genotypes *viz.*, Baruiपुर Local, Mohammad Khaja, Kafri and Khaja were placed in an individual group with their relative performance on plant girth, height and width (E-W and N-S) and leaf length. Most popular genotypes with similar leaf length and breadth were placed in distinct groups (Allahabad Safeda, Shweta, Lucknow 49, Kohlr Safeda and Kohlr Round). These results indicate that the leaf length and plant girth were highly correlated and led to the highest factor loadings in the analysis.

Dendrogram using agglomerative hierarchical clustering (AHC): Three clusters were identified by diversity analysis of the test genotypes (Table 8). The genetic dissimilarity of the 24 genotypes was examined using the Euclidian distance (Fig. 3). The dendrogram revealed three distinct clusters. Cluster II

Table 7. First 6 components from the PCA analysis of qualitative traits of 24 guava genotypes

Variable	F1	F2	F3	F4	F5	F6
Plant girth	0.418	-0.059	-0.145	0.449	0.768	-0.044
Plant height	0.506	0.077	0.100	-0.082	-0.191	0.759
Plant width (E-W)	0.505	-0.011	-0.017	-0.293	-0.193	-0.623
Plant width (N-S)	0.507	-0.046	0.066	-0.349	0.014	-0.037
Leaf length (cm)	0.046	0.595	0.108	0.146	-0.042	-0.077
Leaf breadth (cm)	-0.057	0.428	-0.514	-0.255	0.148	0.043
Petiole length (cm)	0.202	-0.120	-0.543	0.571	-0.541	-0.053
Leaf area (cm ²)	0.010	0.593	-0.168	-0.028	-0.004	-0.008
Leaf length:width ratio	0.103	0.293	0.604	0.413	-0.145	-0.148
Variability (%)	37.120	30.075	18.567	7.157	4.533	1.650

Table 8. Grouping of 24 guava genotypes into different clusters using agglomerative hierarchical clustering analysis.

Cluster Number	Number of Genotypes	Genotypes
I	7	Kohlr Round, Kohlr Red, SRD-1, Arka Mridula, Kohlr Long, Pant Prabhat, Taiwan
II	15	Shweta, Lucknow-49, Hissar Safeda, Lalit, Arka Kiran, Kohlr Safeda, Arka Amulya, Khaja, Kafri, Allahabad Safeda, Safed Jam, Md. Khaja, Hissar Surkha, Baruiपुर Local, Dudh Khaja
III	2	Philippines, China

Table 9. Distances between the class centroids

	I	II	III
I	0		
II	74.44	0	
III	176.42	105.86	0

contained a maximum number of genotypes (15), likely Shweta, Lucknow-49, Hissar Safeda, Lalit, Arka Kiran, Kohlr Safeda, Khaja, Safed Jam, Md. Khaja, Hissar Surkha, Baruiपुर Local, Dudh Khaja; followed by cluster I contained 7 genotypes *viz.*, Kohlr Round, Kohlr Red, SRD-1, Arka Mridula, Kohlr Long, Pant Prabhat, Taiwan. Cluster III comprised only two genotypes, namely Philippines and China. The formation of more clusters with a variable number of entries indicates diversity. The genotypes of clusters I and III exhibited maximum divergence (Table 9) and were indicated by their inter-cluster distance (176.42), followed by clusters II and III (105.86). Whereas the minimum inter-cluster distance between cluster I and II (74.44).

Analysis of cluster means value: The cluster mean value for nine vegetative, 15 fruit characters, three seed characters and yield characters presented in Table 10 indicated considerable differences for all the characters among clusters. Cluster I was characterized by the lowest mean value for fruit weight (116.89 g), fruit length (5.39 cm); fruit width (5.49 cm); outer flesh thickness (10.97 mm), core thickness (30.51 mm); pulp weight (98.22 g); fruit volume (127.18 ml); total seed weight (6.02 g), plant height (2.39 m), plant girth (34.52 cm), plant width (E-W) (3.81 m), plant width (N-S) (3.93 m), petiole length (0.72 cm), total seed number (125.37), total seed weight/fruit (1.15 g), 100 seed weight (0.92 g) and yield (16.84 kg/plant) and moderate mean values for all other characters.

