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RESEARCH ARTICLE

Genetic variability and correlation analysis of diverse Jamun (*Syzygium cumini* L. Skeels) genotypes in southern Rajasthan

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Abstract

In this research study, a survey was conducted in two districts of Rajasthan to evaluate genetic biodiversity of Jamun (*Syzygium cumini*), as it stands as an underutilized minor fruit and very little is known about its genetic diversity, conservation or breeding advancement strategies in this region. The study included forty genotypes of Jamun which were systematically evaluated for over two consecutive fruiting seasons (2022 and 2023) to assess the mean performance, genetic variability and interrelationships among diverse morpho-biochemical traits. The study suggested high values for genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for most of the traits, indicating high genetic variability. Also, the PCV exceeded GCV in most traits suggesting stronger influence of environment in the observed variation. The mean performance demonstrated that the genotypes HMRK-J2 and HMRK-J4 emerged as promising genotypes and exhibited stronger performance across multiple quantitative and qualitative traits. Key attributes including fruit weight, seed weight, total soluble solids, total sugar, titratable acidity, ascorbic acid content and anthocyanin content demonstrated elevated values of heritability, genetic advance and genetic gain suggesting that these traits are controlled by additive gene action, thus offering greater potential for crop improvement through selection. Notably, the fruit weight exhibited strong positive correlation with total soluble solids, fruit length, pulp content, pulp-to-seed ratio and seed weight, suggesting that these traits are genetically linked and could be co-selected in breeding programs targeting towards yield and quality improvement.

Keywords: correlation; genotypic coefficient of variation; genetic diversity; heritability; jamun; phenotypic coefficient of variation

Introduction

Jamun (*Syzygium cumini* L. Skeels) is an underutilized fruit tree with significant nutritional and economic value primarily valued for its fruits and is consumed in both fresh and processed forms. Jamun is a member of genus *Syzygium* and family Myrtaceae with a basic chromosome number (x) of eleven and exhibits different ploidy levels, where diploid forms (2n=22) are the most commonly occurring in nature (1). It originated from India and Indonesia, now growing abundantly throughout Southern Asia, thriving very well in tropical and sub-tropical climates and embracing about 1100 species, most widely known for their fruits (2). Besides *S. cumini*, other important species in India include *S. jambos* (rose apple or safed jamun), *S. javanica* (water apple), *S. uniflora* (Surinam cheery), *S. aromaticum* (clove), *S. densiflora*, *S. fruiticosum*, *S. zeylanicum*, among others. In India, it occurs widely in the states of Punjab, Haryana, Rajasthan, Gujarat, Maharashtra, Bihar, Madhya Pradesh, Chhattisgarh, Karnataka, Jharkhand, Tamil Nadu and Andhra Pradesh.

Jamun fruits are rich in wide range of essential nutrients, minerals and antioxidants. The seeds contain alkaloid called jambosine and glycoside named jambolin (also known as antimellin), which aids in managing insulin resistance and type-II diabetes (3). The different parts of Jamun including bark, leaves and flowers are rich in compounds like glucosides, ellagic acid, isoquercetin, kaempferol and myricetin while, fruits are mainly rich in anthocyanins and ascorbic acid (2). The ripe fruits are eaten fresh and can be consumed in processed form as beverages, ice creams, jellies, jams, flavoured drinks, preserves, herbal teas, squash, wine, vinegar, etc. Being a hardy, evergreen species, it tolerates harsh environmental conditions. This makes it suitable for afforestation, soil conservation and biodiversity maintenance. Additionally, it supports rural livelihoods through fruit collection and trade.

The availability of diverse climatic, soil, temperature and other eco-geographical conditions favours rich gene pool of *Syzygium* which can be found scattered throughout the southern region of Rajasthan in wild and semi-wild, encompassing enormous diversity in terms of morphological and biochemical characters. Despite the huge nutritional and medicinal benefits as well as market demand of Jamun and the presence of diverse gene pool in this region, limited efforts has been conducted on the systemic cultivation, conservation, characterisation and genetic variability evaluation of available Jamun genotypes, which are prerequisite for formulating any breeding strategies for developing improved varieties with desirable quality attributes and high yields. Therefore, to fill this research gap, the knowledge about genetic variability, morpho-biochemical characterisation and its breakdown into various components have been worked in this study. The greater the variability, the greater is the likelihood of selecting desirable genotypes. The components of variation can be evaluated through various metrics, including PCV, GCV, heritability, genetic advance and genetic gain (4). Besides this, correlation studies among different traits also play an important role in determining how yield associates with its component traits and reveal the nature and magnitude of relationships between various pairs of traits. These insights are crucial for formulating precise and target-oriented breeding programs, allowing indirect improvement of one trait through selective focus on genetically linked characteristics. Therefore, in this study, genetic variability parameters and correlation matrix have been worked out for various characteristics at both genotypic and phenotypic levels which will be helpful in formulating targeted selection and breeding strategies for an overall crop improvement in Jamun.

