Heliyon 10 (2024) e26525

Contents lists available at ScienceDirect

Heliyon

journal homepage: www.cell.com/heliyon

Research article

Diversity in morpho-pomological attributes and biochemical profiling of bael (*Aegle marmelos* (L.) Correa) genotypes of North-Western India

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ARTICLE INFO

Keywords:
Bael
Morpho-pomological and biochemical traits
Diversity
Breeding

ABSTRACT

Bael is a medicinal cum fruit tree with multipurpose utility and propagated mostly through seeds. The present study aimed to assess and analyse the morpho-pomological and biochemical traits of eighty seedlings grown bael genotypes comparison with two commercial cultivars (NB-5 and NB-9) of bael. The significant differences were detected among the genotypes based on the measured morpho-pomological and biochemical traits. The morpho-pomological and biochemical traits of bael exhibited variation ranging from 6.17% to 133.65%. Trunk girth ranged from 29.50 to 63.40 cm and tree spread (N–S) varied 1.00–6.30 m. Fruit length ranged from 4.60 to 12.05 cm and fruit width ranged from 4.64 to 11.72 cm. Moreover, fruit weight ranged from 56.33 to 917.65 g and pulp percentage varied from 58.64 to 81.38%. Soluble Solid Content ranged from 25.90 to 36.77 ^{0}brix and ascorbic acid varied from 14.38 to 25.45 mg/100 g. Fruit length was positively correlated with fruit width, fruit weight, pulp percentage, seed length, seed diameter and number of seeds per fruit, while it was negatively correlated with fruit surface and total number of fruit per plant. Principal component analysis showed that 76.66% of the variability observed was explained by the 13 components. Ward cluster analysis using Euclidean distance classified the genotypes into two main clusters. These findings contribute to a better understanding of the diversity and relationships among the studied genotypes, aiding future breeding and selection programs for improved bael cultivation.

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https://doi.org/10.1016/j.heliyon.2024.e26525
Received 9 October 2023; Received in revised form 23 January 2024; Accepted 14 February 2024
Available online 15 February 2024
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1. Introduction

Underutilized fruits mostly found rural areas and in forests in particular under developed countries and they have an important biodiversity sources due to seed propagation characteristics. They are rich for human health promoting substances including non-nutritive, nutritive, and bioactive compounds such as flavonoids, phenolics, anthocyanins, phenolic acids, and as well as nutritive compounds such as sugars, essential oils, carotenoids, vitamins, and minerals. They also have perfect flavor and excellent medicinal value [1–4]. Bael (*Aegle marmelos* (L.) Correa), a member of the Rutaceae family, is an important underutilized fruit crop in India, known for its medicinal and nutritional value [5]. It predominantly thrives in tropical and subtropical regions [6]. Bael has a wide range of adaptability to hostile soil and environment [7]. Temperature tolerances range from −7 to 50 °C and it grows well in alkaline, stony, and shallow soils [8].

Bael is well-suited for regions with limited water resources and is a rich source of essential vitamins and minerals. In today's global market, there is a growing demand for functional foods and natural antioxidants and bael can play a significant role in the development of functional food products [9]. Numerous value-added products, including squash, murabba, fruit slabs, toffees, powders, and jams, are prepared from bael [10]. The ripe pulp of good quality bael cultivars and the "sherbat" made from it are valued for their mild laxative, tonic, digestive and restorative properties, as well as their effectiveness in treating biliousness. Green, unripe bael fruits are commonly used to prepare "murabba", a preserve known for its digestive benefits. In India, a popular beverage referred to as "sherbat" is created by blending seeded bael pulp with milk or water and sugar [11]. In general, the fruits of bael are not consumed as dessert fruit because of its astringent taste, presence of numerous seeds embedded in mucilage and fibre content. However, the fruit pulp contains marmelosin which is restorative, astringent, and laxative properties [8]. Therefore, the bael fruit has great potential for pharmaceutical and processing industries. Morpho-pomological and biochemical profiling is a suitable method to identify the genetic diversity, germplasm conservation and agronomic traits of endangered plants and commercial crops to evaluate the germplasm for future breeding programme. Morpho-pomological characters are one of the most decisive factors for taxonomic classification and for assessing the genetic diversity of the germplasm.

In the present investigation, efforts were made to analyse the morpho-pomological and biochemical diversity among the seedling grown bael genotypes. The Jammu, Samba and Kathua districts of Jammu region exhibit a wide distribution of seedling bael genotypes particularly in dry, undulating, forest and tribal areas which provides a tremendous scope and potential for cultivation of this fruit. This has created the necessity to breed new high yielding varieties. To enhance variety quality in all aspects, the presence of genetic variability within a population is essential for the planning and execution of effective crop improvement programs. Greater variability in crop plants offers an opportunity to select desirable types which may fulfill the needs of the growers. Since, they are all of seedling origin, they have acquired a high level of variability in them. Hence, the documentation and conservation of this groove is important. There is an urgent need to study and analyse the amount of genetic variability present in it and its utilization in crop improvement will be of great significance for formulating an effective breeding strategy for its genetic improvement.

2. Materials and methods

2.1. Plant materials

In the present investigation, a total of eighty bael genotypes originating from seedlings, along with two commercially cultivated varieties known as NB-5 and NB-9 were selected from major bael growing districts of Jammu, Samba and Kathua in the Jammu province of Jammu and Kashmir Union territory in India. Jammu, situated at coordinates 32.73°N 74.87°E, has an average elevation of 300 m (980 feet). Samba, located at coordinates 32.57°N 75.12°E, has an average elevation of 384 m (1259 feet). Kathua, situated at coordinates 32.37°N 75.52°E, has an average elevation of 393 m (1289 feet). The objective of the survey was to identify promising accession among a diverse range of seedling bael genotypes and evaluate the variability in their morpho-pomological and biochemical traits.

2.2. Morpho-pomological and biochemical characterization

For measuring morpho-pomological and biochemical traits, 10 randomly selected flowers, 10 leaves and 5 fruits were taken from each replication and they were collected randomly from 3 different direction of the tree and each direction were considered as one replication.

Trunk girth of bael genotypes was measured at 50 cm above ground level using measuring tape. Tree spread was measured as canopy diameter (average North - South dimensions) during active growth period using measuring tape. Internodal distance of the stem between two successive nodes was measured by measuring scale during active growth period. A total of ten shoots were tagged on each selected tree, with an even distribution of shoots in three different directions and the variable include flower length, flower width, pedicel length, pedicel width, anther length, anther width, ovary length, ovary width measure with help of digital vernier caliper. Leaf length was recorded from petiole base to lamina tip and leaf width was recorded at the widest point and average of 10 fully developed leaves taken from plant and both measure with help of digital vernier caliper and expressed in cm. The fruit length was measured from the base of the fruit to the top of the groove at the calyx end and fruit width taken at the centre of the fruit and both measure with the help of digital vernier caliper and expressed in cm. Fruit weight measured at the harvesting time and mean weight was calculated in grams by using digital electronic balance with 0.01 g precision. The pulp per cent was calculated from the pulp extracted from tagged fruits and the pulp (%) was calculated with the help of the formula: pulp (%) = Pulp weight of the fruit × 100 divided by total weight of

fruit. The shell per cent was calculated by separating the shell of tagged fruits and calculated with the help of the formula: Shell (%) = Shell weight of the fruit × 100 divided by total weight of fruit. Seed length measured from the base to the tip and seed diameter measured at the widest point using digital vernier caliper. Total numbers of seeds per fruit were counted manually and average value was calculated and expressed in numbers. Test seed weight per fruit measured dried hundred seeds weight weighed on digital electronic balance with 0.01 g precision and the average value was calculated and expressed in grams (g). Total no. of fruit/plant measured at the time of harvesting all the fruits were counted manually.