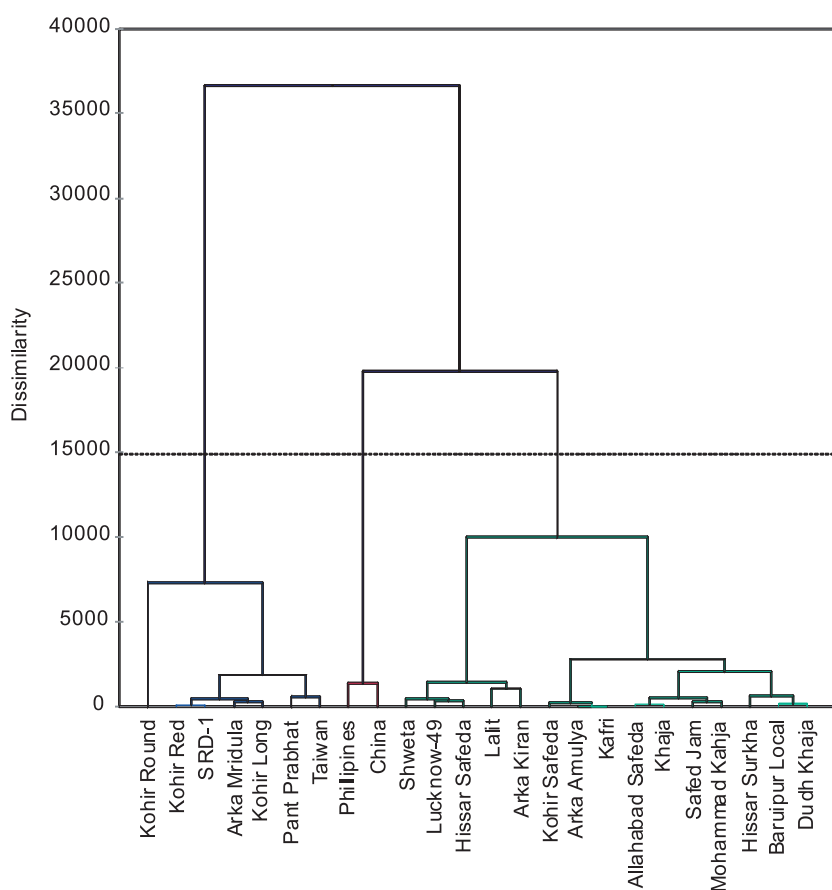


Fig 3. Dendrogram using agglomerative hierarchical clustering (AHC) of 24 guava genotypes based on both quantitative and qualitative traits

The highest mean value for total sugar (6.43 %), reducing sugar (3.43 %), non-reducing sugar (3.12 %), sugar: acid ratio (21.13), leaf length (12.18 cm), leaf area (65.96 cm²), leaf length: width ratio (2.26) and yield (24.17 kg/plant) were represented by Cluster II with moderate mean for rest of the traits.

Cluster III had the highest mean value for fruit weight (153.87 g), fruit length (6.24 cm), fruit width (6.43 cm), outer flesh thickness (14.99 mm), core thickness (37.74 mm), pulp weight (123.26 g), fruit volume (161.61 ml), fruit acidity (0.48 %), plant girth (46.13 cm), plant height (2.83 m), plant width (E-W) (4.95 m), plant width (N-S) (4.66 m), petiole length (1.21 cm), total seed number (290.58), total seed weight/ fruit (2.60 g) whereas, lowest mean value for total soluble solids (8.65), total sugar (4.62 %), sugar: acid ratio (9.80), leaf length (10.05 cm), leaf breadth (4.94 cm), leaf area (49.60 cm²), leaf length: width ratio (2.06) and rest of traits have moderate mean values.

Discussion

Morphological characterization and correlation: The morphological data for the 24 guava genotypes was investigated by measuring 19 quantitative and nine qualitative traits that could be useful for genotypic identification. Most of the traits had potential economic importance for enhancing quality fruit production. They may serve as target traits for guava breeders and growers. The results from the fruits' morphological and physicochemical traits can be used to discriminate genotypes and estimate the genetic relationships across large and diverse guava genotypes. These findings are similar to other studies on quantitative and qualitative traits for evaluating and selecting desirable cultivars (Correa and Santos, 2011; Padilla-Ramirez and Gonzalez-Gaona, 2012). In our studies, first-time evaluation of local germplasms *viz.*, Khaja, Dudh Khaja, Kafri, Mohammad Khaja and Baruiपुर comparison to popular germplasm of India as well as exotic collections. Among the local genotypes, Baruiपुर local has unique characteristics of attractive glossy skin, crispiness of flesh