Materials and Methods

A systematic survey was conducted across Udaipur and Rajsamand districts of Rajasthan to characterize forty regularly fruiting seedling-origin genotypes of Jamun (*S. cumini)*. The study area is situated within the NARP agro-climatic zone IVa, designated as the 'Sub-Humid Southern Plain and Aravalli Hills,' and is geographically located between 24.58° to 25.07° N latitude and 73.71° to 73.88° E longitude, with a mean elevation of 572.50 meters above the mean sea level. The climate of this region is mainly semi-arid and is characterized by moderate rainfall of nearly 600 mm and temperature ranging between 0 °C - 25 °C in winters to 26 °C - 50 °C in summers and the soil type is predominantly claying loam. The genotypes and their location details are given in Table 1. These locations were selected primarily based on the presence of high germplasm diversity of Jamun. The selected genotypes were evaluated for over two consecutive fruiting seasons (2022 and 2023) for a range of morpho-biochemical traits. Data were recorded to assess the mean performance, genetic variability parameters and correlation coefficients at both genotypic and phenotypic levels for all the measured characteristics.

Evaluation of quantitative and qualitative parameters

During the peak fruiting season (June-August), representative samples comprising of ten fully mature and ripe fruits were randomly collected from all four crown orientations for each genotype, with three replications (3 sampling events). The collected fruit samples were washed properly, measured for weight and dimensions and then stored at -80 °C to preserve their integrity for further bio-chemical analysis. Identifying promising Jamun genotypes requires considering specific qualitative and quantitative traits which align with consumer preferences, such as higher fruit weight (>10.0 g), high pulp % (>75), elevated TSS (>15 °B) etc. (5). Therefore, a total of six quantitative parameters namely, fruit length, fruit width, fruit weight, seed weight, pulp content, pulp-to-seed ratio and five qualitative traits namely, total soluble solids (TSS), acidity, total sugar, ascorbic acid content and anthocyanin content were estimated. The fruit length and width were measured using a digital vernier caliper and expressed in cm. The weight of fruits and seeds was determined using a precision analytical balance and expressed in g. The pulp was separated from the seeds, weighed and the proportion of pulp weight to total fruit weight was calculated to determine percent of pulp content. TSS of the fruits was measured in degrees Brix (°Brix) using a digital pocket refractometer (PAL, Atago, Tokyo, Japan; range 0-53%). Acidity in fruits was quantified according to the simple titration process with 0.1N NaOH (6). Total sugar content in the fruit pulp was estimated using the standard titration method described elsewhere (7). The ascorbic acid content was determined using the 2,6-dichlorophenolindophenol dye titration method (8). The total anthocyanin content was quantified using the standard pH differential method (9), with minor modifications.

Table 1. List of genotypes taken under evaluation

S. No.	Genotypes	Source
1	**HMRK-J1**	Ayad, Udaipur
2	**HMRK-J2**	North Ayad, Udaipur
3	**HMRK-J3**	Ganpati Nagar, Udaipur
4	**HMRK-J4**	Panchwati, Udaipur
5	**HMRK-J5**	Fatehpura, Udaipur
6	**HMRK-J6**	Fatehpura, Udaipur
7	**HMRK-J7**	Sardarpura, Udaipur
8	**HMRK-J8**	Raghunathpur, Bardgaon, Udaipur
9	**HMRK-J9**	Bedla, Bardgaon, Udaipur
10	**HMRK-J10**	Hawala Kalan, Bardgaon, Udaipur
11	**HMRK-J11**	Liyo ka Gurha, Bardgaon, Udaipur
12	**HMRK-J12**	Liyo ka Gurha, Bardgaon, Udaipur
13	**HMRK-J13**	Central Area, Udaipur
14	**HMRK-J14**	Bardi pal, Udaipur
15	**HMRK-J15**	Samore Bagh, Udaipur
16	**HMRK-J16**	Samore Bagh, Udaipur
17	**HMRK-J17**	Gulab Bagh, Udaipur
18	**HMRK-J18**	Gulab Bagh, Udaipur
19	**HMRK-J19**	Gulab Bagh, Udaipur
20	**HMRK-J20**	Toola, Girwa, Udaipur
21	**HMRK-J21**	Ora, Kumbhalgarh, Rajsamand
22	**HMRK-J22**	Dhondhi, Kumbhalgarh, Rajsamand
23	**HMRK-J23**	Dowasa, Kumbhalgarh, Rajsamand
24	**HMRK-J24**	Sandukoon Ka Guda, Kumbhalgarh, Rajsamand
25	**HMRK-J25**	Kakerwa, Kumbhalgarh, Rajsamand
26	**HMRK-J26**	Gundi ka Bhilwara, Kumbhalgarh, Rajsamand
27	**HMRK-J27**	Chamboa Sarjela, Kumbhalgarh, Rajsamand
28	**HMRK-J28**	Smeecha, Kumbhalgarh, Rajsamand
29	**HMRK-J29**	Deogarh, Rajsamand
30	**HMRK-J30**	Kelwara, Rajsamand
31	**HMRK-J31**	Lal Bagh, Nathdwara, Rajsamand
32	**HMRK-J32**	Lal Bagh, Nathdwara, Rajsamand
33	**HMRK-J33**	Ganesh Tekri, Nathdwara, Rajsamand
34	**HMRK-J34**	Gunjol, Rajsamand
35	**HMRK-J35**	Gunjol, Rajsamand
36	**HMRK-J36**	Gunjol, Rajsamand
37	**HMRK-J37**	Nichli Oden, Rajsamand
38	**HMRK-J38**	Nichli Oden, Rajsamand
39	**HMRK-J39**	Nichli Oden, Rajsamand
40	**HMRK-J40**	Emdi, Rajsamand

