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Character association and divergence studies in seedling population of Jamun (*Syzygium cumini* L.)

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Abstract

Seedling origin naturally occurring population of jamun was studied in Jammu region of India to assess the divergence and character association for important horticultural traits. The results revealed higher values of phenotypic variance as compared to genotypic variance for all the characters. Maximum genotypic coefficient of variation was found to be 30.12 which was recorded for the character yield efficiency followed by 15.38 for pulp to seed ratio. High heritability (57.00) along-with with high genetic gain (46.90) was recorded for the character yield efficiency, whereas, high heritability along-with medium genetic gain was observed for pulp to seed ratio and ascorbic acid content and high heritability with low genetic gain was recorded in the characters fruit weight, fruit size, total soluble solid content and acidity. Character fruit weight exhibited positive correlation with fruit specific gravity, fruit size, pulp to seed ratio, total soluble solids and yield efficiency but negative correlation with characters ascorbic acid and titratable acidity. Highest direct effect on yield efficiency was observed from size of fruit which was followed by characters total soluble solids, whereas, titratable acidity exhibited highest negative effect on yield efficiency. Maximum positive indirect effect on yield efficiency was found to be from fruit size through fruit specific gravity followed by pulp to seed ratio through size of the fruit. Based on the divergence, forty genotypes of jamun under study were grouped into seven distinct clusters consisting of 3 to 11 genotypes.

Keywords: Jamun, *Syzygium cumini* L., variability, heritability, character association

Introduction

Jamun (*Syzygium cumini* L.) belonging to family Myrtaceae which is also known as Indian blackberry is an important evergreen tropical fruit plant. This fruit has been reported to be native of India, Burma, Ceylon and Andaman Islands. In India, fruits are considered to have nutraceutical properties and all the plant parts are used for different purposes. Ripened fruits are processed into various products viz. juice, sharbat, syrup, jams, jellies, squash, vinegar, puddings and wine. It has many medicinal values as astringent, stomachic, carminative, antiscorbutic, diuretic, anti-diabetic and strong antioxidant potential (Kaur and Kapoor, 2005) [8]. Seeds contain various alkaloids such as Jambosin and glycoside which inhibit the conversion of starch into sugars, therefore, useful for patients suffering from diabetes. Globally, it has been successfully introduced to many tropical countries like West Indies, East and West Africa and some sub-tropical regions like Florida, California, Algeria and Israel for its commercial cultivation. In India, natural populations of jamun exists in ecologically different habitats of Bihar, Jharkhand, Chhattisgarh, Punjab, Haryana, Uttar Pradesh, Gujarat, Madhya Pradesh, Maharashtra, Karnataka, Andhra Pradesh, Tamil Nadu, Jammu Kashmir and North Eastern states up to an elevation of 1300m above mean sea level. Despite its wonderful medicinal properties, the supply of jamun fruit is very limited and in the recent times the demand of quality fruit having good fruit size and other horticultural traits has increased many-folds. Looking at the importance of this fruit, the demand for quality planting material has also increased recently. However, a few known varieties are available in India, despite the existence of a wide variability in jamun throughout the country. To conserve the existing diversity of jamun and to achieve sustainable development based on use of available genetic wealth, promotion and conservation of plant genetic wealth is of immense importance. Genotypes well adapted to local agro-climatic conditions carrying important phenotypic and genotypic traits are being lost due to the ruthless felling of trees.

The ultimate goal is to achieve genetically improved commercially grown jamun with high yield and other quality characteristics through various breeding methods requires a diverse approach involving multipronged strategic actions including assessment of the genetic variability, character identification and association studies and identifying superior genotypes. In India, the majority of the jamun trees growing naturally are of seedling origin. Being allogamous in nature and pre-dominance of seed propagation, enormous genetic variability exists in respect of morphology, floral and physio-chemical characteristics among the seedling origin jamun. In the state of Jammu and Kashmir, it is commonly found growing naturally in different areas of Jammu, Samba and Kathua districts under waterlogged as well as rain-fed sub-tropical conditions. Therefore, present investigations on character association and divergence studies in seedling origin jamun has been carried out in Jammu region with the objective to assess the diversity and character association among the jamun plants of seedling origin.