The observations on inflorescence, leaf colour, lateral leaflet shape, leaf surface, leaf margin, mature fruit colour, fruit surface, fruit shape, arrangement of seed in pulp, seed shape, pulp taste, pulp acridity was recorded as per Guidelines for the Conduct of Test for Distinctiveness, Uniformity and Stability of bael (*Aegle marmelos* Correa) Protection of Plant Varieties and Farmers Right's Authority (PPV&FRA) Government of India [12] and bael descriptor of National Bureau of Plant Genetic Resources [13].

The Soluble solid content (SSC) of the pulp was determined by extracting 20 g of fruit pulp and blending it for 3 min. Afterward, the mixture was wrapped in cheesecloth, hand-squeezed and then expressing juice used for measuring SSC in degrees Brix using a digital refractometer (0–53 °Brix) (pocket PAL-1 ATAGO Corporation, Tokyo, Japan). In addition, titratable acidity (%) was measured by titrating 2 ml of bael fruit juice against a standardized N/10 Sodium Hydroxide (NaOH) solution, using phenolphthalein dye (two drops) as an indicator until an end point was reached (indicated by the persistence of a light pink color for at least 2 s) and expressed as a percentage of citric acid [14]. SSC:acidity ratio was calculated as the ratio of the percentage of Soluble solid content to the percentage of total acid. Ascorbic acid content (Vitamin C) was determined from bael pulp using the 2,6-dichlorophenol indophenols dye (DCPIP) visual titration assay, which involves a reduction reaction. In brief, 5 g of the fruit sample were ground with approximately 25 ml of 4% oxalic acid. The filtrate solution was passed through Whatman No. 4 filter paper and collected in a 50 ml volumetric flask. This resulting solution was titrated against a standard dye until a rose pink color persisted for 5 s and the amount of ascorbic acid was expressed as mg/100 g [14].

2.3. Statistical analysis

The data collected for various characteristics were grouped and subjected to statistical analysis. Descriptive statistics, including minimum and maximum values, mean, standard error (SEM), standard deviation (SD), skewness, kurtosis and coefficient of variation (CV%) were computed for the measured traits. The variance for all the characteristics was assessed using statistical analysis software [15]. Correlations between the traits were determined by pearson correlation coefficients with OriginPro 9.1 software. Relationships between the genotypes were investigated by principal component analysis (PCA) with OriginPro 9.1 software. For cluster analysis, a distance matrix was generated from the phenotypic data and analyzed using the Ward method to better understand the variability patterns among the bael genotypes using OriginPro 9.1 software. In addition, a scatter plot was created according to the PC1 and PC2 using OriginPro 9.1 software.

3. Results and discussion

3.1. Morpho-pomological and biochemical description

Based on analysis of variance, most of the studied bael genotypes showed high variability for most of the traits. The highest coefficient of variation (CV in %) was obtained for leaf surface (133.65) followed by pulp acridity (132.47), fruit surface (113.35) and fruit weight (64.24) while, lowest found in anther length (6.17) (Table 1). In general, a coefficient of variation greater than 10% indicates significant variation in a trait among different germplasm individuals [16]. These results indicated that 35 out of 39 morpho-pomological and biochemical traits, the variation coefficient of the was more than 10% found in trunk girth, tree spread (n-s), internodal distance, inflorescence, flower length, flower width, pedicel length, anther width, ovary length, ovary width, leaf length, leaf width, leaf colour, lateral leaflet shape, leaf surface, leaf margin, fruit length, fruit width, fruit weight, shell percentage, seed length, seed diameter, number of seeds per fruit, test seed weight per fruit, total number of fruit/plant, mature fruit colour, fruit surface, fruit shape, arrangement of seed in pulp, seed shape, pulp taste, pulp acridity, titratable acidity, SSC:acidity, ascorbic acid. The coefficient of variation of 4 morpho-pomological and biochemical traits, pedicel width, anther length, pulp percentage and SSC of pulp were less than 10%, means the genetic performance was relatively stable. The morpho-pomological and biochemical traits of bael exhibited variation ranging from 6.17% to 133.65%, indicating a wide diversity among the individual samples and implied that there was a high breeding potential within bael population studied. These studies are confirmative with fruit crops *viz*., Bael [17,18]; Calamansi [19].

To further analyse the genetic divergence among genotypes, skewness and kurtosis were also calculated. The highest positive skewness was recorded for the traits *viz*., arrangement of seed in pulp (6.28) followed by leaf surface (3.02) and internodal distance (1.45) whereas, highest negative skewness was recorded for leaf margin (−1.57) followed by seed shape (−0.86), trunk girth (−0.79) and SSC pulp (−0.79). Kurtosis indicates the weight of the tails of a distribution and highest platykurtic distribution (positive) pattern was recorded for the traits *viz*., arrangement of seed in pulp (38.40) followed by leaf surface (7.32) and internodal distance (1.63). The highest leptokurtic distribution (negative) was recorded for the traits *viz*., lateral leaflet shape (−1.96) followed by pulp acridity (−1.72) and leaf colour (−1.61) (Table 1). The positive skewness (tree spread, intermodal distance, inflorescence, flower width, pedicel width, anther length, ovary width, leaf length, leaf width, lateral leaflet shape, leaf surface, fruit weight, seed length, number of seeds per fruit, test seed weight per fruit, total number of fruit/plant, fruit surface, arrangement of seed in pulp, pulp taste, pulp acridity, titratable acidity and ascorbic acid) is associated with complementary gene interactions while negative skewness (trunk girth,

Table 1
Descriptive statistics for morpho-pomological and biochemical traits among the studied bael genotypes.