Statistical analysis

The data collected for all the measured traits from the forty Jamun genotypes were subjected to statistical analysis following the methodology as outlined by Panse and Sukhatme (10). The data was analysed using a completely randomized design (CRD) with three replications per genotype, where genotype was considered as the main factor. Analysis of variance (ANOVA) was performed utilizing XLSTAT software which was employed to determine the significance of differences among genotypes for different traits, with statistical significance set at $p \le 0.05$. The coefficient of variation (CV %) was calculated to evaluate the extent of variability present within the dataset. The GCV and phenotypic

PCV, broad-sense heritability (h^{2}bs), genetic advance (GA) and genetic gain (GG) were further computed as per standard methods (4, 11), using INDOSTAT software (Indostat Service, Hyderabad, India). Additionally, the correlation matrix for the various traits was computed (12) as well to evaluate the relationships among various morpho-biochemical characteristics using INDOSTAT software.

Results and Discussion

Mean performance of genotypes

Descriptive statistics which included range, mean, standard deviation along with coefficient of variance were assessed for all the quantitative and qualitative traits, in each of the forty Jamun genotypes (Table 2). Analysis of variance revealed significant difference ($p \leq 0.05$) with pronounced variation across all the evaluated parameters among the selected genotypes. Fruit characteristics, such as size, weight, seed content and pulp recovery greatly impact marketability and consumer preference. Therefore, identifying promising Jamun genotypes requires considering specific traits which align with consumer preferences, such as higher fruit weight (>10.0 g), high pulp % (>75), elevated TSS (>15°B) etc. (5). The findings reveal that the fruit length exhibited a range varying from 2.19 cm in HMRK-J29 to 4.11 cm in HMRK-J2, with an overall mean value of 3.25 cm. The genotype *viz.*, HMRK-J2 (4.11 cm), HMRK-J14 (4.04 cm), HMRK-J11(4.01 cm) and HMRK-J8 (3.93 cm) displayed greater fruit length as compared to the general mean. The fruit width varied between 1.60 cm to 2.88 cm with a mean value of 2.31 cm. The maximum fruit width was exhibited by genotype HMRK-J3 (2.88 cm), followed by HMRK-J11 (2.74 cm). The values of fruit weight spanned from 3.18 g to 12.88 g and seed weight from 1.09 g to 2.73 g. The average values fruit weight and seed weight were recorded as 8.40 g and 1.82 g, respectively. Highest mean performance for average fruit weight was recorded for genotype HMRK-J4 (12.88 g), followed by HMRK-J2 (12.67 g). Further, both genotypes also displayed elevated values for TSS and total sugar suggesting a positive correlation of fruit weight with TSS and sugar. Hence, HMRK-J4 and HMRK-J2 can be considered desirable for both, table purpose and processing. The maximum seed weight was exhibited by HMRK-J5 (2.73 g), followed by HMRK-J15 (2.63 g) and HMRK-J6 (2.51 g) hence, all these three genotypes can be considered for their bold seeds which is highly desirable for making seed powder, which is greatly valued in

Table 2. Descriptive statistics for quantitative and qualitative fruit traits in forty genotypes of Jamun

