BMC Plant Biology

RESEARCH Open Access

Morpho-biochemical insights into globally collected guava germplasm (*Psidium* spp.): opportunities for utilization in breeding

Prabhanshu Mishra[1], Ankita Kashyap[1], Chavlesh Kumar[1*], Amit Kumar Goswami[1*], R. M. Sharma[1], Shruti Sethi[2], Rakesh Singh[3], Gyan Prakash Mishra[4], Virendra Singh Rana[5], Rajeev Ranjan Kumar[6], Kritidipta Pramanik[1], Pragya Ranjan[7], Sanjay Kumar Singh[8], M. K. Sushravya[1] and Dhirendra Rajpoot[9]

Abstract

Background Guava (*Psidium guajava* L.) is a major pantropical fruit crop, valued for its nutritional composition, wider adaptability, and economic significance. Since its introduction in India during the 17th century, guava cultivars have exhibited a narrow genetic base, with most existing genotypes arising from open-pollinated selections or crosses involving a limited number of genotypes. Furthermore, much of the available germplasm has been named based on fruit characteristics or place/regions of origin, leading to confusion in classification and hindering the precise identification and utilization of genetic resources in guava breeding programs. To address this, 49 morpho-biochemical parameters were assessed in 51 diverse *Psidium* genotypes, including cultivars, varieties, hybrids, related wild species, and exotic/USDA introductions.

Results Substantial variability was observed among globally collected guava germplasm for fruit traits, with fruit weight ranging from 11.67 g (*Psidium molle*) to 379 g (S. N90-53), seed number from 8 (S. N11-3) to 512 (S. N15-3), leaf length from 5.57 to 17.17 cm, leaf width from 2.07 to 7.90 cm, and petiole length from 0.17 to 0.77 cm. Germplasm also differed in qualitative descriptors, including branch orientation, bark colour, leaf morphology, tip structure, and fruit surface traits, with wild species forming distinct morphological groups. Additionally, biochemical traits varied widely, including the contents of total soluble solid (6.8–13.8 °Brix), acidity (0.25–1.60%), total sugars (3.62–9.21 g/100 g FW), ascorbic acid (88.36–302.46 mg/100 g FW), ferric reducing antioxidants power (7.74–20.69 µM TE/g FW), free radical scavenging activity (2,2-diphenyl-1-picrylhydrazyl assay)(85.72–98.47%), lycopene (0.05–8.91 mg/100 g FW), and total carotenoids (0.05–2.76 mg/100 g FW). Besides, principal component analysis indicated PC1 (22.1%) related to fruit size and PC2 (15.2%) to biochemical traits. Furthermore, cluster analysis grouped 51 guava genotypes into three clusters, distinguishing wild from cultivated types.

Conclusions The study confirms the presence of wide morpho-biochemical variability in *Psidium* germplasm, offering valuable genetic resources for genetic improvement programs, aimed at enhanced fruit quality with rich

*Correspondence:
Chavlesh Kumar
ckfruits2016@gmail.com
Amit Kumar Goswami
amit.tkg@gmail.com

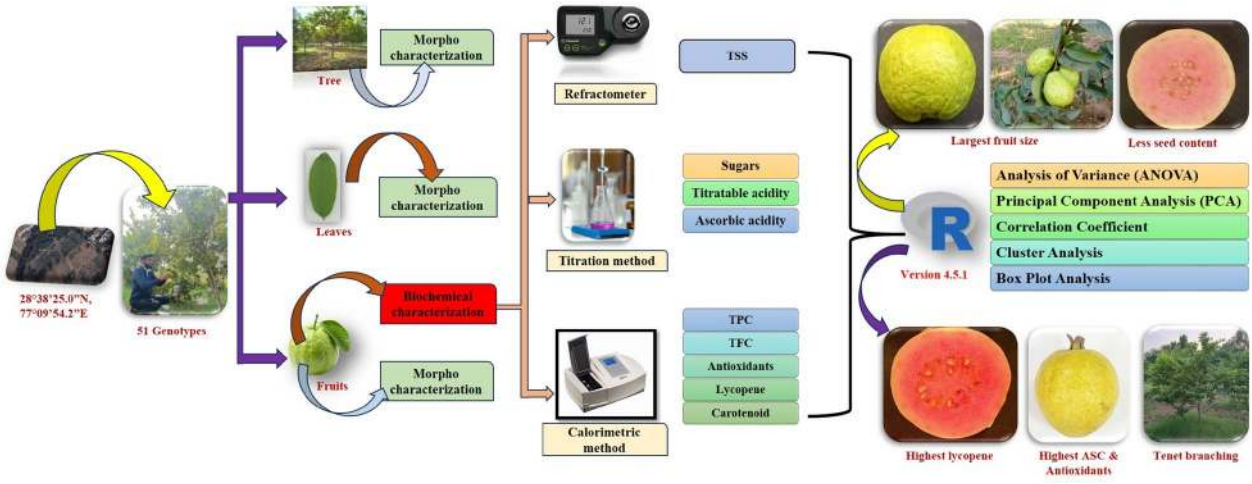
Full list of author information is available at the end of the article

© The Author(s) 2026. **Open Access** This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if changes were made. The images or other third party material in this article are included in the article's Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, visit http://creativecommons.org/licenses/by/4.0/.

antioxidants, bio-fortification, and the tailoring of novel guava genotypes with reduced seed content, enhanced seed mellowness, and tenet branching, fitting in high-density planting and improved yield efficiency.

Keywords Antioxidants, Bio-fortification, Cluster analysis, Genetic resources, Pigments, USDA

Graphical Abstract



Introduction

Guava (*Psidium guajava* L.) ranks among the most extensively cultivated fruit crops across pantropical regions, owing to its prolific yield, rich nutraceutical properties, and remarkable ecological adaptability. It is native to tropical America, which was introduced to India by the Portuguese in the 17th century [1, 2]. Despite the introduced crop species, India has now become a major guava-producing country in the world, with an annual production of 5.35 million metric tons from 358 thousand hectares of area [3]. In the country, guava enjoys high popularity, being regarded as the "super fruit" or "apple of the tropics" due to its exceptional nutraceutical profile, refreshing taste, and pleasant flavour [4–6]. The fruits are also referred to as "poor man's apple" because of their affordability and wider availability. Importantly, guava contributes to nutritional security by supporting the dietary preferences of a galloping, health-conscious population [7]. The fruit is a rich source of vitamins A, C, and B-complex, as well as minerals such as calcium, iron, zinc, and potassium, and dietary fibre [8–10]. Besides, guava contains diverse phytochemicals, including polyphenols, flavonoids, tannins, and phenolic acids, which impart antioxidants, anti-inflammatory, anti-diabetic, and anticancer properties [11–13]. Furthermore, guava leaves, traditionally used in medicine and industry, exhibit anti-diarrheal, antimicrobial, antihypertensive, and hypoglycemic activities [14].

In India, guava possess a narrow genetic base since the crop was introduced, and most varieties have originated either as open-pollinated selections of Allahabad Safeda or from crosses involving only a few guava genotypes. Therefore, at present, many commercial cultivars are deficient in one or more desirable trait(s) in combinations for compact canopy and branching, thick pulp, firm fruit, small seed core with soft seeds, extended shelf life, and resistance to major biotic (nematodes, guava wilt, and fruit fly) as well as abiotic [7, 15–17] stresses. Moreover, the majority of Indian varieties are named after fruit shape, skin colour, or pulp colour, while others are named after their region of origin [18]. Therefore, the Indian guava industry urgently requires novel genetic resources to meet the rising demand of the guava industry and to characterize the existing guava germplasm to develop a comprehensive descriptive database, as considerable ambiguity exists regarding the varietal/germplasm classification and nomenclature of different guava genotypes. Strengthening guava germplasm through augmentation, conservation, detailed characterization, and effective utilization in breeding programs is essential to ensure sustainable guava production.

Efficient characterization of germplasm is the first step in the genetic improvement program for any crop species. Various methods have been employed for the efficient characterization of guava germplasm, among which morphological characterization is considered one of the simplest and easiest [19]. The DUS (Distinctness, Uniformity, and Stability) testing guidelines established by the PPV&FR (Protection of Plant Varieties and Farmers' Rights) authority in India and by UPOV (International Union for the Protection of New Varieties of Plants) internationally outline the procedures

for detailed characterization of guava germplasm [20]. These descriptors were constructed from a set of morphological parameters and appropriate scales to categorize guava germplasm and facilitate efficient germplasm management. The various morphological parameters, supplemented by taxonomic information, provide a true map of the phenotypic diversity in guava germplasm [21, 22]. Although both quantitative and qualitative morphological traits, such as those related to the fruit, seed, leaf, and overall plant characteristics, can aid in identifying closely/distantly related guava germplasm. However, these are often insufficient for precise identification since the environmental variables mostly influence the morphological traits and have pleiotropic effects, epistatic interactions [23]. Additionally, biochemical parameters include primary metabolites (such as sugars, amino acids, proteins, and organic acids), secondary metabolites (like phenolics, flavonoids, alkaloids, and terpenoids), enzymes and isoenzymes, as well as plant pigments (including chlorophylls, carotenoids, and anthocyanins) offer systematic characterization of germplasm and more reliable since they are relatively less affected by the environmental factors [24, 25]. Therefore, in the present investigation, both morphological and biochemical parameters were included to systematically characterize the globally collected guava germplasm (*Psidium* spp.).

Table 1 The details of the guava genotypes undertaken for the morpho-biochemical characterization

Exotic/ USDA introduced guava genotypes		
1. S. Patillo	10. S. Ka Hua Kula	19. S. Portugal
2. S. Khao Niyom	11. S. Beaumont	20. All Time Guava
3. S. 157	12. S. Poamoho Pink	21. *Psidium* genotype 8
4. S. HPSI41	13. *Psidium* genotype 4	22. S. Ruby X Supreme
5. S. Golden	14. S. N90-53	30. Thai Pink
6. S. Kona 1	15. S. Klom Toonklao	39. Thai 7
7. S. Waiakea	16. S. Less Seed Guava	41. Thai Guava
8. *Psidium* genotype 14	17. *Psidium* genotype 6	
9. S. Fan Retief	18. *Psidium* genotype 7	
Indigenously developed/ identified guava genotypes		**Wild guava species/genotypes**
23. *Psidium* genotype 15	35. *Psidium* genotype 10	48. *Psidium molle*
24. *Psidium* genotype 16	36. Hisar Surkha	49. *Psidium pumilum*
25. Super Guava	37. Purple Guava	50. *Psidium guineense*
26. *Psidium* genotype 13	38. Lalima	51. *Psidium genotype* 18
27. *Psidium* genotype 9	40. Dhawal	
28. Punjab Apple	42. *Psidium* genotype 11	
29. Arka Kiran	43. Allahbad Safeda	
31. Shweta	44. Pant Prabhat	
32. Hisar Safeda	45. L-49	
33. Punjab Kiran	46. Lalit	
34. G-Vilas	47. Punjab Pink	

*S indicated the particular guava genotype derived as seedling

Materials and methods

The present study was undertaken on 51 diverse guava germplasm, comprising 22 Indian cultivars, 25 exotics/USDA introduction, and four wild *Psidium* species (Table 1). Among these, exotic germplasm was collected from the United States Department of Agriculture (USDA), Hilo (Hawaii, USA), through the Indian Council of Agricultural Research (ICAR)–National Bureau of Plant Genetic Resources (NBPGR), New Delhi, India, under standard germplasm exchange protocols. Whereas, Indigenous cultivars and wild accessions were maintained in the field gene bank of Division of Fruits and Horticultural Technology (FHT), ICAR–Indian Agricultural Research Institute (IARI), New Delhi, following recommended package of practices. All guava genotypes were established in 2019 in the experimental orchard of the Division of Fruits and Horticultural Technology, ICAR–IARI, New Delhi (28.40°N, 77.10°E). The taxonomic identity of the germplasm, including wild *Psidium* species, was confirmed by Dr Amit Kumar Goswami and Dr Chavlesh Kumar, using morphological descriptors and authenticated reference materials. The collected guava genotypes were evaluated using 49 morpho-biochemical parameters during the winter season fruiting (Mrig bahar) of 2024, and their data were recorded as follows:

Morphological traits

In the present investigation, a total of 37 qualitative and quantitative morphological parameters were recorded, including 17 fruit and seed, 17 leaves, and 3 tree/branch attributes. The details of qualitative and quantitative traits, along with their descriptions, are presented in Supplementary Tables 2a, 2b, 4, and 5. The qualitative parameters were performed based on the Guava Descriptor developed by the Protection of Plant Varieties and Farmers' Rights Authority (PPV & FRA) [26], Government of India, New Delhi, and UPOV, 1987 (International Union for the Protection of New Varieties of Plants). For quantitative parameters, 15 leaves and fruits were randomly selected to record the data. The leaf and fruit size (length and width) and pulp thickness were measured using a digital Vernier calliper (Themisto, Model: TH-M61, India), and their mean values were expressed in centimeter (cm). Fruit weight (g) was measured using a weighing balance (Citizen Scale Pvt. Ltd., India). The fruit peel and pulp colour were recorded by using Royal Horticultural

Society (RHS) colour chart and the visual colour of fruit and pulp was assessed using a Hunter Lab colorimeter (model Labscan XE) in Hunter 'L^*' (lightness), 'a^*' (redness and greenness) and 'b^*' (yellowness and blueness) are coordinates, Lekshmi et al., [27]. Total colour difference (TCD) was calculated using L^*, a^* and b^* values as following equation:

$$\mathrm{TCD} = [(\Delta L^*)2 + (\Delta a^*)2 + (\Delta b^*)2]\,\frac{1}{2}$$

Where, ΔL^*, Δa^*, and Δb^* represent the difference in L^*, a^* and b^* values at a particular interval from the respective initial values.

Biochemical parameters

A total of 12 biochemical parameters were analyzed, including total soluble solids (TSS), titratable acidity (TA), TSS/TA, ascorbic acid (ASC), total phenolics content (TPC), total flavonoids content (TFC), total carotenoids, lycopene, antioxidants activities (FRAP & DPPH), and sugars (total and reducing). For the analysis of biochemical compounds, the fruits were harvested at commercial maturity. Five fruits were picked, wrapped in aluminum foil, and brought to the laboratory just after harvest and subjected to the analysis. Parameters like TSS, TA, lycopene, and carotene were determined from the fresh fruits; the remaining samples were properly labelled and stored at − 80 °C in a deep freezer until the estimation of other parameters.

Total soluble solids (TSS)

The TSS was measured in pulp juice using a digital refractometer (MA871; Milwaukee, Romania). A drop of guava juice was placed on the prism of the refractometer, and the reading was expressed in Brix.

Titratable acidity (TA)

The titratable acidity was determined using the standard procedure [28]. A total of 2.0 g of fruit pulp was crushed with double-distilled water, and the final volume was adjusted to 20.0 mL. The mixture was filtered using Whatman filter paper No. 1, and 10.0 mL of filtrate was titrated against 0.1 M NaOH (ACS grade) using phenolphthalein indicator (ACS grade) until a pale pink colour was developed. The titratable acidity (%) was calculated as citric acid equivalent, using the following formula:

$$\text{Titratable acidity } (\%) = \frac{\text{Titrate} \times \text{ Normality of alkali} \times \text{ Volume made up} \times \text{ Equivalent weight of acid} \times 100}{\text{V (aliquot taken)} \times \text{ W (sample)} \times 1000}$$

Where the equivalent weight of acidity for citric acid was 0.0064, V (aliquot) = 10 mL, and W (sample) = 2 g. The TSS/TA ratio was calculated from the obtained data.

