DIVERSITY OF JAMUN (*Syzygium cumini* L.) FOR HORTICULTURAL TRAITS

By

Madhvi Plathia

(J-11-D-143-A)

Thesis submitted to Faculty of Postgraduate Studies

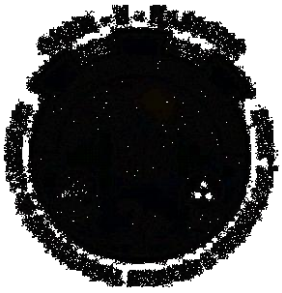
in partial fulfillment of the requirements

for the degree of

DOCTOR OF PHILOSOPHY

IN

HORTICULTURE (FRUIT SCIENCE)



Division of Fruit Science
Sher-e-Kashmir University of Agricultural Sciences & Technology of Jammu
Main Campus, Chatha, Jammu 180009
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Ph.D.

CHARACTERIZATION AND EVALUATION OF GENETIC DIVERSITY OF JAMUN (*Syzygium cumini* L.) FOR HORTICULTURAL TRAITS

Madhvi Plathia

2018

CERTIFICATE-I

This is to certify that the thesis entitled **"Characterization and evaluation of genetic diversity of jamun (*Syzygium cumini* L.) for horticultural traits"** submitted in partial fulfillment of the requirements for the degree of **Doctor of Philosophy in Horticulture (Fruit Science)** to the Faculty of Post Graduate Studies, Sher-e-Kashmir University of Agricultural Sciences and Technology of Jammu, is a record of bonafide research, carried out by **Miss Madhvi Plathia,** Registration No. **J-11-D-143-A**, under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma. It is further certified that help and assistance received during the course of thesis investigation have been duly acknowledged.

Dr. V. K. Wali

(Major Advisor)

Place: Jammu

Date: 4-1-2018

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CERTIFICATE-II

We, the members of advisory committee of **Miss Madhvi Plathia,** Registration No. **J-11-D-143-A,** a candidate for the degree of, **Doctor of Philosophy in Horticulture (Fruit Science)** have gone through the manuscript of the thesis entitled **"Characterization and evaluation of genetic diversity of jamun (*Syzygium cumini* L.) for horticultural traits"** and recommend that it may be submitted by the student in partial fulfillment of requirements for the degree.

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This is to certify that the thesis entitled **"Characterization and evaluation of genetic diversity of jamun (*Syzygium cumini* L.) for horticultural traits"** submitted by **Miss Madhvi Plathia,** Registration No. **J-11-D-143-A,** to the Faculty of Post Graduate Studies, Sher-e-Kashmir University of Agricultural Sciences and Technology Jammu, in partial fulfillment of the requirement for the degree of **Doctor of Philosophy in Horticulture (Fruit Science)**, was examined and approved by the advisory committee and external examiner (s) on 2-04-2018

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None is forgotten but everyone is not included.

Place: Jammu

Date: 4/01/2018

Madhvi Plathia

DEDICATED

TO MY RESPECTED TEACHERS

&

BELOVED FAMILY

ABSTRACT

Title of the Thesis	**:**	**CHARACTERIZATION AND EVALUATION OF GENETIC DIVERSITY OF JAMUN (*Syzygium cumini* L.) FOR HORTICULTURAL TRAITS**
Major Subject	**:**	Fruit Science
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ABSTRACT

The present investigations entitled "Characterization and evaluation of genetic diversity of jamun (*Syzygium cumini* L.) for horticultural traits" were undertaken during 2013-2014 in the jamun growing areas of Jammu district of Jammu and Kashmir. Survey was conducted to locate areas of diversity for jamun and on the basis of expression of different characters forty plants were selected for characterization and evaluation of genetic diversity according to the minimal descriptor jamun published by National Bureau of Plant Genetic Resources. Most of the vegetative, floral and fruit characters recorded as per the descriptor, revealed wide variations among the genotypes studied. Highest heritability (broad sense) was recorded as 67.8 per cent for the character pulp to seed ratio and lowest (28.6%) for specific gravity. Maximum genetic gain (46.9%) was recorded for yield efficiency and minimum (4.7%) for specific gravity. The correlation studies revealed that specific gravity, pulp to seed ratio and TSS exhibited positive and significant correlation whereas fruit weight, fruit size, acidity and ascorbic acid showed negative correlation with yield efficiency at both phenotypic and genotypic levels. Path analysis revealed that maximum positive direct effect on yield efficiency came from fruit size followed by pulp: seed ratio whereas the significant positive indirect effect came from fruit size through pulp: seed ratio. In divergence analysis, all the forty genotypes were grouped into seven clusters. Highest mean values for fruit weight (11.36 g) and fruit size (620.71 cm^2) were recorded in Cluster-II, whereas, Cluster-I recorded maximum pulp to seed ratio (6.71) and ascorbic acid (42.18 mg/100 g). Maximum mean value for TSS (15.04°B) and yield efficiency (0.23) was noted in Cluster-V and for specific gravity (1.06) in Cluster-IV. The

genetic diversity observed during the present investigations can be beneficially exploited either by the way of direct selection of individual superior genotypes or by using them as donor parents in the hybridization programme, keeping in view the high heritability (broad sense) and the magnitude of genetic advance in the different traits of horticultural importance. On the basis of the evaluation of different characters, five jamun genotypes of seedling origin *viz*. SJJS-4, SJJS-10, SJJS-23, SJJS-27 and SJJS-29 have been found promising for different fruit quality parameters.

Keywords: *Syzygium*, heritability, correlation, variability, cluster analysis

Signature of Major Advisor

Signature of the Student

CONTENTS

LIST OF TABLES

LIST OF PLATES

LIST OFABBREVATIONS USED IN THIS MANUSCRIPT

cm^3	Cubic centimetre
cm	Centimetre
cv.	Cultivar
DPPH	2, 2- diphenyl-1-picrylhydrazyl
E.C.	electric conductivity
et al.	*et alia* = and others
ECV	Environmental coefficient of variation
etc.	*et cetera* = and the rest
g	Gram
GA	Genetic advance
GCV	Genotypic coefficient of variation
h^2 (bs)	Heritability in broad sense
HCl	Hydrochloric acid
i.e.	*id est* = that is
Kg	Kilogram
l	Litre
m	Metre
m^3	Metre cube
m^2	Metre square
ml	Millilitre
mg	Milligram
min	Minute
mm	Millimetre
mm^2	millimetre square
nm	Nanometre
N	Normal
NBPGR	National Bureau of Plant Genetic Resources
PCV	Phenotypic coefficient of variation
pH	potential of hydrogen
S.E. m	standard error (mean)
TSS	Total soluble solids

Var.	Variety
viz.	*videlicet* = namely
/	Per
%	Per cent
+	Plus
^{o}B	degree Brix
^{o}C	degree Celsius

Introduction

CHAPTER-1

INTRODUCTION

Jamun (*Syzygium cumini* L.) also known as Indian blackberry, is an important evergreen tropical fruit which belongs to family Myrtaceae. Jamun is believed to be native to India, Burma, Ceylon and Andaman Islands (Zeven and deWet, 1982). It was introduced from India and tropical Asia to southern Africa for its edible and attractive fruits. 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 importance. In India, population of jamun is located in ecologically different habitats and is growing successfully in the states of Punjab, Haryana, Uttar Pradesh, Maharashtra, Gujarat, Madhya Pradesh, Bihar, Chhattisgarh, Jharkhand, Karnataka, Tamil Nadu, Andhra Pradesh including Jammu and Kashmir up to an elevation of 1300m above mean sea level. 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 under rain-fed sub-tropic conditions.

Almost all parts of the jamun tree are used for various purposes. Ripen fruits are very juicy, almost odourless, with a pleasant, slightly bitter, astringent taste and consumed fresh or processed into various products. The fruit pulp is used to make squash, sharbat, syrup, jams, jellies, juice, vinegar and puddings. Fruits are also used to make wine in large quantities in Philippines. Jamun wood being very strong and resistance to water and termite attack, is used to install motors in the wells and being a fast-growing tree, it provides excellent firewood and charcoal to the rural population in India (Chaudhary and Mukhopadhyay, 2012). Jamun has many medicinal values and in the Indian System of Medicine, jamun fruit has been described as astringent, stomachic, carminative, antiscorbutic and diuretic (Singh, 2001). The refreshing and curative properties of jamun make it one of the useful medicinal fruits of India. Jamun fruit is reported to be a good source of minerals, protein and carbohydrate, vitamin C, sugars, phenolic compounds (gallic acid, tannins, flavonoids, anthocyanins) and other antioxidant components.

India ranks on second place in respect of having highest of diabetic people population (63 million aged between 20-79 years) next to China (Sinha, 2012). Jamun

seeds contain various alkaloids such as jambosin and glycoside, which inhibit the conversion of starch into sugars, therefore, useful for patients suffering from diabetes. Also, the juice of the ripe fruit or jamun vinegar may be administered in cases of enlargement of the spleen, chronic diaorrhea, and urine retention. Jamun fruit is an effective food remedy for bleeding piles and correcting liver disorders. The fruit or fruit juice taken with salt every morning for two or three months has been found to affect radical cure and save the user from bleeding piles lifelong (Anonymous, 1954; Joshi, 2001). It has wonderful antihyperglycaemic properties and has also proven to have good anti-oxidant, anti-bacterial, antigenotoxic anti-inflammatory and anti-HIV properties (Sagrawat *et al*., 2006).

Despite such miraculous advantages of consuming jamun fruit, when compared to the extent of increasing demand and growing awareness amongst the masses, the supply is very limited and has created demand for better quality fruit having good fruit size and other horticultural traits. The fruits are being sold from Rs. 40 to 160 per kg depending upon fruit quality as well as location of the material (Patel *et al*., 2005). Looking at the importance of this high value fruit crop, the demand for its planting material is also increasing. However, a few known varieties are available, despite the existence of a wide variability in jamun throughout the length and width of India. Local availability of well-adapted jamun cultivar having good qualitative and quantitative traits is the need of the hour for meeting the demand of ever increasing consumers, especially for health conscious.

Genetic resources of jamun are facing a great threat of extinction due to climate change, large-scale urbanization, developmental projects, lack of commercialization and limited knowledge regarding the importance. To safeguard the existing diversity of jamun and to achieve sustainable development based on use of available genetic wealth, promotion and conservation of genetic diversity 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 for human need and greed. Many local genotypes have completely been lost and many others may be lost in near future. The ultimate goal 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 identifying superior genotypes, protecting and conserving the rich germplasm. To

accomplish this, besides the already existing varieties, local selections need to be identified, evaluated and standardized (Lone and Wafai, 1995) and commercialized. Variations can be successfully utilized for adaptability of a species e.g. drought resistance or selection of a suitable genotype for growth or fruit quality etc. (Sundaram *et al.,* 2003). The success of any improvement programme of fruit crops essentially depends on selection of superior genotypes and to a great extent on the genetic diversity existing in the population. Higher diversity leads to enhanced chances of development of superior and desired genotypes. Both selection and then further hybridization methods require presence of diverse population to choose from.

In India, the majority of the jamun trees growing naturally are of seedling origin. Being underutilized, meager information is available on improvement of jamun fruit crop. Because of allogamous in nature and pre-dominance of seed propagation, enormous genetic variability exists in respect of morphology, floral and physio-chemical characteristics. Jamun cultivation in India is based on very few cultivars and farmer selections *viz*., Ra jamun having oblong deep purple, highly juicy and sweet fruits is grown in North India (Singh *et al*., 2007), large fruited 'Paras' is grown in Gujarat, whereas in Varanasi region Seedless jamun is grown. A selection known as 'Narendra Jamun-6' has been identified with desirable traits at Faizabad. Besides, there are several area-specific local selections identified by the farmers based on fruit size, shape, taste, fruiting period and maturity of fruits etc. For instance, selections growing in Haryana and western Uttar Pradesh are Badama (large size and very juicy fruits), Kaatha (with small and acidic fruits), Jathi (maturing in June or Jeth), Ashada (maturing in June or Ashad) and still late type Bhado (maturing in August). Similarly selections are also found in Konkan area, Pune and Ahmednagar districts of Maharashtra (Keskar *et al*., 1989) and in Gujarat and Rajasthan.

Evaluation and characterization as well as estimation of diversity have been performed for various jamun collections in various parts of Maharashtra, Rajasthan, Gujarat, Uttar Pradesh and West Bengal. Extensive collections and evaluation studies for its characterization have been carried out in eastern Uttar Pradesh (Singh *et al*., 1999), Pune and Ahmednagar districts of Maharashtra (Keskar *et al.,* 1989),West Bengal (Kundu *et al*., 2001), Karnataka (Prabhuraj *et al.,* 2002) and North Goa (Devi *et al.*, 2002). Singh and Singh (2005) collected 33 accessions from Gujarat whereas National Bureau Plant Genetic Resources, New Delhi has made extensive collections from

Haryana and Western Uttar Pradesh in collaboration with Central Horticultural Experimental Station (Central Institute of Arid Horticulture, Bikaner), Godhra and Central Institute of Sub-Tropical Horticulture, Lucknow and 20 elite accessions have been identified. Srivastava *et al*., (2010) studied the physicochemical characteristics of fruits from 25 genotypes of jamun (*Syzygium cumini*) grown in Varanasi, Uttar Pradesh, and Pantnagar, Uttarakhand, India.

In Jammu subtropics, lot of variability is being observed in flowering, fruit size, ripening time, fruit quality characteristics but no systematic studies have been conducted to identify the superior trees for its further promotion. Therefore, present investigation entitled "Characterization and evaluation of genetic diversity of jamun (*Syzygium cumini* L.) for horticultural traits" has been carried out in Jammu district with the following objectives:

1. To survey, map and collect the data on foliage, flowering and fruit characters to assess the distribution range and to record the range of genetic variability in jamun within Jammu district.

2. To select the superior trees based on horticultural traits and consumer preference.

Review of Literature

CHAPTER-2

REVIEW OF LITERATURE

The jamun native to India, Burma, Ceylon and Andaman Islands, is available throughout the Indian plains upto the height of 1300 m. It is found grown wild or semi wild in most of the subtropical and tropical regions of India. Lot of genetic diversity is available in jamun and very little information is available in the crop. However, efforts have been made in the recent past by the breeders to systematically characterize and make selections out of the best genetic resources available in jamun. The diversity in the plant genetic resources also provide an opportunity for the fruit breeders to develop new and improved cultivars with desirable characteristics which include both farmer-preferred traits (yield potential, desired fruit and seed characteristics etc.) as well as breeder-preferred traits (pest and disease resistance, drought tolerance etc.). The characteristics are the depth of the genetic base that enables quick and easy discrimination between the phenotypes which are generally heritable, can be easily seen by the eye and are quickly expressed in all types of environments. According to Frankel (1986) characterization should provide a standardized record of readily accessible plant characters to identify an accession.

A standardized record of readily accessible plant characters to identify an accession is also an important part of characterization. In jamun, there are very few varieties available for cultivation. However, in several areas, specific local selections have been identified by farmers and local people since historical times. All these local selections or types are based on fruit size, shape, taste, fruiting period and maturity of fruits (Keskar *et al*., 1989, Singh *et al*., 2007). Despite of the selections made in different states of India, there is requirement for cultivar distinctness having scientific merits in a system that can ensure the selection of elite cultivars, promote horticultural productivity and contribute to the diversity of plant genetic resources (Smith and Smith, 1988).

Many researchers have collected the jamun germplasm from various resources and characterized for various horticultural traits such as flowering, fruiting, and fruit weight, pulp weight, TSS and acidity etc. On the basis of the characterization of the collected germplasm, several elite genotypes has been identified from Maharashtra

(Keskar *et al*., 1989), eight genotypes grouped into two categories: ovoid and oblong from eastern Uttar Pradesh (Singh *et al*., 1999), from West Bengal germplasm Selection 1 (oval shaped large fruits) and Selection 2 (cylindrical shaped medium sized fruit) proved better for yield and quality fruits (Kundu *et al.*, 2001), RNC-26 and RNC-11 were found promising for higher pulp and fruits weight from Uttar Pradesh and Jharkhand (Devi *et al.*, 2002) whereas five genotypes have been identified from Gujarat (Singh and Singh, 2005) *viz*., GJ-18, GJ-19, GJ-23, GJ-24 and GJ-25. Out of the germplasm screened, a total twenty diverse jamun accessions collected by NBPGR from Haryana and Uttar Pradesh were characterized for fruit and seed characters. These accessions showed a lot of variability. However, Malik *et al*. (2010), in their report on the genetic resources of tropical underutilized fruits in India, have clearly mentioned that the underutilized crops including jamun appears to be the crop of the future and needs focused attention as such type of fruits can meet nutritional needs as well as sustain the effect of climate change. In view of the great importance of underutilized fruit species including jamun, the Indian Council of Agricultural Research showed an urgent need to strengthen the genetic resources and improvement work in such types of fruit crops and launched a National Network Project on Underutilized Fruits including jamun. There is still need to take extensive characterization and field evaluation in local selections for release of area-specific cultivars of jamun.