S. No.	Trait	Abbreviation	Unit	Min.	Max.	Mean	SEM	SD	Skewness	Kurtosis	CV (%)
1.	Trunk girth	TrGi	cm	29.50	63.40	52.15	0.81	7.38	−0.79	0.08	14.14
2.	Tree spread (N–S)	TrSp	m	1.00	6.30	3.02	0.14	1.23	0.50	−0.19	40.57
3.	Internodal distance	InDi	cm	1.90	7.00	3.19	0.12	1.12	1.45	1.63	35.27
4.	Inflorescence	In	Code	1.00	9.00	4.29	0.19	1.70	0.76	1.23	39.68
5.	Flower length	FlLe	mm	12.35	18.73	15.81	0.19	1.73	−0.14	−0.98	10.95
6.	Flower width	FlWi	mm	24.16	36.55	29.96	0.34	3.08	0.04	−0.84	10.30
7.	Pedicel length	PeLe	mm	5.18	9.38	7.40	0.13	1.16	−0.18	−1.02	15.62
8.	Pedicel width	PeWi	mm	2.02	2.58	2.25	0.02	0.15	0.26	−1.02	6.59
9.	Anther length	AnLe	mm	3.29	4.41	3.81	0.03	0.24	0.69	0.00	6.17
10.	Anther width	AnWi	mm	0.50	0.83	0.67	0.01	0.08	−0.04	−0.88	12.44
11.	Ovary length	OvLe	mm	4.25	7.71	6.31	0.09	0.83	−0.46	−0.63	13.21
12.	Ovary width	Ovwi	mm	3.34	4.87	3.92	0.04	0.40	1.04	0.07	10.31
13.	Leaf length	LeLe	cm	3.03	17.63	9.72	0.29	2.63	0.27	0.65	27.01
14.	leaf width	LeWi	cm	1.10	8.67	5.08	0.18	1.59	0.02	−0.41	31.35
15.	Leaf colour	LeCo	Code	3.00	7.00	5.20	0.19	1.71	−0.19	−1.61	32.92
16.	Lateral leaflet shape	LaLeSh	Code	5.00	7.00	5.85	0.11	1.00	0.30	−1.96	17.00
17.	Leaf surface	LeSu	Code	1.00	9.00	1.68	0.25	2.25	3.02	7.32	133.65
18.	Leaf margin	LeMa	Code	3.00	7.00	6.22	0.18	1.59	−1.57	0.47	25.64
19.	Fruit length	FrLe	cm	4.60	12.05	8.29	0.19	1.76	−0.17	−0.85	21.26
20.	Fruit width	FrWi	cm	4.64	11.72	8.01	0.20	1.80	−0.03	−1.07	22.40
21.	Fruit weight	FrWe	g	56.33	917.65	366.51	26.00	235.46	0.63	−0.54	64.24
22.	Pulp percentage	PuPe	%	58.64	81.38	69.07	0.61	5.52	−0.10	−0.75	7.98
23.	Shell percentage	ShPe	%	16.96	30.18	23.38	0.35	3.15	−0.20	−0.91	13.48
24.	Seed length	SeLe	mm	3.70	10.68	6.88	0.15	1.37	0.28	0.05	19.92
25.	Seed diameter	SeDi	mm	2.48	7.12	5.26	0.12	1.04	−0.62	−0.32	19.83
26.	Number of seeds per fruit	NuSeFr	number	23.33	182.33	96.70	4.38	39.66	0.17	−0.97	41.02
27.	Test seed weight per fruit	TeSeWe	g/100 seeds	14.47	25.65	19.72	0.26	2.36	0.17	0.04	11.96
28.	Total number of fruit/plant	TNFP	number	22.00	130.00	48.46	2.17	19.62	1.30	2.65	40.48
29.	Mature fruit colour	MaFrCo	Code	3.00	7.00	4.95	0.12	1.09	−0.02	0.52	21.97
30.	Fruit surface	FrSu	Code	1.00	9.00	3.15	0.39	3.57	1.07	−0.89	113.35
31.	Fruit Shape	FrSh	Code	1.00	9.00	6.00	0.39	3.53	−0.48	−1.59	58.85
32.	Arrangement of seed in pulp	ArSePu	Code	1.00	2.00	1.02	0.02	0.16	6.28	38.40	15.15
33.	Seed shape	SeSh	Code	3.00	7.00	5.78	0.20	1.85	−0.86	−1.29	32.05
34.	Pulp taste	PuTa	Code	3.00	7.00	4.56	0.15	1.37	0.31	−0.84	30.05
35.	Pulp acridity	PuAc	Code	0.00	1.00	0.37	0.05	0.48	0.57	−1.72	132.47
36.	Soluble solid content	SoSoCo	^{0}brix	25.90	36.77	32.89	0.31	2.78	−0.79	0.25	8.44
37.	Titratable acidity	TiAc	%	0.20	0.33	0.25	0.00	0.03	0.52	−0.49	11.66
38.	SSC:acidity	SsAc	ratio	78.48	183.85	132.51	2.67	24.19	−0.18	−0.48	18.26
39.	Ascorbic acid	AsAc	mg/100 g	14.38	25.45	18.76	0.32	2.89	0.55	−0.60	15.43

flower length, pedicel length, anther width, ovary length, leaf colour, leaf margin, fruit length, fruit width, pulp percentage, shell percentage, seed diameter, mature fruit colour, fruit shape, seed shape, SSC pulp and SSC:acidity) is associated with duplicate (additive x additive) gene interactions [20]. Negative (tree spread (n-s), flower length, flower width, pedicel length, pedicel width, anther width, ovary length, leaf width, leaf colour, lateral leaflet shape, fruit length, fruit width, fruit weight, pulp percentage, shell percentage, seed diameter, number of seeds per fruit, fruit surface, fruit shape, seed shape, pulp taste, pulp acridity, titratable acidity, SSC:acidity and ascorbic acid) or close to zero kurtosis value indicated absence of gene interaction whereas positive value (trunk girth, internodal distance, inflorescence, anther length, ovary width, leaf length, leaf surface, leaf margin, seed length, test seed weight per fruit, total number of fruit/plant, mature fruit colour, arrangement of seed in pulp and SSC pulp) indicated presence of gene interactions [20]. The number of genes controlling traits with leptokurtic and platykurtic distributions differs, with leptokurtic traits being controlled by fewer genes and platykurtic traits being controlled by a larger number of genes. Similar studies conducted on bael crop [18].

Variation observed among morpho-pomological traits of bael selections revealed that out of eighty seedling origin bael genotypes compared with two commercial cultivars showed trunk girth ranged from 29.50 to 63.40 cm and tree spread (N–S) varied 1.00–6.30 m. In addition, intermodal distance in selected genotypes ranged from 1.90 to 7.00 cm (Table 1). Among eighty seedling origin bael genotypes compared with two commercial bael cultivars, axillary biparous cyme was observed in four genotypes (4.88%), axillary multiparous cyme in thirty three genotypes (40.24%), terminally biparous cyme in thirty seven genotypes (45.12%), terminally multiparous cyme in four genotypes (4.88%) including NB-5 and axillary uniparous inflorescence in four (4.88%) bael genotypes including NB-9 (Table 2).The variation in the tree characters may be attributed to their genetic constitution and environmental conditions. Singh et al. [21] observed stem girth ranged from 28.95 to 88.39 cm. Pavani et al. [22] also reported stem girth ranged from 0.26 to 0.55 m and tree spread ranged from 4.07 to 6.90 m. Singh et al. [23] found the distance between two internodes ranged between 3.00 and 4.56 cm.