Total phenolics content (TPC)

The total phenolics content (mg GAE/100 g FW) in guava pulp was assayed using the Folin–Ciocalteu colourimetric technique, as outlined by Singleton et al. [29]. For each sample, 1 g of pulp was crushed using a mortar and pestle into 80% ethanol (v/v). The extract was then centrifuged at 10,000 × g for 20 min (Sigma 3–18 K centrifuge, Germany). A 100 µL supernatant and 2.9 mL of double-distilled water were added, along with 0.5 mL of AR grade 0.2 M Folin–Ciocalteu reagent. After allowing the mixture to stand at room temperature for 10 min, 2 mL of a 20% (m/V) sodium carbonate solution (AR grade) was added. The mixture was thoroughly blended and incubated for 30 min at room temperature. The absorbance of the resulting dark blue complex was then recorded at 760 nm using a UV-visible spectrophotometer (GENESYS; Thermo Fisher Scientific). A calibration curve was prepared using AR-grade Gallic acid monohydrate standard (100 µg/mL water).

Total flavonoids content (TFC)

The total flavonoids content (mg QE per 100 g) of the guava pulp was estimated by a calorimetric method using the aluminium chloride reagent and quercetin as standard [30]. A volume of 1 mL of properly diluted extract/supernatant, which was previously prepared for TPC estimation in 80% ethanol, is mixed with 1.4 mL of double-distilled water and 0.3 mL of AR grade $NaNO_2$ (5% m/V). Additionally, 0.3 mL of AR-grade $AlCl_3$ (10% m/V) was added 5 min later and allowed to react for another 6 min. After that, 2.0 mL of 1 M NaOH solution (ACS grade) was added. The resultant mixture was diluted to make a total volume of 5 mL with double-distilled water. The solution was thoroughly mixed, and its absorbance was measured using a UV-vis spectrophotometer (GENESYS; Thermo Fisher Scientific, Waltham, MA, USA) at 510 nm wavelength. Standard quercetin solutions (AR grade) with varying concentrations (0, 10, 25 & 50 ppm) were prepared for making the calibration curve, and absorbance was recorded in the same manner at 510 nm.

Ascorbic acid

The ascorbic acid concentration was determined using the AOAC method [31] with a minor modification. A total of 2.0 g fresh guava pulp was taken and crushed with 20 mL of 3% metaphosphoric acid (laboratory reagent grade). Then, 5mL aliquot of the metaphosphoric extract was titrated with the standard solution of 2, 6-dichlorophenol-indophenol dye (AR grade) until the endpoint appeared as a light pink colour, which persisted for 15 s. The dye was standardized with the standard AR grade ascorbic acid (w/v), and the ascorbic acid content was calculated in mg/100 g fresh fruit pulp.

$$\text{Dye Factor (DF)} = \frac{0.5}{\text{Titre}}$$

Ascorbic acid content in fresh fruit pulp was calculated using the following formula.

$$\begin{aligned}&\text{Ascorbic acid (mg/100 g pulp)}\\&= (\text{DF} \times \text{ Titre value})\\&\quad \times \frac{\text{Volume made (mL)}}{\text{Aliquot volume (mL)} \times \text{Sample weight (g)}} \times 100\end{aligned}$$

DPPH-radical scavenging activity

The 2,2-diphenyl-2-picrylhydrazyl (DPPH) radical-scavenging activity was measured using the procedure outlined by Brand-Williams et al. [32], with a few modifications. The extraction was performed using the same procedure as TPC, and the supernatant (0.1 mL) was mixed with 2.9 mL of DPPH solution, prepared from 0.06 mM of DPPH (analytical standard, 95.2%) dissolved in 80% (v/v) methanol. The absorbance of the reaction mixture was measured using a UV-Vis spectrophotometer (GENESYS; Thermo Fisher Scientific, Waltham, MA, USA) at 517 nm after incubation in the dark for 30 min. The final radical scavenging activity was expressed as the percentage inhibition of DPPH radicals using the following formula:

$$\text{DPPH (\%)} = \frac{\text{Absorbance of control} - \text{Absorvance of reaction mixture}}{\text{Absorvance of control} \times 100}$$

FRAP-Ferric reducing antioxidant potential

The total antioxidant capacity of guava pulp in the different guava genotypes was estimated using the FRAP method described by Benzie and Strain [33]. The FRAP reagent was prepared freshly before use by using 25 mL of AR-grade acetate buffer (300 mM, pH 3.6), 2.5 mL of AR-grade 2,4,6-tripyridyl-s-triazine TPTZ solution (10 mM TPTZ in 40 mM HCl), and 2.5 mL of AR-grade ferric chloride (FeCl3.6H2O) solution (20 mM) in a 10:1:1 ratio. The supernatant (0.1 mL) from the fruit extracts was incubated with 3 mL of FRAP reagent (10:1:1 ratio) for 30 min in the dark. Readings of the coloured product [ferrous tripyridyltriazine complex] were then taken at 593 nm using a UV-vis spectrophotometer (GENESYS; Thermo Fisher Scientific, Waltham, MA, USA). The FRAP was determined using the appropriate formula, and the results were reported as micromoles of Trolox equivalents (μM TE) per g of fresh pulp weight (FW).

$$\begin{aligned}&\text{FRAP (μM TE/g)}\\&= \frac{\text{OD of sample} \times \text{ Volume make up (mL)} \times \text{ Dilution factor}}{1.2 \times \text{ Weight of sample}}\end{aligned}$$

Total carotenoids and lycopene contents

The total carotenoids and lycopene contents in guava pulp were estimated using the methods described by AOAC [34]; Prasad et al. [35] and Pasupuleti & Kulkarni [36]; Akter et al. [37], respectively. For the analysis, 2 g of guava pulp were homogenised in 20 mL of acetone (AR grade, ≥ 99.5% purity) to ensure complete extraction of pigments until the residue turned colourless. The homogenized carotenoid pigments were extracted into petroleum ether (10–15 mL; AR grade, boiling range 40–60 °C), and 2 g of anhydrous sodium sulphate (AR grade) was then added to facilitate pigment separation, and the final volume was adjusted to 50 mL. The absorbance measurements were taken using a UV-Vis spectrophotometer (Model: GENESYS; Thermo Fisher Scientific) at 452 nm for total carotenoids and 503 nm for lycopene, with pure petroleum ether as the blank. The concentrations were calculated separately and expressed as milligrams per 100 g of fresh weight (mg/100 g FW).

$$\begin{aligned}&\text{Total carotenoids (mg/100g)}\\&= \frac{3.8 \times \text{ OD of sample} \times \text{ Volume made up (mL)} \times 0.1}{\text{Weight of sample}}\end{aligned}$$

$$\begin{aligned}&\text{Lycopene content (mg/100g)}\\&= \frac{3.1206 \times \text{ OD of sample} \times \text{ Volume make up (mL)} \times 100}{1 \times \text{ Weight of sample} \times 1000}\end{aligned}$$

Total and reducing sugars

Total and reducing sugars were estimated by the Lane and Eynon titrimetric method [38], where 25 g of guava pulp was homogenized, cleaned with lead acetate and potassium oxalate, diluted to 250 mL with double-distilled water, filtered, and titrated against Fehling's A and B solutions (AR grade) using methylene blue as an indicator. Total sugars were determined by hydrolyzing 25 mL of the filtrate with concentrated HCl for 30 min, neutralizing with NaOH (ACS grade), and titrating under the same conditions. Results were expressed as % fresh pulp weight based on the Fehling's factor.

$$\text{Total sugars (\%)} = \frac{\text{Fehling's factor} \times \text{ Dilution Factor} \times 100}{\text{Titre volume} \times \text{ Weight of sample (g)}}$$

$$\begin{aligned}&\text{Reducing sugars (\%)}\\&= \frac{\text{Fehling's factor} \times \text{ Dilution Factor} \times 100 \times 100}{\text{Titre volume} \times \text{ Weight of sample (g)} \times 50}\end{aligned}$$

Statistical analysis

ANOVA was determined for each quantitative morphological and biochemical parameters for the guava

germplasm using SAS package [39]. The frequency distributions of each qualitative morphological parameter were prepared in Excel 12. Further, the datasets were used for principal component analysis, Pearson's correlation coefficient, cluster analysis, and cluster plot analysis in RStudio. Ver. 4.5.0.

Results

Characterization is the first step in the systematic and meaningful utilization of germplasm; therefore, in the present investigation, morpho-biochemical parameters were taken into consideration to assess genetic diversity among the collected guava germplasm. The findings of the present investigation are given hereunder, following the sub-heads.

Qualitative morphological parameters

The investigated guava genotypes showed significant variation for the studied morphological parameters (Table 2 & Supplementary Table 4). The branch habit varied from drooping to erect, with the maximum (36 No.) genotype having spreading branches, while only three genotypes (S. Portugal, Super Guava, *P. molle*) had drooping branches. Similarly, the outer bark colour showed the maximum frequency for light-green (22 No.) and the minimum for whitish (14 No.). The young shoots were green in most of the guava genotypes (36 No.), whereas it were red in three genotypes (Purple Guava, Lalit, *P. pumilum*). Ovate leaf shape showed the maximum frequency (17 No.), while the minimum was for obovate (6 No.) and oblong (7 No.); similarly, the tip

Table 2 Frequency distribution of the studied qualitative morphological parameters amongst studied guava genotypes

Parameters	1	2	3	4	5	6	7
Tree: attitude of branches	Erect (12)	Spreading (36)	Drooping (3)				
Bark colour	Whitish (14)	Creamy (15)	Light green (22)				
Young shoot: colour of stem	Green (36)	Green with red streaks (12)	Dark red (3)				
Leaf: shape	Ovate (17)	Obovate (6)	Oblong (7)	Lanceolate (10)	Oblanceolate (11)		
Leaf: shape of tip	Apiculate (1)	Acute (21)	Obtuse (23)	Rounded (6)			
Leaf: shape of base	Obtuse (11)	Rounded (20)	Cordate (20)				
Petiole orientation	Twisted (32)	Straight (19)					
Leaf: twisting	Absent (21)	Present (30)					
Young leaf: anthocyanin coloration	Absent (34)	Present (17)					
Leaf: variegation	Absent (51)	Present (0)					
Leaf: colour	Green group (50)	Greyed red Purple (1)					
Leaf: pubescence on lower side	Sparse (43)	Dense (8)					
Colour of lamina	Green (21)	Light green (15)	Dark green (15)				
Lamina thickness	Thin (12)	Intermediate (23)	Thick (16)				
Leaf lamina pubescence	Absent (9)	Sparse (17)	Medium (2)	Dense (15)	Very dense (8)		
Colour of leaf during winter	Pink (1)	Red (13)	Coppery (23)	Brick Red (10)	Brown (4)		
Fruit Shape at stalk end	Broadly rounded (14)	Rounded (21)	Truncate (2)	Pointed (8)	Necked (6)		
Fruit prominence of neck	Absent (40)	Present (11)					
Fruit relief of surface	Smooth (36)	Rough (15)					
Fruit longitudinal ridges	Absent (37)	Present (11)	Prominent (3)				
Fruit longitudinal grooves	Absent (47)	Present (4)					
Fruit puffiness	Absent (49)	Present (2)					
Fruit ridged collar around calyx cavity	Inconspicuous (47)	Conspicuous (4)					
Peel colour	Yellow-Green Group (22)	Yellow Group (28)	Red-Purple Group (1)				
Pulp colour	White Group (25)	Red Group (19)	Orange-Red Group (1)	Orange-White Group (2)	Grayed-Red Group (2)	Yellow-Orange Group (1)	Red-Purple Group (1)

Numbers in parentheses indicate the number of genotypes falling under each category of studied morphological parameters

shapes were predominantly obtuse (23 No.), and only a single genotype, *P. guineense*, had a unique apiculate leaf tip shape. The maximum frequency of leaf-base shapes was rounded and cordate (20 No. each), and the minimum (11 No.) was for obtuse (Fig. 1). Moreover, other notable patterns: variegation was absent in all genotypes, anthocyanin appearance on young leaves occurred only in a few cultivars (e.g., Punjab Apple, Purple Guava), lamina colour was mainly green, lamina thickness was mostly intermediate, and lamina pubescence ranged from none to very dense.

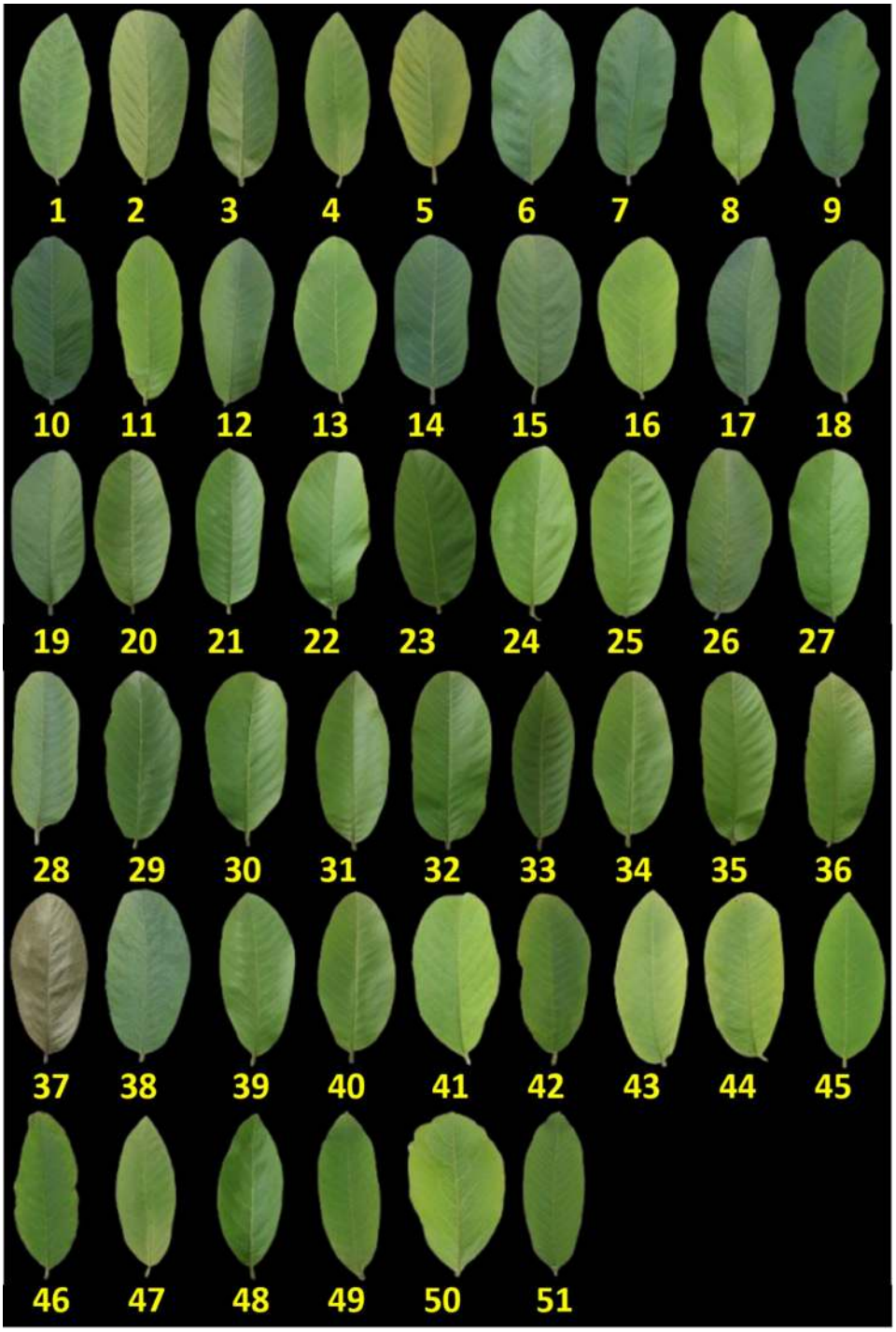


Fig. 1 Variations in leaf morphology of diverse guava genotypes (The serial numbers of the leaf images follow the serial number of guava genotypes presented in Table 1)

The present study revealed the substantial diversity in respect of fruit-related parameters, such as fruit shape at the stalk end, having five categories, with the maximum frequency of rounded (21 No.), the minimum of truncate (2 No.), and only 11 genotypes had a prominent neck. Similarly, fruit surface frequency was predominantly smooth (36 No.) versus rough (15 No.); longitudinal ridges were absent in 37, present in 11, and prominent in three guava genotypes, and the longitudinal grooves occurred only in four guava genotypes (Fig. 2; Table 2 & Supplementary Table 5). Further, the peel colour spanned from yellow (28 No.) to yellow-green (22 No.), and only Purple Guava had a unique purple-colour peel. The maximum frequency was observed for white pulp colour (25 No.), while the minimum was observed with one genotype each for orange-red, yellow-orange, and red-purple pulp colour (Fig. 3 & Supplementary Table 5).