Table 10. Mean performance of different clusters of quantitative and qualitative traits

Variables	Cluster I	Cluster II	Cluster III
Plant girth (cm)	34.52	41.15	46.13
Plant height (m)	2.39	2.81	2.83
Plant width (E-W)	3.81	4.58	4.95
Plant width (N-S)	3.93	4.61	4.66
Leaf length (cm)	11.80	12.18	10.05
Leaf breadth (cm)	5.43	5.39	4.94
Petiole length (cm)	0.72	0.81	1.21
Leaf area (cm ²)	64.18	65.96	49.60
Leaf length:width ratio	2.18	2.26	2.06
Fruit weight (g)	116.89	138.00	153.87
Fruit length (cm)	5.39	6.05	6.24
Fruit Diameter (cm)	5.49	6.10	6.43
Fruit Length:width ratio	0.99	0.99	0.97
Outer Flesh Thickness	10.97	12.40	14.99
Core Thickness (mm)	30.51	34.27	37.74
Pulp weight (gm)	98.22	114.04	123.26
Fruit Volume (ml)	127.18	150.31	161.61
TSS (⁰ B)	10.19	10.19	8.65
Acidity (%)	0.33	0.32	0.48
Ascorbic acid mg/100g	184.67	174.47	173.20
Total sugar (%)	6.02	6.43	4.62
Reducing Sugar (%)	3.20	3.43	2.54
Non Reducing Sugar (%)	2.95	3.12	2.29
Sugar:Acid ratio	18.55	21.13	9.80
Total Seed Number	125.37	189.24	290.58
Total Seed weight/fruit	1.15	1.71	2.60
100 Seed weight (g)	0.92	0.94	0.94
Yield	16.84	24.17	20.16

with a sweet taste and rind on the fruit skin, which makes it different from other genotypes for easy identification. The extensive range of morphological variation of local germplasms revealed many traits related to fruit quality and yield, which may operate the breeding objectives.

Plant breeders should be concerned with more than one character to improve the single character of the genotype. Knowing the relations between the genotype's traits is important to improve fruit production and quality. The present studies revealed that the fruit weight is significantly positively correlated with yield characters, meaning larger fruit size increases the yield but reduces the quality of fruit like TSS, total sugar and non-reducing sugar. For example Philippines genotype has larger fruit size often accompanied by poor accumulation of chemical content, leading to inferior fruit quality. In contrast, Arka Kiran, Baruiपुर Local, and Shweta have medium-sized fruit with good quality. These results are supported by Babu *et al.* (2007) and Afifi *et al.* (2019).

Based on the principal component analysis, some traits had the highest factor loading in the first two components. The traits studied were plant height, leaf area, leaf length and breadth, fruit length and diameter, seed weight, total seed number/fruit, fruit weight, TSS, total sugar, and reducing sugar contents. These findings demonstrated that such

traits are extremely useful for assessing genetic diversity and characterizing guava germplasm.

Genetic diversity: According to the dendrogram, there was wider diversity among the genotypes. Based on quantitative and qualitative data, genotypes were grouped into three clusters. The cluster analysis results were in accordance with the morphological distance. Several forming clusters indicate wider diversity among genotypes. The local genotypes Khaja, Mohammad Khaja, Baruipur Local, Dudh Khaja and Kafri were grouped into one cluster with Allahabad Safeda, Arka Amulya, Safed Jam and Hissar Safeda. The exotic genotypes Philippines and China formed an individual cluster; unexpectedly, Taiwan is merged with other clusters with Pant Prabhat. There was very little dissimilarity between Baruipur and Dudh Khaja; Allahabad Safeda, and Khaja genotypes. Genotypes in the same cluster are less diverse, and crossing between them results in less desirable segregates. These crosses should be performed with parents from different clusters. These results generally agree with those of Mehmood *et al.* (2014), Jana *et al.* (2015) and Rajan *et al.* (2007).

The diversity of genotypes used for breeding is also affected by the environment, which means the lower the environmental effects show, the lower the effect of genotype composition (Perfectii and Camacho, 1999). In this experiment, defined guava genotypes *viz.*, Shweta, China, Philippines, Arka Kiran are adapted to the local environments and perform better than local genotypes.