Flower length varied from 12.35 to 18.73 mm and flower width ranged from 24.16 to 36.55 mm. In addition, the range of pedicel length and pedicel width was 5.18–9.38 mm 2.02–2.58 mm, respectively. Anther length ranged from 3.29 to 4.41 mm and anther width ranged from 0.50 to 0.83 mm. Ovary length varied from 4.25 to 7.71 mm and ovary width ranged from 3.34 to 4.87 mm

Table 2
Frequency distribution for the qualitative traits in the studied genotypes of bael.

Traits	Frequency unit	Categories				
Inflorescence	No.	Axillary biparous cyme (4)	Axillary multiparous cyme (33)	Terminally biparous cyme (37)	Terminally multiparous cyme (4)	Axillary uniparous (4)
	%	4.88	40.24	45.12	4.88	4.88
Leaf colour	No.	Light green (26)	Green (22)	Dark green (34)		
	%	31.71	26.83	41.46		
Lateral leaflet shape	No.	Lanceolate (47)	Ovate (35)			
	%	57.32	42.68			
Leaf surface	No.	Smooth (75)	Rough (7)			
	%	91.46	8.54			
Leaf margin	No.	Crenulate (16)	Crenate (66)			
	%	19.51	80.49			
Mature fruit colour	No.	Green (13)	Greenish pale yellow (58)	Yellowish green (11)		
	%	15.85	70.73	13.41		
Fruit surface	No.	Smooth (60)	Rough (22)			
	%	73.17	26.83			
Fruit Shape	No.	Globose (22)	Ovate (5)	Elliptical (10)	Round (45)	
	%	26.83	6.1	12.2	54.88	
Arrangement of seed in pulp	No.	Arranged in straight line (80)	Distributed in whole pulp (2)			
	%	97.56	2.44			
Seed shape	No.	Round (25)	Oblong (57)			
	%	30.49	69.51			
Pulp taste	No.	Less sweet (30)	Medium sweet (40)	Sweet (12)		
	%	36.59	48.78	14.63		
Pulp acridity	No.	Absent (52)	Present (30)			
	%	63.41	36.59			

(Table 1). Floral traits are believed to be the most conserved traits and affected the least by the environment. Therefore, variation for floral characteristics may be due to variations in genetic makeup among different bael genotypes. Debbarma and Hazarika [17] reported ranged from flower length (13.88–16.63 mm), flower width (22.95–34.41 mm), pedicel length (5.47–8.72 mm), pedicel width (1.86–2.74 mm). Singh et al. [21] reported ranged of anther length (3.50–4.50 mm), anther width (0.50–0.80 mm), ovary length (4.00–8.00 mm), ovary diameter (2.50–5.00 mm).

Leaf length varied from 3.03 to 17.63 cm, while leaf width ranged from 1.10 to 8.67 cm (Table 1). Out of eighty seedling origin bael genotypes compared with two commercial bael cultivars; twenty six genotypes (31.71%) had light green colour, twenty two genotypes (26.83%) had green colour while, thirty four genotypes (41.46%) had dark green colour including NB-5 and NB-9. Furthermore, lanceolate lateral leaflet shape was recorded in forty seven genotypes (57.32%) including NB-5 and ovate shape was found in thirty five (42.68%) genotypes including NB-9. The smooth surface of leaf was recorded in seventy five (91.46%) genotypes including NB-9 and rough surface in seven (8.54%) genotypes including NB-5. The leaf margin observed crenulated in sixteen (19.51%) genotypes while, crenate was found in sixty six (80.49%) genotypes including NB-5 and NB-9 (Table 2). Differences in the leaf morphology in different genotypes are specific characters and adaptability to different agro-climatic conditions. Debbarma and Hazarika [17] reported ranged from leaf length (10.13–14.53 cm) and leaf width (6.21–8.40 cm).

Fruit length ranged from 4.60 to 12.05 cm and fruit width ranged from 4.64 to 11.72 cm. Fruit weight ranged from 56.33 to 917.65 g. Pulp percentage varied from 58.64 to 81.38 %, while shell percentage ranged from 16.96 to 30.18 %. In addition, the range of seed length and seed diameter was 3.70–10.68 mm, 2.48–7.12 mm, respectively. Number of seeds per fruit varied from 23.33 to 182.33 and test seed weight per fruit ranged from 14.47 to 25.65 g/100 seeds. Total number of fruit/plant varied from 22.00 to 130.00 (Table 1). Debbarma and Hazarika [17] reported ranged from fruit length (9.86–15.66 cm), fruit width (8.64–15.51 cm), fruit weight (0.49–1.67 kg), pulp percentage (59.14–84.27 %), seed length (0.73–1.26), seed diameter (0.65–1.07). Amulya et al. [5] reported fruit weight ranged from (54.30–320.00 g), number of seeds per fruit (1.00–84.00). Dhakar et al. [18] reported pulp percentage ranged from (53.72–89.33 %), shell percentage (9.59–42.83 %), number of seeds per fruit (37.67–195.40). Pavani et al. [22] recorded ranged from fruit yield (16.7–209.3 kg).

Among eighty seedling origin bael genotypes compared with NB-5 and NB-9, green colour of mature fruit was found in thirteen (15.85%) genotypes, greenish pale yellow colour in fifty eight (70.73%) genotypes including NB-5 and yellowish green colour in eleven (13.41%) genotypes including NB-9. Smooth fruit surface was observed in sixty (73.17%) genotypes including NB-5, while rough surface was found in twenty two (26.83%) genotypes including NB-9. Among fruit shape, twenty two (26.83%) genotypes had globose fruit shape, five (6.10%) genotypes had ovate fruit shape including NB-9, ten (12.20%) genotypes had elliptical fruit shape and the remaining forty five (54.88%) genotypes had round fruit shape including NB 5. Arrangement of seed in pulp were found eighty (97.56%) bael genotypes having seeds arranged in straight line including NB-5 and NB-9 while, seeds were distributed in whole pulp was found in two (2.44%) bael genotypes. Among seed shape, twenty five (30.49%) genotypes had round seed shape including NB-5 and remaining fifty seven (69.51%) genotypes had oblong seed shape in all bael genotypes including NB-9. Pulp taste showed thirty

(36.59%) genotypes had less sweet pulp taste, forty (48.78%) genotypes had medium sweet pulp taste including NB-9 and the remaining twelve (14.63%) genotypes had sweet pulp taste including NB-5. Pulp acridity was absent in fifty two (63.41%) seedling origin bael genotypes including NB-5 and NB-9 while, pulp acridity was present in thirty (36.59%) among all the seedling bael genotypes (Table 2). Mani et al. [24] found 7 genotypes had dull green fruit colour and 18 genotypes had dull yellow fruit colour. Based on fruit shape, 4 genotypes had oblong fruit shape, 11 genotypes had round shape, 6 genotypes had oval fruit shape, 1 genotype had globose fruit shape and 3 genotypes had slightly pear shaped fruit shape. Kumar et al. [25] found NB-5, CISHB-1, NB-16, Pant Aparna, Pant Sujata had round fruit shape, NB-9 had ovate fruit shape, NB-17 had elliptical fruit shape and NB-17 genotypes had globose fruit shape. Uddin et al. [6] found 1 genotype had less sweet, 4 genotypes had medium sweet, 5 genotypes had sweet and 4 genotypes had very sweet sweetness.