Quantitative morphological parameters

The evaluated guava genotypes expressed substantial variability in quantitative morphological traits (Supplementary Table 2a & 2b). The leaf-related traits, viz., leaf blade length, leaf blade width, leaf shape index, and petiole length, had coefficient of variation (CV) greater than 9.8%, indicating considerable diversity among the genotypes, with the highest CV observed for petiole length (20.32%; Table 3). The leaf blade length was recorded in the range of 5.57–17.17 cm and width 2.07–7.90 cm, with the minimum length and width observed in the wild species *P. pumilum*, while the maximum length was recorded in S. Patillo and width in S. Ruby × Supreme. The leaf shape index also varied from 1.56 to 2.69, with a maximum in *P. pumilum*, which was at par with Shweta (2.68 cm), while the minimum was measured in *P. guineense*. However, the petiole length ranged from 0.17 to 0.77 cm; *P. pumilum* had the shortest length, and *Psidium* genotype 11 and S. Ruby × Supreme had the longest.

Fruit-related parameters such as fruit length, width, weight, pulp thickness, calyx diameter, and fruit peel and pulp colour are important traits for the consumer preference; therefore, these parameters are valuable for the development of novel guava genotypes. The CV values for most of the fruit-related parameters exceeded 20%, indicating high genetic diversity; however, the fruit shape index and fruit width exhibited lower CVs (13.26 and 18.16%, respectively), suggesting relatively moderate variability for these traits (Table 3). Fruit length and width varied widely, 2.77–9.48 cm and 2.68–8.84 cm, respectively; the smallest values were observed in wild species *P. molle*, while the largest value was recorded in *Psidium* genotype 16 and S. N90-53, respectively (Supplementary Table 2a). However, the fruit shape index varied widely, ranging from 0.82 to 1.38. The highest fruit weight was observed in S. N90-53 (379 g), which was comparable to *Psidium* genotype 16 (330.0 g); and the lowest fruit weight was recorded in *P. molle* (11.67 g). The total colour difference of peel and pulp was observed, which varied from 47.40 to 88.65 and 51.37–85.53, respectively; the lowest peel and pulp colour difference was observed in Purple Guava, while the highest was in Thai Guava and S. Less Seed Guava, respectively. Pulp thickness and calyx cavity diameter also showed significant variation, the maximum pulp thickness 2.62 cm, was observed in *Psidium* genotype 16, which was statistically at par with S. N90-53 (2.43 cm), while it was thinnest in wild species *P. molle*. The maximum calyx cavity 2.47 cm was observed in Arka Kiran, and was noticed < 1.00 cm in only four genotypes (Supplementary Table 2b).

There was a significant difference in seed-related parameters (weight, size and count/number) among the studied guava genotypes (Supplementary Table 2b). The seed count per fruit ranged from 30 (*P. guineense*) to 463 (S. Poamoho Pink), with S. Golden and S. Fan Retief having very high counts, while S. HPSI41 (80) and *Psidium* genotype 18 (86) genotypes proved low seeded. Furthermore, the ratio of seed number per fruit-to-fruit weight was highest in the wild species *P. pumilum (*12.67), while it was lowest in *Psidium* genotype 16 (0.39), followed by S. N90-53 (0.41) and S. HPSI41 (0.46). Seed weight per fruit ranged from 0.33 g in S. HPSI41 to 4.30 g in Thai 7. The seed weight of the majority of the indigenously developed guava genotypes ranged between 1.00 and 3.00 g, whereas it was 1.4 to 3.5 g in exotic genotypes (USDA). Seed size (length and width) showed a significant variation, with maximum guava genotypes having length > 3.5 mm, and ranged from 3.07 mm (*P. molle*) to 5.91 mm (S. 157). Similarly, the seed width ranged from 2.32 mm (*Psidium* genotype 14) to 3.90 mm (*P. guineense*). The maximum seed hardiness was observed in genotype *P. guineense* (17.41 kg/cm^2), while the softest seed was noticed in S. Poamoho Pink (6.26 kg/cm^2), followed by *Psidium* genotype 10 (6.32 kg/cm^2). The coefficient of variation (CV) of these seed-related parameters ranged from 12.18 to 88.96%, indicating substantial diversity among the studied guava genotypes.

Summary statistics of the biochemical parameters

The evaluated guava genotypes exhibited substantial variability for their biochemical parameters (Supplementary Table 3). The biochemical parameters, viz. TSS, titratable acidity, TSS/TA ratio, total sugars, reducing sugars, ascorbic acid, total phenols, total flavonoids, FRAP, DPPH, total carotenoids, and lycopene had coefficient of variation (CV) ranging from 2.71 to 99.08, indicating moderate to high diversity in the studied set of guava genotypes. The highest TSS was recorded in *Psidium* genotype 18 (14.77 °Brix), followed by S. HPSI41 (12.83 °Brix) and *Psidium* genotype 10 (12.17 °Brix),

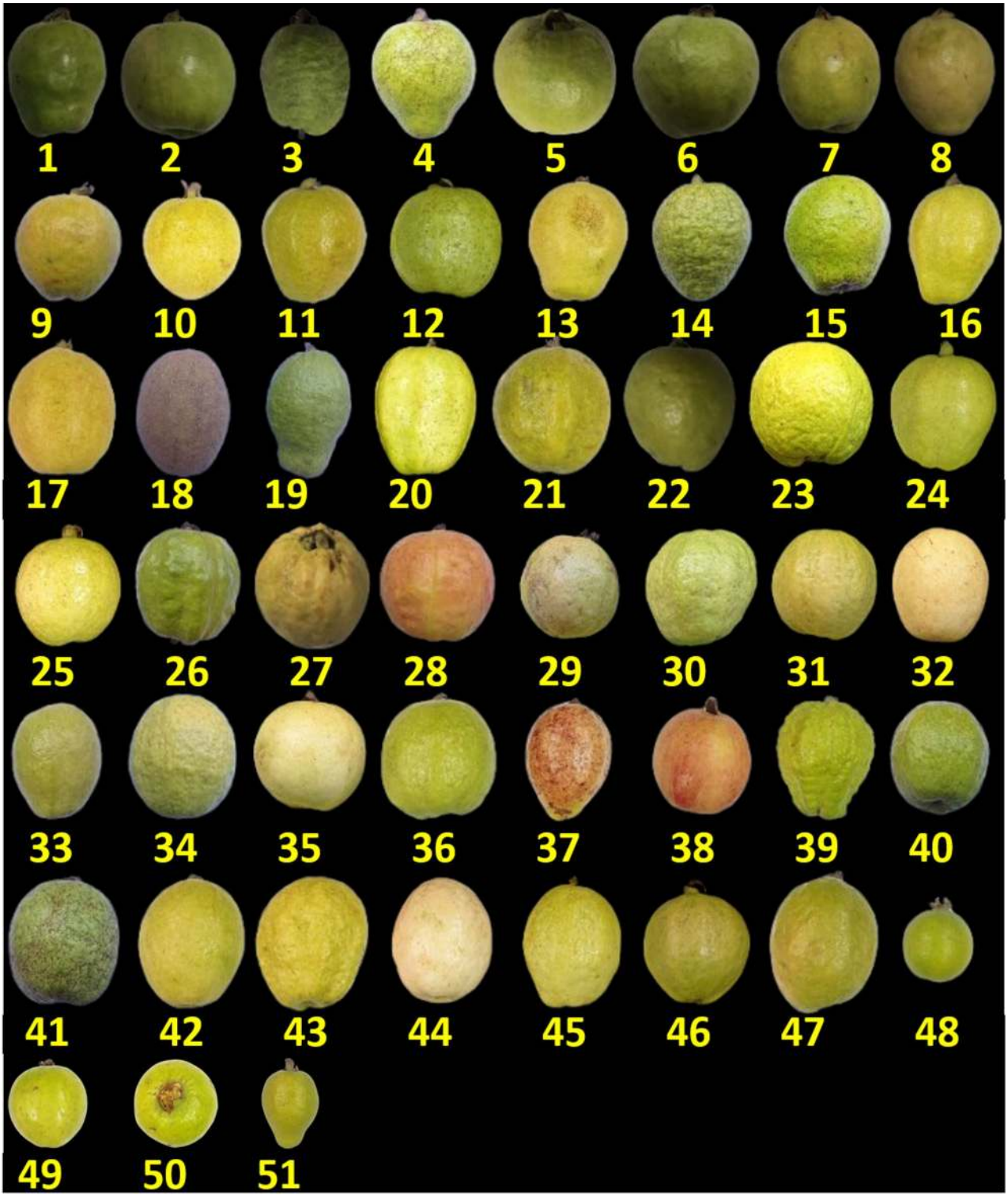


Fig. 2 Variations in fruit morphology of diverse guava genotypes (The serial numbers of the fruit images follow the serial number of guava genotypes presented in Table 1)

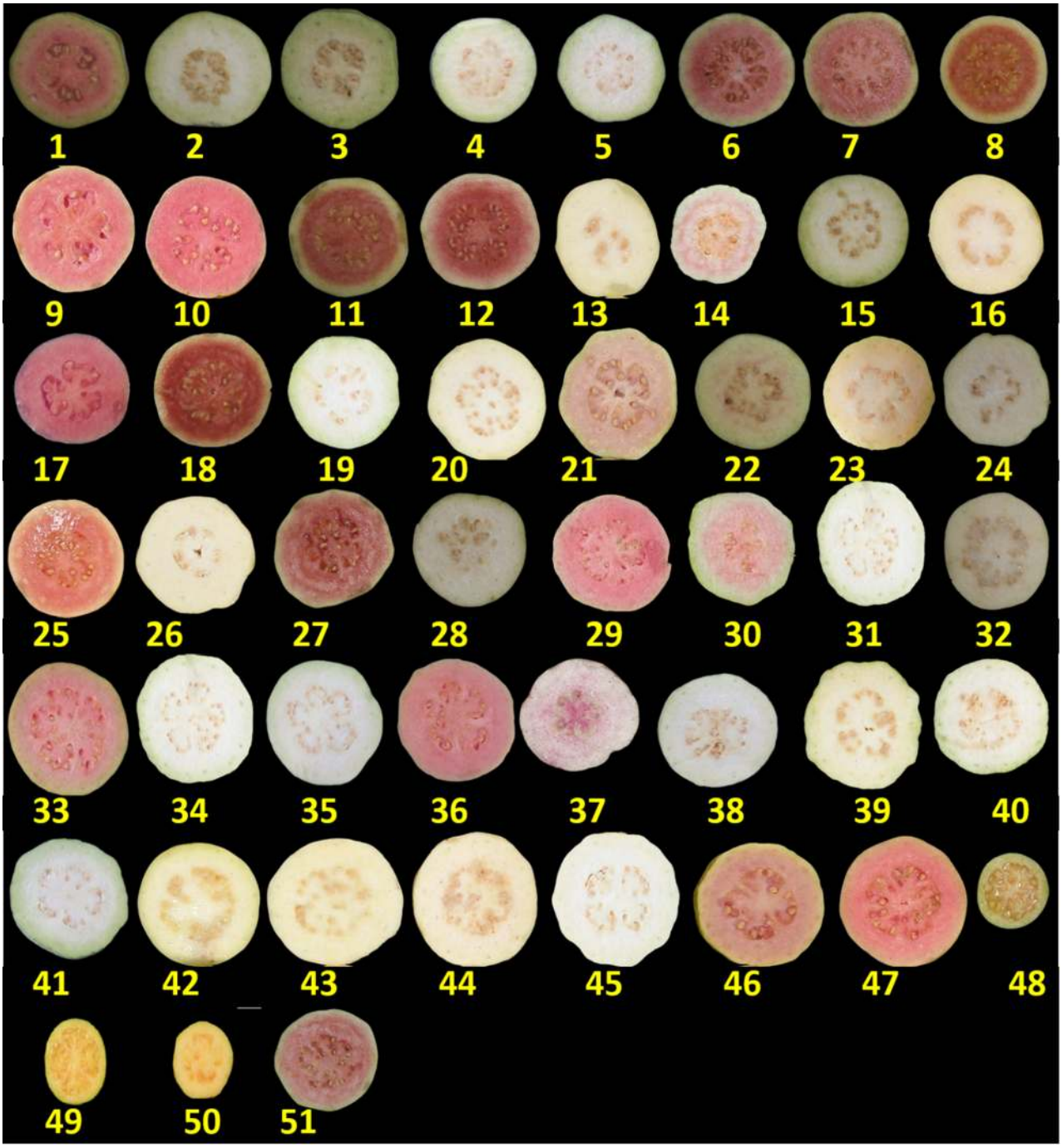


Fig. 3 Variations in fruit pulp colour of diverse guava genotypes (The serial numbers of the fruit pulp images follow the serial number of guava genotypes presented in Table 1)

while the lowest was observed in S. Fan Retief (8.13 °Brix). The highest fruit acidity (1.60%) was recorded in the wild genotype *P. guineense*, followed by S. Fan Retief (1.41%), *Psidium* genotype 6 (1.40%), and S. Ka Hua Kula (1.34%); although the lowest in *Psidium* genotype 15(0.25%), which was statistically at par with Super Guava (0.26%). The *Psidium* genotype 15 had the highest TSS/acid ratio (50.19), followed by Super Guava (43.62), S. Ruby × Supreme (42.97), and was lowest (5.75) in S. Fan Retief. Ascorbic acid was found to be the highest in S. Ka Hua Kula (338.93 mg/100 g FW), followed by Arka Kiran (279.67 mg/100 g FW), and the lowest content was observed in Thai Pink (72.67 mg/100 g FW). Total sugars content in fruit ranged from 5.41 to 10.21%, with the highest in *Psidium* genotype 18(10.21%), followed by S. HPSI41 (9.34%), and the lowest (3.20%) in S. Fan Retief.