Materials and Methods

The present investigations were undertaken during in the subtropical zone of Jammu region lying between 32°40' North longitude and 74°58' East latitude where seedling origin natural population of jamun is found growing. It is categorized under subtropical zone in fruit growing regions of Jammu province of Jammu and Kashmir state. During summers (May to June) the maximum temperature rises upto 47 °C and minimum temperature falls to 1 °C during winters. The mean annual rainfall is about 1000-1200 mm. During the first year, a survey was conducted in Jammu, Samba and Kathua districts of Jammu region to locate areas of diversity for jamun. During the preliminary survey, ninety trees of seedling origin of almost uniform age were identified of which 40 trees were selected for data collection. Horticulturally important fruit and tree characters of identified genotypes were recorded as per minimal descriptors for jamun published by NBPGR (Mahajan *et al.*, 2002) [9] during. The data collected during July-August on different horticultural traits *viz.* fruit weight (g), fruit size (fruit length × fruit breadth), specific gravity, pulp: seed ratio, TSS, acidity, ascorbic acid and yield efficiency of the selected trees were analyzed for various statistical parameters such as mean, range, coefficients of variation, heritability, genetic advance, correlations, path and cluster analysis using multivariate statistical analysis. Components of variance was worked out according to the method suggested by Al-Jibouri *et al.* (1958) [2]. Heritability in broad sense was estimated according to the method suggested by Johnson *et al.* (1955) [7]. Genetic advance at 5 percent selection intensity was worked out using the formula suggested by Johnson *et al.* (1955) [7]. Procedure suggested by Singh and Chaudhary (1985) [16] was employed to estimate genetic divergence and genotypes were assigned to different clusters according to Tocher's method.

Results and Discussion

Range and Mean: Results regarding scale of variability present among important horticultural traits presented in Table 1 revealed that significant variability exists among all the characters studied. Fruit weight, fruit size (fruit length × fruit breadth), specific gravity, pulp: stone ratio, TSS, titratable acidity, ascorbic acid and yield efficiency ranged

between 8.30 - 11.47 g, 416.85 - 629.62 cm², 0.94 - 1.18, 4.75 - 7.71, 10.00 -17.35°B, 0.47 - 0.94 percent, 22.71 - 45.93 mg/100 g and 0.19 - 0.26 respectively with a mean of 10.04± 0.34 g, 537 ± 34.67cm², 1.05 ± 0.06, 5.89 ± 0.61, 14.19 ± 1.01°B, 0.64 ± 0.01 percent, 29.93 ± 1.83 mg per 100 g and 0.21 ± 0.02 respectively. In seedling origin jamun, Shah Nawaz and Sheikh (2011) [14] also recorded mean values of fruit weight (gm) specific gravity, TSS (°B), titratable acidity (%) of improved cultivars as 9.55±0.685, 1.26±0.031, 13.75±0.501 and 1.26±0.120 respectively and of indigenous cultivars as 6.71±0.520, 1.58±0.021, 15.82±0.505 and 1.25±0.048 respectively. Improved cultivars showed better horticultural traits as they had already been selected for better horticultural traits from the vast gene pool. While studying different seedling origin accessions of Jamun, Anushama and Sane (2018) [3] recorded mean values of fruit weight, fruit length, fruit diameter, pulp content and TSS as 5.58-11.18g, 2.25-3.87cm, 1.68-3.42cm, 70.84-79.24 percent and 11.25-13.62°B respectively. Slight variations from the present observations may be due to difference in the genetic makeup of seedling origin jamun trees and climatic influence of different locations.