SSC of pulp ranged from 25.90 to 36.77 ^{0}brix and titratable acidity ranged from 0.20 to 0.33%. SSC:acidity varied from 78.48 to 183.85%, while ascorbic acid ranged from 14.38 to 25.45 mg/100 g (Table 1). Singh et al. [21] reported SSC of mucilage ranged from 37.00 to 49.50 °brix and SSC of pulp ranged 37.45–30.57 °brix. Dhakar et al. [18] reported ranged from SSC (24.40–47.80 °brix) and titratable acidity (0.15–0.40%). Debbarma and Hazarika [17] reported ranged from SSC (30.95–39.96%), titratable acidity (0.220–0.457%), ascorbic acid (14.54–21.97 mg/100 g). Pavani et al. [26] recorded ranged from ascorbic acid (12.23–29.00 mg/100 g). The pictures of tree, leaf and fruit of the studied bael genotypes are shown in Fig. 1.

Fig. 1. Vivid presentation of seedling bael genotypes (A) Tree, (B) Leaf, (C) Fruit.

3.2. Correlation between the variables

The correlation observed between traits serves the purpose of examining and establishing a meaningful and logical relationship among them. By establishing a relationship between several traits can pave the way for examining traits that may be difficult to measure. Additionally, in cases where a trait's appearance is time-specific or requires precise measurements for identification, selecting correlated traits with a meaningful correlation can be chosen as suitable indicators. This approach proves particularly useful when measuring a trait directly is expensive, complex, time-consuming, or difficult. The presence of correlation between two traits indicates a linear relationship, ranging from −1 to +1, and the relationship between them can be used in the breeding programs. The positive and negative correlations were discovered between the studied 39 morpho-pomological and biochemical traits (Table 3). Trunk girth was positively correlated with tree spread (N–S) ($r = 0.34$) and intermodal distance ($r = 0.22$). Flower length was positively correlated with flower width ($r = 0.84$), anther length ($r = 0.68$), anther width ($r = 0.32$), ovary length ($r = 0.44$) and ovary width ($r = 0.55$). Leaf length was positively correlated with leaf width ($r = 0.80$). Fruit length was positively correlated with fruit width ($r = 0.81$), fruit weight ($r = 0.84$), pulp percentage ($r = 0.65$), seed length ($r = 0.52$), seed diameter ($r = 0.58$), number of seeds per fruit ($r = 0.26$) and pulp taste ($r = 0.39$), while it was negatively correlated with fruit surface ($r = -0.43$) and pulp acridity ($r = -0.46$). SSC of pulp was positively correlated with SSC:acidity ($r = 0.92$) and ascorbic acid ($r = 0.76$), while it was negatively correlated with titratable acidity ($r = -0.81$). Similar studies conducted on fruit crops *viz*., *Pyrus syriaca* [27]; Fig [28]; Cornelian cherry [29].

3.3. Principal component analysis

The use of Principal component analysis (PCA) allows for a more realistic interpretation of relationships among individuals by plotting them in two or more dimensions. PCA reduces dimensionality which explores data to identify relationships between objects along with estimation of correlation structure of variables and determines the minimum number of components (a linear combination of original features) necessary to explain most of the variance with minimal information loss [30,31]. Identifying and describing genetic variability in bael is crucial for exploiting useful traits to develop better quality bael genotypes. PCA indicates the genetic diversity among the genotypes could be due to factors like heterogeneity, genetic architecture of the populations and developmental traits [32]. In present study, principal component analysis was performed on 39 morpho-pomological and biochemical traits, the eigenvalues of the first 13 principal components were greater than 1, and the cumulative contribution rate reach 76.66%, indicating that the first 13 principal components can represent most of the trait information about the 39 morpho-pomological and biochemical traits of bael (Table 4). The PC1 exhibited significant factor loadings for fruit length (0.33), fruit width (0.31), fruit weight (0.31), seed diameter (0.27) and pulp percentage (0.26), contributing 16.37% of the total variance. Similarly, PC2 showed significant factor loadings for anther length (0.37), ovary width (0.35), flower length (0.31) and ovary length (0.30), contributing 11.17% of the total variance. PC3 demonstrated significant factor loadings for titratable acidity (0.37), ovary length (0.27) and flower width (0.23), contributing 9.44% of the total variance. The important traits including fruit length, fruit width, fruit weight and pulp percentage were found to be influential for PC1. Through this analysis, those individuals with higher scores from comprehensive evaluation were selected. The Scatter plot constructed based on PC1 and PC2 illustrates the diversity in morpho-pomological and biochemical traits among the bael genotypes (Fig. 2). It has been previously reported on fruit crops *viz*., Bael [17,18]; Apricot [33]; Calamansi [34]; *Camellia oleifera* [35].

3.4. Cluster analysis

The application of PCA and cluster analysis unveiled significant variations within bael genotypes. The observed genetic diversity among these genotypes may be attributed to factors such as heterogeneity, the genetic makeup of the populations and developmental traits [32]. In present study, the Ward method was used for conducting cluster analysis of 39 morpho-pomological and biochemical traits of the eighty seedling bael genotypes and two commercial cultivars NB-5 and NB-9. The eighty seedling origin bael genotypes and two commercial cultivars based on morpho-pomological and biochemical traits under two main clusters with sub-clusters (Fig. 3). In Cluster I comprised of thirty one genotypes and Cluster II consists of fifty one bael genotypes. Similar studies conducted on fruit crops *viz*., Bael [17,18]; Apricot [33]; Calamansi [34]; *Camellia oleifera* [35].

4. Conclusions

The genotypes of seedling origin bael from Jammu region were diversified, indicating they have high genetic potential. From an agronomic perspective, this might be exploited to uncover numerous valuable, well-adapted genotypes suited for significantly increasing production. This diversity also makes it possible to choose parents for various breeding programmes with regard to fruit quality and high production. Thus, the present study emphasizes the importance of preservation of genetic resources for any fruit tree breeding program. Hence, this study underscores the significance of conserving genetic resources for fruit tree breeding initiatives. The research has demonstrated that morpho-pomological and biochemical traits are valuable for phenotypic assessments of bael. By incorporating fruit traits into breeding programs, it is possible to create superior genotypes suitable for fresh consumption or processing. To ensure the continuity of successful breeding programs, the preservation of existing genetic material is essential, as it will play a crucial role in the development of productive varieties, fully adapted to the needs of commercial growers.

Table 3
Correlations between the morpho-pomological and biochemical traits in the studied genotypes of bael.