S.No.	Genotype	Fruit length (cm)	Fruit width (cm)	Fruit weight (g)	Seed weight (g)	Pulp content (%)	Pulp-to-seed ratio	TSS (°Brix)	Total sugar (%)	Acidity (%)	Ascorbic acid content (mg/100g)	Anthocyanin content (mg/100g)
1	HMRK-J1	3.30	2.09	8.83	1.81	79.49	4.04	15.06	23.55	0.23	13.62	76.56
2	HMRK-J2	4.11	2.59	12.67	2.38	81.25	4.35	22.38	24.25	0.11	9.55	50.28
3	HMRK-J3	3.11	2.88	7.49	1.63	78.23	3.61	13.21	7.88	0.30	18.57	84.49
4	HMRK-J4	3.72	2.30	12.88	1.94	84.94	5.67	21.82	15.43	0.12	10.23	46.10
5	HMRK-J5	3.34	2.50	8.53	2.73	67.95	2.13	13.73	11.55	0.24	13.41	96.79
6	HMRK-J6	3.81	2.12	10.85	2.51	76.69	3.36	17.53	7.34	0.17	11.82	48.20
7	HMRK-J7	3.46	2.69	8.02	1.09	86.34	5.75	14.85	19.88	0.22	14.11	87.83
8	HMRK-J8	3.92	2.34	11.56	1.62	86.00	6.34	19.03	7.20	0.12	10.61	77.37
9	HMRK-J9	3.58	2.49	8.73	2.31	73.59	2.77	13.96	12.38	0.26	14.22	82.88
10	HMRK-J10	3.83	2.40	9.98	1.75	82.51	4.75	16.07	15.49	0.17	12.78	56.28
11	HMRK-J11	4.01	2.74	11.00	1.35	87.72	7.65	19.02	12.73	0.14	11.41	65.29
12	HMRK-J12	3.12	2.29	8.11	2.15	73.37	2.77	13.77	17.28	0.24	17.88	96.01
13	HMRK-J13	3.50	2.41	9.10	1.40	84.64	5.76	14.64	16.04	0.22	13.94	74.72
14	HMRK-J14	4.05	2.59	11.65	1.94	83.30	5.02	16.36	14.61	0.23	13.09	53.66
15	HMRK-J15	3.60	2.47	8.58	2.63	69.27	2.27	13.19	20.27	0.30	15.65	96.15
16	HMRK-J16	3.40	2.65	7.63	2.40	68.45	2.20	13.98	22.34	0.26	14.67	93.52
17	HMRK-J17	3.61	2.51	11.85	1.66	85.95	6.15	18.73	15.30	0.13	11.22	63.55
18	HMRK-J18	3.03	2.36	8.66	1.68	80.51	4.16	12.25	18.22	0.37	21.20	83.46
19	HMRK-J19	3.59	2.49	10.65	2.38	77.54	3.47	17.55	23.00	0.14	11.78	54.72
20	HMRK-J20	2.53	1.76	5.90	1.48	74.96	3.19	10.76	17.82	0.51	30.06	115.48
21	HMRK-J21	2.49	1.77	4.73	1.29	74.30	2.94	9.88	8.75	0.64	28.00	113.12
22	HMRK-J22	2.83	2.43	6.55	1.43	77.94	3.65	12.50	21.95	0.35	20.71	96.87
23	HMRK-J23	3.70	2.19	11.47	2.43	78.83	3.75	20.18	10.99	0.13	10.83	76.19
24	HMRK-J24	2.52	2.15	4.81	1.33	73.33	2.79	10.06	7.51	0.39	31.55	113.72
25	HMRK-J25	3.60	2.63	9.90	2.34	76.33	3.25	16.38	9.50	0.17	12.48	54.84
26	HMRK-J26	3.16	2.38	7.24	2.09	71.08	2.46	12.07	10.45	0.38	19.61	95.32
27	HMRK-J27	3.24	2.35	11.98	1.70	85.75	6.28	12.05	21.95	0.32	19.05	110.00
28	HMRK-J28	2.84	2.02	5.81	1.61	73.59	2.82	10.37	14.53	0.55	28.27	124.67
29	HMRK-J29	2.19	2.21	3.17	1.25	62.30	1.73	8.69	6.50	0.64	35.82	125.05
30	HMRK-J30	3.02	2.28	6.45	1.56	75.76	3.17	12.98	16.65	0.44	18.41	84.91
31	HMRK-J31	3.36	1.85	9.73	2.27	76.59	3.36	16.16	14.79	0.17	12.77	86.40
32	HMRK-J32	2.76	2.33	5.34	1.30	75.23	3.17	10.38	20.12	0.51	25.06	52.67
33	HMRK-J33	3.67	2.16	10.61	2.41	77.29	3.42	10.63	16.91	0.52	28.40	99.80
34	HMRK-J34	2.48	1.93	6.01	1.29	79.63	3.98	11.35	13.42	0.56	23.20	95.67
35	HMRK-J35	2.69	2.38	5.62	1.58	71.85	2.60	10.01	15.34	0.54	25.33	104.70
36	HMRK-J36	2.60	2.40	5.91	1.15	79.99	4.03	10.93	19.34	0.57	22.82	108.79
37	HMRK-J37	2.54	2.27	5.16	1.47	70.26	2.60	12.12	23.10	0.25	28.86	95.63
38	HMRK-J38	3.29	1.60	7.75	2.42	68.76	2.32	12.21	10.76	0.53	25.60	87.25
39	HMRK-J39	3.40	2.02	6.86	1.31	82.53	4.80	11.56	9.88	0.45	24.07	83.61
40	HMRK-J40	2.84	2.28	8.11	1.58	81.55	5.01	13.59	18.29	0.28	15.82	105.53
Range		2.19-4.11	1.60-2.88	3.18-12.88	1.09-2.73	62.30-87.72	1.73-7.65	8.69-22.38	6.50-24.25	0.11-0.64	9.55-35.82	46.10-125.05
General mean		3.25	2.31	8.40	1.82	77.39	3.84	14.05	15.33	0.32	18.66	85.45
SE±		0.08	0.03	0.15	0.08	1.21	0.25	0.31	0.50	0.01	0.48	1.87
CD (5%)		0.23	0.09	0.41	0.22	3.38	0.71	0.85	1.40	0.03	1.35	5.23
CV (%)		6.14	3.33	4.31	10.71	3.83	16.21	5.28	7.96	8.80	6.34	5.37