Variance and coefficient of variation: Improvement in important characters through associated character can be brought only if genetic information regarding magnitude and type of variability present in the population is available. A better idea of available variability in a population can be understood by comparing the relative magnitude of PCV, GCV and ECV for understanding the variability. Phenotypic variance, genotypic variances, phenotypic variation and genotypic coefficient of variation for different horticultural traits among natural population of jamun are presented in Table 1. The values for phenotypic coefficient were recorded to be higher as compared to the values of genotypic coefficient of variations for all the characters indicating additive gene action and influence of environment on the expression of these traits. Similarly, higher phenotypic coefficient values as compared to genotypic coefficient values have been reported by Devi (2019) [5] while studying the genetic diversity of jamun germplasm. All the characters under study *viz.*, fruit weight, fruit size, specific gravity, pulp to seed ratio, total soluble solids, acidity, ascorbic acid and yield efficiency showed positive phenotypic and genotypic variances. Values recorded for phenotypic and genotypic coefficient of variation indicates the presence of significant variability for the character yield efficiency. Since yield is a quantitative trait and controlled by additive gene action so the variability among the contributing traits also contribute towards yield and yield efficiency. Values of phenotypic coefficient of variation and genotypic coefficient of variation were low (<10%) for fruit weight and specific gravity, whereas, moderate in case of fruit size, pulp: seed ratio, TSS, titratable acidity, ascorbic acid and was high *i.e.* more than 30 percent for yield efficiency. Similarly, Devi (2019) [5] also reported moderate to high PCV and GCV values for anthocyanin content, reducing sugar, non-reducing sugar, total sugar, TSS/acidity ratio, pulp/seed ratio and fruit/seed ratio. Slight variation in the values of PCV and GCV under different studies may be due to the fact that different genes are involved in the phenotypic expression of a quantitative trait. Higher variability for a trait in the population is

observed if more number of genes are involved in its expression. Similarly, Srivastava *et al.* (2014) [17] also reported similar findings while undertaking survey of natural population of jamun.

Heritability and genetic gain: It is the amount of heritable portion of variation which is of value in a breeding programme. This heritable portion of variation cannot be predicted only with the help of PCV and GCV, but requires estimation of heritability along-with genetic advance. It helps in the prediction of selection on phenotypic expression of a trait. Heritability in broad sense and percent genetic gain recorded in present study are shown in Table 1. Highest heritability of 85.00 percent was recorded ascorbic acid content followed by pulp:seed ratio (68.00%), fruit weight (61.00%), fruit size (58.00%), yield efficiency (57.00%), T.S.S. (56.00%), titratable acidity (53.00%) and specific gravity (28.6%). Heritability was grouped in three classes, wherein, less than 10 percent heritability was classified as low, 10-30 percent as medium and 30-60 percent as high heritability (Robinson, 1966) [13]. Similarly, Devi (2019) [5] reported broad sense heritability of different characters among jamun genotypes ranging between 56.82 – 99.91 percent. Abengmeneng *et al.* (2015) [1] reported that high heritability may not be coupled with high genetic advance and heritability estimates in case of quantitative traits may be used to indicate the reliability of phenotypic value to predict the breeding value. The GCV along with heritability provides reliable estimates of the amount of genetic advance expected in a cycle of phenotypic selection. Estimates of genetic gain for a trait indicates the amount of improvement in which is expected by selecting a particular part of the population. Based on the magnitude, genetic gain is grouped into three groups, *i.e.* low (<20%), medium (20-40%) and high (>40%). In the present study, the genetic gain was found to be low for fruit size (15.86%), fruit weight (12.17%), fruit specific gravity (4.70%), total soluble solids (17.81%) and acidity (19.73%). Genetic gain was medium for pulp to seed ratio (26.08%), ascorbic acid (25.76%) and high for yield efficiency (46.89%). High heritability (broad sense) along-with high genetic gain was recorded for the characters average fruit volume, average fruit weight and yield efficiency, whereas, high heritability (broad sense) along-with medium genetic gain was observed for the characters stone weight, pulp to stone weight ratio and titratable acidity. For total soluble solids, high heritability was recorded along-with low genetic gain.

Johnson *et al.*, (1955) [7] suggested that high heritability along-with high genetic gain is the better predictor of result of selection as compared when these parameters are taken into consideration individually. High heritability of a trait indicates that it is less influenced by the environment and hence there is a better scope for the improvement through direct selection. Higher heritability (broad sense) along-with high genetic advance was observed for fruit yield per plant (table 1), which may be due to presence of additive gene action, and therefore, selection would be effective for the characters. High values of genetic advance are indicators of additive gene action, whereas, low values are indicator of non-additive gene action.