In summary, this study explored the diversity among 24 guava genotypes based on various morphological and physicochemical traits. Analysis of descriptive statistics and correlations revealed significant variability in traits like fruit weight, volume, seed number, and acidity. The principal component analysis highlighted the key traits driving the observed differences. Genotypes were grouped into clusters, showcasing varying levels of genetic diversity. The findings emphasize the importance of considering multiple traits in breeding programs to enhance fruit quality and yield while maintaining genetic variability. Utilizing quantitative and qualitative data alongside multivariate analyses, this approach offers insights into genotype relationships and informs future breeding strategies.

References

- Afifi Eman H., N.A. Awad, Y.S.G. Abd El-Aziz, E.H. El-Bassel, A.S.M. Ismail and M.M. Abdal-Galeel, 2019. Selection and evaluation of some guava strains under Behera Governorate condition. *Middle East J. Agric. Res.*, 8(2): 469-481.
- Babu, K.D., R.K. Patel, and D.S. Yadav, 2007. Comparative evaluation of guava selection under the northeastern region of India. *Acta Hort.*, 735: 99-103.
- Correa, L.C., C.A. Santos, E. Vianello and G.P.P. Lima, 2011. Antioxidant content in guava (*Psidium guajava*) and arara (*Psidium* spp.) germplasm from different Brazilian regions. *Plant Genetic Resources: Characterization and Utilization*, 9(3): 384-391. <http://dx.doi.org/10.1017/S1479262111000025>
- Dinesh M.R. and C. Vasugi, 2010. Guava improvement in India and future needs. *J. Hort. Sci.*, 5(2): 94-108.
- Dubois, M.K., J.K. Gilles, P.A. Robers and F. Smith, 1951. Calorimetric determination of sugar and related substances. *Analyt. Chem.*, 26: 351-356.
- Jana, B.R., P.S. Munsu, D.C. Manna, H. Sarkar and B. Das, 2015. Genetic Divergence Studies in Guava (*Psidium guajava* L.). *Electronic J. Plant Breed.*, 6(1): 161-166.
- Mehmood, A., I.A. Muhammad Khan, S. Ahmad., R. Ahmad, S. Luo and N.M. Ahmad, 2014. Genetic diversity of Paistani guava (*Psidium guajava* L.) germplasm and its implications for conservation and breeding. *Sci Hort.*, 177: 221-232.
- Menzel, C.M. and B.F. Paxton, 1985. The pattern of growth, flowering and fruiting of guava varieties in sub-tropical Queensland. *Aus. J. Expt. Agric.*, 26: 123-127.
- NHB, 2019. Horticultural Statistics at a Glance. National Horticulture Board. Govt. of India. <http://nhb.gov.in>
- Perfecti, F and J.P.M. Camacho, 1999. Analysis of genotypic differences in developmental stability in *Annona cherimola*. *Evolution*, 53(5): 1396-1405.
- Prakash, D.P., P. Narayanaswamy and S.N. Sondur, 2002. Analysis of molecular diversity Inguava using RAPD markers. *J. Hort. Sci. Biotechnol.*, 77: 287-293.
- Rajan S., L.P. Yadava., Ram Kumar and S.K. Saxena, 2007. Genetic divergence in seed characteristics of guava: A basis for parent selection in hybridization, *Indian J. Hort.*, 64(3): 290-293.
- Ruck, J.A. 1969. Chemical Methods for Analysis of Fruits and Vegetables Products. Department of Agriculture, Canada SP50 Summerland Research Station, Ontario.
- Sadasivam S and A. Manickam, 1996. *Biochemical Methods*, New Age International (P) Limited, New Delhi., 2:124-126.
- Saxena, S.K., S. Rajan., R. Chandra., N. Srivastava and A. Bajpai, 2007. Molecular characterization of closely related open pollinated seedling selections in guava. *Acta Hort.*, 735: 49-55.
- Santos, C.A.F. and Correa, L.C. 2012. Antioxidant and biochemical content in Brazilian guava germplasm with white, red and pink pulps. *Acta Hort.*, 959: 125-130.
- Shiguera, G.T. and M.R. Bullock, 1983. Guava (*Psidium guajava* L.) in Hawaii history and production. *Res. Ext. Series*, pp-1-32.
- Singh, S.P. 2011. Guava. In: *Postharvest Biology and Technology of Tropical and Subtropical Fruits*. Woodhead Publishing Limited. pp. 214-226.

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