Trait	TrGi	TrSp	InDi	In	FlLe	FlWi	PeLe	PeWi	AnLe	AnWi	OvLe	Ovwi	LeLe	LeWi	LeCo	LaLeSh	LeSu	LeMa	FrLe	FrWi
TrGi	1																			
TrSp	0.34*	1																		
InDi	0.22*	0.21	1																	
In	0.1	−0.13	0.12	1																
FlLe	−0.07	0.21	0.13	−0.21	1															
FlWi	0.02	0.19	0.22	−0.18	0.84*	1														
PeLe	0.05	0.05	−0.1	0.06	0.2	0.04	1													
PeWi	0.12	0.04	0.03	−0.21	0.02	0.13	0.15	1												
AnLe	0.04	0.17	0.01	−0.14	0.68*	0.60*	0.21	0.06	1											
AnWi	−0.16	−0.02	−0.03	−0.2	0.32*	0.23*	0.14	0.12	0.64*	1										
OvLe	−0.04	0.1	0.07	−0.03	0.44*	0.46*	0.05	−0.15	0.67*	0.53*	1									
Ovwi	−0.14	0.02	0.13	−0.12	0.55*	0.52*	0.09	−0.03	0.71*	0.57*	0.68*	1								
LeLe	0.1	0.11	−0.07	−0.27*	0.16	0.13	0.04	0.08	0.05	−0.1	−0.06	−0.09	1							
LeWi	0.14	0.08	−0.05	−0.17	0.11	0.07	0.09	0.03	−0.01	−0.2	−0.14	−0.21	0.80*	1						
LeCo	−0.02	0.08	−0.12	0.15	0.03	0.02	0.04	−0.18	0.21	0.1	0.21	0.12	−0.09	−0.01	1					
LaLeSh	0.04	−0.04	−0.02	0.24*	0.1	0.06	−0.02	−0.26*	0.15	−0.02	0.07	0.18	0.08	0.22*	0.13	1				
LeSu	0.02	−0.03	−0.08	−0.13	0.06	0.13	−0.18	−0.03	0.06	−0.1	0.09	−0.07	−0.15	−0.19	−0.04	−0.18	1			
LeMa	0.06	−0.06	−0.1	0.23*	−0.05	0.01	0.14	0.14	0.05	0.01	0.02	−0.03	−0.19	−0.13	0.02	0.05	0.04	1		
FrLe	0.02	0.17	0.11	−0.05	0	0.01	0.03	0.14	0.03	−0.03	−0.15	−0.1	0.37*	0.48*	0.15	0.06	−0.26*	−0.03	1	
FrWi	−0.09	0.21	0.14	0	0.06	0.04	0.03	0.01	0.1	0.02	0.01	−0.08	0.22*	0.38*	0.18	0.17	−0.21	−0.07	0.81*	1
FrWe	−0.01	0.15	0.1	−0.01	−0.07	−0.06	0.06	0.1	0.02	0.02	−0.05	−0.13	0.29*	0.40*	0.12	0.09	−0.21	−0.06	0.84*	0.91*
PuPe	0	0.34*	0.22	−0.08	0.07	0.04	0.1	0.16	0.16	0.19	−0.01	0	0.33*	0.34*	0.04	0.07	−0.18	−0.13	0.65*	0.63*
ShPe	0.06	−0.13	−0.12	0.06	−0.05	−0.13	−0.09	−0.12	−0.16	−0.19	−0.25*	−0.2	0	0.09	0.1	0.06	0.04	0.08	0.1	0.05
SeLe	0.01	0.23*	−0.05	−0.12	0.08	0.01	0.15	0.08	0.07	−0.04	−0.01	0.06	0.33*	0.28*	0.11	−0.01	−0.24*	0	0.52*	0.46*
SeDi	−0.06	0.18	−0.14	−0.17	0.04	−0.01	0.2	0.16	0.05	0.02	−0.08	−0.08	0.30*	0.34*	0.11	0.01	−0.21	0.05	0.58*	0.55*
NuSeFr	−0.13	−0.06	−0.13	−0.01	−0.04	0	−0.01	−0.02	−0.09	−0.1	0.07	−0.03	0.11	0.19	0.14	0.17	−0.17	−0.07	0.26*	0.41*
TeSeWe	0.01	−0.08	0.11	−0.05	0	0.06	−0.18	−0.18	0.03	−0.03	0.23*	−0.05	−0.1	0.02	0.11	−0.04	0.09	0.05	−0.01	0.11
TNFP	0.36*	0.21	0.15	−0.01	0.07	0.15	0.06	0.03	0.2	0.07	0.17	0.18	−0.07	−0.16	−0.06	0.03	0.16	0.15	−0.13	−0.11
MaFrCo	0.07	−0.03	−0.1	−0.1	0.16	0.13	−0.01	0.03	0.05	0.01	−0.05	0.04	0.29*	0.19	−0.07	0.04	−0.23*	−0.08	0.19	0.06
FrSu	0.04	0.02	−0.21	0.12	−0.15	−0.09	−0.03	−0.03	−0.07	−0.03	0.02	0.01	−0.28*	−0.28*	0.22*	−0.08	0.21	0.09	−0.43*	−0.44*
FrSh	0.08	0.09	−0.03	0.14	−0.06	−0.02	−0.01	0.1	0.13	0.14	0.24*	0.12	−0.04	−0.12	0.04	−0.06	0.11	−0.07	−0.19	−0.08
ArSePu	−0.02	−0.05	0.09	−0.03	0.09	0.11	−0.08	−0.09	−0.07	−0.12	0.06	0.05	−0.03	0.07	−0.11	0.18	−0.05	−0.12	0.01	0.03
SeSh	−0.01	−0.15	0.13	−0.15	0.07	−0.04	0.04	−0.13	0.01	0.07	0.07	0.12	0.01	0.03	0.08	0.14	−0.08	−0.26*	0.16	0.17
PuTa	−0.04	−0.04	0.16	−0.18	0.06	0.03	0.01	0.11	0.06	0.06	0.04	0.06	0.39*	0.41*	−0.09	0.21	−0.09	−0.07	0.39*	0.42*
PuAc	0	0	−0.09	0.02	0.01	0.06	−0.05	−0.02	−0.03	−0.04	−0.06	−0.05	−0.31*	−0.33*	0	−0.14	0.13	0.05	−0.46*	−0.46*
SoSoCo	0.22*	0.14	0.05	0.01	0.1	−0.05	0.07	0.06	0.16	0.03	−0.02	0.02	0.05	0.02	−0.04	0.03	−0.15	−0.12	0.27*	0.19
TiAc	−0.29*	−0.08	−0.1	−0.02	−0.09	0	−0.12	−0.09	−0.16	−0.01	0.11	−0.04	0	0.01	0.21	−0.04	0.1	0.08	−0.2	−0.13
SsAc	0.28*	0.11	0.11	−0.01	0.12	0	0.11	0.1	0.19	0.03	−0.05	0.08	0.03	0.01	−0.15	0.04	−0.09	−0.09	0.25*	0.17
AsAc	0.29*	0.11	0.18	−0.02	0.11	0.04	0.1	0.12	0.21	0.05	−0.03	0.14	−0.04	−0.04	−0.2	0.03	0	−0.1	0.18	0.16