Table 3 Descriptive statistics for the morpho-biochemical characters in the studied guava genotypes

S. No.	Parameters	Min	Max	Mean	LSD ($p \leq 0.05$)	CV (%)
1	**Leaf: ength (cm)**	5.57	17.17	12.97	0.82	15.15
2	**Leaf: width (cm)**	2.07	7.90	5.92	0.49	15.99
3	**Leaf: length/width**	1.56	2.69	2.21	0.19	9.82
4	**Petiole length (cm)**	0.17	0.77	0.54	0.16	20.32
5	**Fruit length (cm)**	2.78	9.48	6.64	0.73	20.75
6	**Fruit width (cm)**	2.68	8.84	6.40	0.60	18.16
7	**Fruit: length/ width**	0.82	1.38	1.04	0.09	13.26
8	**Fruit weight (g)**	11.67	379	162.13	17.34	45.33
9	**Pulp thickness (cm)**	0.30	2.62	1.60	0.17	27.21
10	**Calyx cavity diameter (cm)**	0.70	2.47	1.55	0.13	22.52
11	**TCD of Peel**	47.40	88.65	80.79	1.23	9.10
12	**TCD of Pulp**	51.37	85.53	76.41	1.22	10.01
13	**Seed weight/ fruit (g)**	0.33	4.30	2.12	0.57	37.99
14	**Number of seeds/fruits**	30.67	463.33	283.84	63.66	34.78
15	**Seed number/fruit weight**	0.39	12.67	2.30	0.76	88.96
16	**Seed length (mm)**	3.07	5.91	3.78	0.87	12.18
17	**Seed width (mm)**	2.32	3.90	2.89	0.43	13.59
18	**Seed hardiness (kg/cm^2)**	6.26	17.41	10.18	0.44	26.16
19	**TSS (° Brix)**	8.13	14.77	10.85	1.16	10.79
20	**Titratable acidity (%)**	0.25	1.60	0.50	0.09	63.01
21	**TSS/TA ratio**	5.75	50.19	27.02	7.09	39.02
22	**Total sugar (%)**	5.41	10.21	7.72	0.62	12.68
23	**Reducing sugar (%)**	3.17	5.65	4.29	0.51	12.82
24	**Ascorbic acid (mg/100g)**	72.67	338.93	165.52	10.92	36.93
25	**Total phenolic (mg GAE/100 g)**	117.93	449.63	288.63	9.09	26.22
26	**Total flavonoid (mg QE/ 100 g)**	54.99	242.77	159.69	13.92	30.43
27	**FRAP (µ M TE/g)**	7.74	20.69	13.28	1.06	23.04
28	**DPPH-radical scavenging activity (%)**	85.72	98.47	93.24	1.97	2.71
29	**Carotenoid (mg/100g)**	0.48	10.66	3.03	0.38	99.08
30	**Lycopene (mg/100g)**	0.59	9.97	4.72	0.30	52.43

Where: *Max* Maximum, *Min* Minimum, *LSD* Least Significant Difference, *CV* Coefficient of Variation

However, the maximum reducing sugars were observed in *Psidium* genotype 18(5.65%), which was at par with Thai 7 (5.27%), while it was lowest in S. Ka Hua Kula (3.17%).

Total phenolics content (TPC) and total flavonoids content (TFC) are the indicators of antioxidants potential of guava fruits, showing substantial variation from 117.93 to 449.63 mg GAE/100 g FW phenols in S. Poamoho Pink and *Psidium molle*, respectively; and 54.99 to 242.77 mg QE/100 FW flavonoids in S. N90-53 and Punjab Kiran, respectively. The DPPH and FRAP assays revealed antioxidants activity; the highest DPPH scavenging activity was assayed in Punjab Kiran (98.47%), which was statistically comparable to *Psidium* genotype 7 (97.93%) and the lowest was observed in Super Guava (85.72%). However, the genotype Arka Kiran had the highest FRAP antioxidant activity (20.69 µM TE/g FW), followed by Dhawal (19.24 µM TE/g FW), which was at par with S. Ka Hua Kula (18.45 µM TE/g FW), while the lowest in S. Beaumont (7.74 µM TE/g FW), which was statistically similar lwith Thai Pink (7.79 µM TE/g FW). Total carotenoids content was noted highest in S. Ka Hua Kula (10.66 mg/100 g), followed by Arka Kiran (9.56 mg/100 g FW), *Psidium* genotype 7 (9.13 mg/100 g FW), and Punjab Pink (8.85 mg/100 g FW), although it was recorded lowest in *Psidium* genotype 4 (0.48 mg/100 g), and a high CV of 99.08% was observed for this parameter (Table 3). Regarding lycopene content, of the 51 genotypes, 22 were pink-fleshed and were included in the lycopene assessment. The highest lycopene content was observed in S. Ka Hua Kula (9.97 mg/100 g), followed by Arka Kiran (8.70 mg/100 g), which was statistically at par with *Psidium* genotype 7 (8.07 mg/100 g) while the lowest value was recorded in Purple Guava (0.59 mg/100 g), followed by S. N90-53 (1.64 mg/100 g).

Principal component analysis

Principal component analysis (PCA) was employed to assess the relative contributions of 18 morphological and 12 biochemical parameters toward overall variability among guava genotypes. Of the 30 principal components (PCs), nine had eigenvalues greater than 1.0, and together

explained 80.54% of the total morpho-biochemical variation. Each PC accounted for a specific proportion of variance, with the first component capturing the largest share (22.10%), followed by successive components describing progressively smaller proportions. The first five PCs alone accounted for 61.82% of the total variation (Table 4; Fig. 4). The variables with the strongest contributions to each component (eigenvalues ≥ 0.5), as suggested by Wu et al. [40], were considered significant and are highlighted in bold. The PC1 was strongly and positively associated with fruit morphological traits, particularly fruit width (0.91), fruit weight (0.84), pulp thickness (0.85), fruit length (0.77), calyx diameter (0.71), Leaf length (0.65), and leaf width (0.58); explaining 22.1% of the total variation. In contrast, seed number per fruit (–0.79) showed a strong negative association. This component, therefore, primarily represents fruit size and yield-related traits. The PC2 showed high positive association for lycopene (0.57), total carotenoids (0.55), fruit length/width ratio (0.58), and seed weight/fruit (0.59), However the negative associations were observed for TSS (–0.69), TSS/TA ratio (–0.64), TSC (–0.70), and RSC (–0.65); explaining 15.2% of the total variation. Thus, PC2 captures a contrast between fruit quality (sugars, TSS, sweetness index) versus fruit pigment parameters (lycopene, total carotenoids). Component PC3 was positively influenced by seed-related traits such as seed number (0.60) and leaf length/width ratio (0.56), whereas strong negative loadings were recorded for seed hardiness (–0.57), total phenolics (–0.55), and seed width (–0.47), and accounted for 10.39% of total variation. Component PC4 was primarily associated with ascorbic acid (0.60) and explained 8.54% of the total variation. Moreover, PC5 explained an additional 5.5% of the variability through moderate positive contributions from total flavonoids (TFC, 0.41), total phenolics (TPC, 0.31), leaf traits (leaves L/W, 0.45), and seed weight per fruit (0.34). Negative loadings were noted for fruit sugars components and seed width. Hence, the morpho-biochemical parameters could effectively explain the existing variability among the studied guava genotypes.

Table 4 Eigenvalues, variance (%) and cumulative variance (%) for five principal components axes from the PCA of morpho-biochemical parameters in the studied guava genotypes

Parameters	Principal component				
	Dim.1	Dim.2	Dim.3	Dim.4	Dim.5
TSS	0.31	**-0.69****	0.25	0.24	0.12
TA	-0.46	**0.51****	-0.44	0.18	-0.01
TSS.TA	0.44	**-0.64****	0.39	-0.06	-0.17
TSC	0.44	-0.70	0.25	0.25	0.06
RSC	0.46	**-0.65****	0.21	0.18	0.03
ASC	0.15	0.24	0.09	**0.60****	0.23
TPC	-0.40	-0.11	**-0.55****	0.24	0.31
TFC	-0.34	-0.21	-0.23	0.09	0.41
FRAP	0.15	0.08	0.10	0.37	0.37
DPPH	0.03	0.17	-0.02	0.37	0.13
Carotenoid	-0.01	**0.55****	0.43	**0.51****	-0.14
Lycopene	-0.02	**0.57****	0.41	**0.52****	-0.14
Fruit_length	**0.77****	0.42	-0.10	0.08	0.25
Fruit_width	**0.91****	0.09	0.04	-0.07	0.08
Fruit_L/W	-0.01	**0.58****	-0.16	0.23	0.32
Pulp_thickness	**0.86****	0.00	-0.13	0.03	-0.10
Calyx_diameter	0.72	-0.06	0.15	0.13	0.09
Fruit_weight	**0.84****	0.21	-0.17	-0.14	0.09
TCD_Peel	0.19	-0.01	-0.17	-0.33	0.41
TCD_Pulp	0.18	-0.30	-0.42	-0.47	0.39
Leaves_Length	**0.66****	0.37	0.12	-0.12	-0.04
Leaves_width	**0.58****	0.43	-0.19	-0.20	-0.28
Leaves_L/W	-0.03	-0.16	**0.56****	0.14	0.45
Petiole_length	0.43	0.33	-0.01	-0.34	-0.13
Seed_weight/fruit	0.20	**0.59****	0.32	-0.34	0.34
Seed_Number/fruit	-0.02	0.39	**0.60****	-0.49	0.25
Seed_lengh	0.32	-0.28	-0.35	0.18	0.20
Seed_width	0.36	-0.12	-0.47	0.25	-0.27
Seed_hardiness	0.31	0.07	**-0.57****	0.25	0.04
S_No/F_W	**-0.79****	-0.09	0.27	-0.19	0.11
Eigenvalue	6.63	4.54	3.11	2.57	1.67
Variance (%)	22.10	15.15	10.39	8.57	5.5
Cumulative variance (%)	22.10	37.26	47.65	56.23	61.82

** Eigenvalues are significant ≥ 0.5

Bi-plot analysis

The Principal Component Analysis (PCA) biplot illustrates the relationships among the studied guava genotypes and the measured parameters, were distributed throughout all four quadrants of the biplot, indicating high morpho-biochemical diversity (Supplementary Fig. 1). The horizontal axis (Dim1) explains 22.1% of the total variation, while the vertical axis (Dim2) explains 15.2%, together accounting for 37.3% of the variability in the dataset. In this biplot, parameters such as fruit weight, fruit length, fruit width, and pulp thickness cluster together, showing strong positive correlations; and the guava genotypes, *Psidium* genotype 16, Thai 7, and S. N90-53 are well aligned with these parameters in the positive axis of PC1, reflecting more association with higher fruit weight and pulp thickness. In contrast, lycopene and total carotenoids are located in opposite directions to TSS and total sugars content, indicating a negative correlation, which means the guava genotypes having higher lycopene content such as S. Ka Hua Kula, S. Fan Retief and Punjab Pink tend to contained lower TSS; however, the guava genotype with higher TSS such as *Psidium* genotype 18, S. HPSI41 and *Psidium* genotype 15 tend to have lower lycopene content. Several genotypes, including S. Patillo, S. Poamoho Pink, S. Kona 1, and Lalit, positioned in the upper left quadrant near antioxidant-related traits (DPPH, ASC, and FRAP) showed a strong

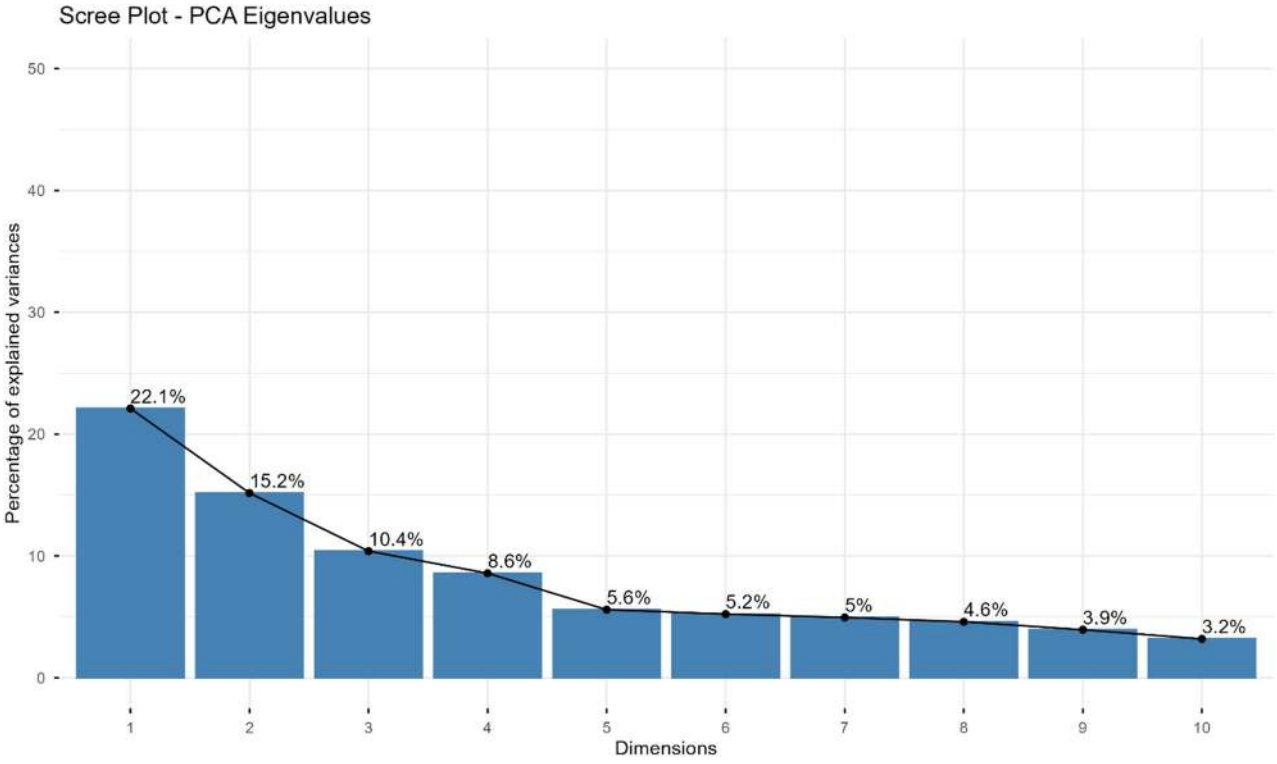


Fig. 4 Scree plot analysis derived from studied morpho-biochemical parameters in guava genotypes based on first two principal components that accounted for 22.1% (PC1) and 15.2% (PC2) of the total variance

association with antioxidants, reflecting their potential as bioactive-rich genotypes. However, the genotype *P. molle*, *P. pumilum* and *P. guineense* clustered distinctly towards the negative axis of Dim. 1 and in TPC, TFC and seed number per fruit-to-fruit weight ratio point direction and also opposite to fruit weight, fruit width and leaf length in the bottom right quadrant, indicating the genotype having small fruit weight had higher TPC and TFC. The guava genotypes, viz. Hisar Surkha, *Psidium* genotype 11, and *Psidium* genotype 10 clustered near the origin and displayed an intermediate combination of traits, with no extreme values and balanced expression of characteristics. Moreover, the distribution of biochemical parameters such as TPC, TFC, lycopene, total carotenoids, and total sugars content, as well as superior morphological parameters such as fruit weight, pulp thickness, and seed number per fruit, aligned in separate axes reflecting their independent variation, thereby providing opportunities for the concurrent selection of quality and functional attributes.