Correlation

Genotypic and phenotypic correlation coefficients of eight horticulturally important quantitative traits were estimated

and the results are presented in table 2. The results on correlation coefficients revealed that fruit weight showed a positive correlation with fruit size, specific gravity, pulp to seed ratio, T.S.S. and yield efficiency. At both genotypic and phenotypic levels, correlation of ascorbic acid and titratable acidity is negative. Average fruit size exhibited positive correlation with total soluble solids, pulp to seed ratio, fruit specific gravity and yield efficiency at both genotypic and phenotypic levels but had negative correlation with acidity and ascorbic acid. Fruit specific gravity revealed positive correlation with pulp to seed ratio, total soluble solid content and yield efficiency at both phenotypic and genotypic levels but negative with titratable acidity and ascorbic acid content. Total soluble solid content revealed negative values with titratable acidity for both genotypic and phenotypic correlation but had positive correlation with yield efficiency. At both genotypic and phenotypic levels, titratable acidity and ascorbic acid exhibited negative correlation with yield efficiency. Mir *et al.* (2009) [10] also observed significantly positive correlation between yield/plant and plant height, plant spread, fruit weight, fruit diameter, fruit volume and number of fruits/plant. Srivastava *et al.* (2010) [18] while studying correlation coefficient among important characters of jamun also recorded significantly positive correlation between fruit weight, pulp weight and pulp to seed ratio. Phenotypic correlation coefficients were higher or same as that of genotypic correlation coefficients, indicating that genotypic and environmental correlations acted in the same direction maximizing their phenotypic expression because phenotypic expression of a trait is the outcome of genotype of an individual, environment and genotype and environmental interaction.

Path analysis: Path coefficient analysis yields better picture of character association revealing the cause and effect relationship among different parameters. It splits correlation coefficients into direct and indirect components indicating direct and indirect contribution of dependent traits towards independent trait which is to be improved. Path coefficient analysis was performed to assess direct and indirect effect of various characters on yield efficiency of jamun. Direct and indirect contribution of different horticulturally important traits involving average fruit size, average fruit weight, fruit specific gravity, pulp to seed ratio, total soluble solid content, titratable acidity and ascorbic acid content towards yield efficiency were estimated through fractioning of genotypic correlation coefficients and the results obtained are given in table 3. Fruit size recorded the maximum positive direct effect (0.35) on yield efficiency followed by pulp: seed ratio (0.32) whereas titratable acidity revealed highest negative effect (-0.26) on yield efficiency. Maximum positive indirect effect on yield efficiency yielded by average fruit size through pulp to seed ratio. Highest negative indirect effect came from acidity through fruit size. Path analysis exhibited 18.09 percent residual variance indicating that 89.01 percent of the total variance was explained by path analysis. Highest positive, direct effect towards fruit weight has been reported to be contributed by pulp to seed ratio followed by total sugar content, pulp weight, seed length, fruit length, leaf width, reducing sugar, seed width, leaf length, seed weight, anthocyanin content and fruit volume of jamun by Devi (2019) [5].

Divergence and cluster analysis

Genetic divergence refers to the genetic distance between two individuals. Smaller genetic distances indicate a close genetic relationship, whereas, large genetic distances indicate a more distant genetic relationship. Information about genetic divergence is critical for a productive breeding programme as genetically diverse parents can produce high heterotic effects among the progeny. Based on the cluster analysis, 40 jamun genotypes were grouped into seven distinct clusters (Table 4). Cluster-IV had highest number of genotypes (11) viz., SJJS-1, SJJS-3, SJJS-5, SJJS-7, SJJS-11, SJJS-13, SJJS-17, SJJS-18, SJJS-20, SJJS-21, SJJS-39 followed by Cluster-III with seven genotypes viz., SJJS-6, SJJS-8, SJJS-15, SJJS-19, SJJS-22, SJJS-30, SJJS-38 and Cluster-VII with seven genotypes as well viz., SJJS-2, SJJS-9, SJJS-14, SJJS-16, SJJS-26, SJJS-35, SJJS-37. Cluster-V was comprised of six genotypes viz., SJJS-23, SJJS-25, SJJS-29, SJJS-33, SJJS-34, SJJS-40. Cluster-I, Cluster-II and Cluster-VI comprised of three genotypes each with Cluster-I comprising SJJS-4, SJJS-12, SJJS-31 genotypes, Cluster-II comprising SJJS-10, SJJS-27, SJJS-28 genotypes and Cluster-VI having SJJS-24, SJJS-32, SJJS-36 genotypes. Cluster analysis in present study revealed that spatial divergence is not responsible for grouping of genotypes into different clusters, however, genotypes from different geographical locations got clustered into same group. The grouping of different genotypes from different geographical locations into a cluster can be attributed to the free exchange of plant material and admixture. It was also observed that many genotypes found growing in the nearby geographical locations were scattered in different clusters. It has been hypothesized by Murty and Arunachalam (1966) [11] that genetic architecture, developmental traits and heterogeneity of the populations are the possible reasons for the prevalence of this type of genetic diversity. The perusal