In state of Jammu and Kashmir, a lot of genetic diversity is available in jamun which can be evaluated for making a selection in jamun having desirable horticultural traits *viz*. bigger fruit size, small seed with higher TSS etc. The present investigation entitled "Characterization and evaluation of genetic diversity of jamun (*Syzygium cumini* L.) for horticultural traits" was undertaken during 2013 and 2014 in the jamun growing areas of Jammu district. The relevant information pertaining to the horticultural characterization of jamun is limited, however in other fruit crops, a lot of work is reported. The literature utilized for the planning and execution of present studies is reviewed in this chapter under suitable headings.

2.1 Vegetative and yield characteristics

2.1.1 Tree characteristics

To identify and analyze the genetic diversity in any living species, including

jamun, both the phenotypic traits and genotypic traits are the basic indicators. Genetic variability is essentially the first step of plant breeding for crop improvement which is immediately available from germplasm. The germplasm may be defined as the material that forms the physical basis of heredity for species and is transmitted from one generation to next. Germplasm is considered as the reservoir of variability for different characters. Vavilov (1951) was the first to accept the fact that broad genetic base of germplasm is the basic need for plant breeder. Morphological analysis is quick and commonly used method to identify and characterize the germplasm through phenotyping. Phenotypic characteristics that are influenced by environmental factors, however, may cause elevated diversity in the desirable agronomic traits (Marinoni *et al*., 2003), thus lowering the reliability of the method.

In litchi, the growth behaviour of a genotype may vary in a climate other than it originated. Rai *et al.* (2001) also reported that genetic variation in 13 litchi genotypes were found under Ranchi condition for various traits including tree spread and volume.

Sanou *et al.* (2006) studied variability of agromorphological traits of shea trees in Mali and reported that the range of plant height, circumference and crown diameter was 6-25 m, 40-320 cm and 2-22.5 m respectively. The mean of plant height and circumference was 10.8 m and 142.7 cm, respectively.

Athani *et al*. (2009) carried out an experiment from May 2003 to July 2004 at Arabhavi in Gokak taluk of Belgaum district, Karnataka to know the morphological and physical characters of jamun strains (*Syzygium cumini*). Out of ten strains, seven were found large and three medium with respect to height of the plant. Shape of the canopy was round in five strains, while five strains had oval shaped canopy. Five strains had spreading habit and five had erect branching habit. All the ten strains had greyish white bark colour. The maximum tree girth was noticed in strain KLV-9 (94.4 cm).

Swamy *et al.* (2017) reported that among fifteen jamun genotypes studied, the highest spread of 9.50 m was recorded in KJS-45 and KJS-48, which were old trees and lower height was recorded in KJS- 45a, KJS-45b and KJS-20 (2.00-2.65 m) which were young trees. Five genotypes were of large size and ten were of small stature.

2.1.2 Yield characteristics

Tree yield is a complex character and is a function of both number of fruits on the tree and their weight. The number of fruits in turn depends on the flower density, tree size and percentage of fruit set (Lombard *et al*., 1998). Usually the percentage of fruit set decreases as the flower density increases, but this relationship is heavily influenced by climate (Chang *et al*., 1987; Dennis, 1986). When the fruit set is too large for the tree to handle, thinning becomes necessary to ensure that the remaining fruit attains marketable size (Costa and Vizzotto, 2000). Only tree size, plantation density and number of flower buds after pruning are available at the beginning of the active period to estimate the potential yield in a simple rapid way. Potential yield increases with tree size, although not linearly since bigger trees are less efficient (Lombard *et al*., 1998). Positive correlations were observed between all the growth indices, especially trunk girth and yield in different apple genotypes. Silva *et al*. (1980) reported that in of crown weight and the number of branches had a significant correlation with the total number of fruits. They also suggested that by using girth measurements one young orchard of apple (Golden Delicious), yield became increasingly a function of trunk girth during first three cropping years.

Athani *et al*. (2009) studied leaf characters of ten jamun strains under Karnataka conditions and reported that maximum yield (260 kg/plant) was noticed in strain GLH-85.

Blazkova *et al*. (2010) conducted the survey of cherry and found that quantities of fruits harvested from trees were mainly dependent on the cultivar and its canopy volume. In some cases, however, rootstock and tree training also had a significant influence on this characteristic. Real incidence of these influences ensues from some assessments done in USA as well (Lang, 2005).

Singh and Singh (2012) studied variability in sixteen jamun genotypes and revealed that maximum yield (152.00 kg/plant) was recorded in GJ-2 and minimum (90.00 kg/plant) in GJ-4.

Lawande *et al.* (2014) studied uniformly grown, 9 years old grafted plants of jamun var. Konkan Bahadoli at two locations and concluded that vigorous jamun plants of 6.5 m height beheaded back at 3.6 m and less vigorous jamun plants of 3.6 m

height should be pruned to 2.7 m height for obtaining more number of flowered plants, higher flowering intensity, more number of flowers and fruits per branch let and yield as well as for more number of sellable fruits and less time required for harvesting the fruits.

2.1.3 Leaf characteristics

Leaves, through photosynthesis, produce the structural carbohydrates and sugars that are critical for the growth of a fruit. They not only produce the food but also aid in mobilizing nutrients and reserves from the rest of the tree and the soil.

Lone and Wafai (1995) reported that cherries show remarkable diversity in leaf size and divided the varieties into two groups, small and large leaved. The small leaved varieties included Awal Number Gilas and Acc.CITH whereas large leaved varieties included Gole, Makhmali, Mishri, Tontal, Double and Gogji Makhmali Gilas.

Among the 55 jamun trees which were sampled around Gokak taluk of Belgaum district for variability studies, it was seen that each differed distinctly in morphological leaf traits which included leaf length, breadth and petiole length (Prabhuraj *et al*., 2002).

Sanou *et al.* (2006) studied variability of agromorphological traits of shea trees in Mali and reported that the range of leaf length, leaf width and petiole length was 5.4-21.3 cm, 2.2-6.8 cm and 3.7-17.0 mm respectively. The mean of leaf length, leaf width and petiole length was 13.6 cm, 4.1 cm, 7.2 mm respectively. The variance components showed that variation among populations represented the smaller percentage of the total variation with most of the values varying between 15 and 30 per cent. The repeatability coefficient was generally high for tree within populations with values ranging between 0.23 and 0.78. Although genetic correlations cannot be accurately estimated, due to difficulties in separation from environmental effects, the results indicate that there is a very low genetic relation between the three kinds of traits, i.e. between those related to tree and those related to leaf and those related to fruit.

The shape and size of leaf play an important role in the growth of plants. Leaves having less width with more length are important features to control the process of transpiration in case the field having water scarcity (Singh, 2007). It had been accepted

by the earlier workers that the leaf area was a linear function of leaf characters in different fruit crops (Fulger, 1965, Holland, 1968).

Athani *et al*. (2009) studied leaf characters of jamun strains under Karnataka conditions and reported that with respect to orientation, shape and colour of leaf, all the selected 10 strains showed the intermediate, oblong lanceolate and dark green colour of leaf. The highest leaf length (14.7 cm) was noticed in strain DPD-25, while highest leaf breadth (6.5 cm) was in strain DPD-20. Leaf length to breadth ratio was maximum (2.7) in strain GLH-85. The strain KLV-9 had the highest leaf area (85.3 cm^2). Maximum petiole length (2.0 cm) was observed in strain GLH-58, while strain DPD-24 had maximum leaf length to petiole length ratio (8.7).

Sharma *et al*. (2010) reported that guava genotypes Allahabad Safeda and Smooth Green showed green shade of foliage and genotypes Nasik and Apple Colour showed pale green shade, whereas Spear Acid and Lucknow-49 exhibited dark green foliage. Wani *et al*. 2010 studied variation in leaf shape in thirty three seedling origin quince genotypes and found ovate oblong leaf shape in thirty two genotypes and oblate in one of them.

Ayyanar and Subash-Babu (2012) reviewed various characteristics of jamun and found that leaves vary were leathery, oblong, ovate to elliptic or obovate elliptic with 6 to 12 cm long (extremely variable in shape, smooth and shining with numerous nerves uniting within the margin) and the tip being broad and less acuminate.

Preisigke *et al*. (2013) compared the different clustering methods in assessing genetic divergence among mango accessions, as well as identify the minimum efficient descriptors for the crop. A total of 20 mango accessions in Cáceres, Mato Grosso state of Brazil were evaluated. When building dissimilarity matrices, the descriptors were divided according to the following groups: leaf, flower/inflorescence, fruit, seed and growth habit and ripening period. With these divisions, combinations were performed among the groups of descriptors. The similarity index was used to obtain the dissimilarity matrices. Later, the accessions were clustered using the methods of Tocher, Ward and UPGMA. The study observed that the use of only the fruit descriptors, in detriment of the 64 overall descriptors, makes it possible to obtain, with greater efficiency, the genetic dissimilarity among accessions of *Mangifera*

indica L. The Tocher, UPGMA and Ward methods were in agreement in allocating the 20 evaluated accessions.

Ribeiro *et al*. (2013) characterized 103 mango accessions of the field germplasm using 50 morphological descriptors established by the Brazilian Ministry of Agriculture, livestock and supply to help in the development of new mango cultivars for the Northeastern region of Brazil. Four trees were selected for each accession and eight adult leaves, eight flowers and 16 fruits were collected from each tree. Morphological characteristics ranging from plant size to seed embryo were evaluated. Simple percentages were estimated for all the descriptors. Only the descriptors for leaf symmetry and fruit waxiness did not show variability among the accessions.

Singh *et al*. (2017) carried out a study to investigate morpho-physiological and productivity characteristics of four genotypes of five years old guava (*Psidium guajava* L.) trees, grown under hot-arid zone of Rajasthan. Preliminary investigation indicated that all four cultivars of guava could survive except merely 10.0 per cent field mortality in guava cv. L-49. The maximum increase in plant height (25.93%) and number of new leaves/branch (4.66) over six months of planting were recorded in Shweta, followed by Lalit, while during fruiting (August for rainy season guava) highest number of new shoot sprouts/branch was found in Allahabad Safeda, followed by Shweta. Lalit and Shweta also produced substantial number of new leaves/branch during fruiting, than the other cultivars. The leaves produced on Sweta received lesser photosynthetically active radiations (PAR) but had highest leaf area (80.91 cm^2), specific leaf area (36.61 cm2/g) and relative water content (60.19%). Although L-49 had thicker leaves (lowest SLA; 33. 29 cm2/g), indicating better adaptation towards resource poor environment but other cultivars of guava also had SLA at par among other three cultivars. They concluded that guava cultivars Sweta followed by Lalit performed better under hot-arid environment with better growth and physiological adaptation. L-49 was not found suitable for the area.

2.3 Floral characters

Flowering is one of the most important jamun phenophases, because yield depends on the start, duration and abundance of flowering. The flowering time is greatly influenced by weather, particularly by temperature and relative humidity before the beginning of flowering and during flowering. Teotia and Pandey (1970)

also found that variation in duration of flowering and number of days of flowering differed due to climatic variations in guava crop. According to Chaudhary and Mukhopadhyay (2012) jamun flowers are rich in nectar and are useful in the apiculture for their yield of high quality honey. Flowering occur from March to May and flowers get pollinated by honey bees, house flies and wind. Fruit formation takes place about 32 days after flowering.

Majumder *et al*. (2012) studied plant, inflorescences and fruit characteristics of sixty mango genotypes during the period 2007 to 2008. There were distinct variations among the studied gemplasm interms of plant, leaf, inflorescence, fruit characters and yield. Wide variations were observed in relation to the percent flowering shoot, percent perfect flower, percent fruit set per panicle, number of harvested fruits per plant, individual fruit weight, per cent edible portion and per cent total soluble solid ranging from 24.00 to 71.33%, 8.10 to 19.17%, 9.07 to 29.27%, 21.33 to 60.33, 365.33 to 219.00g, 45.22 to 79.83% and 16.90 to 28.26%, respectively. The germplasm MI28 was on the top of the list in case of number of panicles, number of main branch per panicle, percent perfect flower and fruits harvested per plant. The maximum and minimum number of fruit set per panicle was noted in MI28 and MI92, respectively. The maximum percentage of fruit harvested per panicle was found in MI94 (5.46) but the germplasm MI28 gave the highest number of fruits per plant (60.33). Moreover, the germplasm MI09 had the highest percentage of fruit pulp portion (79.83).

In jamun, flowering start in February-March and fruiting in May to July. The sessile whitish-yellow flowers emerge in clusters; have a funnel-shaped calyx and 4 to 5 united petals. The flower appears during the month of March to April and the fruit formation takes place about 32 days after flowering during the month of May to July. (Chaudhary and Mukhopadhyay, 2012).

Singh and Singh (2012) studied flowering in sixteen jamun genotypes and revealed wide variation in flowering and fruiting among them. Earliest flowering took place (mid February) in GJ-1, GJ-2, GJ-3 and GJ-10. The genotypes GJ-3, GJ-2, GJ-10 and GJ-14 found to be earliest to ripen (First week of May) and GJ-16 and GJ-13 ripened at last (Last June).

Devi *et al*. (2016) conducted an experiment to know the variability on flowering and physical characters of jamun genotypes. Observation on the flowering and

physical characters of fruits were recorded on six genotypes wherein significant differences were observed among the genotypes for the characters studied. Month of flower initiation among the selected genotypes ranged from last week of February to mid-April. Genotype AJG-58 showed early initiation of flower (Late February), maximum number of panicles (94.00) and higher number of flowers (2983.25). Other genotypes showing early initiation of flower (Late February) was AJG-45 while three genotypes *viz*. AJG-85, T.C-85 and Konkan Bahadoli revealed late initiation (mid-April). Genotypes AJG-20 found to be recorded maximum number of fruit (1644), number of fruit harvested (882) and fruit length (33.32 mm) whereas maximum fruit width was recorded in Konkan Bahadoli (21.62 mm). Maximum fruit weight and pulp weight was recorded in AJG-85 as 9.50 g and 6.93 g, respectively. Seed length and seed width was found maximum in Konkan Bahadoli as 17.93 mm and 10.43 mm, respectively, followed by AJG-20. Maximum seed weight (2.40 g) was recorded in AJG- 20 followed by AJG-85 with 2.37 g. These two genotypes can be utilized in making jamun seed powder which is of high medicinal importance for diabetic patients. These characters could be considered as important traits for breeding programmes.

Tolli *et al*. (2016) in their study concluded that morphological characterization allows for the study of plant variation using visual attributes. Fruits have been the major descriptors for identification of different varieties of fruit crops. However, even in their absence, farmers, breeders and interested stakeholders require to distinguish between varieties. This study aimed at determining diversity in mango germplasm from the Upper Athi River (UAR) and providing useful descriptors for the identification of different mango varieties in the absence of fruits. A total of seventeen IPGRI descriptors for mango were selected for use in visual assessment of 98 mango accessions from fifteen sites of the Upper Athi River (UAR) region of Eastern Kenya. Purposive sampling was used to identify farmers growing diverse varieties of mangoes. Evaluation of descriptors was performed on site and data collected was subjected to multivariate analysis including Principal Component analysis (PCA) and cluster analysis. Results classified the accessions into two major groups corresponding to indigenous (17.35%) and exotic (82.65%) varieties. The PCA showed the first seven principal components accounting for 82.87% of the total variance. A strong and highly significant correlation was also found between the colors of young leaves, stem

circumference, tree height, leaf margin type and fragrance strength. Four leaf descriptor traits namely pulvinus thickness, leaf pubescence, angle of secondary veins to midrib and presence of secondary veins on leaf, were discarded for presenting only one phenotypic class and hence ineffective in distinguishing between mango varieties in that region. These results reveal that mango germplasm in that region possesses significant diversity and that other morphological traits apart from fruits are useful in determining significant morphological variation that can be incorporated in mango breeding programs in Kenya.

2.4 Fruit characters

The physico-chemical traits serve as traditional markers for discriminating different germplasm or accessions. The enormous variability was observed with respect to morphology and physico-chemical attributes of fruits due to pre-dominance of seed propagation in jamun trees. The study of physico-chemical attributes screening are very useful for the selection of high yielding accessions of jamun.

Noomrio and Dahot (1996) studied chromatographic analysis of jamun and reported that fruit contained different types of sugars *viz.*, glucose, mannose and sucrose and amino acids *viz*., alanine, arginine, asparagine, tyrosine, glutamine and cysteine.

Devi *et al.* (2002) collected ripe fruits from 18 selected trees and analyzed for physico-chemical traits like fruit weight, length, width, pulp and seed content, pulp: seed ratio, TSS (°B), titratable acidity and carbohydrates in terms of total sugars and reducing sugars. The study revealed that there was a wide variation among its accessions in terms of fruit weight (3.42-13.67 g), length (3.31-5.26 cm), girth (5.21 to 9.82 cm), length: width ratio (1.44-2.3) and pulp percentage (58.57-84.55%) Total soluble solids (12.0-26.8 °B), titratable acidity (0.59-1.63%), total sugars (6.87-25.31%) and sugar: acid ratio (15.39-27.92).