Correlation matrix analysis

Pearson's correlation analysis revealed significant interrelationships among the studied quantitative morpho-biochemical parameters among the guava genotypes. Based on the Pearson's correlation coefficients between the morpho-biochemical variables, a heat map was created (Fig. 5 and Supplementary Table 6). The colour scale moves from blue (negative correlation) to red (positive correlation); where the pale blue/red colour indicates weak correlation ($-0.30 < r < +0.30$), dark blue colour indicates strong negative correlation ($r < -0.70$) while the dark red shows strong positive correlation ($r > 0.70$), with the colour intensity indicating the strength of association. Statistical significance is indicated by asterisks ($^{*}p < 0.05$, $^{**}p < 0.01$, $^{***}p < 0.001$). Fruit weight exhibited a strong positive correlation with fruit width ($r = 0.90^{***}$) and fruit length ($r = 0.84^{***}$), and pulp thickness ($r = 0.78^{***}$), indicating that larger fruit dimensions contributed substantially to overall fruit mass. Similarly, seed width was positively correlated with seed length ($r = 0.47^{***}$), while there is no relationship observed between the seed width and seed hardiness ($r = 0.28^{*}$), However Number of seed/ fruit was negative correlated with seed width (r = -0.45***) and seed hardiness (r = -0.45***), while it was strongly positive correlated with seed weight ($r = 0.74^{***}$). Leaf length was positively correlated with leaf width ($r = 0.83^{***}$) and positively correlated with petiole length ($r = 0.52^{***}$), fruit weight ($r = 0.48^{***}$), fruit length ($r = 0.55^{***}$), and fruit width ($r = 0.51^{***}$), suggesting that plants with longer leaves tend to produce heavier fruits. Similarly, the seed number per fruit to fruit weight ratio is strongly negative correlated with pulp thickness (r = -0.72***) and negative correlated with

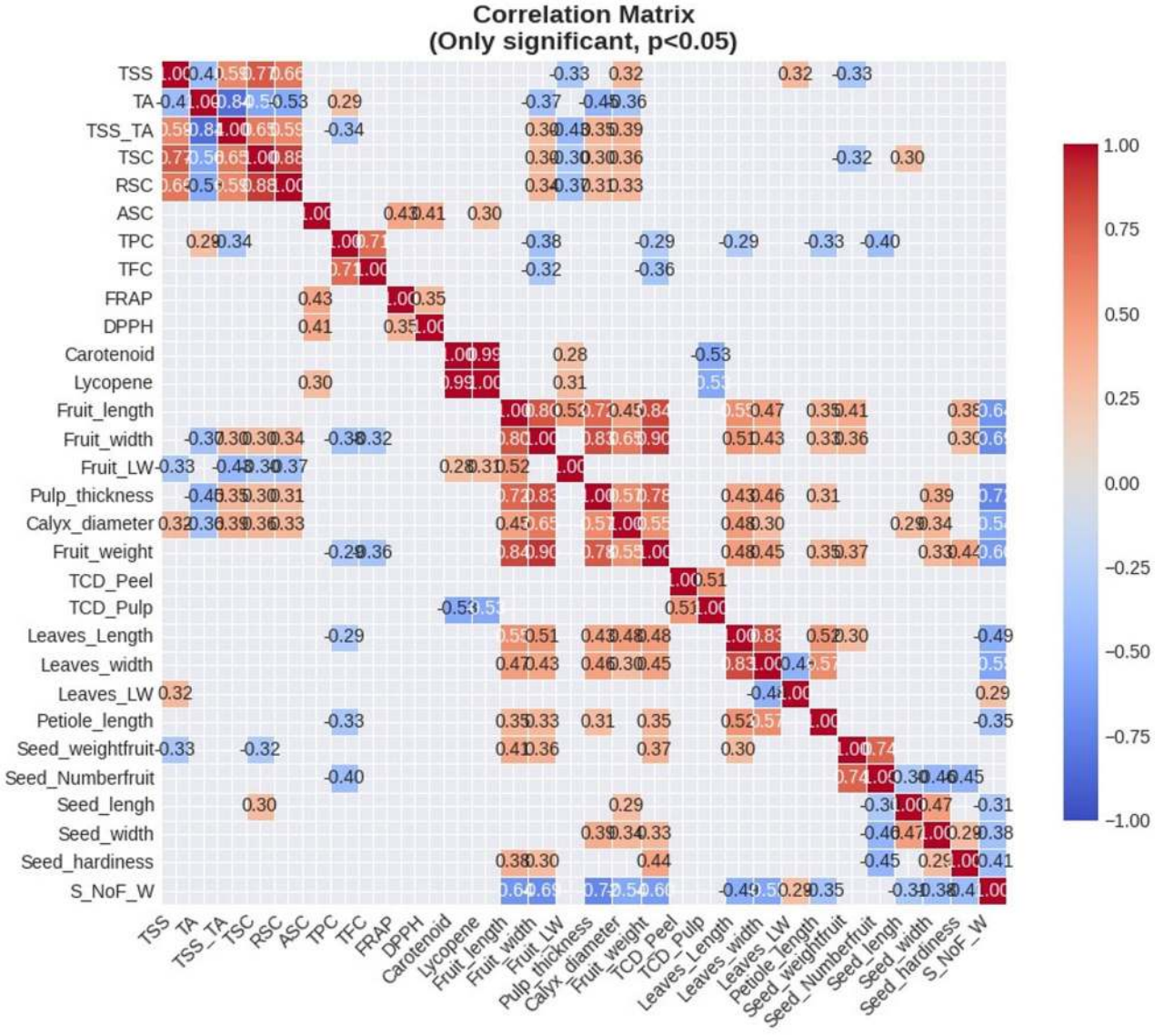


Fig. 5 Simple correlations among the quantitative morpho-biochemical parameters among the guava genotypes (Stronger positive correlations are shown in deeper red, while negative correlations are indicated by dark blue shades. Significance levels are denoted by asterisks ($p < 0.05$, $p < 0.01$, $p < 0.001$)

fruit width (r = -0.69***), fruit length (r = -0.64***), fruit weight (r = -0.60***), leaves width (r = -0.55***), leaves length (r = -0.49***) and seed hardiness (r = -0.41**). This finding suggests that selecting genotypes with a lower seed-to-fruit weight ratio holds considerable promise for improving fruit quality traits. Amongst studied biochemical parameters, total phenolics content (TPC) showed a significant positive relationship with total flavonoids content (TFC) (r = 0.71***), implying coordinated biosynthesis of phenolics compounds. Conversely, total soluble solids to titratable acid ratio (TSS/TA) had a significant negative correlation with titratable acidity (TA) (r = -0.84***), reflecting the expected inverse relationship between sweetness-acidity balance in fruit quality; however TSS content strong positively correlated with total sugars content (TSC) (r = 0.77***) and negative correlated with titratable acidity (r = -0.41**), showing its significance in fruit sensory qualities. A negative significant correlation was observed between total colour difference of pulp and lycopene content (r = -0.53***) and total carotenoid content (r = -0.53***) that revealed genotypes with a higher pigment may contain lower total colour difference, moreover the total colour difference of peel is positively correlated with total colour difference of pulp (r = 0.51***); and a significant strong positive correlation observed between total carotenoid content and lycopene content (r = 0.89***), indicating that the genotype having higher lycopene content had also higher carotenoid. The ascorbic acid content was positively correlated with antioxidants activity DPPH (r = 0.41**), and FRAP (r = 0.43**),

which revealed that the guava genotypes with higher vitamin C content may had higher antioxidants activity. Interestingly in the present study, we observed that pulp thickness is negatively correlated with TA ($r = -0.46^{***}$), and seed number per fruit is also negatively correlated with TPC ($r = -0.40^{**}$).

Box plots analysis

The standardized boxplot summarizes the distribution of all evaluated morph-biochemical parameters across the studied guava genotypes (Fig. 6). The majority of parameters were centered around zero, with comparable interquartile ranges, confirming the effectiveness of standardization. However, the biochemical parameters such as total carotenoids, FRAP, lycopene, ASC, TFC, TPC, RSC, TSS, and TSS/acid ratio as well as in majority of morphological parameters except calyx cavity diameter and seed number per fruit to fruit weight ratio, exhibited broader dispersions and a higher frequency of outliers, indicating moderate to high variability among the studied guava genotypes. In contrast, the other parameters, such as DPPH, TA, TSC, and morphological parameters, showed relatively narrower distributions, reflecting lower variability. Moreover, the whiskers extend to the minimum and maximum values, and the parameters like fruit weight, lycopene, seed number per fruit to fruit weight ratio, seed length, seed weight per fruit, TA, TSC, and TSS had several high outliers beyond the whiskers, elucidating the presence of exceptional genotypes with extreme values. In contrast, the other parameters, such as DPPH, fruit length, fruit weight, leaf length, leaf width, pulp thickness, seed number/fruit, TCD pulp, and TCD peel, show several lower outliers beyond the whiskers, indicating the presence of exceptional genotypes with lower values. The presence of outliers for certain parameters points to unique genotypes with extreme high or low values that may offer potential for guava breeding or the selection of superior genetic resources.

Cluster composition and D^2 distance matrix analysis

The dendrogram presented herein delineates the morpho-biochemical relationships among diverse guava genotypes and related species, constructed using the data from 51 guava genotypes (Fig. 7). The clustering pattern clearly shows the extent of morpho-biochemical similarity or divergence among the accessions, as indicated by the vertical scale (Height), where lower joining points correspond to higher similarity. The dendrogram divided 51 guava genotypes into five major clusters, which are further simplified into several clades at higher hierarchical levels. The cluster 1 contained three wild genotypes, *P. pumilum*, *P. molle*, and *P. guinense*, which were distinctly separated from the main guava group, highlighting their distant morpho-biochemical relationships. Similarly, the cluster 4 also contained only three guava genotypes, two exotic (S. Fan Retief, S. Ka Hua Kula) and one wild type (*Psidium* genotype 6), that were markedly separated from the other three major clusters. In contrast, cluster

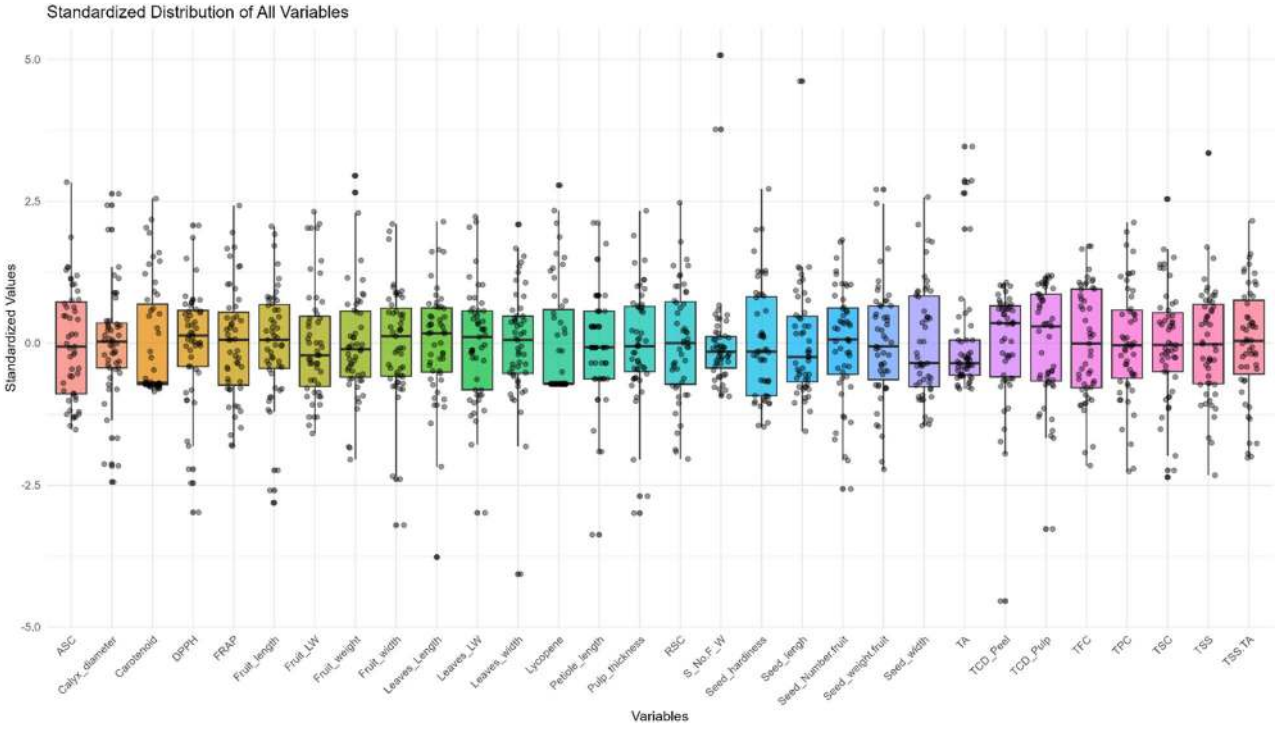


Fig. 6 Box plots indicating distribution of morpho-biochemical variables of studied guava genotypes

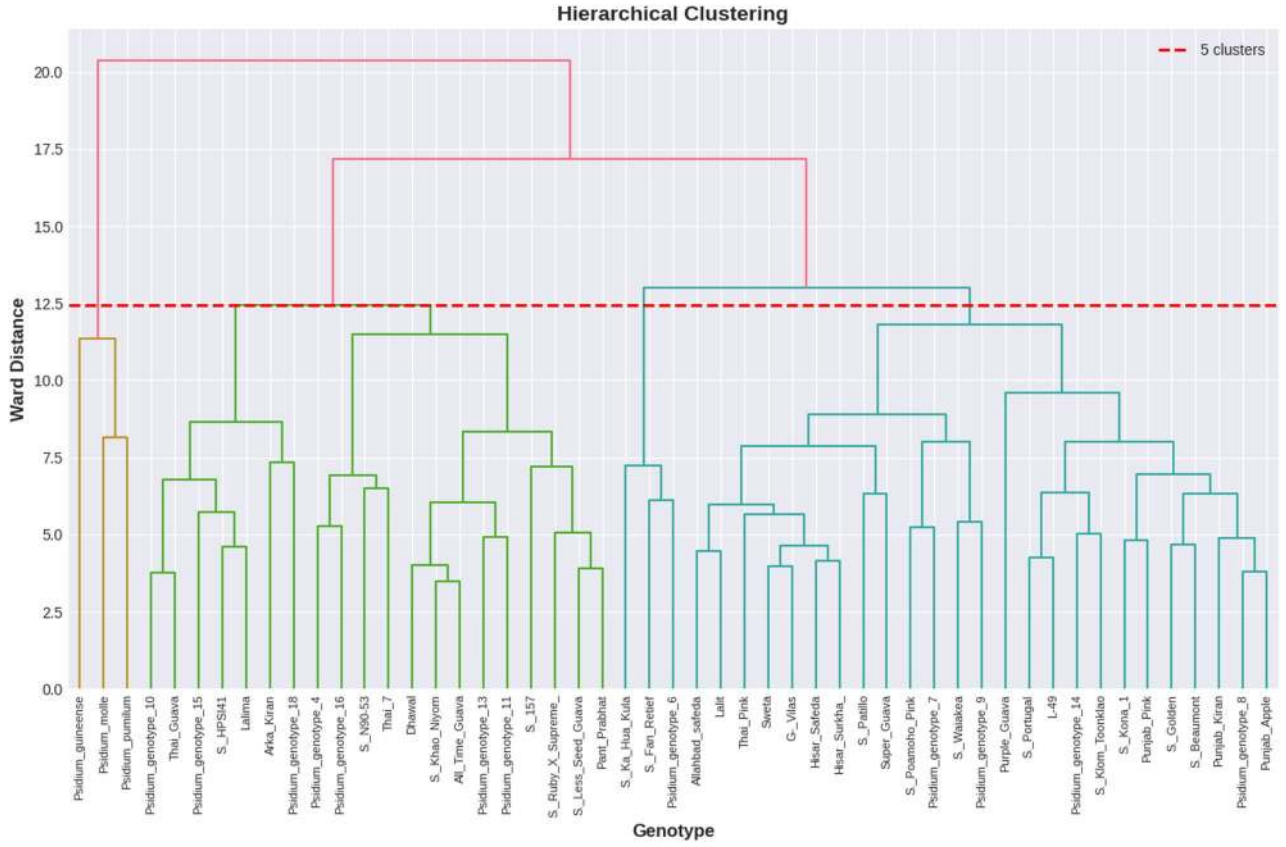


Fig. 7 Cluster analysis based on the morpho-biochemical parameters of the studied guava genotypes

Table 5 D^2 statistics and genetic distance between clusters

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
Cluster 1	0.00	21.85	19.03	29.39	17.63
Cluster 2	21.85	0.00	9.20	21.16	7.76
Cluster 3	19.03	9.20	0.00	19.38	5.15
Cluster 4	29.39	21.16	19.38	0.00	17.06
Cluster 5	17.63	7.76	5.15	17.06	0.00

2 comprised 7 guava genotypes, cluster 3 comprised 13 guava genotypes, and cluster 5 was the largest, comprising 25 genotypes, including both indigenously developed and exotic/USDA introductions. These clusters formed at lower hierarchical distances, suggesting morpho-biochemical similarity within clusters but considerable divergence among them. Overall, the majority of guava genotypes aggregated within three large clusters, reflecting broad morpho-biochemical affinities among the studied genotypes. The D^2 distance matrix further corroborated these findings, revealing distinct patterns of genetic divergence among clusters (Table 5). The cluster 1 exhibited the highest overall divergence from all other clusters, recording maximum inter-cluster distances with Cluster 4 (D^2 = 29.39), Cluster 2 (D^2 = 21.16), and Cluster 3 (D^2 = 19.38), indicating that cluster 1 is genetically most distinct. Conversely, cluster 3 and cluster 5 showed the least divergence, as evidenced by the lowest D^2 value (5.15), indicating a high degree of genetic similarity between them. Additionally, cluster 2 demonstrated close affinity with cluster 5 (D^2 = 7.76) and cluster 3 (D^2 = 9.20), further confirming the genetic relatedness among these clusters. Notably, clusters 2, 3, and 5 formed a cohesive group characterized by low inter-cluster distances, whereas clusters 1 and 4 were comparatively more divergent from the rest. These results collectively provide valuable insights into morpho-biochemical diversity and relationships amongst the studied guava genotypes, which could be strategically utilized in breeding programs by selecting genetically diverse parents from highly divergent clusters to maximize genetic variability in segregating populations.