of the results on intra and inter cluster distances presented the table 5 revealed that Cluster-III had the maximum intra cluster distance (3.56) followed by Cluster-V (2.99). Highest inter-cluster distance was observed between Cluster-V and Cluster-VI which was 200.92 followed by Cluster-II and Cluster-VI as 188.62, Cluster-III and Cluster-VI as 155.65, Cluster-II and Cluster-V as 135.00 and Cluster-V and Cluster-VII as 130.30. It is clear from the results obtained on cluster analysis that inter-cluster distances were much higher than intra-cluster distances and parent selection for hybridization programme from clusters having highest inter-cluster distance would help to develop new hybrids. Hybridization attempted among the parents selected from clusters having large inter-cluster distances may lead to heterogenous progeny which is useful for isolating superior recombinants from the segregating populations. Similar findings were also observed by Rajan *et al.* (2009) [12] who advised to select parents for hybridization which are distantly related based on D² analysis. Data presented in table 6 pertaining to percent contribution of different parameters towards total divergence reveal that ascorbic acid content is the main contributor (32.69%) towards total divergence, followed by fruit weight (20.00%), yield efficiency (13.59%), acidity (11.41%), specific gravity (8.85%), total soluble solid content (8.33%) and fruit size (2.69%). Lowest contribution towards total divergence came from pulp to seed ratio (2.44%). Higher values for some parameters indicate their importance as main contributors towards genetic diversity available in natural population. De *et al.* (1988) [4] suggested that such traits which are contributing most towards total divergence should be given greater importance while choosing clusters for selection and as prospective parents for hybridization programmes.

Table 1: Variability parameters, heritability and genetic gain for important traits in seedling jamun genotypes.

Characters	Range	Mean	Components of Variance		Components of coefficient of variation		Heritability (Broad sense)	Genetic gain (percent of mean)
			σ^2_g	σ^2_p	GCV	PCV		
Fruit weight	8.30 - 11.47	10.04 ± 0.34	0.57	0.93	7.54	9.62	61.00	12.17
Fruit size	416.85 – 629.62	537 ± 34.67	29.38	50.04	10.09	13.22	58.00	15.86
Specific gravity	0.94 – 1.18	1.05 ± 0.06	0.002	0.007	4.27	7.99	29.00	4.70
Pulp: seed ratio	4.75 – 7.71	5.89 ± 0.61	0.82	1.21	15.38	18.68	68.00	26.08
TSS	10.00 – 17.35	14.19 ± 1.01	2.67	4.73	11.51	15.32	56.00	17.81
Acidity	0.47 – 0.94	0.64 ± 0.04	0.007	0.013	13.05	17.79	54.00	19.73
Ascorbic acid	22.71 – 45.93	29.93 ± 1.83	16.75	19.8	74.81	81.34	85.00	25.76
Yield efficiency	0.19 – 0.26	0.21 ± 0.02	0.004	0.007	30.12	39.84	57.00	46.90

Table 2: Genotypic and phenotypic correlation coefficients for various traits in jamun genotypes.

Characters	Correlation	Fruit weight	Fruit size	Specific gravity	Pulp: seed ratio	TSS	Acidity	Ascorbic acid	Yield efficiency
Fruit weight	G	-	0.852*	0.671*	0.559	0.562	-0.388	-0.403	0.698*
	P	-	0.874*	0.693*	0.586	0.586	-0.432	-0.445	0.721*
Fruit size	G		-	0.587	0.622	0.076	-0.233	-0.174	0.749*
	P			0.643	0.651	0.347	-0.441	-0.385	0.753*
Specific gravity	G			-	0.567	0.394	-0.359	-0.123	0.491
	P				0.583	0.422	-0.369	-0.156	0.533
Pulp: seed ratio	G				-	0.485	0.143	0.372	0.753
	P					0.543	0.165	0.432	0.599
T.S.S.	G					-	-0.236	-0.160	0.595
	P						-0.283	-0.187	0.662
Acidity	G						-	0.538	-0.219
	P							0.546	-0.378
Ascorbic acid	G							-	-0.138
	P								-0.308

*Significant at 5%

Table 3: Path analysis of various traits on yield efficiency in jamun genotypes.