Patel *et al*. (2005) conducted survey in Uttar Pradesh (Lucknow, Varanasi and adjoining areas) and Jharkhand (Ranchi and adjoining areas) to find out the existing natural variability among the jamun seedling trees and to identify superior genotypes with good fruit qualities. The data pertaining to physical and chemical quality attributes of fruits from 32 jamun genotypes showed significant differences and a high

degree of variability for all the characters studied. The fruit weight varied from 2.20 g in RNC-29 to 13.80 g in RNC-26 genotypes. The genotypes, RNC-26 and RNC-11 were found promising and had higher fruit and pulp weight with sweet fruits. Highest pulp content (97.71%) was recorded in V-8 followed by V-6 (95.84 %) and V-7 (93.81%) genotypes collected from Varanasi region. Thin seed with almost negligible seed weight (0.12 g) was observed in V-8 followed by V-6 (0.16 g) and V-7 (0.31 g).

Chowdhury and Ray (2007) studied composition of jamun fruit (cv. Jamun) harvested locally in May for preparing wine. They found that per 100 g of jamun fruit contains: 83.20 g moisture, 14.00 g reducing sugars, 0.90 g crude fibre, 0.25 g ascorbic acid, 0.14 g anthocyanin, 0.33 g ash, 0.13 g nitrogen, 1.90 g tannin and 0.30 g fat.

Shahnawaz *et al.* (2009) studied composition of fresh jamun (improved variety) fruit pulp along with various jamun prossessed products like jam, squash juice, pulp powder, seed powder stored under various conditions. They reported that fresh jamun pulp contained 0.32 per cent ash, 19.14 mg Vitamin C per 100 g, 5.72 per cent reducing sugars, 8.58 per cent non-reducing sugars, 14.31 per cent total sugars, 17.37 per cent carbohydrates, 0.72 per cent proteins, 0.27 per cent fats, 18.68 per cent total solids and 0.22 per cent crude fibres.

Malik *et al*. (2010) compiled genetic resources studies of various underutilized fruits including jamun. They reported that total of 20 diverse jamun accessions collected by NBPGR from Haryana and Uttar Pradesh were characterized for fruit and seed characters. Fruit size (length x width) varied from 2.12 cm × 5.44 cm to 3.35 cm × 7.52 cm. The lightest fruit weighed 3.04 gm and heaviest weighed 8.84 gm which depicted a large variation. Seed length x width ranged from 1.62 cm x 3.02 cm to 2.62 cm x 4.30 cm. The pulp weight showed large variation from 1.24 to 6.96 gm. The accessions which showed largest fruits with highest pulp weight were IC537858, IC537848, IC537846 and IC537853. Smallest seeds were seen in accessions IC537860, IC537849 and IC537850. TSS in fruits was also variable ranging from 5.96 to 14.2 ºB. Fruits with high TSS value were found in accessions IC537842, IC537854 and IC537845.

Srivastava *et al*. (2010) studied the physico-chemical characteristics of fruits from 25 genotypes of jamun grown in Varanasi, Uttar Pradesh, and Pantnagar, Uttarakhand, India from June to July 2006. Fruit weight ranged from 2.24 g in genotype VJ-1 5 to

7.05 g in genotype PJ-24. Fruit length was greatest for genotype PJ-22 (2.66 cm) and lowest for genotype VJ-4 (1.97 cm), whereas fruit breadth was greatest for genotype PJ-24 as 2.07 cm and lowest for genotype PJ-25 as 1.26 cm. Genotype PJ-25 had cylindrical fruits, whereas genotypes PJ-24 and VJ-19 had round fruits. Pulp weight was greatest for genotypes PJ-23 (5.82 g), PJ-24 (5.54 g) and PJ-2 1 (5.32 g). Pulp content ranged from 47.76 to 83.5 per cent, with maximum value for genotype PJ-23. The correlation of pulp weight and pulp to seed ratio with fruit weight was highly significant and positive. The lowest percentage of seeds (16.5%) was recorded for genotype PJ-23. The total soluble solids content varied from 14.3% in genotype VJ-12) to 26.2% in genotype VJ-14. The total sugar content was lowest (9.94%) for genotype VJ-12 and highest (25.46%) for genotype VJ-14. The reducing sugar content was highest (20.54%) for genotype VJ-14 and lowest (8.14%) for genotype VJ-12. The sugar: acid ratio ranged from 13.42 in genotype PJ-25 to 37.45 in genotype VJ-5. Acidity value was highest (1.14%) for genotype VJ-20 and lowest (0.37%) for genotype VJ-5. The TSS: acid ratio ranged from 14.50 in genotype PJ-25 to 43.78 in genotype VJ-5. The ascorbic acid content varied from 30.0/100 g pulp in genotypeVJ-10 to 45.3/100 g pulp in genotype PJ-23.

Wide variation of physico-chemical composition in thirty three seedling origin quince genotypes from Budgam district of Jammu and Kashmir has been reported by Wani *et al*., 2010. They found variability in fruit shapes i.e., ovate oblong, globose, flat and pyriform and ovate oblong fruit shape as dominant. They also reported wide range of variability in physico-chemical characters. Fruit weight ranged from 62.5 in genotype SKAUQ-026 to 274.5 g in genotype SKAUQ-028. Total soluble solids content was highest (18^{o}B) in genotype SKAUQ-031whereas lowest (5 ^{o}B) in genotype SKAUQ-026. The acidity value varied from 3.02 mg/100 g in genotype SKAUQ-027 to 18.3 mg/100 g in genotype SKAUQ-034. Ascorbic acid was highest (18.3 mg/100 g) for genotype SKAUQ-034 and lowest (3.02 mg/100 g) for genotype SKAUQ-027.

Shahnawaz and Sheikh (2011) while studying the improved (V1) and indigenous (V2) cultivars of Jamun observed significantly higher edible portion in V1 (69.10%) than V2 (39.19%), besides having larger fruits (9.55 g in weight, 3.88 cm × 2.98 cm in size).

Singh and Singh (2012) studied flowering, fruiting and fruit quality attributes of sixteen jamun genotypes in Gujarat to identify the elite genotypes and revealed that there was a wide variation among the genotypes. Earliest flowering (Mid February) took place in GJ-1, GJ-2, GJ-3 and GJ-10. Maximum panicle length (15.50 cm) and number of fruits per panicle (28.00) were found in GJ-2. Fruits of genotypes GJ-3, GJ-2, GJ-10 and GJ-14 ripened earliest (First Week May), while GJ-16 and GJ-13 ripened at the last (last June). Maximum yield per plant (152.00 kg) was recorded in genotype GJ-2. Individual fruit weight ranged from 9.80 to 21.50 g, length from 1.98 to 3.20 cm and pulp percentage from 79.67 to 86.37 percent, TSS from 9.60 to 12.30^{o}B, total sugar 7.40 to 9.14% and vitamin C 33.00 to 43.00 mg/100g. On the basis of overall performance GJ-2, GJ-3 and GJ-8 were found to be promising among all the genotypes.

Ali *et al*. (2013) undertook studies to assess some compositional properties and antioxidant potentials of jaman fruit parts. Proximate composition in terms of crude protein, fat, fiber and ash content were estimated in pulp, skin and seed portions and found in the range of 3.57-5.05%, 1.60-8.00%, 3.09-3.33%, 4.51-6.21% respectively. Seed was leading in protein, fat, ash and crude fiber, whereas varying levels were found in pulp and skin. Among the chemical attributes, total sugars, titratable acidity and ascorbic acid were assessed only in fruit pulp on dry weight basis that were 52.48%, 5.66% and 187.63 mg/100g, while total soluble solids (9.11^{o}B) were estimated in fresh pulp. Bioactive composition revealed that jamun fruit parts were rich in phenolics (4812.03- 5103.03 mg Gallic Acid Equivalent/100g), flavonoids (2380-3920 mg Quercetin Equivalent/100g), anthocyanins (272.26-384.32 mg/100g) and antioxidant activity (82.52-90.66%). Fruit skin had higher amounts of bioactive components and antioxidant capacity followed by pulp and seed.

Patel and Rao (2014) observed that jamun exhibited a gradual decrease in the pigments, chlorophylls, and carotenoids, while the accumulation of anthocyanin changed the color of the fruit from green to deep purple in color. Rai *et al.* (2011) found that 100 g jamun fruit pulp at harvest contains 55.48 mg ascorbic acid, 1175.17 mg phenol, 115.11 mg flavinoid, 7.25 mg anthocyanin. They also recorded 61.56 percent DPPH inhibition antioxidant activity in ripe jamun pulp.

Rakesh and Shivanna (2015) studied variations in important fruit and seed traits of jamun undertaking an extensive survey across eight different localities spread over different taluks in Uttar Kannada. Fruiting season varied in different localities. Fruit length showed significant variation among the different seed sources varying from 12.18 to 21.26 mm. Significantly higher fruit length was recorded from Mundgod (21.26 mm) followed by Yellapur (20.31 mm) as compared to the other seed sources. The lower seed length was recorded in the seeds collected from Sirsi (12.16 mm). Maximum fruit diameter and higher fruit test weight were recorded in fruits collected from Mundgod as 14.79 mm and 370.71 g respectively, followed by Yellapur (14.35 mm and 366.38 g, respectively. Higher test weight was recorded in Mundgod (32.85 g) and least seed weight was recorded in Sirsi seed source (32.85 g). Similarly, higher seed diameter (8.42 mm) and seed length (15.20 mm) were recorded in Mundgod. Lower seed length and diameter was recorded in the seed collected from Sirsi as 12.16 and 7.51 mm respectively.

Singh *et al*. (2015) studied variability in respect to physico-chemical and phytochemical characteristics of jamun. The enormous variability was observed with respect to morphology and physico-chemical attributes of fruits due to pre-dominance of seed propagation in jamun trees. The fruit weight was recorded in the range of 11.65 to 20.74 g with maximum fruit weight as 20.74 g in J–37 followed by J–36 (19.65 g), while, the minimum fruit weight was found in J–51 (11.65 g). There were wide variations in fruit size (length and breadth) observed among different accessions. The fruit length and breadth was recorded maximum in J-37 as 3.97 cm and 2.91 cm, respectively with big size fruit (11.83 cm^2) whereas the length breadth ratio was found maximum in J–23 (1.48 cm) which exhibited oblong fruits shape while minimum fruit length and breadth were recorded in accession J-49 (1.11 cm) which exhibited fruits towards the round shape. The maximum pulp weight (17.09 g) was recorded in J-37, however, highest pulp content (93.75%) was recorded in J–42 followed by J-44 (92.94 %) and J–43 (92.66 %). The lowest pulp content was recorded (70.21%) in accession J-49. Though the maximum weight of the fruit was observed in J–37 but maximum pulp content was recorded with the accessions J–42, J–43 and J–44 in which fruit weight was 13.28 g, 12.26 g and 13.46 g respectively, which was due to seedlessness of these accessions. The seed weight ranged from 2.79 to 4.10 g, however, in case of seedless accessions J–42, J–43 and J–44, whole seed was not

found, only the seed coat weight was recorded that ranged from 0.83 to 0.95 g. The maximum seed weight (4.10 g) was recorded in J–34, however, maximum seed length, breadth was found in J–51 as 2.37 and 1.52 cm respectively. Data revealed that pulp: seed ratio in various accessions ranged from 2.36 to 15.00 that showed the wide range of variability. The TSS was recorded in the range of 15.65 to 11.60^{o}B. TSS was found maximum (15.65^{o}B) in J–37, whereas, minimum TSS (11.60^{o}B) recorded in accession J–55. Titratable acidity content of the fruit varied from 0.90 to 1.08 percent. Titratable acidity was found maximum (1.08%) in J–40 followed by 1.06% in J–42, while it was the lowest (0.90 %) in accession J–51. The TSS: acid ratio ranged from 16.13 to 11.15. The maximum TSS:acid ratio (16.13) was noted in J-37 and minimum in J–55 as 11.15. A wide range of variability was also recorded in total sugar content among selected accessions of jamun. Total sugars were estimated to be highest (16.57 %) in J-37, whereas lowest sugar content (9.29%) recorded in J-55. The reducing sugars were found to be maximum (14.83%) in J-37 followed by J–23 as 13.55% and it was observed minimum (7.26 %) in J–55, however, the non-reducing sugar found maximum (2.36%) in accession J–49 and lowest in accession J–42 as 1.52%. The sugar: acid ratio also showed considerable variability among accessions and ranged from 17.08 to 8.90 in J-37 and J–26 respectively. There was a considerable variability in ascorbic acid content of fruit, which ranged from 25.74 to 37.68 mg/100g fruit pulp among the accessions. The maximum ascorbic acid content was recorded in J–37 (37.68 mg/100g) followed by 35.65 mg/100 g in J-23 and 34.85 mg/100g in J–49 while, it was minimum (25.74 mg/100g) in J–26.

Singh *et al*. (2015) identified sixteen superior mango varieties of endemic value and importance were evaluated for table, sucking and pickling purposes on the basis of physical appearance and chemical attributes. Out of these, six were found suitable for table, five for sucking, three for pickle and two for dual purpose (sucking and table). Studies revealed a clone from Bhuskaul community with fruit weight up to 420.0 g with TSS 27.40^{o}B and having very thin stone and maturing by the end of August. Study highlighted the need for and demands of diversity rich areas to conserve and protect seedling mangoes for the benefit of posterity with high value traits for future promotion.

Devi *et al*. (2016) observed significant difference among the genotypes for different characters in jamun. Genotypes AJG-20 found to have maximum number of

fruit (1644), number of fruit harvested (882) and fruit length (33.32mm) whereas maximum fruit width was recorded in Konkan Bahadoli as 21.62mm. Maximum fruit weight and pulp weight was recorded in AJG-85 as 9.50 and 6.93g respectively. Seed length (17.93mm) and seed width (10.43mm) was found maximum in Konkan Bahadoli followed by AJG-20 as 11.10 and 4.36mm respectively. Maximum seed weight was recorded in AJG- 20 as 2.40g followed by 2.37g in AJG-85. It was concluded that AJG-20 and AJG-85 can be utilised in making jamun seed powder which is of high medicinal importance for diabetic patients.

An investigation on morphological and physico-chemical characters of 15 elite jamun genotypes was undertaken at University of Horticultural Sciences, Bagalkot by Swami *et al.* (2017). They reported that among 15 genotypes observed, five were of old age (more than 40 years), one of medium age (20-40 years) and nine were of young age (less than 20 years). Genotype KJS-48 recorded significantly higher fruit weight (10.76 g), fruit length (3.48 cm), fruit breadth (2.27 cm), fruit volume (11.03 ml), pulp weight (9.02 g), pulp per cent (83.50%) and pulp to seed ratio (5.13) and lower seed weight and seed content (16.50%). KJS-89a recorded lowest fruit weight (3.60 g), fruit length (2.30 cm), fruit breadth (1.46 cm), fruit volume (3.66 ml) and minimum pulp weight (2.60 g). Lowest pulp content (68.08%) and pulp to seed ratio (2.33) was recorded in KJS-58. High TSS was recorded in KJS-48 (16.95°B) while lowest in KJS-89a (9.66°Brix). Significant differences were observed for total, reducing and non-reducing sugar content among the genotypes. Highest acidity was recorded in KJS-65 (1.03%) and lowest in KJS-20 (0.51%). Highest TSS to acid ratio was recorded in KJS-89 (26.39) and the lowest in KJS-58 (10.85). Highest phenol content was recorded in KJS-44 (1.65 mg/gram) and lowest in KJS-65 (0.281 mg/gram).

Agrawal *et al.* (2017) carried out a survey during 2016 in Madhya Pradesh, India to identify elite genotypes of jamun. Morphological qualitative, quantitative characteristics and biochemical attributes of sixteen genotypes were studied. The study revealed that there was a wide variation among the accessions. JJ-5 was the most promising genotype among the 16 accessions for average fruit weight (55.40 g), fruit length (27.78 mm), fruit width (22.01 mm), pulp weight (31.60 g) and seed weight (14.70g). This genotype can be used for table purpose as well for preparation of seed powder. The biochemical characteristics also showed high variability among all the

accessions of jamun. Maximum TSS was found in JJ-4 (21.25°B) and JJ-3 (19.85°B). Acidity was highest (0.53%) in JJ-9 and ascorbic acid in JJ-15 (42.30 (mg/100 g).

2.5 Organoleptic evaluation

Nisar *et al*. (2015) conducted the sensory evaluation of *Prunus domestica* fruits on the basis of aroma, consistency and flavor, fruit excellence and was assessed by a team of judges. Fruits of the genotypes DR3 and DR4 scored the maximum value of ranking as 9.33 followed by those of LY4 (9.27), SY2 (8.83) and RB1 (8.07). The minimum score were achieved by the fruits of RB2 (2.43), LY1 (2.83) and LY3 (3.20). The genotypes with higher sugar content (reducing and/or non-reducing) had the higher organoleptic score as compared with those with lower sugar content.

Swami *et al.* (2017) reported that organoleptic evaluation of fifteen elite jamun genotypes revealed no significant differences among the genotypes with respect to colour and taste however, overall acceptance showed significant difference among the genotypes. Significantly high score for overall acceptability was recorded in the genotype KJS- 45 as 4.17 and lowest score of 2.90 was recorded in KJS-84 and KJS-20a. They attributed it to the comparatively bigger size of the fruit with higher pulp content, higher TSS and moderate acidity in the genotype KJS-45 when compared to other genotypes.