medicinal and plant-based supplement industry. The values for pulp content demonstrated considerable variation, ranging from 62.30 % to 87.72 %, with a mean of 77.39 %. The most promising genotypes in terms of higher pulp content were found to be HMRK-J11 (87.72 %), followed by HMRK-J7 (86.34 %), HMRK-J8 (86.00 %), HMRK-J17 (85.95 %), HMRK-J27 (85.75 %), HMRK-J4 (84.94 %) and HMRK-J13 (84.64 %), hence making them suitable for pulp processing. The values for pulp-to-seed ratio varied from 1.73 to 7.65, with a mean of 3.84. The maximum value was for pulp-to-seed ratio was observed for the genotype HMRK-J11 (7.65), followed by HMRK-J8 (6.34), both exhibiting greater pulp recovery as compared to other genotypes due to their relatively smaller seeds. The genotypes having fruits with high-pulp content and those with high pulp-to-seed ratio are particularly preferred because of their increased yield per fruit and pulp recovery, making them more suitable for processing and value addition (5). Similar range of variations with respect to the above traits have also been reported in previous studies on Jamun (13-15).

Consumer preferences for fruit are greatly driven by their palatability, flavour, taste, colour and nutritional values which are often dependent upon biochemical traits like TSS, sugars, acidity and antioxidant content. The knowledge of variability for these biochemical traits could be utilized as an index for guiding selection and breeding for enhanced fruit quality and suiting market demands. The results based on ANOVA revealed significant difference ($p \leq 0.05$) with pronounced variation for different biochemical parameters across the selected genotypes (Table 2). Parameters like TSS indicates sweetness while sugars and acids determine taste and flavour balance. Therefore, in this study these qualitative traits in Jamun have been estimated, where the values for TSS across all the genotypes varied from 8.69 °Brix to 22.38 °Brix with an overall mean of 14.05 °Brix. The highest value for TSS was recorded for genotype HMRKJ-2, (22.38 °Brix), followed by HMRKJ-4 (21.82 °Brix). These two genotypes were comparatively sweeter in taste and could be preferred for table purpose and processing. Titratable acidity values displayed a wide range varying from 0.11 % in HMRKJ-2 to 0.64 % in HMRKJ-29 and HMRKJ-21, with an overall mean of 0.32 %. The total sugar content exhibited values ranging from 6.50 % to 24.25 % with a mean of 15.33 %. The maximum value for total sugar was recorded for genotype HMRKJ-2 (24.25 %), followed by HMRKJ-1 (23.55 %), HMRKJ-37 (23.10 %) and HMRKJ-19 (23.00 %). Anthocyanins and ascorbic acid contribute to nutritional value and health benefits. It was observed that the values for anthocyanin concentration varied significantly from 46.10 mg/100 g to 125.04 mg/100 g with a mean value of 85.45 mg/100 g. The maximum value for anthocyanin content was recorded for genotype HMRKJ-29 (125.05 mg/100 g), followed by HMRKJ-28 (124.67 mg/100 g). The values for ascorbic acid content widely ranged from 9.55 mg/100 g to 35.82 mg/100 g with a mean of 18.66 mg/100 g. The maximum value for ascorbic acid content was obtained for genotype HMRKJ-29 (35.82 mg/100 g), followed by HMRKJ-24 (31.55 mg/100 g). All the above results with respect to variation in different qualitative traits are in accordance with the previous studies in Jamun (15, 16). Overall, among all the genotypes, HMRK-J2 and HMRK-J4 consistently exhibited strong performance across multiple traits like fruit weight, pulp weight, total sugar and TSS and genotypes HMRK-J5, HMRK-J6 and HMRK-J15 displayed bold seeds. The genotypes HMRK-J8 and HMRK-J11 displayed higher pulp content and pulp recovery and HMRK-J29 exhibited maximum ascorbic acid and anthocyanin content. All these genotypes demonstrated high potential to be used in breeding programs aimed at enhancing both yield and quality traits in Jamun making them valuable prospects for future crop improvement efforts. Also, the presence of these variations in different quantitative and qualitative parameters in fruits play a crucial role in adaptation of a genotype in different environmental conditions, selection of superior genotypes and formulating suitable breeding programmes aimed at improving fruit yield, quality, consumer preference and marketability (13). These variations can be primarily attributed to the genetic makeup of the individual plant which is also modulated by high magnitude of cross pollination, varied environmental factors (soil, temperature, light reception & rainfall), growing conditions during and biochemical processes within the plant during fruit development (17, 18).