Discussion

Morpho-biochemical characterization is crucial for grouping and distinguishing germplasm of perennial fruit crops, including jamun [41], jackfruit [42], mulberry [43], persimmon [44], and guava [45]. In the present study, tree, leaf, fruit, and seed morphological parameters are extensively used to characterize 51 diverse guava germplasm. Most of the parameters had potential economic importance for high-quality fruit production and

may serve as cultivar identification tools for evaluating guava germplasm and as target traits for guava breeders and growers [46, 47]. Tree architecture is an important consideration when characterizing guava germplasm because branch orientation includes a spreading of canopy with strong angles that reduce breakage and suit, especially for growing under high-density systems [48, 49]. In previous studies, the tree growth habit, tree height, tree volume, and shoot length have been proved reliable traits for guava germplasm characterization [23, 40–52]. In the present investigation, the guava genotypes studied showed substantial variation in tree habit, including branch orientation (from erect to drooping), bark and young-shoot colour. This prominent variation indicates useful tree structural diversity, which agrees with the prior reports of high diversity in *Psidium* germplasm [53–56] and Kidaha et al. [55] also made selection in guava germplasm for reducing branch breakage and decreasing labour intensity when it will be trained in high-density systems. Moreover, Ran et al. [51] found that a few guava genotypes, viz., Hisar Surkha and Strawberry guava had drooping growth habit; Allahabad Safeda, Hisar Safeda, Banarasi Surkha, Lalit, and Chinese guava have upright growth; whereas, Patillo, Supreme, Shweta, and Lucknow-49 showed spreading growth habit, which was aligned with similar findings by Daulta et al. [57].

Similarly, there was a wide variation in leaf morphology recorded among the studied guava genotypes. Earlier, Nikhil et al. [58] used leaf shape, leaf apex shape, leaf base shape, lamina colour, and petiole orientation for the characterization of guava germplasm. Recently, Gethe et al. [59] reported the highest leaf length 12.76 cm and width 5.99 cm, the leaf shape from lanceolate to oblanceolate, the leaf apex shape from rounded to acute, and the leaf base shape from obtuse to rounded, from the 20 guava genotypes. In the present study, leaf blade lengths ranged from 5.57 to 17.17 cm, widths from 2.07 to 7.90 cm, and the length/width ratio varied from 1.56 to 2.69. There were five distinct leaf-shape classes and significant differences in petiole length, which ranged from 0.17 to 0.77 cm, along with twisting and leaf pubescence among the studied guava genotypes. These findings support earlier studies that reported considerable variation in leaf morphology among *Psidium* germplasm [51, 54, 56, 58]. The present study highlights that the maximum leaf length observed in S. Patillo (17.17 cm) and S. Waiakea (16.13 cm) exceeds the longest leaves reported in previous surveys, like the 14.9 cm reported by Nikhil et al. [58], 12.76 cm by Gethe et al. [59], and 12.18 cm by Sarkar and Sarkar [46]. This suggests that these genotypes may be potential sources of large-leaved plants that could be valuable for tailoring the development of photosynthetically efficient plants. The significant variation in leaf and shoot characteristics offers additional markers for describing and classifying guava germplasm. These variations are consistent with earlier findings about pigment and shoot colour diversity in both cultivated and wild plants [53, 55, 58, 60]. In this study, the dominance of intermediate lamina thickness and mostly sparse pubescence on the lower side provides additional criteria for selecting plants based on texture for pest resistance and other agronomic traits. These traits were mentioned in previous studies, Sohi et al. [61] and Gangappa et al. [45]. From a breeding strategy perspective, the observed diversity supports the use of both cultivated and wild plants to broaden the genetic base and introduce desirable traits [56, 62]. Specifically, genotypes with a spreading growth habit and suitable branch angles should be prioritized to tailor guava genotypes for high-density planting and improve yield efficiency. Meanwhile, large-leaved types and those with longer petioles should be evaluated for their vigour and photosynthetic ability. Rare traits, such as drooping plants, dark red shoots, and unique winter pigmentation, are useful for identifying germplasm and may aid in classifying guava accessions.

The fruit parameters of the 51 guava genotypes studied, showed the significant variation for fruit length (2.77 to 9.48 cm), width (2.68 to 8.84 cm), and weight (11.67 to 379.0 g), which is consistent with earlier findings by Delgado et al. [53] and Rajore et al. [50]. Kumari et al. [56] noted the maximum fruit weight (450.6 g) in the Thai variant 2 genotype with fruit length (8.21 cm) and width (7.27 cm), while the minimum was in *P. pumilum*. Some guava accessions in this study, such as S. N90-53, Thai 7, and *Psidium* genotype 16, produced the heaviest fruit with the thickest pulp. These traits are noted in exotic and Thai germplasm, which are valuable for breeding aimed at increasing pulp content and fruit weight [45, 56, 59]. In contrast, wild species like *P. molle* produced tiny fruits, which supports descriptions of wild *Psidium* often having small fruit but may provide other beneficial traits [62]. However, fruit size is primarily a varietal trait, though it can be partly influenced by factors such as total fruit load on the tree, soil moisture availability, and the source–sink balance [51, 63]. The fruit surface characteristics, including relief and longitudinal ridges or grooves, were consistent with the qualitative fruit trait differences noted in earlier studies [45, 51, 56]. The colour and shape of fruits are vital ripening markers, frequently utilized for cultivar identification [64]. The fruit pulp and peel colours displayed a wide variability, along with large total colour difference (TCD) values amongst the studied guava genotypes. This finding aligns with reports linking colour variation to differences in composition, such as carotenoids and lycopene, and consumer preference [45, 61]. Recently, Sharma et al. [23] observed three different pulp colours, with pink pulp being prominent among the six guava cultivars/hybrids; Ran et al. [51] recorded

peel colour variation from yellowish green to saffron yellow, with red spots on some genotypes, such as Shweta. Moreover, these fruit traits, including large fruit size, thick pulp, favourable pulp-to-seed ratio, low seed count, and vibrant pulp colour (TCD), highlight clear targets for parent selection in breeding programs focused on fruit quality and processing potential [52, 65].

The current research findings also revealed significant differences in seed-related traits that align with previous descriptions of guava germplasm. Several exotic/USDA introductions showed high seed counts and seed weights, for example, S. Poamoho Pink with 463 seeds and S. Golden with 459 seeds. Seed weights range from 4.1 to 4.3 g, higher in Thai 7 and S. Fan Retief. This contrasts with the very low seed numbers in genotypes *P. guineense* (30 seeds) and S. HPSI41 (80 seeds), and the small seed weight in S. HPSI41 (0.33 g). These findings reflect a notable phenotypic diversity found in regional collections [53, 56, 62]. The wide range in seed dimensions and hardness, seed length from 3.07 to 5.91 mm, and hardness from 6.26 to 17.41 kg/cm², supports earlier results that suggest wild species often have harder seeds even less number and also some wild types produce more seeds, while cultivated and hybrid germplasm typically have softer seeds and higher pulp proportions [45, 52, 65]. The current research findings indicate that genotypes with a higher seed count may have softer seeds, as observed in S. Poamoho Pink (463 seeds and 6.26 kg/cm² hardness), S. Golden (459 seeds and 10.66 kg/cm² hardness), and All Time Guava (386 seeds and 7.36 kg/cm² hardness). In contrast, genotypes with a lower seed count tend to have harder seeds, such as *Psidium* genotype 13 (146 seeds and 15.53 kg/cm² hardness) and *P. guineense* (30 seeds and 17.1 kg/cm² hardness). Rajan et al. [66] reported that the positive association existing between the fruit weight and number of seed per fruit, which was coincide with present study, however in our study the seed number and fruit weight ratio varies from 0.39 to 12.67, with some genotypes like *Psidium* genotype 16, S. N90-53, and S. HPSI41 had the lowest ratio 0.39, 0.41 and 0.46, respectively, indicating these genotypes has highest fruit weight with comparative lower seed content, suggesting valuable germplasm. From a germplasm utilization perspective, the existing patterns for the seed-related traits suggest that some USDA lines and Thai variants could provide useful traits for seed-based processing, such as those with acceptable seed mass. Meanwhile, low-seed genotypes with higher fruit weight, such as S. HPSI41, S. N90-53 and *Psidium* genotype 16 are promising candidates for improving edible quality by decreasing seed number or size and increasing the pulp/seed ratio. This goal has also been highlighted by other researchers aimed at developing fruit crop varieties for table and processing purposes [59, 61, 67].

The present study revealed substantial variability in the biochemical parameters of the studied guava genotypes, consistent with earlier findings by Corrêa et al. [68] and Chiveu et al. [69]. The wide range in total soluble solids (8.13–14.77 °Brix) and acidity (0.25–1.60%) observed in the present investigation parallels the reports of Singh et al. [70], Sarkar and Sarker [46], and Parveen et al. [71], who also documented significant inter-genotypic diversity for these traits. Similarly, the high variability in TSS/acid ratio (5.75–50.19), total sugars content (5.41–10.21%), and reducing sugars content (3.17–5.16) aligns with the results of Kumari et al. [6] and Pagi et al. [72], underscoring their importance in determining fruit sweetness and consumer acceptability. Considerable differences in ascorbic acid levels (72.67–338.93 mg/100 g) further support earlier reports by Yousaf et al. [73]; Ravi et al. [74]; Vishwakarma et al. [75], and they have also emphasized that guava as a rich and highly variable source of vitamin C. Likewise, the broad range of total phenols (117.93–449.6 mg GAE/100 g) and total flavonoids (54.99–242.77 mg QE/100 g FW) corresponds with the antioxidants diversity and radical scavenging potential of guava germplasm [45, 76–78], reaffirming guava's nutraceutical potential; However, in the present study, higher phenolics content was reported in wild species, reaching up to 449.6 mg GAE/100 g in *P. molle* and 436.9 mg GAE/100 g FW in *P. guineense*. Similarly, some USDA-collected guava genotypes also exhibited high phenolics values, such as 382.2 mg GAE/100 g and 381.13 mg GAE/100 g in *Psidium* genotype 13 and S. Portugal, respectively. These values are higher than those reported in previous research findings by Verma et al. [78] (up to 305.4 mg GAE/100 g) and Sanguansil et al. [76] (276.5 mg GAE/100 g FW). However, Chiveu et al. [69] observed that the red-fleshed fruits have higher phenolics content than white fleshed, but in our study, there were no such relations observed. Furthermore, the significant variation in total carotenoids (0.48–10.66 mg/100 g) and lycopene (0.59–9.97 mg/100 g) agrees with previous findings [72, 79], however higher antioxidants (20.69 µmol TE/g FW) reported in pink fleshed guava genotype Arka Kiran, indicating the genetic basis for pigmentation and antioxidants capacity in pink-fleshed genotypes; beside these pink flesh guava are preferred for processing because of their attractive pulp colour, rich total carotenoids, abundance of phytochemicals, and valuable minerals [45, 80]. The strong DPPH (85.72–98.47%) and FRAP (7.74–20.69 µmol TE/g FW) activities observed in this study are in close agreement with earlier antioxidants activity reports in guava genotypes [73, 76], highlighting the potential of specific genotypes such as Punjab Kiran, Arka Kiran, and S. Ka Hua Kula for use in breeding programs aimed at improving both fruit quality and bio-fortification of the existing guava cultivars.

Multivariate, correlation and cluster analysis

PCA is an efficient multivariate technique that clusters correlated variables into principal components to reduce data complexity and is frequently used to elucidate relationships among fruit genotypes and the correlations among traits within subsets [41, 81]. Earlier, Yousaf et al. [73] found 44.28%, 21.71%, and 12.1% variability in the total genetic variation for the first three components, respectively, across 31 traits in indigenous guava germplasm. However, Santos et al. [12] applied principal component analysis to quantify phenolics compounds in 96 guava pulps and found that two principal components explained 60% of the data variability. In the present study, first three principal components in this study accounted for 47.65% of the observed variation (Table 4). PC1 predominantly captured morphological traits, while PC2 consolidated fruit-quality and pigment attributes, underscoring the value of these trait groups for characterizing guava germplasm. Strong correlations among several traits and their principal components indicate that the number of variables needed for effective evaluation of guava germplasm could be reduced. The PCA results, therefore, provide a practical basis for breeders to select a limited set of highly diverse populations for further genotype screening [82, 83].

Presently, PCA biplot is commonly used to illustrate the distribution of genotypes and their association with different traits. In the current findings, the first two principal components together explained 37.3% of the total variation; they were sufficient to capture the major trends and associations between traits and genotypes. Consistent with the present findings, Paras et al. [79] reported a total of 74.5% variation, Verma et al. [78] recorded a total of 28.99% variation, and Chandana et al. [84] observed 34.9% of total variation contributing to the first two principal components, from 12, 18 and 31 guava genotypes, respectively. Traits related to fruit size (fruit weight, length, width, and pulp thickness) are tightly clustered together, confirming their strong positive association, as also observed in the correlation analysis, a pattern also emphasized in earlier studies by Kumari et al. [56] in guava and Kumar et al. [41] in jamun. Furthermore, lycopene content was inversely correlated with TSS, indicating a negative relationship between fruit sweetness and pigment accumulation. Genotypes such as *P. molle*, *P. pumilum*, and *P. guineense* had higher total phenolics (TPC) and total flavonoids content (TFC) but opposite to fruit size traits, implying that smaller-fruited *Psidium* genotypes are rich in secondary metabolites and antioxidants, which is congruent with the findings of Paras et al. [79] and Chandana et al. [84].