2.6 Genetic variability

The success of any breeding programme depends on the presence of sufficient genetic variability to make effective selection. It is important to assess the relative magnitude of components of variability in order to use such information, together with other selection parameters for improvement of plant type through adoption of effective breeding methods (Johnson *et al*., 1955; Hanson *et al*., 1956; William, 1964; Briggs and Knowles, 1967). It is necessary to divide total phenotypic variance of the entire characters into its components as these are the basis for the genetic analysis and the dimensions of these components divide the breeding behavior of the populations. Such selection parameters particularly genetic coefficient of variability (GCV) helps to choose a potential genotype whereas heritability (h^2), genetic advance (GA) are useful in predicting the resultant effect from selection of best genotypes (Ganesan *et al*., 1996; Saravanan and Senthil, 1997).

Genotypic coefficient of variation is the relative measure of the extent of variability contributed by the genotype of the population. The phenotypic coefficient of variation provides knowledge of variability at phenotypic level including both genotypic and environmental variability. The high magnitudes of GCV and PCV have been reported for different fruit characters in litchi (Sarkar *et al.,* 1991) and mango (Attri *et al.,* 1999). The phenotypic variance gives the magnitude of phenotypic differences among the individuals in a population which can be attributed to both genetic and environmental sources. The genotypic and phenotypic variance has been evaluated in many fruit crops *i.e.* Japanese persimmon (Yamada *et al.,* 1993), strawberries (Sacks and Shaw, 1994), peach (DeSouza *et al.,* 1998), grape (Sato *et al.,* 2000), blueberry (Connor *et al.,* 2002), guava (Thaipong and Boonprakob, 2006) and mango (Majumder *et al.,* 2012). Such studies on variance analysis help in selecting an efficient breeding strategy. The phenotypic coefficient of variation provides knowledge of variability at phenotypic level including both genotypic and environmental variability.

Rajan *et al.* (2005) recorded high variability among sixty eight guava genotypes for all the traits with high GCV and PCV. High GCV (559.84%) was noticed for pulp to seed weight ratio. The phenotypic coefficient of variation (PCV) varied from 33.85 in average fruit weight to 609.75 percent in pulp: seed weight ratio. The high PCV (48.02) was also observed for seed percentage, number of seeds per fruit (44.49) and 100 seed weight (39.83).

Baruah *et al.* (2007) assessed the extent of genetic variation among twenty banana cultivars. The growth parameters of local banana cultivars of Assam *viz*., Bhutmanohar, Bharatmoni and Kachkal were superior as compared to commercial cultivars. Yield and yield attributing parameters was most promising in commercial cultivar Barjahaji as compared to local ones. The GCV and PCV were highest for leaf area and finger weight of the banana.

Singh and Mishra (2010) estimated genetic variability, heritability and genetic advance of the important morphological traits in 15 year old grafted trees of Bael. Phenotypic and genotypic coefficients of variation were observed higher for fruit set, followed by leaf number per shoot, yield, fruit drop, shoot length and tree height. Barhate *et al.* (2011) observed higher degree of phenotypic and genotypic coefficient

of variation for the traits number of fruits per tree and yield per tree in mango genotypes.

According to Murty and Arunachalam (1966) genetic drift and selection in different environments could cause greater drift than geographical distance. The value of phenotype is resultant of genotype and environment and their interaction. If there is no genotype x environment interaction, the average difference between genotypes is estimated through phenotypic stability in different environments is constant. The significance of G x E interaction results from changes in the magnitude of the difference among genotypes in different environments or from changes in sedative ranking of the genotypes. The G x E interaction reduces the correlation between phenotype and genotype and decreases selection progress. Srivastava *et al*. (2014) studied genetic variability for fruit weight, fruit length, fruit diameter, TSS, annual extension growth, girth, height, number of primary and secondary branches per plant and yield per tree in twenty one sweet cherry selections during 2009-12 at CITH, Srinagar. Analysis of variance revealed highly significant differences among the genotypes for all the traits under study. The range of variation was high for annual extension growth (67.66-112.15 cm) followed by yield (1.45-6.60 kg/plant) and TSS (11.31-17.18 per cent). The comparison of relative magnitude of phenotypic and genotypic co-efficient of variations for the actual strength of variability can be better understood. The estimates of phenotypic coefficient were observed to be higher in magnitude than their corresponding estimates of genotypic coefficient of variations for all the traits, which indicates the influence of additive effect of the environment on the expression of these traits. The estimates of PCV and GCV indicated the presence of fairly high degree of variability for yield per plant, trunk girth, annual extension growth and number of secondary branches. Moderate variability was observed for fruit weight, fruit length, TSS, tree height and number of primary branches, while for rest of the traits the estimates of PCV and GCV were relatively low. The difference between PCV and GCV was minimum for yield per plant, annual extension growth and trunk girth suggesting that these traits were least affected by environment. These observations draw support from the high value of heritability recorded for these traits.

2.7 Components of variability

One of the important considerations in the formulation of complete breeding programme is the knowledge regarding the relative contribution of genes in the

expression of a particular trait. Genetic advance i.e. the improvement in genetic value of the new population as compared with base population depends among other things, on the magnitude of differences among genotypic values of individuals in the base population. If all or most of the variability among the individuals in the base population is attributable to non heritable agencies, selection of phenotypically superior individuals from the population will not lead to desired improvement. Success of breeder in changing the characteristics of population therefore depends upon the correspondence between phenotypic values and genotypic values.

2.8 Heritability

The concept of heritability is important to determine whether phenotypic differences observed among individuals are due to genetic or environmental factors. Heritability is the transmissibility of traits or characters from parents to offsprings. The quantitative measures which provide information about the correspondence between genotypic variance and phenotypic variance is called heritability. The concept was originally presented by Lush (1945) to describe the ratio between genotypic and phenotypic variance and is now known as broad sense heritability. However, mean genotypic value of the progeny is determined by the average effects of genes transmitted by the parents in question. In other words it is the breeding value of the parents which determines the genetic properties of the progeny. Hence it is the proportion of phenotypic variance that is made up of variation attributable to the breeding values (additive genetic variance) which is of the prime importance from breeder's point of view.

Generally, heritability is used to specify the relative degree to which a character is conveyed from parent to offspring. The ample information on extent and type of genetic variability and their corresponding heritability is very important for any future breeding programme. The selection of elite accession is proportional to the sum of genetic variability present and the extent to which the traits are inherited. The degree of such estimation also implies the extent to which development is possible through selection (Omoigui *et al.*, 2006).

Raghava and Tiwari (2008) analyzed heritability for thirteen fruit characters in 15 guava genotypes. Higher estimates of heritability were observed for all the fruit traits which ranged from 90.27 to 99.97 percent. Singh and Mishra (2010) studied

heritability of the important morphological traits in 15 year old grafted trees of Bael (*Aegle marmelos*) for genotypes and reported that broad sense heritability ranged from 48.29 percent for tree height to 99.30 percent for ascorbic acid. Ibrahim (2012) noticed high heritability for fruit weight and yield per plant in sweet melon.

Nayak *et al.* (2013) evaluated physico-chemical characteristics of fruits of F1 mango progenies. High to moderate broad sense heritability was reported for quality traits of different fruits *i.e.* fruit weight (0.82), fruit volume (0.80), total carotenoids (0.97), ascorbic acids (0.83), stone width (0.71), fruit length (0.70), fruit width (0.62), total soluble solids (0.69), stone length (0.68), stone thickness (0.62). titratable acidity (0.58) and peel thickness (0.53). Srivastava *et al.* (2014) evaluated twenty one sweet cherry (*Prunus avium* L.) cultivars and low to moderate heritability was observed for several traits, whereas high broad sense heritability of four traits *viz*. fruit length (71 %), TSS (68 %), annual extension growth (65 %) and trunk girth (74%) was observed.

2.9 Genetic advance

Sarkar *et al.* (1991) studied genetic variability with respect to fruit characters in nine litchi cultivars. The study revealed higher genetic advance for fresh seed weight, fruit weight, fruit volume and pulp weight. These characters allow for selection of improved cultivars.

Attri *et al.* (1999) studied the genetic variability of fourteen collections of mango for various fruit characters *viz.* fruit length, fruit breadth, peel, pulp, stone weight, TSS, sugars, ascorbic acid, carotenoids and overall quality. The genetic advance was highest for carotenoids, fruit weight, fruit volume and ascorbic acid content.

Kumar *et al.* (2002) recorded high genetic advance for bunch width, number of berry per bunch, 100 berry weight, 100 seed weight, juice content, total soluble solids, reducing sugar, organic acid content and berry yield among fourteen early maturing grape genotypes. Genetic advance was highest for different fruit characters of guava (Raghava and Tiwari, 2008).

Bala *et al.* (2009) reported that among different vegetative and fruit characteristics of different genotypes of aonla, fruit weight, TSS, reducing and non reducing sugars exhibited high genetic advance, however, genetic advance was moderate for fruit set and acidity of fruit. While, fruit length, fruit width, ascorbic acid and total sugars were

exerted low genetic advance. Simultaneously, high heritability with high genetic advance was estimated by Ara *et al.* (2009) in seven exotic genotypes of strawberry.

Singh and Mishra (2010) evaluated genetic advance of the important morphological traits in 15 year old grafted trees of Bael (*Aegle marmelos*). Higher genetic advance estimates as percentage of mean was observed for fruit weight (70.78), leaf number per fruit (70.00), leaf fresh weight (64.12) and fruit volume (63.72)

Rajan *et al.* (2012) studied genetic advance for different traits of fruits of guava (*Psidium guajava L.*). All the traits except 100 seed weight, almost similar extent of genetic advance and remarkably highest genetic advance was observed for the traits of fruit weight, number of seeds per fruit and fruit to seed weight ratio.

Majumder *et al.* (2012) reported high genetic advance for different characters of mango *i.e.* weight of harvested fruits per plant (81.07%), per cent fruit harvested per inflorescence (67.02%), initial fruit set per inflorescence (66.84), number of fruits per plant (61.53%), per cent flowering shoot (55.20%) and number of inflorescences per shoot (52.12 %).

Srivastava *et al*. (2014) while investigating the heritability in twenty one sweet cherry selections during 2009-12 at CITH Srinagar, stated that the amount of heritable portion of variation cannot be predicted with the help of PCV and GCV alone, but by estimating heritability along with genetic advance which inturn helps in predicting the resultant effect of selection on phenotypic expression. They observed that estimates of heritability in broad sense were high for trunk girth, fruit length, yield per plant, annual extension growth and total soluble solids; whereas, these estimates for fruit weight and number of primary and secondary branches were low.

2.10 Correlation

Correlation is association between the two pairs of characters which helps the plant breeder to improve the crop, on the basis of significant correlation co-efficient between yield and other traits, the procedure to improve yield is simplified because the latter is complex in inheritance. The phenotypic correlation indicates the extent of observed relationship between the two characters and these include both hereditary and environmental influence, however genotypic correlation co-efficient provides a

real association between the two characters and is most useful in selection (Johnson *et al*., 1955).

In genetic studies it is not uncommon to find correlation between two or more characters. Genotypic correlation between two or more characters may result from pleiotropic effects of genes or linkage of genes governing inheritance of two or more characters (Stebbins, 1950; Adams, 1967). Correlation due to linkage is relatively ephemeral, whereas correlation resulting from pleiotropy is long lasting. Although the immediate effect of pleiotropism and close linkage may be generally similar in the first segregation generations following a cross, their consequences in regard to the potential breeding value of the material may be rather different. If the character combination of high and low values is due to pleiotropic effects, it would appear to be extremely difficult, if not possible, to ever obtain the desired combinations from the population. On the other hand if linkage appears to be the cause of correlation, then breeding procedures would be needed which would maximise the opportunities for the breaking up of these linkage blocks. In this respect potentialities of an inter-crossing programme among segregates should be considered rather than either continued selfing or recurrent back crossing (Al-Jibouri *et al*., 1958).

Srivastava *et al*. (2014) worked out correlation coefficients among different traits in all the possible combinations at both the phenotypic and genotypic levels and they found that the magnitudes of genotypic correlation coefficients were higher than their corresponding values at phenotypic level. Seed yield/plant exhibited significant and positive correlation with fruit weight, TSS, tree girth, and tree height at both phenotypic and genotypic levels. The positive association indicated that the selection for these traits would result in increased yield per plant. The interrelation of these characters with another character may provide likely consequences of selection for simultaneous improvement of desirable traits. The rate of influence of one component character over another can be studied by estimating the inter-correlation among different components of total yield per plant. Fruit weight, fruit length and tree height had significant positive association with yield per plant and were also found to be significant and positively associated with each other. Similarly, TSS and tree height were significant and positively correlated with each other and had positive and significant association with yield per plant. The correlation between annual extension of growth and yield per plant was non-significant and negative. These results

suggested that these characters could be considered as major yield contributing traits in cherry, indicating improvement in the characters, *i.e*. fruit weight, fruit length, TSS and tree height, would bring an enhancement in yield per plant. Fruit weight and diameter were significant and positively associated with each other at both the levels. Similarly, fruit length and tree height were also positive and significantly associated with each other.

2.11 Path coefficient analysis

The path coefficient divides the correlation between two parts *i.e.* direct and indirect effects and thus determines the exact magnitude of association. The method of path coefficient was first established by Wright (1921). Previously known results of various mating systems, obtained by laborious arithmetic procedures were confirmed by the more elegant method and many new results were reached, some of which were later collaborated by the method of matrix algebra. It is specific type of multivariate analysis- a system of dealing with a closed system of variables that are linearly related. In other words the system is formally complete, enclosing all the basic factors and their resultant variables. The practical application of this method is greatly facilitated by the formulation of a casual network showing the inter relationship of the variables concerned. Li (1956) emphasized that the employment of this method must be preceded by the formulation of a casual scheme, relations are based on a hypothesis which the investigator chooses to accept or test. Consequently, the more we know of the true relationship among the variables, the more meaningful will be the result of path analysis. The technique has been employed to study the direct and indirect effect of various traits on the ultimate product of economic importance in cherry by several workers and the information is reviewed in the present section. Correlation studies alone are not adequate to establish clear-cut associations among the traits as more variables need to be considered. Srivastava *et al*. (2014) carried out the path coefficient analysis during their investigation on twenty one sweet cherry genotypes and they recorded appreciable amount of direct positive effect of fruit diameter, tree height, TSS and annual extension of growth on yield per plant. Significant genotypic correlation coefficients of TSS, tree height and fruit diameter and number of secondary branches contributing maximum towards yield per plant and are having no significant positive association with yield per plant and would also be reliable in the process of selection for higher yield per plant. Overall results indicated that the greater emphasis

should be given to traits like, fruit diameter, TSS, plant height and number of secondary branches. The direct effect of remaining component traits on yield per plant was either negligible as that of number of primary branches or negative as that of fruit length.

2.12 Divergence

The variability present among the different genotypes of a species is known as genetic diversity. Genetic diversity arises either due to geographical separation or due to genetic barrier to crossability. Variability differs from diversity in the sense that one has observed phenotypic differences; however after sometime he may not have such an expression. Hybridization involving genetically diverse parents is known to provide an opportunity for bringing together gene constellation yielding desirable transgressive segregants in advanced generations. However, postulation of a rational criterion for identification of such parents is still a lying problem in plant breeding. To consider geographic diversity among parents as an index of genetic diversity has been equally acclaimed and disclaimed in numerous published reports.

Hybrid development requires parents with greater genetic diversity. One of the potent techniques of assessing genetically divergent parents for hybridization is the multivariate analysis proposed by Mahalanobis (D^2 statistics, 1936). D^2 statics has been used as a tool for estimating genetic divergence by plant breeders, being a numerical estimate which permits precise comparison among all possible pairs of populations. As the estimate are obtained from the study of potential parent themselves, the required information is available before attempting any cross and thus it can be used with advantage in the choice of the parental combination of promise (Rao, 1952).

Experimental evidences in Drosophila (Brunic, 1954; Wallse, 1955) have demonstrated that crosses of diverse origin exhibited greater heterotic response than crosses of strains of same origin. The variability present among the different genotypes of a species is known as genetic diversity. Genetic diversity arises either due to geographical separation or due to genetic barrier to crossability. Variability differs from diversity in the sense that one has observed phenotypic differences; however after sometime he may not have such an expression. Murty and Arunachalam (1965) hypothesized that Mahalanobis (1928) generalized distance, measure of metric

distance between population centriods, could be very useful multivariate statistical tool for effective discrimination among parents on the basis of genetic diversity. Precise information about genetic divergence is critical for a productive breeding programme as genetically diverse parents are known to produce high heterotic effects increasing consequently yield desirable segregants. Studies in a number of crop species with different breeding systems by means of D^2 statistics suggested that genetic diversity need not to be directly related to geographic diversity (Murty and Arunachalam, 1965). In understanding the nature of genetic divergence and for selecting diverse parents for successful hybridization in out breeding population such as self-incompatible Brassica (Murty and Arunachalam, 1966) and in self pollinated crops like linseed (Anand and Murty, 1968). The biological populations may undergo genetic diversity by a number of causes. Human selection has lead to quite a big array of varieties grown for the same end product and thus, affected their diversity, whereas stress conditions, natural selection and genetic drift maintained divergence (Ram and Panwar, 1970; Das and Borthakur, 1973). Eleven litchi genotypes were grouped in four clusters on the basis of the Tocher's method. Cluster I was the largest with five genotypes and all other clusters had two genotypes each. The inter cluster D2 values varied from 213.9 (between Clusters II and III) to 1373.4 (between Clusters I and IV); the intra cluster D2 values varied from 79.7 (Cluster I) to 138.8 (Cluster IV). Crossing between genotypes belonging to Cluster I with those of Cluster IV is expected to give maximum extent of heterosis (Dwivedi and Mitra, 1996**).**

Sharma and Sharma (2001) studied genetic divergence in seedling trees of Persian walnut (*Juglans regia* L.) for various metric nut and kernel characters in Himachal Pradesh. The nature and magnitude of genetic divergence was assessed using non – hierarchical Euclidean cluster analysis in 229 seedling trees of Persian walnut growing naturally in four districts of Himachal Pradesh for 15 nut and kernel characters. Minimum and maximum values of coefficient of variability were recorded for nut width and kernel weight and wide range of variation was observed in nut and kernel characters from different locations. All genotypes were grouped into 16 different clusters.