Genetic variability parameters

The nature as well as extent of genetic variability in plant species is important criteria in formulating an efficient breeding programme as greater the variability, greater is the likelihood of selecting desirable genotypes. In any genetic stock evaluation, PCV and GCV serve as critical metrics for predicting phenotypic and genotypic variability. Therefore, GCV and PCV for different characters have been worked out in this study (Table 3). In general, the estimates of PCV were observed to be higher in magnitude than their corresponding estimates of genotypic coefficient for most of the traits, suggesting a stronger influence of environmental factors (soil, climate & cultural practices) on expression of these traits (16). High magnitudes (>20 %) of genotypic as well as phenotypic coefficient of variation were recorded for characters, *viz*., acidity (49.82 % & 51.93 %), ascorbic acid content (37.81 % & 38.36 %), pulp-to-seed ratio (35.68 % & 38.95 %) total sugar (33.80 % & 34.48 %), fruit weight (29.45 % & 30.12 %), seed weight (25.87 % & 27.53 %), anthocyanin content (25.52 % & 26.25 %) and total soluble solids (23.25 % & 25.64 %). This indicates the existence of high genetic variability, offering

Table 3. Genetic variability parameters (GCV, PCV, heritability in broad sense, genetic advance & genetic gain) for different traits in Jamun

S.No.	Characters	GCV (%)	PCV (%)	h^{2}bs (%)	GA	GG (%)
1	Fruit length (cm)	15.35	16.51	86.38	0.95	29.38
2	Fruit width (cm)	12.05	12.48	93.23	0.55	23.96
3	Fruit weight (g)	29.45	30.12	95.62	4.98	59.33
4	Seed weight (g)	25.87	27.53	88.27	0.91	50.07
5	Pulp content (%)	7.65	8.51	80.76	10.95	14.16
6	Pulp-to-seed ratio	35.68	38.95	83.90	2.58	67.32
7	Total soluble solid (^{0}Brix)	23.25	25.64	82.20	6.15	43.42
8	Total sugar (%)	33.80	34.48	96.08	10.46	68.25
9	Acidity (%)	49.82	51.93	92.01	0.32	98.44
10	Ascorbic acid content (mg/100g)	37.81	38.36	97.14	14.33	76.77
11	Anthocyanin content (mg/100g)	25.52	26.25	94.48	43.66	51.09

h2bs: heritability (broad sense); ga: genetic advance; gg: genetic gain greater potential for crop improvement in Jamun from selection for these traits. High values of GCV and PCV for different yield attributes have also been reported in other fruit crops (19, 20).

The GCV explains the existence of genetic variability which arises due to genetic make-up of individual plant whereas, PCV highlights the influence of environment on expression of given characters. Both parameters give valuable insights into the extent of variability among different traits, but they do not offer any information regarding nature of inheritance of that trait. However, by estimating heritability along with genetic advance and genetic gain, the impact of selection on phenotypic expression can be anticipated more accurately (10). Most of the yield traits are quantitative in nature, complex in inheritance and largely influenced by environmental conditions (21), therefore, heritability (broad sense) can play a useful role to estimate the scope of improvement by selection, as it measures the magnitude inherent part of variation which is stable and transferred from one generation to another (20). The broad-sense heritability (h^2bs) estimates for all the characters were estimated (Table 3). All the observed traits displayed high (>60 %) heritability estimates. The highest was recorded for ascorbic acid content (97.14 %), total sugar (96.08 %), fruit weight (95.62 %), anthocyanin content (94.48 %), fruit width (93.23 %), acidity (92.01 %), seed weight (88.27 %), fruit length (86.38 %), pulp-to-seed ratio (83.90 %), total soluble solid (82.20 %) and pulp content (80.76 %). High values of heritability estimate for different characters have also been reported in fruits crop like cherry (21) and annona (22). Traits with high heritability indicate a strong association between phenotype and genotype, suggesting greater genetic control and stable inheritance for such traits (23). This indicates that selection will be effective for selecting genotypes having such traits with high heritability (22).