Trait	FrWe	PuPe	ShPe	SeLe	SeDi	NuSeFr	TeSeWe	TNFP	MaFrCo	FrSu	FrSh	ArSePu	SeSh	PuTa	PuAc	SoSoCo	TiAc	ScAc	AsAc
TrGi																			
TrSp																			
InDi																			
In																			
FlLe																			
FlWi																			

(*continued on next page*)

Table 3 (*continued*)

PeLe																			
PeWi																			
AnLe																			
AnWi																			
OvLe																			
Ovwi																			
LeLe																			
LeWi																			
LeCo																			
LaLeSh																			
LeSu																			
LeMa																			
FrLe																			
FrWi																			
FrWe	1																		
PuPe	0.58*	1																	
ShPe	0.11	−0.45*	1																
SeLe	0.47*	0.33*	0.07	1															
SeDi	0.55*	0.41*	−0.01	0.66*	1														
NuSeFr	0.40*	−0.13	0.07	0.24*	0.30*	1													
TeSeWe	0.13	−0.14	0.05	−0.05	0.04	0.31*	1												
TNFP	−0.13	−0.01	−0.21	−0.12	−0.15	−0.2	−0.14	1											
MaFrCo	0.06	0.05	0.26*	0.07	−0.04	−0.01	−0.13	−0.02	1										
FrSu	−0.40*	−0.37*	−0.01	−0.21	−0.34*	−0.21	−0.02	0.08	−0.28*	1									
FrSh	−0.09	−0.08	−0.04	−0.11	−0.12	0.06	−0.19	0.09	−0.03	0.06	1								
ArSePu	−0.03	0.01	−0.11	−0.08	−0.01	0.11	0.01	0.1	0.15	−0.1	−0.23*	1							
SeSh	0.17	0.12	0.09	0.28*	−0.05	0.1	0.12	−0.01	0.12	−0.08	−0.19	0.1	1						
PuTa	0.47*	0.26*	0.2	0.24*	0.32*	0.16	0.03	0	0.15	−0.41*	−0.02	−0.07	−0.02	1					
PuAc	−0.48*	−0.29*	−0.2	−0.36*	−0.41*	−0.13	0.04	0.02	−0.11	0.40*	−0.06	0.04	0.06	−0.87*	1				
SoSoCo	0.18	0.2	0.02	0.23*	0.23*	−0.06	−0.13	0.23*	0.12	−0.16	−0.07	0.07	0.05	0.15	−0.25*	1			
TiAc	−0.1	−0.14	0.01	−0.07	−0.2	0.08	0.15	−0.25*	−0.13	0.19	0.03	−0.04	0.13	−0.13	0.19	−0.81*	1		
SsAc	0.15	0.18	0	0.14	0.21	−0.08	−0.16	0.29*	0.13	−0.17	−0.04	0.05	−0.03	0.17	−0.24*	0.92*	−0.96*	1	
AsAc	0.13	0.18	−0.06	0.04	0.14	−0.1	−0.13	0.38*	0.07	−0.15	0.02	−0.02	−0.11	0.2	−0.22*	0.76*	−0.92*	0.93*	1

For the explanation of character symbols, see Table 1.

* Correlation is significant at the 0.05 level.

Table 4
Eigenvectors of principal component axes from PCA for the morpho-pomological and biochemical traits in the studied genotypes of bael.

	Component												
Traits	1	2	3	4	5	6	7	8	9	10	11	12	13
Trunk girth	0.04	0.08	−0.20	−0.07	−0.06	0.18	0.40	0.19	0.10	−0.09	0.17	0.14	0.30
Tree spread (N–S)	0.10	0.10	0.00	−0.05	−0.30	0.27	0.24	0.15	0.12	−0.16	−0.01	0.09	−0.14
Internodal distance	0.06	0.09	−0.03	−0.01	0.02	0.41	0.17	−0.30	−0.12	0.10	0.34	0.10	−0.01
Inflorescence	−0.06	−0.05	−0.10	0.36	0.05	0.04	0.27	0.13	−0.33	0.17	0.04	0.11	−0.20
Flower length	0.08	0.31	0.22	−0.18	0.11	0.02	0.01	0.14	0.13	0.14	0.04	−0.01	−0.23
Flower width	0.04	0.29	0.23	−0.20	0.06	0.09	0.12	0.06	0.17	0.23	0.03	0.08	−0.21
Pedicel length	0.06	0.08	0.01	0.03	−0.18	−0.18	−0.09	0.32	−0.13	0.18	0.07	0.01	0.30
Pedicel width	0.06	0.04	−0.05	−0.20	−0.34	−0.15	−0.09	−0.08	0.06	0.22	0.18	0.25	0.14
Anther length	0.08	0.37	0.21	0.05	−0.02	−0.09	0.04	0.08	0.04	−0.02	0.00	−0.06	−0.05
Anther width	0.03	0.26	0.20	0.10	−0.10	−0.18	−0.21	−0.13	−0.14	−0.09	0.10	−0.04	0.07
Ovary length	0.00	0.30	0.27	0.16	0.06	−0.01	0.09	−0.10	0.02	−0.09	−0.11	0.07	0.14
Ovary width	0.01	0.35	0.22	0.08	0.10	−0.08	−0.07	−0.03	−0.11	−0.03	0.04	0.01	0.07
Leaf length	0.20	−0.08	0.09	−0.40	0.01	−0.06	0.14	0.14	−0.03	−0.15	−0.19	−0.05	0.09
leaf width	0.22	−0.15	0.09	−0.30	0.06	0.00	0.20	0.18	−0.02	−0.04	−0.20	−0.08	0.07
Leaf colour	0.01	−0.01	0.17	0.34	−0.04	−0.01	0.12	0.27	0.09	−0.26	0.02	−0.11	−0.16
Lateral leaflet shape	0.07	0.01	0.07	0.14	0.31	0.05	0.21	0.20	−0.32	0.06	−0.21	−0.17	0.06
Leaf surface	−0.13	0.06	−0.01	−0.07	−0.05	0.01	0.16	−0.23	0.37	−0.07	−0.11	−0.31	−0.09
Leaf margin	−0.05	0.00	0.00	0.15	−0.16	−0.19	0.21	0.14	0.02	0.54	0.17	−0.15	0.09
Fruit length	0.33	−0.12	0.04	0.07	−0.08	0.08	−0.03	0.03	0.02	0.03	0.12	−0.02	−0.15
Fruit width	0.31	−0.10	0.11	0.20	−0.04	0.13	0.01	−0.07	0.02	0.03	0.02	0.04	−0.15
Fruit weight	0.31	−0.14	0.09	0.18	−0.07	0.07	0.02	−0.09	0.05	0.01	0.08	0.05	−0.03
Pulp percentage	0.26	0.01	0.06	−0.02	−0.29	0.25	−0.10	−0.07	−0.26	−0.06	−0.02	−0.18	−0.13
Shell percentage	0.01	−0.15	−0.04	0.02	0.31	−0.28	0.19	0.11	0.24	−0.08	0.41	−0.01	−0.17
Seed length	0.24	−0.07	0.08	0.07	−0.12	−0.04	−0.10	0.21	0.15	−0.09	0.11	−0.01	0.16
Seed diameter	0.27	−0.09	0.05	0.09	−0.18	−0.12	−0.11	0.10	0.17	0.12	−0.17	−0.03	0.04
Number of seeds per fruit	0.11	−0.14	0.15	0.19	0.16	−0.03	−0.01	0.01	0.21	0.09	−0.29	0.48	0.19
Test seed weight per fruit	−0.02	−0.06	0.14	0.18	0.17	0.17	0.05	−0.17	0.42	0.15	−0.02	0.05	0.17
Total no. of fruit/plant	0.00	0.23	−0.15	0.00	−0.06	0.14	0.23	0.00	−0.02	0.00	0.00	−0.12	0.38
Mature fruit colour	0.09	0.01	−0.01	−0.26	0.26	−0.11	−0.04	0.19	−0.12	−0.07	0.28	0.26	−0.15
Fruit surface	−0.23	0.03	−0.04	0.12	−0.13	−0.02	0.06	0.21	0.13	−0.19	−0.06	−0.18	0.05
Fruit Shape	−0.05	0.08	0.01	0.06	−0.16	−0.22	0.26	−0.16	−0.14	−0.34	−0.12	0.48	−0.02
Arrangement of seed in pulp	0.01	0.02	0.00	−0.09	0.27	0.30	−0.12	0.07	−0.10	0.23	−0.25	0.07	0.09
Seed shape	0.05	−0.03	0.11	0.06	0.22	0.24	−0.27	0.09	0.01	−0.27	0.36	−0.07	0.38
Pulp taste	0.25	−0.04	0.05	−0.08	0.14	−0.24	0.21	−0.33	−0.08	0.02	0.04	−0.19	0.16
Pulp acridity	−0.26	0.05	−0.01	−0.03	−0.10	0.26	−0.21	0.27	0.11	0.04	−0.02	0.17	−0.10
Soluble solid content	0.20	0.17	−0.31	0.11	0.10	−0.02	−0.12	0.08	0.09	−0.10	−0.05	−0.02	−0.04
Titratable acidity	−0.18	−0.20	0.37	−0.05	−0.10	0.06	0.08	−0.02	−0.07	−0.04	0.10	−0.04	0.08
SSC:acidity	0.20	0.21	−0.35	0.07	0.10	−0.04	−0.09	0.03	0.09	−0.03	−0.07	0.00	−0.04
Ascorbic acid	0.17	0.24	−0.34	0.07	0.06	−0.03	−0.03	−0.08	0.07	0.00	−0.07	−0.01	−0.02
Eigen Value	6.38	4.36	3.68	2.08	2.04	1.83	1.67	1.61	1.51	1.34	1.22	1.12	1.07
% of Variance	16.37%	11.17%	9.44%	5.33%	5.22%	4.70%	4.29%	4.12%	3.86%	3.44%	3.13%	2.86%	2.73%
Cumulative Variance %	16.37%	27.54%	36.98%	42.31%	47.53%	52.22%	56.52%	60.63%	64.49%	67.93%	71.06%	73.92%	76.66%