Based on the physical and chemical characteristics, thirty one genotypes of mango were constructed four uniform clusters. Large table fruit varieties like Mulgoa,

Phirangiladua, and Banganapalli formed a single group, while Totapuri, Gudad, and Chotta Jehangir deviated considerably from that (Pradeepkumar *et al*., 2006).

The genetic relationship among twenty genotypes of *Psidium guajava* and two species namely *P. friedrichsthalianum* and *P. catleianum* by means of morphological characters were measured. The similarity matrix was ranged from 0.06 to 0.50 and cluster analysis grouped into two major clusters. Cluster I included Chakaiya Rehmannagar, Gutaniwala, Super Max Ruby and Spear Acid and cluster II grouped eighteen genotypes (Sharma *et al.,* 2010).

Sixty-nine guava accessions collected in six Brazillian states were analyzed by two non-hierarchical clustering methods (Santos *et al.,* 2011). They studied genetic divergence of genus *Psidium* based on biochemical and agronomic variables. The variables were ascorbic acid, lycopene, total phenol, total flavonoids, anti-oxidant activity, acidity, T.S.S., diameter of fruit, fruit pulp and seed weight, fruit number and weight. There was no specific grouping according to their origin, indicating the absence of barriers in the guava propagation accessions. The analyses suggested that the collection of a greater number of guava germplasm samples from smaller number of regions and divergent accessions with high nutritional compound levels to develop new cultivars.

Barhate *et al.* (2011) reported that cluster analysis grouped the twelve mango genotypes into four clusters. Among the four clusters, cluster I was the biggest one, consisting of six genotypes and cluster II contained four genotypes, while cluster three and four had one genotype each. The data of morphological traits of sixty accessions of papaya were subjected for cluster analysis is based on similarity indices of horticultural traits. In order to classify the accessions single linkage cluster analysis was used to generate five cluster groups with specific characteristics (Aikpokpodion, 2012).

Evica *et al*. (2012) analyzed ten wild growing sweet cherry (*Prunus avium* L.) genotypes from South-East Serbia with different fruit skin color for their phenological, morphological and chemical traits. Agronomic evaluation of germplasm accessions revealed considerable diversity among different accessions for all the characters studied. The analysis of variance revealed significant differences among all genotypes for almost all examined properties. Cluster analysis showed adequate

grouping of wild sweet cherry genotypes according to pomological characterization and distinguished them into two distinct groups. The first group had two subgroups and consisted of seven genotypes, while the second one included only three accessions. Despite of the significant differences among genotypes, the total concentration of phenols made a clear separation between the clusters. The level of genetic diversity in these wild sweet cherry genotypes is very high and therefore these trees are useful sources of variability for attributes studied and can be employed in further breeding programs or conservation.

Bayazit and Sumbul (2012) conducted experiment to determine correlations among important fruit and plant characteristics using 12 walnut genotypes (Bilecik, Malatya 1, Şebin, Tokat 1, Kaplan 86, Yalova 1, Yalova 3, Yalova 4, Şen 1, 65/4, 77H1, KR 2). Twelve traits viz., fruit weight, fruit diameter, fruit length, fruit height, shell thickness, kernel weight, shell weight, kernel percentage, shoot length, trunk diameter, tree canopy volume, total number of fruits per tree, and yield per tree were evaluated for correlation and path analysis. Results depicted that kernel percentage and yield were influenced by direct and indirect effects of different characters. Fruit weight and shell weight of walnut were the most important properties that directly reduced the kernel percentage whereas kernel percentage increased as the kernel weight increased. Kernel percentage increased as shell thickness decreased. Total fruit number per tree, fruit height, and kernel percentage were determined as the most important characters that directly affected the yield per tree. Kernel percentage and yield per tree were the most important characters for walnut breeding researches and were positively associated. Fruit and shell weight had negative effect on both the kernel percentage and the yield per tree whereas fruit weight and tree canopy volume had the positive effect on both of kernel percentage and yield per tree.

Bootprom *et al.* (2014) evaluated genetic diversity among twenty one varieties of mulberry for horticultural traits (fruit weight, length and width) and total soluble solid at immature, medium ripe and fully ripe stages. They found that twenty one varieties of mulberry were grouped into 6 distinct clusters.

Verma *et al.* (2014) assessed the cluster analysis among twenty four accessions of Kashmiri Nakh pear (*Pyrus pyrifolia*). Cluster analysis grouped the accessions in two major groups. The accessions with superior quality in terms of fruits total soluble

solids (TSS), TSS to acidity ratio and yield related characteristics were included in first group. The large size fruits producing accessions were placed in second group. Najafzadeh *et al.*, (2014) reported that Iranian superior sour cherry genotypes formed different clusters when studied alongwith other foreign cultivars wherein all the cultivars formed three clusters.

Sharma *et al.* (2015) studied that dendrogram based on physicochemical data of grape fruit grouped all the six cultivars into two major clusters A and B at genetic similarity of 0.48. Major cluster A is further subdivided into one out group A1 and cluster A2 with genetic similarity value of 0.34. Cluster A2 consisted of three cultivars namely Foster, Duncan and Imperial, whereas, Star Ruby was presented as an out group A1. Major cluster B was also subdivided into two out groups B1 and cluster B2 with genetic similarity value of 0.35. Cluster B2 comprised the cultivar Marsh Seedless along with four variants whereas, Redblush separated as an out group B1. In minor cluster B2 variant GS1 and GS3 showed 100% genetic similarity.

The pooled divergence of all the characters within different cherry cultivars tested by Wilk's criterion reported by Srivastava *et al*. (2014) was found relevant. On the basis of relative magnitude of D^2 values, 21 genotypes were grouped by using Tocher's method into six clusters with maximum number of genotypes (9) in Cluster-I and 8 in Cluster-II; while, rest of the clusters were mono-genotypic. Murty and Arunachalam (1966) described heterogeneity, genetic architecture of the populations and developmental traits as possible reasons for the prevalence of diversity. The intra-cluster distance was maximum (16.76) in Cluster II followed by in Cluster-I (11.62). The mean inter-cluster distance was highest between clusters III and VI (41.22), followed by Cluster-III and V (37.76), Cluster-III and VI (37.58) and cluster V and VI (36.28). The clusters were found to have more inter-cluster distances hence the selection of parents for hybridization from such clusters would helps to evolve novel hybrids. The parents for hybridization could be selected on the basis of their large inter-cluster distance for isolating useful recombinants in the segregating generations. Inter-cluster distance was minimum between clusters III and IV indicating close relationship and similarly for most of the traits in these genotypes. Hence, selection of parents from such clusters should be avoided. Similar findings have been reported in cherry by Lacis *et al*. (2009), Singh *et al*. (2003) in pomegranate; Rai and Mishra (2005) in bael; Lal *et al*. (2006) in fennel., Dar *et al*. (2015) in tomato and Nagar and

Fageria (2006) in lehsua suggested selection of distant parents based on D^2 analysis. During their investigation they found considerable amount of variation among cluster means for different traits which is strong evidence for genetic divergence. Cluster III showed the highest mean for annual extension growth, trunk girth and tree height, Cluster-V for yield per plant, fruit weight and number of primary branches and Cluster-II for fruit length and fruit diameter. This indicates that these clusters had genotypes with the respective desirable traits. Hence, for the improvement of any particular trait should be selected from their respective genotypes cluster showing highest cluster mean for those traits. Their experimental observations further revealed that character trunk girth contributes maximum towards the genetic divergence (19.52 per cent) followed by annual extension growth (19.05 per cent). Thus, importance of these traits is emphasized as principal contributors to genetic diversity prevalent in such germplasm.

Materials and Methods

CHAPTER-3

MATERIALS AND METHODS

The present investigations entitled "Characterization and evaluation of genetic diversity of jamun (*Syzygium cumini* L.) for horticultural traits" were undertaken during 2013 and 2014 in the jamun growing areas of Jammu district, located between 32º40' North longitude and 74º58' East latitude at the elevation of 332 m above mean sea level. It is categorized under subtropical zone in fruit growing regions of Jammu province of Jammu and Kashmir state. The maximum temperature rises upto 45ºC during summers (May to June) and minimum temperature falls to 1ºC during winters. The mean annual rainfall is about 1000-1200 mm.

3.1 Experimental material

Survey was conducted in the subtropical areas of Jammu to locate areas of diversity for jamun during the year 2012. During the preliminary survey, ninty plants of seedling origin were identified. On the basis of expression of different characters, forty plants were selected for characterization and evaluation of genetic diversity during 2013 and 2014.

Different vegetative, floral and fruit characteristics of identified genotypes were recorded as per minimal descriptors for jamun published by NBPGR (Mahajan *et al.*, 2002). The procedures followed for recording different characters is as follows:

3.1.1 Vegetative and yield characteristics

Tree characteristics were recorded for different genotypes under the following parameters study.

3.1.1.1 Tree height

Tree height was recorded with the help of marked bamboo stick/ measuring staff from the ground surface to the maximum height attained by the plant and recorded in metre (m).

3.1.1.2 Tree spread

Tree spread was recorded for each tree by putting the marked bamboo stick horizontally with the tree from east-west and north-south and mean spread was worked out in metre (m).

3.1.1.3 Canopy volume

Canopy volume (m^3) of the respective trees was calculated as per the following formula given by Westwood (1963)

$$\text{Canopy Volume} = 4/3\pi a^2 b$$

where 'a' = represent radius of the crown of plant which was found by measuring the maximum spread in North-South and East-West direction adding these values and dividing the sum by 4. 'b' = denotes height of the plant (m).

3.1.1.4 Yield efficiency

Yield efficiency was calculated by dividing the yield of each tree by trunk cross sectional area of the same tree.

$$\text{Yield efficiency} = \frac{\text{Yield}}{\text{Trunk cross sectional area}}$$

3.1.2 Leaf characteristics

Observations on leaf characteristics were recorded on mature fully expanded leaves collected during July-August.

3.1.2.1 Leaf shape

Leaf shape of mature fully expanded leaves was recorded as under:

1. Broadly ovate
2. Elliptic oblong
3. Elliptic
4. Lanceolate

3.1.2.2 Leaf colour

Leaf colour was visually observed and categorised as following description:

1. Light green
2. Dark green

3.1.2.3 Leaf Size (L × B)

The leaf length and breadth was measured with the help of a measuring scale and the size determined in centimetres (cm).

3.1.2.4 Leaf area

Leaf area was determined by randomly selecting 20 leaves from all over the tree canopy of experimental trees and their cumulative area was recorded with the help of leaf area meter, Systronics-211 model and expressed as average leaf area in square centimetres (cm^2).

3.1.2.5 Petiole length

Petiole length was recorded with the help of a digital vernier calliper and expressed in centimetre (cm).

3.1.2.6 Leaf length to petiole length ratio: Leaf length to petiole length ratio was obtained by dividing leaf length with petiole length.

3.1.3 Floral characteristics

3.1.3.1 Full bloom time

Date of full bloom was recorded as on the date when more than 80 per cent flowering was obtained.

3.1.4 Fruit Characteristics

3.1.4.1 Duration of fruiting

The duration of fruiting was noted at the start and end of fruiting period and expressed as date of start and ending of fruiting.

3.1.4.2 Fruit Shape

The shape was determined through visual observation from the frontal view and categorised as per the shapes provided in the descriptor (Mahajan et al., 2002) as under:

1. Round
2. Oblong
3. Oval
4. Ellipsoid

3.1.4.3 Fruit weight

The weight of 20 randomly selected healthy fruits was measured using electronic weighing balance and the average fruit weight was calculated by dividing total fruit weight by 20 and expressed in gram (g).

3.1.4.4 Fruit size

The fruit length and breadth of 20 healthy fruits was measured using digital vernier calliper and expressed as length × breadth (cm^2).

3.1.4.5 Fruit volume

Fruit volume was determined by water displacement method using a measuring cylinder and result was expressed as cubic centimetres (cm^3).

3.1.4.6 Specific gravity

Specific gravity was calculated by dividing fruit weight by fruit volume as per the following formula:

$$\text{Specific gravity} = \frac{\text{Weight of the fruit (g)}}{\text{Volume of the fruit (cm}^3\text{)}}$$

3.1.4.7 Proportion of consumable matter (pulp)

Fruit pulp was separated and scraped from seed and weighed to calculate proportion of consumable matter (pulp)

$$\text{Per cent consumable matter} = \frac{\text{Weight of the consumable matter (g)}}{\text{Weight of the whole fruit (g)}} \times 100$$

3.1.4.8 Moisture content of fruit and seed

Moisture content of fruit and seed was determined by weighing the fresh fruits and seeds separately and then drying in the hot air oven at 100^{o}C for 4 hours. The process was repeated till a constant weight was obtained.

$$\text{Moisture content (\%)} = \frac{\text{Fresh weight – Dry weight (g)}}{\text{Fresh weight (g)}} \times 100$$

3.1.4.9 Proportion of non-edible contents (seed)

Seed was separated and scraped carefully to remove pulp and was weighed to calculate proportion of non-edible contents as per following formula:

$$\text{Per cent consumable matter} = \frac{\text{Weight of the non-edible matter (g)}}{\text{Weight of the whole fruit (g)}} \times 100$$

3.1.4.10 Seed weight

Seed weight was determined with an electronic weighing balance on the basis of 20 randomly selected healthy fruits and average seed weight was calculated by dividing total seed weight by 20 and the results were expressed in grams (g).

3.1.4.11 Seed size

The length and girth of 20 seed taken from randomly selected healthy fruits was measured using digital vernier calliper and expressed in cm.

3.1.4.12 Pulp: seed ratio

The fruit flesh was separated from the stone and the ratio between weights of pulp and stone was worked out.

3.1.4.13 Juice content

The juice content was measured by pressing out juice from known pulp weight minced thoroughly with the help of a blender and filtered through a muslin cloth. The quantity of juice obtained was expressed as per cent unit of pulp.

$$\text{Per cent Juice} = \frac{\text{Volume of juice obtained}}{\text{Weight of pulp}} \times 100$$

3.1.4.14 Juice pH

Juice was determined by using digital pH meter (Elico, India) calibrated with a standard buffer solution of pH 4.0, 7.0 and 9.0 as described in A.O.A.C. (1995).

3.1.4.15 Total soluble solids (^{o}B)

The total soluble solids (TSS) of the fruit pulp was recorded with the help of Erma hand refractometer (0-32^{o}B) according to standard procedure as given in A.O.A.C (1995) in terms of degree Brix (^{o}B) at room temperature. A temperature correction was applied when the readings were taken at a temperature other than 20^{o}C. The refractometer was calibrated with double distilled water before use.

3.1.4.16 Titratable Acidity

Titratable acidity in fresh fruits was determined by the method as suggested in A.O.A.C (1995). Twenty five gram of fruit pulp was taken in blender, homogenized in distilled water and the volume was made 250 ml and then, filtered through Whatman no. 1 filter paper. The colouration of juice is removed by mixing with activated charcoal before the filteration. Twenty-five ml of filtered solution was titrated against 0.1 N NaOH solution using phenolphthalein as an indicator. The total per cent titratable acidity was calculated on the basis of one ml NaOH equivalent to 0.0064 g of anhydrous citric acid. The results were expressed as per cent total titratable acidity.

3.1.4.17 Ascorbic acid

The standard method as suggested by A.O.A.C (1995) using 2, 6-dichlorophenol indophenols (0.04%) was followed for estimation of ascorbic acid. A known quantity of sample (10 g) was made to 100 ml with 0.4% oxalic acid and filtered. A known volume

of aliquot (10 ml) was mixed with 15 ml of oxalic acid (0.4%) and titrated against the standardized dye to a light pink colour persisting for at least 15 seconds.

3.1.4.18 Sugars

3.1.4.18.1 Reducing sugars

Twenty five grams of fruit pulp was thoroughly homogenized with distilled water. To this, 2 ml of saturated lead acetate solution was added and the precipitate was filtered into flask containing 5 ml of potassium oxalate solution. The filtrate was shaken and re-filtered. Boiling mixture containing 5 ml each of Fehling A and Fehling B reagents was titrated against un-hydrolyzed but de-leaded and clarified aliquot by using methylene blue as an indicator. The end point was marked by the appearance of brick red colour. Volume of aliquot used was noted and the reducing sugars were calculated as per the procedure described in A.O.A.C. (1995).