Genetic advance, governed by variability and heritability, measures the potential gains from selection within a given population. The data on expected genetic advance (Table 3) for different traits ranged from 0.32 in acidity to 43.66 in anthocyanin content. Higher values (>20) of expected genetic advance were recorded for anthocyanin content (43.66) and moderate (10-20) for characters *viz*., ascorbic acid content (14.33), pulp content (10.95) and total sugar (10.46). High heritability coupled with high genetic advance was observed for anthocyanin content. Also, a high heritability coupled with moderate genetic advance was recorded for ascorbic acid content, total sugar and pulp content. In any breeding program, the selection for any trait is based on its high heritability in combination with high or moderate genetic advance. The presence of high heritability coupled with high genetic advance is indicative of a strong additive genetic control and high selection efficiency, as expression of such traits is strongly influenced by genetic factors rather than the environmental factors (19). On the other hand, moderate genetic advance indicates a mix of both additive and non- additive gene action and a moderate response to selection. Both are valuable for designing breeding strategies in fruit and other crops (22). In addition, information regarding genetic advance as a percent of mean (genetic gain), allows breeders to predict and achieve tangible improvements that can be anticipated in a specific crop trait through selection of segment of the population (19). High (>20 %) genetic gain was recorded for traits like acidity (98.44 %), followed by ascorbic acid content (76.77 %), total sugar (68.25 %), pulp-to-seed ratio (67.32 %), fruit weight (59.33 %), anthocyanin content (51.09 %), seed weight (50.07 %), total soluble solid (43.42 %), fruit length (29.38 %), fruit width (23.96 %) while moderate (10 -20 %) for pulp content (14.16 %).

Correlation coefficient analysis

By analysing correlation coefficients, it can be quantified that how yield associates with its component traits, as it reveals the nature and magnitude of relationships between pairs of traits. This insight informs strategic breeding decisions, allowing indirect improvement of one trait through selective focus on genetically linked characteristics. The analysis of genotypic and phenotypic correlation coefficients revealed significant positive and negative associations between different characters at both genotypic and phenotypic levels. For most of the traits, genotypic correlation coefficient (rg) was higher than the phenotypic correlation coefficient (rp). The lower values of phenotypic correlation over genotypic correlation may result from the masking effect of environment on the inherent association of traits at genetic level (24). In essence, the environmental variation tends to obscure the underlying genetic relationships, leading to lower phenotypic correlations as compared to genotypic ones. Fruit weight is an important trait that has a direct bearing on total fruit crop yield (22, 25). Therefore, for all the conceivable combinations, the correlation coefficient between fruit weight and its component characters have been estimated (Table 4). The fruit weight displayed highly significant positive genotypic and phenotypic correlation with TSS (rg = 0.95, rp = 0.84), fruit length (rg = 0.91, rp = 0.83), pulp content, pulp-to-seed ratio, seed weight. Hence, these traits could be utilized in future breeding programs as key factors for indirect selection, aimed at enhancing overall yield via fruit weight. Similar results have also been obtained in earlier studies (14, 26). In contrast, a highly significant negative correlation was observed with ascorbic acid content (rg = -0.82, rp = -0.79), acidity (rg = -0.80, rp = -0.76) and anthocyanin content (rg = -0.69, rp = -0.66), which indicates that selection based on these traits might lead to a decrease in yield attributing trait like fruit weight.

Other yield attributing traits like fruit length, fruit width, seed weight, pulp content and pulp -to-seed ratio also displayed positive and negative correlations, where fruit length showed strong positive genotypic and phenotypic correlation with fruit weight (rg = 0.91, rp = 0.83), TSS (rg = 0.85, rp = 0.77), seed weight, pulp content, pulp-to-seed ratio and, fruit width. While strong negative correlation was obtained with ascorbic acid content (rg = -0.83, rp = -0.75), acidity (rg = -0.79, rp = -0.68) and anthocyanin content (rg = -0.75, rp = -0.65). Fruit width showed highly significant positive correlation with fruit length, TSS and a significant positive correlation with fruit weight. Seed weight exhibited a highly significant positive correlation with fruit length, fruit weight and TSS. On the other hand, highly significant negative correlations were recorded with ascorbic acid content, acidity, pulp-to-seed ratio and pulp content. Similar associations were reported for fruit weight and fruit length in ber (24). The pulp content displayed strong positive correlation with pulp-to-seed ratio (rg = 0.96, rp = 0.90), TSS, fruit weight and fruit length. The pulp-to-seed ratio showed highly significant positive correlation with pulp content (rg = 0.96, rp = 0.90), fruit weight, TSS and fruit length. While, a strong negative association was observed with ascorbic acid content, acidity, anthocyanin content and seed weight. Thus, the results suggest that some yield attributing traits share mutual positive correlation enabling breeders to exercise multi-trait selection.