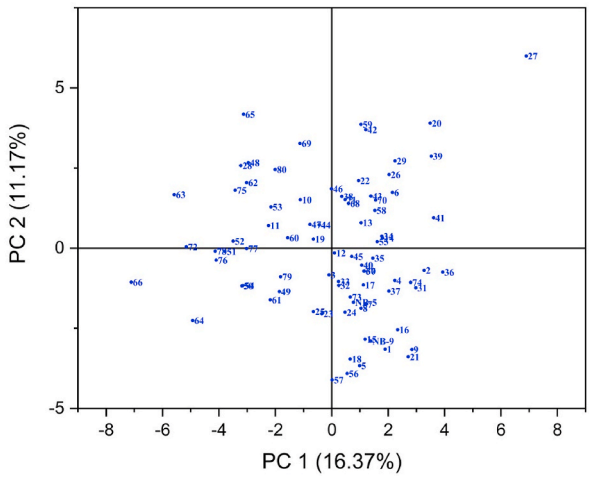

Fig. 2. 2-Dimensional scatter plot for the studied of bael genotypes based on PC1/PC2.

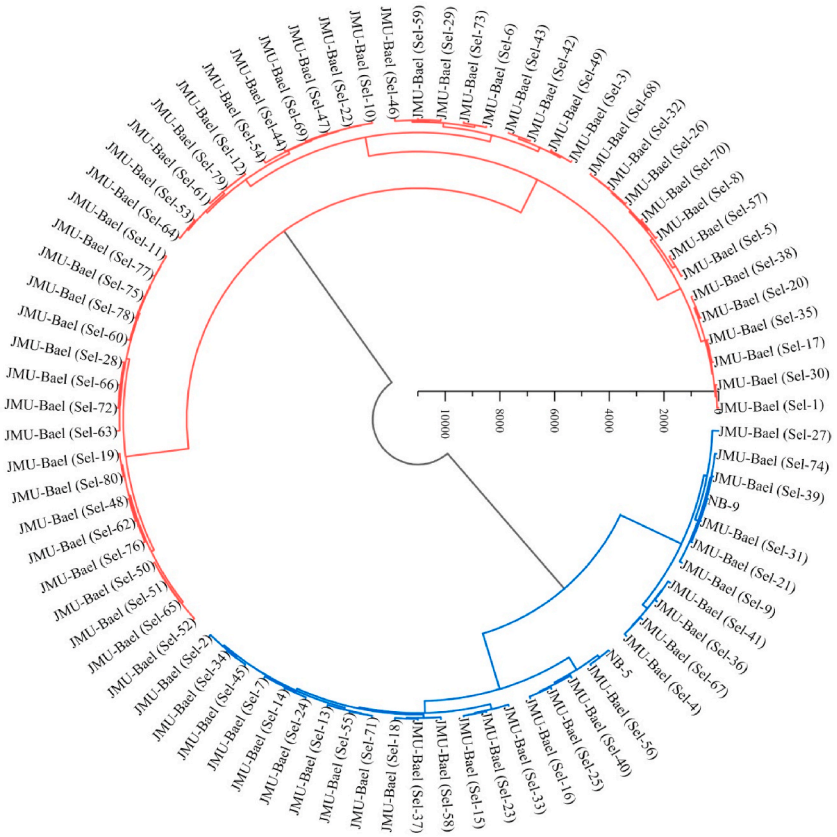

Fig. 3. Ward cluster analysis of the studied bael genotypes based on morpho-pomological and biochemical traits using Euclidean distances. The results show that the populations were divided into 2 categories, which was indicated by red and blue colors. (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)

CRediT authorship contribution statement

Prabhdeep Singh: Writing – original draft, Software, Methodology, Formal analysis, Data curation, Conceptualization. **Akash Sharma:** Writing – review & editing, Project administration, Investigation. **Amit Jasrotia:** Supervision, Investigation. **Romesh Kumar Salgotra:** Validation, Supervision, Data curation, Conceptualization. **Manish Sharma:** Visualization, Software, Formal analysis, Data curation. **Vishal Gupta:** Visualization, Investigation.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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