3.1.4.18.2 Total Sugars

100 ml of de-leaded and clarified filterate was hydrolyzed by adding 5 ml concentrated HCl and leaving it overnight. The excess of HCl was neutralized with concentrated sodium hydroxide solution. Total sugars were estimated by titrating boiling mixture of 5 ml each of Fehling A and Fehling B solution against a hydrolyzed aliquot, using methylene blue as an indicator. The end point was marked by the appearance of brick red colour. Total volume of aliquot used was noted and total sugars were calculated by the procedure described in A.O.A.C. (1995).

3.1.4.18.3 Non-reducing sugars

The non-reducing sugars were obtained by subtracting reducing sugars from total sugars and multiplying the difference by standard factor 0.95. The calculation was done as per the procedure described in A.O.A.C (1995).

3.1.4.19 Total anthocyanin content

The total anthocyanin content was determined as per the method of Swain and Hillis (1959). 1 g of fruit was extracted with 10 ml of methanol and centrifuged. 1 ml of supernatant was mixed with 3 ml of HCl in aqueous methanol (0.5N HCl in 80–85 per cent methanol) and 1 ml of anthocyanin reagent [1 ml of 30 per cent H_2O_2 in 9 ml of methanolic HCl (5:1, 3N)]. After 15 min of incubation in the dark, optical density of the reaction mixture was measured against blank at 525 nm with the help of SHIMAZDU UV-Vis spectrophotometer.

3.1.4.20 Total tannins

The total tannin contents of the fruit were determined using the Folin-Ciocalteu method (Singleton and Rossi, 1965), reading samples on a SHIMAZDU UV-Vis spectrophotometer at 760nm. 5 ml of fruit juice extracted from fresh fruit. Juice samples were centrifuged at 2000 x g (4°C, 5 min) and diluted by a factor 10 with distilled water. The final results were expressed as mg/100 g fresh fruit weight.

3.1.4.21 Antioxidant activity

Antioxidant activity was determined through assessment of free radical-scavenging effect on 2,2-diphenyl-1-picrylhydrazyl (DPPH) radical (HiMedia Laboratories, India) as per the method of De Ancos *et al.* (2000). One g of fruit was extracted with 5 ml of methanol. The extract solution was centrifuged and refrigerated. Aliquots of 0.01 ml of supernatant so obtained were mixed with 3.9 ml of methanolic DPPH (0.025 g/l) and 0.090 ml of distilled water. Absorbance of the mixture was measured against the blank at 515 nm using SHIMAZDU UV-Vis spectrophotometer. The results were obtained as the percentage decrease with respect to the absorbance of a reference DPPH solution.

3.1.4.22 Organoleptic evaluation

To assess consumer preference, the fruits were examined and evaluated by panel of 7-8 judges who scored the ripe fruit of jamun genotypes for quality characteristics colour, texture, taste, aroma and overall acceptability. Samples were served on coded plates. The judges scored the quality characteristics on nine-point hedonic scale. The scores obtained from all characteristics under test given by judges were averaged to calculate the overall acceptability and consumer preference. The overall score of five or above was considered acceptable.

3.2 Statistical analysis

The data recorded on different horticultural traits on the selected trees was analyzed for various statistical parameters such as mean, range, coefficients of variation, heritability, genetic advance, correlations, path correlation and cluster analysis using multivariate statistical analysis.

3.2.1 Genotypic variance

Genotypic variance was calculated using the method suggested by Al-Jibouri *et al.* (1958) for the data as per the following formula:

$$\sigma^2 g = \frac{MSg - MSe}{R}$$

where,

$\sigma^2 g$ = genotypic variance

MSg = mean sum of squares for genotypes

MSe = mean sum of squares for G x E interaction

R = number of replications

3.2.3 Genotypic coefficient of variation (GCV)

$$GCV = \frac{\sqrt{\sigma^2 g}}{\overline{X}}$$

Where,

$\sigma^2 g$ = genotypic variance and

$\overline{X}$ = mean of trait

3.2.4 Phenotypic variance

Phenotypic variance was calculated by the formula given by Al-Jibouri *et al*. (1958) for the data.

$$\sigma^2_p = \sigma^2_g + \sigma^2_e$$

where,

σ^2_p = phenotypic variance

σ^2_g = genotypic variance

σ^2_e = error variance

3.2.5 Phenotypic coefficient of variation (PCV)

$$GCV = \frac{\sqrt{\sigma^2 p}}{\overline{X}}$$

where,

σ^2_p = phenotypic variance

$\overline{X}$ = mean of trait

3.2.6 Heritability (broad sense)

Broad sense heratibility was estimated as per the procedure given by Burton and Vane (1953), Johnson *et al*. (1955) and Hanson *et al.* (1956).

$$h^2(b.s) = \frac{\sigma^2 g}{\sigma^2 p}$$

where,

h^2 = estimate of heritability in broad sense

$\sigma^2 g$ = genotypic variance and

$\sigma^2 p$ = phenotypic variance

3.2.7 Genetic advance (GA)

Genetic advance at 5 per cent selection intensity was worked out using the formula given by Lush (1949) and Johnson *et al.* (1955).

$$G.A = \frac{\sqrt{\sigma^2 p}}{\overline{X}} \times h^2(b.s) \times K$$

Where,

G.A = genotypic advance of the trait

$\sigma^2 p$ = phenotypic variance of the trait

$\overline{X}$ = mean of the trait

h^2 = estimate of heritability in broad sense

K = selection differential and value of K at 5 per cent selection intensity being 2.06

3.2.8 Expected genetic gain (genetic advance as per cent of mean)

It was estimated as per the method suggested by Johnson *et al.* (1955) and worked out with the help of following formula

$$\text{Genetic gain} = \frac{\text{G.A.}}{\overline{X}} \times 100$$

Where,

G.A = genetic advance of the trait and

$\overline{X}$ = mean of the trait

3.2.9 Correlation analysis

Correlation analysis followed the same pattern as that of variance analysis. The genotypic and phenotypic covariances between the two characters were obtained in the same fashion as the corresponding variances. Estimates of genotypic and phenotypic variances and covariances were substituted in the following formulae suggested by Al-Jibouri *et al*. (1958) to calculate the correlation coefficients between all the possible pairs of characters.

3.2.9.1 Genotypic and phenotypic correlation coefficient

$$\text{Genotypic correlation coefficient } r_{xy\,(g)} = \frac{\sigma^2 xy_{(g)}}{[\sigma^2 x_{(g)} \times \sigma^2 y_{(g)}]^{0.5}}$$

$$\text{Phenotypic correlation coefficient } r_{xy\,(p)} = \frac{\sigma^2 xy_{(p)}}{[\sigma^2 x_{(p)} \times \sigma^2 y_{(p)}]^{0.5}}$$

where,

$r_{xy\,(g)}, r_{xy\,(p)}$ = Genotypic and phenotypic correlation coefficient respectively between pair of characters x and y

$\sigma^2 x_{(g)}, \sigma^2 y_{(p)}$ = Genotypic and phenotypic covariances for a pair of characters x and y respectively

$\sigma^2 x_{(g)}, \sigma^2 y_{(g)}$ = Genotypic variances for the pair of characters x and y respectively

$\sigma^2 x_{(p)}, \sigma^2 y_{(p)}$ = phenotypic variances for the characters x and y respectively

3.2.9.2 Test of significance of correlation coefficient

The significance of correlation coefficient was tested by 't' test.

t = $r(n-2)^{0.5}/(1-r^2)^{0.5}$, for (n-2) degrees of freedom

Where,

n = number of treatments and

r = value of correlation coefficient

This 't' value is tested against the table value of 't' for (n-2) degrees of freedom. If the observed value is more than the tabulated one, the correlation coefficient is said to be significant.

3.2.10 Estimates of genetic divergence

The genetic divergence was calculated using the procedure described by Rao (1952) and Singh and Chaudhary (1985). The ranking of differences in uncorrelated means between all the characters for all pair wise combinations of genotypes was carried out, with first rank being assigned to the highest differences. Finally relative contribution of a character towards total divergence was estimated by calculating the percentage of first rank in that character.

3.2.11 Group constellation

Tocher's method was used for assigning various genotypes to different clusters. This method starts with a pair of genotypes showing the smallest D^2 value to which the third genotype showing the smallest average D^2 value increased. The remaining genotypes were then considered for the next cluster and the process was continued till all genotypes were included in various clusters. The spatial distances between clusters were arrived at by taking square root of average intra and inter cluster D^2 values.

Results

CHAPTER-4

RESULTS

The present investigations entitled “Characterization and evaluation of genetic diversity of jamun (*Syzygium cumini* L.) for horticultural traits” were undertaken during 2013 and 2014 in the jamun growing areas of Jammu district in order to screen the available germplasm of jamun to obtain the quantitative measures of the degree of variability of various morphological and horticultural traits; predict heritability and estimate possible association among morphological and phenological traits in jamun germplasm. The observations for various parameters were recorded as per the objectives and aims of the present investigation. During the course of survey, identification and documentation, ninty genotypes of jamun were covered. On the basis of expression of different characters, forty plants were selected for characterization and evaluation of genetic diversity during 2013 and 2014. The results of the investigations are presented as under.

4.1 Vegetative and yield characteristics

The vegetative characteristics *viz*., tree height, tree spread, canopy volume, yield efficiency, leaf shape, leaf colour, leaf length, leaf breadth, leaf area, petiole length, leaf length: petiole ratio were recorded during 2013 and 2014 and the results thus obtained for each selection are described under suitable headings.

4.1.1 Tree characteristics

4.1.1.1 Tree height

The tree height of the jamun selections ranged from 6.55 to 16.5 m (Table 1). Out of forty genotypes, maximum tree height was recorded in SJJS-12 and SJJS-15 genotypes followed by SJJS-38, SJJS-11 and SJJS- with tree height of 16.4 m, 15.5 m and 15.4 m, respectively. Minimum tree height was noted in genotype SJJS-34, preceded by SJJS-21 with 7.4 m.

4.1.1.2 Tree spread

The data presented in Table 1 revealed substantial amount of variability in tree spread ranging from 5.25 to 17.95 m. Maximum tree spread was observed in SJJS-2 followed closely by SJJS-12 and SJJS-40 with tree spread of 17.20 m and 17.05 m,

respectively whereas minimum tree spread was recorded as 5.25 m in SJJS-28 and 6.70 m in SJJS-29.

4.1.1.3 Canopy volume

Canopy volumes of jamun genotypes are presented in Table 1. The canopy volume in the studied genotypes ranged from 305.59 to 4905.13 m^3. The maximum canopy volume has been recorded in SJJS-12 followed by SJJS-38 (3944.30 m^3) whereas minimum values were recorded in SJJS-34.

4.1.1.4 Yield efficiency

The results pertaining to yield efficiency of jamun showed variation among the studied genotypes as presented in Table 1. The highest yield efficiency of 0.26 was observed in genotype SJJS-40 followed by 0.25 each in SJJS-23 and SJJS-29 respectively whereas the lowest yield efficiency of 0.19 was recorded in eight genotypes *viz*., SJJS-1, SJJS-2, SJJS-8, SJJS-9, SJJS-10, SJJS-12, SJJS-16 and SJJS-25.

4.1.2 Leaf Characters

The various leaf characteristics were recorded during two successive years (2013 and 2014). The leaf characteristics of each selection studied are given Table 2 and described under different headings.

4.1.2.1 Leaf shape

So far as leaf shape is concerned which is expressed as the ratio of leaf length to leaf width, genotypes ranged from elliptic and broadly ovate in leaf shape. Among forty genotypes studied twenty five genotypes *i.e.*, SJJS-1, SJJS-2, SJJS-3, SJJS-4, SJJS-5, SJJS-6, SJJS-7, SJJS-8, SJJS-9, SJJS-10, SJJS-11, SJJS-12, SJJS-16, SJJS-17, SJJS-18, SJJS-25, SJJS-26 SJJS-27, SJJS-30, SJJS-32, SJJS-33, SJJS-35, SJJS-37, SJJS-38, SJJS-39 had elliptic leaf shape whereas in fifteen genotypes *viz*., SJJS-13, SJJS-14, SJJS-15, SJJS-19, SJJS-20, SJJS-21, SJJS-22, SJJS-23, SJJS-24, SJJS-28, SJJS-29, SJJS-31, SJJS-34, SJJS-36, SJJS-40, the shape of the leaf was broadly ovate (Table 2).

4.1.2.2 Leaf colour

In all the genotypes studied, no variation in the leaf colour was observed and had dark green colour (Table 2).

Table 1: Tree characteristics of jamun genotypes

S. No.	Genotype	Tree height (m)	Tree Spread (m)	Canopy volume (m^3)	Yield Efficiency
1	SJJS-1	11.50	12.60	1745.50	0.19
2	SJJS-2	13.30	17.95	3326.00	0.19
3	SJJS-3	8.90	8.75	726.01	0.24
4	SJJS-4	12.00	15.93	2402.88	0.20
5	SJJS-5	12.70	14.20	2399.11	0.20
6	SJJS-6	14.80	12.80	2936.89	0.20
7	SJJS-7	15.40	12.30	3055.63	0.21
8	SJJS-8	13.30	15.93	2951.71	0.19
9	SJJS-9	13.15	8.40	1521.55	0.19
10	SJJS-10	14.80	11.00	2523.89	0.19
11	SJJS-11	15.50	10.05	2529.20	0.21
12	SJJS-12	16.50	17.20	4905.13	0.19
13	SJJS-13	13.90	10.09	2041.08	0.21
14	SJJS-14	12.70	7.83	1322.04	0.20
15	SJJS-15	16.50	11.40	3251.07	0.21
16	SJJS-16	13.50	11.50	2195.43	0.19
17	SJJS-17	12.70	15.80	2669.43	0.20
18	SJJS-18	11.50	12.45	1724.72	0.20
19	SJJS-19	11.50	9.50	1316.05	0.20
20	SJJS-20	8.90	8.07	669.17	0.21
21	SJJS-21	7.40	9.95	570.74	0.22
22	SJJS-22	8.00	9.25	620.12	0.20
23	SJJS-23	8.00	6.80	455.87	0.25
24	SJJS-24	12.40	11.85	1908.60	0.20
25	SJJS-25	11.80	15.60	2275.32	0.19
26	SJJS-26	12.10	11.58	1775.96	0.20
27	SJJS-27	13.65	8.50	1658.97	0.20

28	SJJS-28	7.75	5.25	330.31	0.21
29	SJJS-29	9.90	6.70	687.86	0.25
30	SJJS-30	10.20	7.15	779.22	0.22
31	SJJS-31	11.50	11.55	1600.04	0.21
32	SJJS-32	10.00	7.49	784.05	0.22
33	SJJS-33	10.40	7.75	878.06	0.21
34	SJJS-34	6.55	6.80	305.59	0.23
35	SJJS-35	8.00	9.45	633.53	0.21
36	SJJS-36	10.60	10.40	1224.05	0.22
37	SJJS-37	15.50	13.50	3397.44	0.21
38	SJJS-38	16.40	14.00	3944.30	0.20
39	SJJS-39	14.90	16.30	3790.65	0.20
40	SJJS-40	13.00	17.05	3018.32	0.26

Table 2: Leaf and floral characteristics of jamun genotypes

S. No.	Genotype	Leaf shape	Leaf colour	Leaf length (cm)	Leaf breadth (cm)	Leaf area (cm^2)	Petiole length (cm)	Leaf length: petiole length ratio	Full bloom (80 %)
1	SJJS-1	Elliptic	Dark green	15.0	6.7	36.4	2.2	6.7	1-3 May
2	SJJS-2	Elliptic	Dark green	15.1	6.8	45.3	2.2	6.7	30 April-2 May
3	SJJS-3	Elliptic	Dark green	14.0	7.2	45.5	1.8	7.9	8-10 May
4	SJJS-4	Elliptic	Dark green	14.3	7.2	47.1	1.9	7.4	6-8 May
5	SJJS-5	Elliptic	Dark green	13.5	7.1	45.9	1.8	7.5	30 April-2 May
6	SJJS-6	Elliptic	Dark green	15.9	7.6	43.2	1.7	9.4	29 April-1 May
7	SJJS-7	Elliptic	Dark green	12.5	6.4	47.1	1.9	6.7	29 April-1 May
8	SJJS-8	Elliptic	Dark green	18.0	8.1	51.3	1.6	11.5	6-8 May
9	SJJS-9	Elliptic	Dark green	17.5	8.2	50.4	1.9	9.1	2-4 May
10	SJJS-10	Elliptic	Dark green	17.9	8.3	52.3	1.4	12.8	29 April-1 May
11	SJJS-11	Elliptic	Dark green	18.3	9.1	58.4	1.9	9.6	6-8 May
12	SJJS-12	Elliptic	Dark green	18.9	9.9	66.2	1.8	10.7	6-8 May
13	SJJS-13	Broadly ovate	Dark green	18.7	10.7	70.3	1.9	9.7	1-3 May
14	SJJS-14	Broadly ovate	Dark green	17.5	9.9	60.7	1.7	10.1	6-8 May
15	SJJS-15	Broadly ovate	Dark green	16.3	9.2	52.6	1.7	9.4	1-3 May
16	SJJS-16	Elliptic	Dark green	15.6	8.1	44.7	1.5	10.2	6-8 May
17	SJJS-17	Elliptic	Dark green	16.9	8.7	51.9	1.7	9.7	28-29 April
18	SJJS-18	Elliptic	Dark green	18.2	8.6	55.1	1.9	9.8	10-12 May
19	SJJS-19	Broadly ovate	Dark green	20.2	9.2	65.8	1.9	10.5	30 April-2 May