Characters	Fruit weight	Fruit size	Specific Gravity	Pulp: Seed ratio	TSS	Acidity	Ascorbic acid	Genetic correlation of yield efficiency
Fruit weight	0.244	0.148	0.110	0.178	0.201	-0.019	-0.018	0.698
Fruit size	0.122	0.352	0.102	0.262	0.120	-0.001	-0.001	0.749
Specific gravity	0.218	0.290	0.103	-0.0004	0.034	-0.0003	0.0001	0.533
Pulp: seed ratio	0.152	0.143	0.384	0.320	-0.008	-0.002	0.007	0.599
T.S.S	0.165	0.122	-0.057	-0.092	0.269	-0.031	0.002	0.662
Acidity	-0.114	-0.196	-0.097	0.029	0.048	-0.263	-0.075	-0.377
Ascorbic acid	-0.090	-0.109	-0.012	-0.100	-0.002	-0.064	-0.223	-0.308

Residual: 18.09

Bold figures in the diagonal are direct effects and others are indirect effects.

Table 4: Distribution of different seedling origin jamun genotypes into clusters based on D² statistics.

Cluster	Number of genotypes in the cluster	Accession number of the genotype
I	3	SJJS-4, SJJS-12, SJJS-31
II	3	SJJS-10, SJJS-27, SJJS-28
III	7	SJJS-6, SJJS-8, SJJS-15, SJJS-19, SJJS-22, SJJS-30, SJJS-38
IV	11	SJJS-1, SJJS-3, SJJS-5, SJJS-7, SJJS-11, SJJS-13, SJJS-17, SJJS-18, SJJS-20, SJJS-21, SJJS-39
V	6	SJJS-23, SJJS-25, SJJS-29, SJJS-33, SJJS-34, SJJS-40
VI	3	SJJS-24, SJJS-32, SJJS-36
VII	7	SJJS-2, SJJS-9, SJJS-14, SJJS-16, SJJS-26, SJJS-35, SJJS-37

Table 5: Average inter and intra cluster distance values among different jamun genotypes

Clusters	I	II	III	IV	V	VI	VII
I	2.52	103.75	101.39	93.91	107.47	111.43	95.27
II		2.75	117.38	119.74	135.00	188.62	110.77
III			3.56	112.38	110.51	155.65	107.34
IV				2.51	152.75	106.59	95.13
V					2.99	200.92	130.30
VI						2.70	120.19
VII							2.50

Table 6: Percent contribution of individual traits towards total divergence in jamun genotypes.

Traits	Number of times appearing first in ranking	Percent contribution towards total divergence
Fruit weight	156	20.00
Fruit size	21	2.69
Specific gravity	69	8.85
Pulp: seed ratio	19	2.44
T.S.S.	65	8.33
Acidity	89	11.41
Ascorbic acid	255	32.69
Yield efficiency	106	13.59

Conclusion

It was concluded from the study that huge genetic variations exists among the seedling origin population of jamun in Jammu region. High heritability along-with with high genetic gain was recorded for the character yield efficiency, whereas, high heritability coupled with moderate genetic gain was recorded in case of pulp to seed ratio and ascorbic acid content. Average fruit weight revealed significant, positive correlation with fruit size, fruit specific gravity, pulp to seed ratio, total soluble solid content, yield efficiency and negative correlation with ascorbic acid content and acidity at both genotypic and phenotypic levels. Highest positive direct effect on yield efficiency was yielded by fruit size followed by total soluble solid content, whereas, titratable acidity exhibited highest negative effect on yield efficiency. Maximum positive indirect effect on yield efficiency was recorded from fruit size through fruit specific gravity followed by pulp to seed ratio through fruit size.

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