The correlation analysis revealed strong and meaningful associations among the morpho-biochemical parameters of guava genotypes, highlighting key trait linkages important for breeding and useful for characterizing the large germplasm. Positive correlation facilitates the concurrent enhancement of multiple traits, whereas negative correlation necessitates compromise among desirable characteristics [19]. In the present investigation, the fruit weight showed strong positive correlations with fruit dimensions (length, width, and pulp thickness), confirming that overall fruit size is the main contributor to higher fruit mass [85, 86]. Similarly, leaf length and width exhibited positive associations with several fruit traits, suggesting that vegetative vigour may support better fruit development. For seed traits, seed number per fruit showed a negative association with both seed width and seed hardness, but a strong positive correlation with seed weight. This suggests that fewer seeds per fruit may favour larger individual seeds, which could influence perceptions of fruit quality. These observations were aligned with previous reports on fruit quality assessment in guava germplasm [45, 46, 56, 84, 87]. Similarly, among biochemical parameters, total phenolics content was highly correlated with total flavonoids content, reflecting coordinated biosynthetic pathways for secondary metabolites [84]. Recently, Kumar et al. [41] also reported strong inter-correlation among traits like total phenols, total flavonoids, and antioxidants content in jamun. However, fruit quality traits, such as the TSS/TA ratio, were negatively correlated with titratable acidity, confirming their inverse role in determining the sweetness-acidity balance. Likewise, TSS was positively related to total sugars content and negatively to acidity, aligning with consumer preference for sweeter fruits. Pigment-related parameters showed clear interrelationships: lycopene and total carotenoids were almost perfectly correlated, and both were negatively related to the total colour difference of guava pulp, suggesting that high pigment content improves colour uniformity [88]. Further, antioxidant-related parameters showed positive associations with ascorbic acid, suggesting a synergistic effect of vitamin C on antioxidants activity. These findings are in close agreement with earlier reports on the correlation of different fruit biochemical parameters [45, 69, 73, 78].

The dendrogram analysis showed clear grouping patterns of morpho-biochemical diversity among the studied guava genotypes. The 51 guava genotypes were sorted into five major clusters, which were further divided into several clades, highlighting both similarities and differences within the germplasm. The clustering of most cultivated genotypes into three large groups suggests significant morpho-biochemical affinities, reflecting their shared ancestry, gene flow, and similar selection pressures during domestication; this finding aligns with previous research on guava and other fruit crops [70, 89]. In contrast, the two distinct small clusters demonstrate unique morpho-biochemical profiles that may serve as

useful parental sources for broadening the genetic base in breeding programs. The separation of wild species *P. pumilum*, *P. molle*, and *P. guinense* from the main guava clusters underscores their distant relationships with cultivated genotypes, reaffirming the value of wild relatives as sources of new alleles for improving fruit quality, stress tolerance, and adaptability [75, 90]. Recently, Gangappa et al. [45] found that wild species formed separate clusters, while other genotypes clustered together, indicating close phylogenetic relationships. In contrast, Kumari et al. [56] reported that all studied wild species formed a single cluster along with some cultivated guava genotypes, and only a single wild species, *P. quadrangularis*, formed a separate cluster with other cultivated genotypes. Additionally, the clustering of indigenously developed cultivars with exotic/USDA introductions indicates overlapping genetic backgrounds and shared selection for desirable traits, as observed in previous studies of guava germplasm [70, 91]. Overall, these findings provide valuable insights into the morpho-biochemical relationships among guava genotypes and related species, and also highlight the practical benefits of dendrogram-based clustering for guiding parental selection, efficient germplasm characterization, conservation, and management, and developing breeding strategies to improve varietal diversity in guava.

Conclusion

This study revealed considerable diversity in morpho-biochemical traits, such as fruit width, fruit length, pulp thickness, seed characteristics, and key biochemical components including sugars, acids, antioxidants, total carotenoids, and lycopene, across globally collected guava germplasm. Distinct guava genotypes exhibiting extreme values for desirable traits were identified; S. N90-53, Thai 7, and *Psidium* genotype 16 for large fruit size; *Psidium* genotype 16, S. N90-53, and S. HPSI41 for reduced seed count coupled with higher fruit weight; S. Ka Hua Kula, Arka Kiran, and *Psidium* genotype 7 for enrichment of total carotenoids, lycopene, and vitamin C; and wild species such as *P. molle* and *P. guineense* as potential donor parents for enhanced nutraceutical properties (phenolics and antioxidants). Collectively, these findings provide morpho-biochemical insights into globally collected guava germplasm and highlight key genotypes that may serve as a basis for developing novel guava genotypes with superior fruit quality, improved nutraceutical value, and enhanced processing traits in future breeding programs.

Abbreviations

USDA	United States Department of Agriculture
TSS	Total soluble solids
TA	Titratable acidity
TPC	Total phenolics content
TFC	Total flavonoids content
ASC	Ascorbic acid
TCD	Total colour difference
TSC	Total sugars content
DPPH	2,2-diphenyl-1-picrylhydrazyl
FRAP	Ferric reducing antioxidant potential
QE	Quercetin equivalent
GAE	Gallic acid equivalent
PC	Principal Component

Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s12870-026-08167-9.

Supplementary Material 1

Acknowledgements

The authors wish to convey their profound gratitude to the ICAR–Indian Agricultural Research Institute (IARI), New Delhi, for providing the requisite facilities and institutional support that enabled the successful completion of this research. They further extend their sincere gratitude to the Indian Council of Agricultural Research (ICAR) and the Department of Agricultural Research and Education (DARE), Government of India, for their invaluable administrative supports. The senior author gratefully acknowledges the award of the Junior Research Fellowship (JRF) by ICAR in support of the M.Sc. degree. The authors also express their deep appreciation to the USDA, Hilo, for generously providing guava germplasm, and to the ICAR-National Bureau of Plant Genetic Resources (NBPGR), New Delhi, for their efficient coordination and facilitation of the regulatory procedures.

Authors' contributions

PM, CK, AKG: Conceptualization, Visualization, Methodology, Data curation, Writing – original draft. AK, RMS, GPM, RS, SS, VSR, RRK, KP, PR: Supervision, Resources, Writing – review & editing. DR, SKS, SMK: Formal analysis, Writing – review & editing.

Funding

Not applicable.

Data availability

The data that support the findings of this study are available from the corresponding author upon reasonable request.

Declarations

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

Competing interests

The authors declare no competing interests.

Author details

[1]Division of Fruits and Horticultural Technology, ICAR-Indian Agricultural Research Institute, New Delhi 110012, India
[2]Division of Food Science & Post-Harvest Technology, ICAR-Indian Agricultural Research Institute, New Delhi 110012, India
[3]Division of Genomic Resources, ICAR- National Bureau of Plant Genetic Resources, New Delhi 110012, India
[4]Division of Genetics, ICAR-Indian Agricultural Research Institute, New Delhi 110012, India
[5]Division of Agricultural Chemicals, ICAR-Indian Agricultural Research Institute, New Delhi 110012, India
[6]Division of Forecasting & Agricultural Systems Modelling, ICAR-Indian Agricultural Statistics Research Institute, New Delhi 110012, India
[7]Division of Germplasm Exchange & Policy Unit, ICAR- National Bureau of Plant Genetic Resources, New Delhi 110012, India

[8]Horticultural Science Division, ICAR-Krishi Anusandhan Bhawan-II, New Delhi 110012, India
[9]Department of Fruit Science, Central Agricultural University, Rani Lakshmi Bai, Jhansi 284003, Uttar Pradesh, India

Received: 29 October 2025 / Accepted: 12 January 2026
Published online: 03 February 2026

References

1. Rymbai H, Reddy GS. Effect of IBA concentrations on guava stooling and plantlets survival under open and polyhouse conditions. Indian J Hortic. 2010;67:443–6.
2. Menzel CM, Paxton BF. The pattern of growth, flowering and fruiting of guava varieties in subtropical Queensland. Aust J Exp Agric. 1986;26:123–7. https://doi.org/10.1071/EA9860123.
3. Anonymous. (2024-25). India: First Advance Estimate, Area and production of horticulture crops. https://agriwelfare.gov.in/en/Hirticulture
4. Nakasone HY, Paull RE. Tropical Fruits. Wallingford: Cab International. 1998; 132–148.
5. Radha T, Mathew L, Fruit Crops. (Vol. 3). New India Publishing Agency, New Delhi, India. 2007.
6. Kumari P, Mankar A, Karuna K, Homa F, Meiramkulova K, Siddiqui MW. Mineral composition, pigments, and postharvest quality of guava cultivars commercially grown in India. J Agric Food Res. 2020;2:100061. https://doi.org/10.1016/j.jafr.2020.100061.
7. Kumar C, Kumar R, Singh SK, Goswami AK, Nagaraja A, Paliwal R, Singh R. Development of novel g-SSR markers in guava (*Psidium Guajava* L.) cv. Allahabad Safeda and their application in genetic diversity, population structure and cross-species transferability studies. PLoS ONE. 2020;15:e0237538. https://doi.org/10.1371/journal.pone.0237538.
8. Bihari M, Narayan S, Pandey AK. Path coefficient and correlation studies in guava crop (Psidium Guajava L). Progressive Hortic. 2009;41:107–9.
9. VijayaAnand A, Velayuthaprabhu S, Rengarajan RL, Sampathkumar P, Radhakrishnan R. Bioactive compounds of guava (*Psidium guajava* L.). In Bioactive Compounds in Underutilized Fruits and Nuts. 2020; 503–527.https://doi.org/10.1007/978-3-030-30182-8_37
10. Jamieson S, Wallace CE, Das N, Bhattacharyya P, Bishayee A. Guava (*Psidium Guajava* L.): a glorious plant with cancer preventive and therapeutic potential. Crit Rev Food Sci Nutr. 2022;63:192–223. https://doi.org/10.1080/10408398.2021.1945531.
11. Flores G, Wu SB, Negrin A, Kennelly EJ. Chemical composition and antioxidant activity of seven cultivars of guava (*Psidium guajava*) fruits. Food Chem. 2015;170:327–35. https://doi.org/10.1016/j.foodchem.2014.08.076.
12. Dos Santos WNL, Silva Sauthier MC, Santos AMP, Andrade Santana D, Azevedo A. & Cruz Caldas, J. Simultaneous determination of 13 phenolic bioactive compounds in guava (*Psidium Guajava* L.) by HPLC-PAD with evaluation using PCA and neural network analysis (NNA). Microchem J. 2017;133:583–92. https://doi.org/10.1016/j.microc.2017.04.029.
13. Shukla S, Kushwaha R, Singh M, Saroj R, Puranik V, Agarwal R, Kaur D. Quantification of bioactive compounds in guava at different ripening stages. Food Res. 2021;5:183–9. https://doi.org/10.26656/fr.2017.5(3).554.
14. Eze UN, Chukwuebuka VU, Maxwell O, Stanley MU. Anti-hyperglycaemic effects of *Psidium Guajava* L. crude leaf extracts and fractions in alloxan-induced diabetic mice. J Chem Nutritional Biochem. 2021;2:1–27. https://doi.org/10.48185/jcnb.v2i2.283.
15. Dinesh MR, Vasugi C. Guava improvement in India and future needs. J Hortic Sci. 2010;5:94–108. https://doi.org/10.24154/jhs.v5i2.454.
16. Rajan S, Hudedamani U. Genetic resources of guava: importance, uses and prospects. Conserv Utilization Hortic Genetic Resour. 2019;363–83. https://doi.org/10.1007/978-981-13-3669-0_11.
17. Kavino M, Sanjana U, Auxcilia J, Raveendran M. Evaluation and selection in half-sib progenies of *Psidium Guajava* aiming to identify Pink pulp with soft seed progeny. Sci Hort. 2023;315:111972. https://doi.org/10.1016/j.scienta.2023.111972.
18. Pramanik K, Goswami AK, Kumar C, Singh R, Prabha R, Jha SK, Kashyap A. Development of genome-wide SSR markers through in Silico mining of guava (*Psidium Guajava* L.) genome for genetic diversity analysis and transferability studies across species and genera. Front Plant Sci. 2025;16:1527866. https://doi.org/10.3389/fpls.2025.1527866.
19. Mehmood A, Jaskani MJ, Khan IA, Ahmad S, Ahmad R, Luo S, Ahmad NM. Genetic diversity of Pakistani guava (*Psidium Guajava* L.) germplasm and its implications for conservation and breeding. Sci Hort. 2014;172:221–32. https://doi.org/10.1016/j.scienta.2014.04.005.
20. Rajan S, Misra AK, Ravishankar H. Guava Descriptor. Lucknow: AICRP (STF), CISH. 2011; 19 p.
21. Fernandes-Santos CA, Cunha-Castro JM, Franca-Souza F, Alcantara-Vilarinho A, Ferreira FR, Gomes-Padua J, Estigarribia-Borges RM, Barbieri RL, de Claret ADG, Amorim-Rodrigues M. Prospecting and morphological characterization of Brazilian *Psidium* germplasm. Acta Hort. 2010;849:63–8. https://doi.org/10.17660/ActaHortic.2010.849.6.
22. Thakur S, Yadav IS, Jindal M, Sharma PK, Dhillon GS, Boora RS, Mittal A. Development of genome-wide functional markers using draft genome assembly of guava (*Psidium Guajava* L.) cv. Allahabad Safeda to expedite molecular breeding. Front Plant Sci. 2021;12. https://doi.org/10.3389/fpls.2021.708332.
23. Sharma S, Kumari R, Prasad H, Walia A, Kumar R, Dobhal S. Characterization of guava (*Psidium Guajava* L.) germplasm through morphological traits and scot markers. J Hortic Sci Biotechnol. 2023;98:374–83. https://doi.org/10.1080/14620316.2022.2139767.
24. El-Tody G, Khalid A, Elwakil H, Abdelsalam N. Genetic description of acacia species based on different markers. J Adv Agricultural Researches. 2014;19:82–99. https://doi.org/10.21608/jalexu.2014.160312.
25. Sadia B, Awan FS, Saleem F, Altaf J, Umar AB, Nadeem M, Nasir M. Exploring plant genetic variations with morphometric and molecular markers. In Genetic variation. IntechOpen, 2021. https://doi.org/10.5772/intechopen.95026
26. PPV & FRA. Guidelines for the conduct of test for Distinctiveness, uniformity and stability on guava (Psidium Guajava L.). Government of India, New Delhi.
27. Lekshmi SG, Sethi S, Asrey R, Singh KP, Kumar R, Sindhu PM, Goswami. A. K. Comprehensive characterization of biodegradable edible films activated with Rose and marigold extracts and application of active edible coatings to extend the postharvest storage life of guava. Food Res Int. 2025;203:115895. https://doi.org/10.1016/j.foodres.2025.115895.
28. AOAC Official Method. 947.05. Titrimetric method. Rockville, MD, USA: AOAC International; 2000.
29. Singleton VL, Orthofer R, Lamuela-Raventós RM. Analysis of total phenols and other oxidation substrates and antioxidants by means of Folin-Ciocalteu reagent. In methods in enzymology. Acad Press. 1999;299:152–78. https://doi.org/10.1016/S0076-6879(99)99017-1.
30. Zhishen J, Mengcheng T, Jianming W. The determination of flavonoid contents in mulberry and their scavenging effects on superoxide radicals. Food Chem. 1999;64:555–9. https://doi.org/10.1016/S0308-8146(98)00102-2.
31. AOAC Official Method 967.21. Ascorbic acid in vitamin preparations and juices. Rockville, MD, USA: AOAC International; 2000.
32. Brand-Williams W, Cuvelier ME, Berset CL. W. T. Use of a free radical method to evaluate antioxidant activity. LWT-Food Sci Technol. 1995;28:25–30. https://doi.org/10.1016/S0023-6438(95)80008-5.
33. Benzie IF, Strain JJ. The ferric reducing ability of plasma (FRAP) as a measure of antioxidant power: the FRAP assay. Anal Biochem. 1996;239:70–6. https://doi.org/10.1006/abio.1996.0292.
34. AOAC. (2000) Official and tentative methods of analytical chemists, Washington, D.C., USA, 17th Edition.
35. Prasad K, Singh G, Singh SK, Pradhan J, Kumar U, Singh H. Plant extract and essential oil coating prolongs shelf life and maintains keeping quality of Papaya fruit during storage. J Food Process Preservation. 2022;46:e17015. https://doi.org/10.1111/jfpp.17015.
36. Pasupuleti V, Kulkarni SG. Lycopene fortification on the quality characteristics of beverage formulations developed from Pink flesh guava (*Psidium Guajava* L). J Food Sci Technol. 2014;51:4126–31. https://doi.org/10.1007/s13197-013-0932-z.
37. Akter MK, Motalab M, Zubair MA, Haque MZ, Saha BK, Mumtaz B. Isolation and quantification of lycopene and determination of B-carotene and total phenolic contents from tomato (*Lycopersicum esculentum*) by using various methods. Int J Food Sci Nutr Dietetics. 2020;442–7. https://doi.org/10.19070/2326-3350-2000079.
38. Lane JH, Eynon J. Determination of reducing and total sugars by fehling's solution with methylene blue as indicator. J Soc Chem Ind. 1923;42:32–7.
39. SAS® Procedures. Version 6. 3rd ed. Cary, NC: SAS Institute; 1990.
40. Wu J, Zhang C, Chen J, Cai C, Wang L, Fu D, Ou L. Morphological diversity within Litchi (*Litchi chinensis* Sonn.) based on leaf and branch traits. Sci Hort. 2016;207:21–7. https://doi.org/10.1016/j.scienta.2016.05.004.