20	SJJS-20	Broadly ovate	Dark green	19.8	8.6	59.8	1.8	11.2	10-12 May
21	SJJS-21	Broadly ovate	Dark green	19.9	8.8	61.7	1.8	11.3	4-6 May
22	SJJS-22	Broadly ovate	Dark green	19.1	8.4	56.8	1.8	10.4	2-4 May
23	SJJS-23	Broadly ovate	Dark green	19.5	8.5	58.3	1.6	12.2	2-4 May
24	SJJS-24	Broadly ovate	Dark green	18.6	8.0	52.7	2.2	8.3	24-26 April
25	SJJS-25	Elliptic	Dark green	17.4	7.5	46.2	2.4	7.2	26-28 April
26	SJJS-26	Elliptic	Dark green	16.6	7.3	42.7	1.4	11.6	23-25 April
27	SJJS-27	Elliptic	Dark green	16.0	7.0	39.4	2.1	7.6	28-30 April
28	SJJS-28	Broadly ovate	Dark green	18.7	8.3	54.7	1.7	11.0	27-29 April
29	SJJS-29	Broadly ovate	Dark green	19.7	8.4	58.1	1.8	10.8	20-22 April
30	SJJS-30	Elliptic	Dark green	16.7	8.0	47.0	1.9	8.8	20-22 April
31	SJJS-31	Broadly ovate	Dark green	19.6	10.1	69.9	2.0	10.0	3-5 May
32	SJJS-32	Elliptic	Dark green	20.2	8.6	61.0	1.5	13.3	26-28 April
33	SJJS-33	Elliptic	Dark green	18.9	8.6	56.9	2.3	8.2	28-30 April
34	SJJS-34	Broadly ovate	Dark green	19.2	8.4	56.7	3.0	6.4	28-30 April
35	SJJS-35	Elliptic	Dark green	18.1	7.6	48.2	2.0	9.1	27-29 April
36	SJJS-36	Broadly ovate	Dark green	17.9	7.6	47.9	2.3	7.8	23-25 April
37	SJJS-37	Elliptic	Dark green	18.1	7.6	48.2	2.3	8.0	29 April-1 May
38	SJJS-38	Elliptic	Dark green	17.8	7.5	46.7	2.2	8.2	29 April-1 May
39	SJJS-39	Elliptic	Dark green	18.1	8.2	52.3	2.2	8.4	3-5 May
40	SJJS-40	Broadly ovate	Dark green	16.4	7.1	41.2	2.2	7.6	29 April-1 May

SJJS- 12

SJJS-27

SJJS-34

SJJS- 35

Plate 1: Variation in tree characters of Jamun (*Syzygium cumini* L.) genotypes selected for evaluation

SJJS-13

SJJS-19

SJJS-31

SJJS-32

Plate 2: Variation in leaf characters of Jamun (*Syzygium cumini* L.) geno selected for evaluation

4.1.2.3 Leaf size

The data on the leaf length and leaf breadth of the selected jamun genotypes are presented in Table 2. From the perusal of the data, maximum leaf length of 20.2 cm was observed in SJJS-19 and SJJS-32 jamun genotypes followed by19.9 cm, 19.8 cm, 19.7 cm in SJJS-21, SJJS-20 and SJJS-29 respectively whereas minimum leaf length of 12.5 cm was recorded in SJJS-7 genotype.

The leaf breadth varied between 6.4 to 10.7 cm with minimum leaf breadth in genotype SJJS-7 and maximum in SJJS-13 followed by SJJS-31 with 10.1 cm.

4.1.2.4 Leaf area

The leaf area in the studied jamun genotypes ranged from 36.4 to 70.3 cm^2 (Table 2). From the data obtained in the present study, the leaf area can be grouped into large, medium and small.

The leaf area of the forty genotypes studied, presented in Table 2 revealed that the large leaf area (>60 cm^2) was recorded in seven jamun genotypes *viz*., SJJS-12, SJJS-13, SJJS-14, SJJS-19, SJJS-21, SJJS-31 and SJJS-32 followed by medium sized (40-60 cm^2) in rest of the genotypes except SJJS-27 which had small leaf area.

4.1.2.5 Petiole length

Petiole length in forty jamun genotypes ranged from 1.4 to 3.0 cm with maximum petiole length of 3.0 cm recorded in SJJS-34 followed by 2.4 cm, 2.3 cm and 2.3 cm in SJJS-25, SJJS-36 and SJJS-37 genotypes respectively while minimum petiole length (1.4 cm) was observed in SJJS-10 and SJJS-26 genotypes (Table 2).

4.1.2.6 Leaf length: petiole length ratio

The range of leaf length: petiole length ratio varied between 6.4 and 13.3 as revealed by the data presented in Table 2. The genotype SJJS-32 recorded maximum leaf length: petiole length ratio as 13.3 followed by 12.8 in SJJS-10. Minimum leaf length: petiole length ratio of 6.4 was observed in genotype SJJS-34 preceded by 6.7 in SJJS-1 and SJJS-2 each. The leaf length: petiole length ratio of the forty genotypes studied, presented in Table 2 reveal that the medium length: petiole length ratio (8-10) was recorded in fifteen jamun genotypes *viz*., SJJS-6, SJJS-9, SJJS-11, SJJS-13, SJJS-15, SJJS-17, SJJS-18, SJJS-24, SJJS-30, SJJS-31, SJJS-33, SJJS-35, SJJS-37, SJJS-38 and SJJS-39 followed by large leaf length: petiole length ratio (>10) in thirteen genotypes *viz*., SJJS-8, SJJS-10, SJJS-12, SJJS-14, SJJS-16, SJJS-19, SJJS-20, SJJS-21,

SJJS-22, SJJS-23, SJJS-26, SJJS-29 and SJJS-32 whereas rest of the genotypes showed small leaf length: petiole length ratio (>8) *viz*., SJJS-1, SJJS-2, SJJS-3, SJJS-4, SJJS-5, SJJS-7, SJJS-25, SJJS-27, SJJS-34, SJJS-36 and SJJS-40.

4.3 Floral character: Full bloom time

The floral characteristic studied was full bloom recorded as the date when 80 per cent flowers on the selected branches have opened and the results are presented in Table 2. The full bloom in jamun genotypes studied ranged from 20 April to -12 May. The date of full bloom was earliest in genotypes SJJS-29 and SJJS-30 between 20-22 April while in the genotypes SJJS-18 and SJJS-20 the time of full bloom was 10-12 May. In genotypes SJJS-26, SJJS-24, SJJS-28, SJJS-17, SJJS-27, SJJS-33 and SJJS-34 full bloom time was recorded in 4^{th} week of April.

4.4 Fruit Characters

A wide range of variation is present in horticultural traits such as fruiting duration, fruit weight, fruit size, fruit volume, specific gravity, percent consumable and non-consumable matter, seed weight, seed length, seed breadth, pulp: seed ratio, moisture content and seed, juice content, juice pH, T.S.S., titratable acidity, TSS: acidity ratio, ascorbic acid, total, non-reducing and reducing sugars, total antocyanin content, antioxidant activity, total tannins, organoleptic evaluation. The results regarding fruit characters of jamun genotypes studied are described in this section under suitable titles.

4.4.1 Duration of fruiting

The results pertaining to duration of fruiting in selected genotypes are presented in Table 3. A close observation of the data disclosed that the duration of fruiting starts earliest from 3^{rd} of June in genotype SJJS-29 and it concludes on 2^{nd} of August in genotypes SJJS-18 and SJJS-20 which were the latest in fruiting. The earliest fruiting genotype recorded the ending of fruiting on 20 July. The other early bearing genotypes were SJJS-24, SJJS-26, SJJS-30 and SJJS-36 while the late bearing genotypes were SJJS-9, SJJS-10, SJJS-13, SJJS-14, SJJS-15, SJJS-16 and SJJS-39.

4.4.2 Fruit Shape

Fruit shape varied from ellipsoid to oval. Among the forty genotypes eighteen genotypes *viz*., SJJS-1, SJJS-2, SJJS-4, SJJS-7, SJJS-8, SJJS-9, SJJS-11, SJJS-14, SJJS-16, SJJS-20, SJJS-22, SJJS-25, SJJS-29, SJJS-30, SJJS-33, SJJS-34 and SJJS-35 SJJS-

Table 3: Fruit physical characteristics of jamun genotypes- I

S. No.	Genotype	Duration of fruiting	Fruit shape	Fruit weight (g)	Fruit size (LxB) (mm^2)	Fruit volume (cc)	Specific gravity	Per cent consumable matter (pulp)	Per cent Non-edible matter (seed)
1	SJJS-1	29 June-27 July	Ellipsoid	10.34	573.16	10.00	1.05	85.62	14.38
2	SJJS-2	25 June-15 July	Ellipsoid	11.14	629.62	10.50	1.06	86.31	13.69
3	SJJS-3	25 June-15 July	Oval	9.43	513.03	9.33	1.01	85.74	14.26
4	SJJS-4	22 June-25 July	Ellipsoid	10.09	553.57	9.33	1.08	87.88	12.12
5	SJJS-5	26 June-26 July	Oval	9.92	563.16	9.33	1.07	82.80	17.20
6	SJJS-6	23 June-20 July	Oval	8.98	509.06	8.50	1.06	85.48	14.52
7	SJJS-7	25 June-22July	Ellipsoid	10.11	560.40	9.33	1.09	85.57	14.43
8	SJJS-8	28 June-25 July	Ellipsoid	8.73	491.09	8.67	1.01	85.73	14.27
9	SJJS-9	29 June-30 July	Ellipsoid	10.96	587.26	10.00	1.10	86.67	13.33
10	SJJS-10	26 June-28 July	Oval	10.97	616.97	11.33	1.01	84.89	15.11
11	SJJS-11	30 June-27 July	Ellipsoid	10.33	512.91	9.67	1.07	84.58	15.42
12	SJJS-12	30 June-30 July	Oval	10.80	581.06	10.33	1.05	86.48	13.52
13	SJJS-13	29 June-31 July	Oval	10.64	584.73	10.00	1.07	83.76	16.24
14	SJJS-14	29 June-31July	Ellipsoid	10.65	573.16	10.67	1.00	83.51	16.49
15	SJJS-15	29 June-31 July	Oval	9.05	472.48	8.67	1.05	86.85	13.15
16	SJJS-16	30 June-31 July	Ellipsoid	10.41	558.65	10.00	1.04	83.49	16.51
17	SJJS-17	16 June-18 July	Oval	10.05	524.38	10.00	1.01	85.35	14.65
18	SJJS-18	3 July-2 August	Oval	10.45	540.26	10.00	1.06	85.99	14.01
19	SJJS-19	27 June-31 July	Oval	8.80	492.88	8.33	1.06	85.89	14.11

20	SJJS-20	1 July-2 August	Ellipsoid	10.49	551.36	9.67	1.09	85.60	14.40
21	SJJS-21	28 June-25 July	Oval	10.80	416.85	10.00	1.08	82.15	17.85
22	SJJS-22	24 June-27 July	Ellipsoid	9.74	527.23	9.00	1.08	84.37	15.63
23	SJJS-23	25 June-29 July	Oval	10.23	543.95	9.67	1.06	86.16	13.84
24	SJJS-24	9 June-21 July	Oval	8.86	462.98	8.33	1.07	84.01	15.99
25	SJJS-25	10 June-25 July	Ellipsoid	9.56	514.41	10.17	0.95	84.76	15.24
26	SJJS-26	8 June-24 July	Oval	11.05	549.28	11.00	1.01	82.73	17.27
27	SJJS-27	17 June-25 July	Oval	11.40	622.64	11.33	1.01	86.58	13.42
28	SJJS-28	14 June-23 July	Oval	11.21	622.51	10.67	1.05	84.95	15.05
29	SJJS-29	3 June-20 July	Ellipsoid	10.02	539.33	9.33	1.08	85.80	14.20
30	SJJS-30	5 June-22 July	Ellipsoid	9.21	494.46	8.67	1.06	84.35	15.65
31	SJJS-31	26 June-27 July	Oval	9.58	519.09	9.33	1.03	85.36	14.64
32	SJJS-32	10 June-19 July	Oval	8.40	434.97	8.00	1.05	85.14	14.86
33	SJJS-33	17 June-27 July	Ellipsoid	9.71	529.70	9.00	1.09	83.26	16.74
34	SJJS-34	15 June-30 July	Ellipsoid	9.96	546.05	9.00	1.11	86.24	13.76
35	SJJS-35	10 June-22 July	Ellipsoid	10.66	572.17	9.67	1.10	86.71	13.29
36	SJJS-36	8 June-15 July	Oval	8.30	423.85	8.33	1.00	88.38	11.62
37	SJJS-37	18 June-20 July	Oval	10.65	563.87	10.50	1.02	83.93	16.07
38	SJJS-38	20 June-25 July	Oval	9.08	490.29	9.00	1.01	82.51	17.49
39	SJJS-39	25 June-31 July	Ellipsoid	10.32	554.16	9.00	1.19	84.70	15.30
40	SJJS-40	20 June-27 July	Oval	10.30	566.56	10.00	1.04	84.34	15.66

SJJS-1

SJJS-2

Plate 3(A) : Variation in fruit characters of Jamun (*Syzygium cumini* L.) genotypes selected for evaluation

SJJS-3

SJJS-4

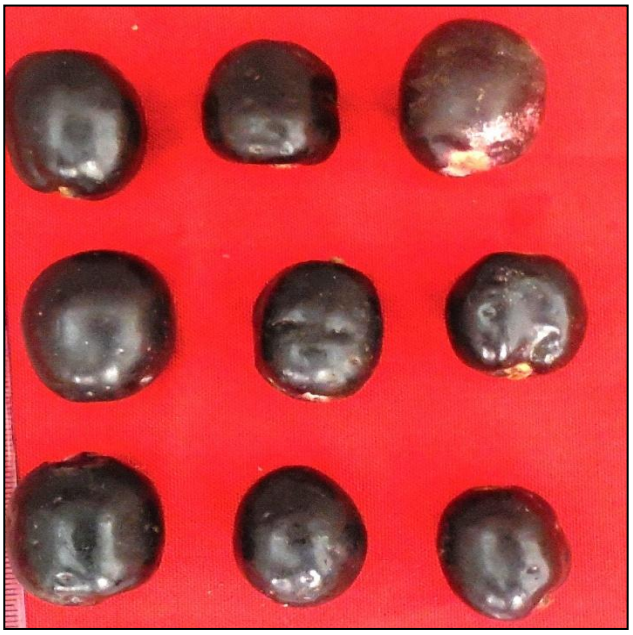
Plate 3(B): Variation in fruit characters of Jamun (*Syzygium cumini* L.) genotypes selected for evaluation

SJJS-5

SJJS-6

Plate 3© : Variation in fruit characters of Jamun (Syzygium cumini L.) genotypes selected for evaluation

SJJS-7



SJJS-8

Plate 3(D) : Variation in fruit characters of Jamun (*Syzygium cumini* L.) genotypes selected for evaluation

SJJS-9

SJJS-10

Plate 3(E) Variation in fruit characters of Jamun (*Syzygium cumini* L.) genotypes selected for evaluation

SJJS-11

SJJS-12

Plate 3(F) Variation in fruit characters of Jamun (*Syzygium cumini* L.) genotypes selected for evaluation

SJJS-13

SJJS-14

Plate 3(G) Variation in fruit characters of Jamun (*Syzygium cumini* L.) genotypes selected for evaluation

SJJS-16

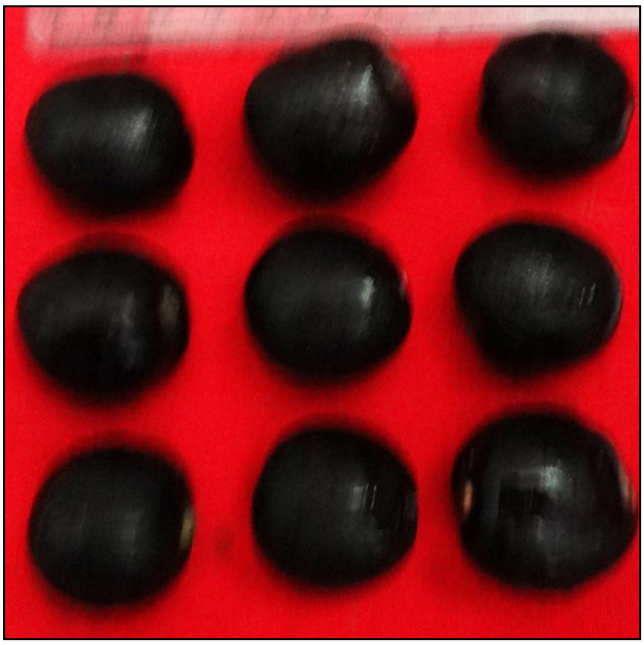
Plate 3(H) Variation in fruit characters of Jamun (*Syzygium cumini* L.) genotypes selected for evaluation