Table 4. Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficient matrix for different traits in Jamun

S.No.	Character	Fruit length (cm)	Fruit width (cm)	Fruit weight (g)	Seed weight (g)	Pulp content (%)	Pulp-to-seed ratio	T.S.S (°Brix)	Total sugar (%)	Acidity (%)	Ascorbic acid content	Anthocyanin content (mg/100g)
1	Fruit length (cm)		0.43**	0.91**	0.57**	0.50**	0.49**	0.85**	0.02	-0.79**	-0.83**	-0.75**
2	Fruit width (cm)	0.38**		0.34*	0.07	0.27	0.30*	0.38**	0.20	-0.52**	-0.51**	-0.37**
3	Fruit weight (g)	0.83**	0.32*		0.52**	0.61**	0.60**	0.95**	0.12	-0.80**	-0.82**	-0.69**
4	Seed weight (g)	0.49**	0.07	0.48**		-0.30*	-0.34*	0.42**	0.02	-0.43**	-0.46**	-0.32*
5	Pulp content (%)	0.42**	0.22	0.57**	-0.34**		0.96**	0.62**	0.15	-0.48**	-0.54**	-0.48**
6	Pulp-to-seed ratio	0.42**	0.26	0.56**	-0.37**	0.90**		0.60**	0.10	-0.48**	-0.50**	-0.41**
7	TSS (°Brix)	0.77**	0.35**	0.84**	0.34**	0.50**	0.53**		0.12	-0.92**	-0.90**	-0.77**
8	Total sugar (%)	0.06	0.19	0.11	0.02	0.12	0.08	0.13		-0.15	-0.14	-0.07
9	Acidity (%)	-0.68**	-0.48**	-0.76**	-0.39**	-0.42**	-0.43**	-0.81**	-0.13		0.89**	0.70**
10	Ascorbic acid content (mg/100g)	-0.75**	-0.48**	-0.79**	-0.42**	-0.48**	-0.45**	-0.81**	-0.13	0.86**		0.73**
11	Anthocyanin content (mg/100g)	-0.65**	-0.35**	-0.66**	-0.29*	-0.43**	-0.37**	-0.67**	-0.05	0.66**	0.70**	

*, ** significant at 5% and 1% respectively

TSS which is key indicator of sweetness, fruit quality and hence overall consumer preference, displayed strong positive correlation with fruit weight (rg = 0.95, rp = 0.84), fruit length (rg = 0.85, rp = 0.77), pulp content, pulp-to-seed ratio, seed weight and fruit width. Hence, these traits could be utilized in breeding programs for indirect selection, aimed at enhancing overall fruit quality in accordance with market preference. These results are in line with the similar studies conducted in ber (24) and litchi (20). The biochemical traits especially acidity, ascorbic acid and anthocyanin content showed a strong mutual positive correlation with one another. A mutual significant positive correlation between ascorbic acid and titratable acidity have also been reported in ber (24) and pomegranate (25). Conversely, all three of these qualitative traits displayed a strong negative correlation with fruit weight and most of the other yield-attributing traits, which suggests that selection for traits like acidity, ascorbic acid and anthocyanin content might lead to a decrease in overall yield attributing traits. These results resonate with the findings for similar traits in Jamun (14).

Conclusion

The present study highlights considerable genetic variability among all the observed forty genotypes of Jamun with respect to different qualitative and quantitative traits. Traits such as acidity, ascorbic acid content, total sugar content, pulp-to-seed ratio, fruit weight, anthocyanin content, seed weight, total soluble solid, fruit length and fruit width displayed elevated values for PCV, GCV, heritability and genetic gain suggesting that these traits could offer a positive response to direct selection. A strong positive association was obtained between fruit weight and TSS, fruit length, fruit width, pulp content, pulp-to-seed ratio and seed weight. Hence, these traits can prove as key factors for indirect selection. Among all genotypes, HMRK-J2 and HMRK-J4 consistently performed well across multiple traits like fruit weight, pulp content, fruit size, total sugar and TSS. The genotypes HMRK-J5, HMRK-J6 and HMRK-J15 exhibited bold seeds, HMRK-J8 and HMRK-J11 displayed higher pulp recovery and, HMRK-J29 exhibited high antioxidant potential. All these genotypes demonstrated high potential to be used in breeding programs aimed at enhancing both yield and quality traits in Jamun hence, making them valuable prospects for future crop improvement endeavours.

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Authors' contributions

HM developed the protocol for systematic field survey, data collection, designed the experiment and prepared the original draft, RAK conceptualised, validated the experiment and reviewed the original draft, RRB helped in statistical analysis, SP helped with the methodology and formal analysis, TB helped in data curation and MKG helped in manuscript preparation. All authors read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interests to declare.

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