41. Kumar A, Singh K, Prakash J, Goswami AK, Patel VB, Ingole AD, Singh AK. Multivariate assessment of morpho-biochemical and bioactive diversity in *Syzygium cumini* (L.) Skeels for the selection of superior genotype and breeding applications. BMC Plant Biol. 2025;25962. https://doi.org/10.1186/s12870-025-06977-x.
42. Kaur J, Singh Z, Mazhar MS, Afrifa-Yamoah E, Woodward A. Variability in fruit quality traits of tropical Australian jackfruit (*Artocarpus heterophyllus* Lam.) genotypes. Sci Hort. 2024;338:113771. https://doi.org/10.1016/j.scienta.2024.113771.
43. Krishna H, Singh D, Singh RS, Kumar L, Sharma BD, Saroj PL. Morphological and antioxidant characteristics of mulberry (*Morus* spp.) genotypes. J Saudi Soc Agricultural Sci. 2020;19:136–45. https://doi.org/10.1016/j.jssas.2018.08.002.
44. Tunç Y, Aydınlıoğlu C, Yılmaz KU, Khadivi A, Mishra DS, Sakar EH, Vyhnánek T. Determination of genetic diversity in persimmon accessions using morphological and inter simple sequence repeat markers. Sci Rep. 2025;15:2297. https://doi.org/10.1038/s41598-025-86101-z.
45. Gangappa ND, Singh C, Verma MK, Thakre M, Sevanthi AM, Singh R, Nagaraja A. Assessing the genetic diversity of guava germplasm characterized by Morpho biochemical traits. Front Nutr. 2022;9:1017680. https://doi.org/10.3389/fnut.2022.1017680.
46. Sarkar T, Sarkar SK. Genetic diversity analysis of guava (*Psidium Guajava* L) genotypes in West Bengal, India. J Appl Hortic. 2022;24:381–7. https://doi.org/10.37855/jah.2022.v24i03.69.
47. Krause W, Ramos Cavalcante N, PioViana A, Ambrosio M, Azevedo Santos E, Duarte Vieira H. Genetic variability in inbred guava families mediated by agronomic traits. Funct Plant Breed J. 2021;3:2. https://doi.org/10.35418/2526-4117/v3n2a5.
48. Nimisha S, Kherwar D, Ajay KM, Singh B, Usha K. (2013). Molecular breeding to improve guava (*Psidium guajava* L.): current status and future prospective. Scientia Horticulturae. 2013; 164, 578–588.https://doi.org/10.1016/j.scienta.2013.10.017
49. Dinesh MR, Iyer CP. A. Significant research achievement in guava—improvement and future needs. In Souvenir 1st International Guava Symposium. Lucknow, India. 2005; (pp. 7–16).
50. Rajore M, Kanwar J, Rathore GPS, Kachouli B. Evaluation of guava (Psidium Guajava L.) cultivars for morphological, yield and quality attributes under Malwa plateau conditions. J Pharmacognosy Phytochemistry. 2021;10:483–5.
51. Ran S, Sharma JR, Jakhar MS. Assessment of genetic diversity and diversity relationship in different varieties of guava using morphological characterization. Plant Archives. 2017;17:307–11.
52. Patel RK, Maiti CS, Deka BC, Deshmukh NA, Roy D. Variability studies in guava (Psidium Guajava L.) genotypes for Growth, yield and quality attributes at mid-hills of Meghalaya. Indian J Hill Farming. 2011;24(12):24–8.
53. Hernandez-Delgado S, Padilla-Ramirez JS, Nava-Cedillo A, Mayek-Perez N. Morphological and genetic diversity of Mexican guava germplasm. Plant Genetic Resour. 2007;5:131–41. https://doi.org/10.1017/S1479262107827055.
54. Mani A, Mishra R, Thomas G. Elucidation of diversity among Psidium species using morphological and SPAR methods. Journal of phytology. 2011; 3(8).
55. Kidaha LM, Alakonya AE, NyendeA B. Morphological characters of guava landraces in Western and coastal Kenya. Am J Experimental Agric. 2015;9:1–11. https://doi.org/10.9734/AJEA/2015/12674.
56. Kumari S, Nagaraja A, Singh R, Srivastav M, Banoth S, Mithra AC, Arun MB, Goswami AK, Khan YJ. Diversity analysis of guava (*Psidium guajava*) germplasm collection. Indian J Agric Sci. 2018;88:489–97. https://doi.org/10.56093/ijas.v88i3.78740.
57. Daulta BS, Godara NR, Bhatia SK, Singh HK. and S. S. Bisla. New guava hybrids hisar Safeda and hisar Surkha. Indian Hortic. 1998; 22–3.
58. Nikhil, H. N., Goswami, A. K., Singh, S. K., Kumar, C., Goswami, S., Singh, R., … Maurya, N. K. Assessment of morpho-genetic diversity of guava (*Psidium guajava*) hybrids and genotypes. The Indian Journal of Agricultural Sciences. 2021; 91, 1640–1645.https://doi.org/10.56093/ijas.v91i11.118576.
59. Gethe AS, Patil SD, Magar SD, Jadhav SB, Kshirsagar DB. Morphological characterization of different guava genotypes based on leaf and fruit parameters. Int J Adv Biochem Res. 2024;8:538–44. https://doi.org/10.33545/26174693.2024.v8.i11g.2879.
60. Shiva B, Nagaraja A, Srivastav M, Kumari S, Goswami AK, Singh R, Arun MB. Characterization of guava (*Psidium guajava*) germplasm based on leaf and fruit parameters. Indian J Agric Sci. 2017;87:634–8. https://doi.org/10.56093/ijas.v87i5.70172.
61. Sohi HS, Gill MIS, Singh D, Arora NK. Characterization of F1 hybrids of guava (Psidium Guajava L.) on the basis of phenotypic and biochemical parameters. Chem Sci Rev Lett. 2019;8:335–9.
62. Nogueira AM, Ferreira A, Ferreira MFS, Mangaravite E. Preliminary study of wild guava from Espírito Santo and Minas Gerais by continuous descriptors. Acta Hort. 2012;959:35–40. https://doi.org/10.17660/ActaHortic.2012.959.3.
63. Singh BK, Singh S, Pal AK. Morphological chemical attributes of guava (Psidium Guajava L.) cultivars. Indian Hortic J. 2014;4:2249–6823.
64. Agarwala P, Gaurb PK, Tyagia N, Purib D, Kumar N, Kumard SS. An overview of phytochemical, therapeutic, Pharmacological and traditional importance of syzygium cumini. Asian J Pharmacognosy. 2019;3:5–17.
65. Methela NJ, Faruk O, Islam MS, Hossain MM. (2019). Morphological characterization of guava germplasm (*Psidium* sp.). Journal of Bioscience and Agriculture Research. 2019; 20, 1671–1680.https://doi.org/10.18801/jbar.200119.203
66. Rajan S, Yadava LP, Kumar R, Saxena SK. Direct and indirect effects of seed related characters on number of seed in guava (*Psidium Guajava* L.) fruits. Sci Hort. 2008;116:47–51. https://doi.org/10.1016/j.scienta.2007.10.024.
67. Jana BR, Munsi PS, Manna DC, Das B. Evaluation of guava (*Psidium Guajava* L.) genotypes based on fruit morphology, physico-chemical properties and yield under Eastern plateau condition. Indian J Plant Genetic Resour. 2010;23:25–9. https://ispgr.in/index.php/ijpgr/article/view/1614.
68. Corrêa LC, Santos CAF, Lima GPP. Chemical and biochemical characterization of guava and araca fruits from different regions of Brazil. In III International Symposium on Guava and other Myrtaceae. 2012; 959(pp. 103–109).https://doi.org/10.17660/ActaHortic.2012.959.12
69. Chiveu J, Naumann M, Kehlenbeck K, Pawelzik E. Variation in fruit chemical and mineral composition of Kenyan guava (*Psidium Guajava* L.): inferences from Climatic conditions, and fruit morphological traits. J Appl Bot Food Qual. 2019;92. https://doi.org/10.5073/JABFQ.2019.092.021.
70. Singh DS, Gill MIS, Boora RS, Arora NK. Genetic diversity analysis in guava (*Psidium guajava*) on the basis of morphological and physico-chemical traits. Indian J Agricultural Sci. 2015;85:717–22. https://doi.org/10.56093/ijas.v85i5.48504.
71. Parveen C, Jitarwal OP, Deepak S, Baloda S. Bio-Chemical characterization of guava cultivar's under Semi-Arid ecosystem of Haryana. Int J Hortic Crop Sci Res. 2023;1941–6. https://doi.org/10.60151/envec/FZGJ1225.
72. Dhruv PNK, Patel JJ, M. J., Patel HR. Nutritional characterization of guava (*Psidium Guajava* L.) under middle Gujarat condition. Indian J Agricultural Biochem. 2021;34:96–101. https://doi.org/10.5958/0974-4479.2021.00013.7.
73. Yousaf AA, Abbasi KS, Ahmad A, Hassan I, Sohail A, Qayyum A, Akram MA. Physico-chemical and nutraceutical characterization of selected Indigenous guava (*Psidium Guajava* L.) cultivars. Food Sci Technol. 2020;41:47–58. https://doi.org/10.1590/fst.35319.
74. Ravi GK, Jholgiker P, Thippanna KS, Kumar BP, Pattepur S. Evaluation of red fleshed guava (*Psidium Guajava* L.) varieties for their processing potential. Int J Curr Microbiol Appl Sci. 2023;7:3475–83. https://doi.org/10.20546/ijcmas.2018.711.397.
75. Vishwakarma PK, Vasugi C, Shivashankara KS. Morpho-biochemical characterization of psidium species. J Hortic Sci. 2023;18(2). https://doi.org/10.24154/jhs.v18i2.1435.
76. Sanguansil S, Boonprakob U, Thaipong K. Quantification of antioxidant content in fruit of guava germplasm. In International Symposium on Tropical and Subtropical Fruits. 2011; 1024(pp. 385–390).https://doi.org/10.17660/ActaHortic.2014.1024.53
77. Mishra DS, Berwal MK, Singh Anshuman, Singh AK, Appa Rao VV, Yadav V, Sharma BD. Phenotypic diversity for fruit quality traits and bioactive compounds in red-fleshed guava: insights from multivariate analyses and machine learning algorithms. South Afr J Bot. 2022;149:591–603. https://doi.org/10.1016/j.sajb.2022.06.
78. Verma, V. K., Rymbai, H., Deshmukh, N. A., Bhattacharjee, B., Jha, A. K., Patel,R. K., … Mishra, V. K. (2024). Genetic diversity and stability analysis of the improved cultivars of guava and their related species. Scientia Horticulturae. 2024; 333, 113260.https://doi.org/10.1016/j.scienta.2024.113260.
79. Paras, Kaur K, Kaur G, Singh D, Brar JS. (2024). Heritability and Principal Component Analysis of Phytochemical Traits in Guava under Indian Subtropics. Applied Fruit Science. 2024; 66, 193–202.https://doi.org/10.1007/s10341-023-01012-5
80. Duke GO, George OA, Michael WO, Charles KG, Agnes WM. Physico-chemical and processing qualities of guava varieties in Kenya. Int J Fruit Sci. 2022;22:329–45. https://doi.org/10.1080/15538362.2022.2039342.

81. Ruiz D, Egea J. Phenotypic diversity and relationships of fruit quality traits in apricot (*Prunus Armeniaca* L.) germplasm. Euphytica. 2008;163:143–58. https://doi.org/10.1007/s10681-007-9640-y.
82. Iezzoni AF, Pritts MP. Applications of principal component analysis to horticultural research. HortScience. 1991;26:334–8. https://doi.org/10.21273/HORTSCI.26.4.334.
83. Kumar, C., Singh, S. K., Pramanick, K. K., Verma, M. K., Srivastav, M., Singh, R.,… Naga, K. C. Morphological and biochemical diversity among the *Malus* species including indigenous Himalayan wild apples. Scientia Horticulturae. 2018;*233*, 204–219.https://doi.org/10.1016/j.scienta.2018.01.037.
84. Chandana MR, Goswami AK, Rana VS, Kumar C, Singh SK, Goswami S, Sushravya MK. Unravelling the physicochemical and antioxidant profiles of guava genotypes across developmental stages and seasonality. Food Bioscience. 2025;71(107097). https://doi.org/10.1016/j.fbio.2025.107097.
85. Raghava M, Tiwari JP. Genetic variability and correlation analysis in guava. Indian J Hortic. 2008;65:263–70.
86. Bihari M, Suryanarayan S. Genetic diversity, heritability, genetic advance and correlation coefficient in guava (*Psidium guajava*). Indian J Agricultural Sci. 2011;81:107–10. https://epubs.icar.org.in/index.php/IJAgS/article/view/3986.
87. Gupta N, Kour A. Genetic parameters, character association and path analysis for fruit yield and its component characters in guava (*Psidium Guajava* L). Electron J Plant Breed. 2019;256–63. https://doi.org/10.5958/0975-928X.2019.00030.9.
88. Pandurangaiah S, Sadashiva AT, Shivashankar KS, Sudhakar Rao DV, Ravishankar KV. Carotenoid content in Cherry tomatoes correlated to the color space values l*, a*, b*: A non-destructive method of Estimation. J Hortic Sci. 2020;15:27–34. https://doi.org/10.24154/jhs.v15i1.779.
89. Sharma A, Sehrawat SK, Singhrot RS, Tele A. Morphological and chemical characterization of *Psidium* species. Notulae Botanicae Horti Agrobotanici Cluj-Napoca. 2010;38:28–32. https://doi.org/10.15835/nbha3813569.
90. Vishwakarma PK, Vasugi C, Umamaheswari R, Sriram S, Nandeesha P, Sankaran M, Shivashankara KS. Screening of *Psidium* species and their interspecific hybrid progenies for resistance to *Fusarium oxysporum* f. sp. *psidii* and Southern root-knot nematode. South Afr J Bot. 2023;155:249–60. https://doi.org/10.1016/j.sajb.2023.02.027.
91. Sitther V, Zhang D, Harris DL, Yadav AK, Zee FT, Meinhardt LW, Dhekney SA. (2014). Genetic characterization of guava (*Psidium guajava* L.) germplasm in the United States using microsatellite markers. Genetic Resources and Crop Evolution. 2014; 61, 829–839.https://doi.org/10.1007/s10722-014-0078-5

Publisher's Note

Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.