SJJS-17

SJJS-18

Plate 3(I): Variation in fruit characters of Jamun (*Syzygium cumini* L.) genotypes selected for evaluation

Plate 3(J): Variation in fruit characters of Jamun (*Syzygium cumini* L.) genotypes selected for evaluation



SJJS-21

SJJS-22

Plate 3(K): Variation in fruit characters of Jamun (*Syzygium cumini* L.) genotypes selected for evaluation

SJJS-23

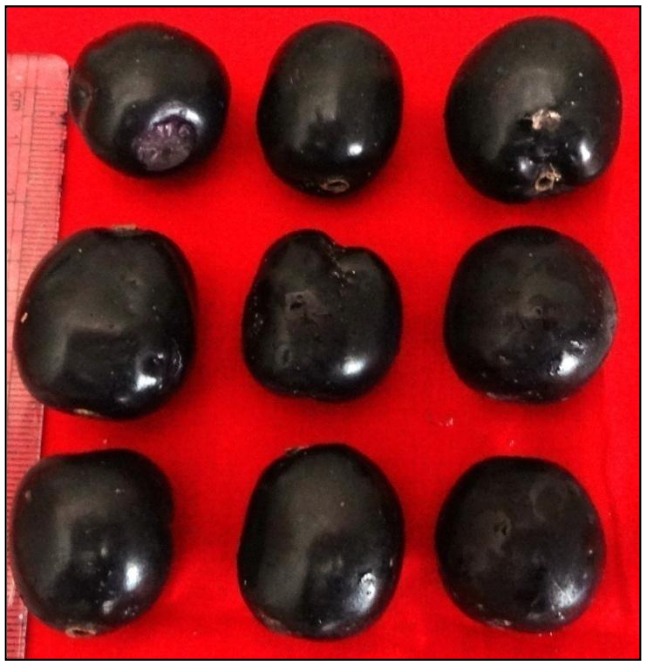
SJJS-24

Plate 3(L): Variation in fruit characters of Jamun (*Syzygium cumini* L.) genotypes selected for evaluation

SJJS-25

SJJS-26

Plate 3(M): Variation in fruit characters of Jamun (*Syzygium cumini* L.) genotypes selected for evaluation



SJJS-27

SJJS28

Plate 3(N): Variation in fruit characters of Jamun (*Syzygium cumini* L.) genotypes selected for evaluation

SJJS-27

SJJS-30

Plate 3(O): Variation in fruit characters of Jamun (*Syzygium cumini* L.) genotypes selected for evaluation

SJJS-31

SJJS-32

Plate 3(P): Variation in fruit characters of Jamun (*Syzygium cumini* L.) genotypes selected for evaluation

SJJS-33

SJJS-34

Plate 3(Q): Variation in fruit characters of Jamun (*Syzygium cumini* L.) genotypes selected for evaluation

SJJS-35

SJJS-36

Plate 3(R): Variation in fruit characters of Jamun (*Syzygium cumini* L.) genotypes selected for evaluation

SJJS-37

SJJS-38

Plate 3(S): Variation in fruit characters of Jamun (*Syzygium cumini* L.) genotypes selected for evaluation

SJJS-39

SJJS-40

Plate 3(T): Variation in fruit characters of Jamun (*Syzygium cumini* L.) genotypes selected for evaluation

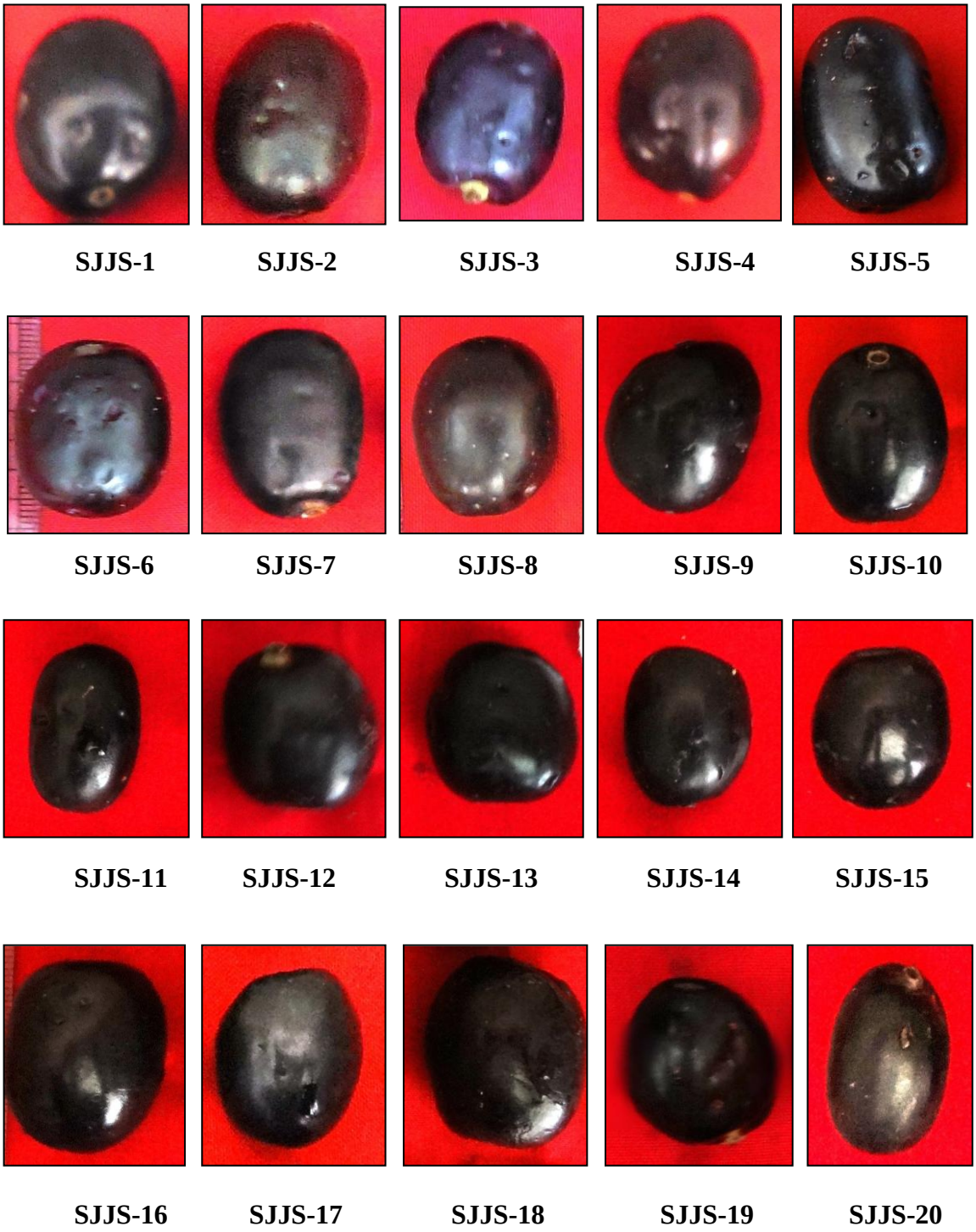
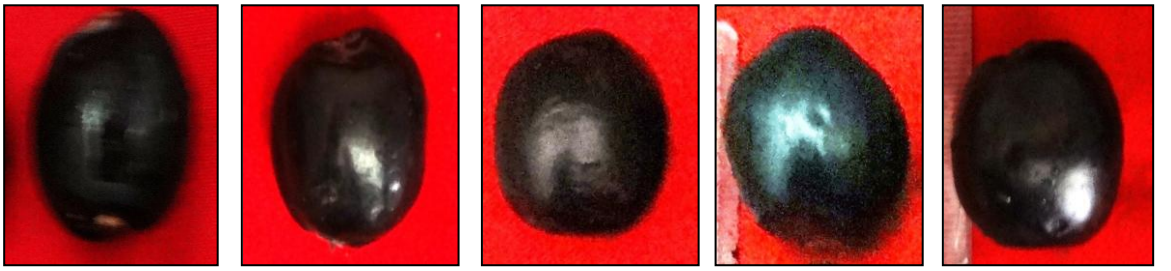


Plate 4(A): Variation in fruit shape of individual Jamun (*Syzygium cumini* L.) genotypes selected for evaluation



SJJS-21 SJJS-22 SJJS-23 SJJS-24 SJJS-25

SJJS-26 SJJS-27 SJJS-28 SJJS-29 SJJS-30

SJJS-31 SJJS-32 SJJS-33 SJJS-34 SJJS-35

SJJS-36 SJJS-37 SJJS-38 SJJS-39 SJJS-40

Plate 4(B): Variation in fruit shape of individual Jamun (*Syzygium cumini* L.) genotypes selected for evaluation

39 had ellipsoid fruit shape whereas twenty two genotypes had oval shape *viz*., SJJS-3, SJJS-5, SJJS-6, SJJS-10, SJJS-12, SJJS-13, SJJS-15, SJJS-17, SJJS-18, SJJS-19, SJJS-21, SJJS-23, SJJS-24, SJJS-26, SJJS-27, SJJS-28, SJJS-31, SJJS-32, SJJS-36, SJJS-37, SJJS-38 and SJJS-40 (Table 3).

4.4.3 Fruit weight

The data on the fruit weight selected jamun genotypes are presented in Table 3. From the perusal of the data, maximum fruit weight was recorded as 11.40 g in SJJS-27 followed by SJJS-28 (11.21 g) and SJJS-2 (11.14 g) genotypes respectively while minimum fruit weight of 8.40 g was noted in SJJS-32 genotype.

4.4.4 Fruit size

The results with respect to fruit size are presented in Table 3. The observation of results revealed that fruit size was recorded maximum in genotype SJJS-2 with 629.62 mm^2 followed by SJJS-27 and SJJS-28 with 622.64 mm^2 and 622.51 mm^2, respectively whereas minimum fruit size was recorded in SJJS-21(416.85 mm^2) genotype.

4.4.5 Fruit volume

The perusal of data presented in Table 3 showed that maximum fruit volume was recorded in genotypes SJJS-10 and SJJS-27 with 11.33 cc whereas minimum fruit volume of 8.00 cc is observed in genotype SJJS-30.

4.4.6 Specific gravity

The variation of specific gravity of forty studied genotypes is given in Table 3. Specific gravity ranged from 0.95 to 1.19. The maximum value of specific gravity was observed as in genotype SJJS-39 whereas minimum value was recorded in genotype SJJS-25.

4.4.7 Proportion of consumable matter (pulp) and proportion of non-edible matter (seed)

The results obtained with respect to, proportion of consumable matter (pulp) and proportion of non-edible matter (seed), are presented in Table 3. The data showed that genotype SJJS-36 had maximum consumable and minimum non-edible matter with 88.38 per cent and 11.62 per cent respectively followed by genotype SJJS-4 with 87.88 per cent and 12.12 per cent consumable and non-edible matter respectively. The

minimum value of consumable matter and maximum non-edible matter was observed in SJJS- 21 with 82.15 per cent.

4.5.2 Seed weight

The perusal of data presented in Table 4 showed that seed weight varied from 0.96 g to 1.93 g. Minimum seed weight of .096 g was recorded in SJJS- 36 preceded by 1.19 g and 1.22 g in genotypes SJJS-15 and SJJS-4 respectively. Maximum seed weight of 1.93 g was recorded in genotype SJJS-26 followed by 1.91 g in genotype SJJS-21.

4.5.3 Seed size

The results pertaining to seed length showed that it varied between 15.30 to 20.83 mm. Minimum seed length was observed in genotype SJJS-8 followed by SJJS-36 (15.52 mm) and genotype SJJS-19 (15.84 mm). Maximum seed length of 20.83 mm was observed in genotype SJJS- 5 followed by genotypes SJJS-26 (20.63 mm) and SJJS-16 (20.35 mm).

Seed breadth ranged from 9.52 to 12.57 mm. Minimum seed weight was observed in SJJS-8 followed by SJJS-36 (9.74 mm) and SJJS-24 (9.86 mm) whereas maximum seed weight was noted in SJJS-21 followed by SJJS-26 (12.04 mm).

4.5.4 Pulp: seed ratio

The pulp: seed ratio showed a range of 4.75 to 7.71. Minimum pulp: seed ratio was noted in genotype SJJS-21 followed by genotype SJJS-38 (4.86) and maximum pulp: seed ratio was observed in genotype SJJS-36 followed by genotype SJJS-4 (7.44).

4.4.7 Moisture content of fruit and seed

The results related to moisture content of fruit and seed of genotypes studied are presented in Table 4. The maximum moisture content of fruit in per cent was found in genotype SJJS-25 (92.04 per cent) followed by SJJS-15 (89.41 per cent) while minimum moisture content was noted in SJJS-30 (74.91 per cent).

The range of moisture content of seed between 53.41 to 62.79 per cent with maximum moisture content of seed in genotype SJJS-36 followed by SJJS-33 (62.54 per cent) whereas minimum moisture content of seed was observed in genotype SJJS-21.

4.6.1 Juice content

The perusal of data of selected jamun genotypes is presented in Table 4 revealed that maximum juice content was observed in genotype SJJS-36 (37.47 per cent) whereas minimum juice content was found in genotype SJJS-14 (27.77 per cent).

Table 4: Fruit physical characteristics of Jamun genotypes- II

S. No.	Genotype	Seed weight (g)	Seed length (mm)	Seed breadth (mm)	Pulp : seed Ratio	Moisture content of fruit (%)	Moisture content of seed (%)	Juice Content (%)
1	SJJS-1	1.48	19.09	10.41	6.07	86.42	53.85	32.13
2	SJJS-2	1.52	19.64	10.36	6.49	84.36	55.98	32.17
3	SJJS-3	1.34	18.45	9.95	6.13	85.98	55.95	32.97
4	SJJS-4	1.22	17.57	10.04	7.44	85.13	59.34	34.23
5	SJJS-5	1.70	20.83	10.88	4.94	83.68	55.60	31.64
6	SJJS-6	1.30	17.70	10.48	6.09	84.51	57.13	32.82
7	SJJS-7	1.46	18.84	10.19	5.98	85.96	55.20	32.58
8	SJJS-8	1.25	15.30	9.52	6.10	85.69	56.57	33.13
9	SJJS-9	1.47	19.06	10.13	6.64	83.14	54.16	30.65
10	SJJS-10	1.74	19.03	11.42	5.77	87.59	59.49	35.54
11	SJJS-11	1.59	17.44	11.81	5.49	85.86	57.52	33.69
12	SJJS-12	1.45	18.44	10.94	6.80	86.65	56.29	33.47
13	SJJS-13	1.73	19.99	11.19	5.17	82.31	54.89	30.60
14	SJJS-14	1.76	19.58	11.14	5.11	76.93	54.61	27.77
15	SJJS-15	1.19	16.57	10.12	6.64	89.41	54.90	34.16
16	SJJS-16	1.72	20.35	11.04	5.29	86.35	55.10	32.72
17	SJJS-17	1.47	17.63	11.59	5.87	85.86	55.96	32.91
18	SJJS-18	1.45	18.33	11.78	6.33	84.29	56.17	32.23
19	SJJS-19	1.26	15.84	11.05	6.22	85.51	60.02	34.77

20	SJJS-20	1.51	19.01	10.02	6.04	84.57	56.18	32.37
21	SJJS-21	1.91	18.96	12.57	4.75	85.80	53.41	31.60
22	SJJS-22	1.52	17.94	10.84	5.42	85.59	58.56	34.08
23	SJJS-23	1.43	17.90	11.15	6.33	82.71	56.41	31.56
24	SJJS-24	1.42	18.39	9.86	5.28	84.13	55.46	31.79
25	SJJS-25	1.47	16.97	11.75	5.70	92.04	57.83	36.94
26	SJJS-26	1.93	20.63	12.04	5.08	86.35	61.00	35.68
27	SJJS-27	1.54	19.65	11.28	6.63	84.12	58.39	33.26
28	SJJS-28	1.69	19.01	11.25	5.65	84.69	57.54	33.12
29	SJJS-29	1.42	18.08	10.62	6.12	81.98	55.65	30.81
30	SJJS-30	1.44	17.97	10.59	5.41	74.91	56.43	27.67
31	SJJS-31	1.40	17.54	10.89	5.90	82.96	56.18	31.57
32	SJJS-32	1.25	16.56	10.11	5.74	85.70	58.94	34.32
33	SJJS-33	1.63	18.10	10.12	5.03	82.20	62.54	34.37
34	SJJS-34	1.37	16.93	10.39	6.31	80.45	60.92	32.69
35	SJJS-35	1.42	18.35	11.08	6.60	84.78	59.80	34.29
36	SJJS-36	0.96	15.52	9.74	7.71	88.15	62.79	37.47
37	SJJS-37	1.71	19.89	11.91	5.24	85.25	56.57	32.91
38	SJJS-38	1.56	19.35	11.28	4.86	87.82	57.10	34.46
39	SJJS-39	1.57	18.61	11.84	5.66	85.52	56.41	32.96
40	SJJS-40	1.61	18.78	11.18	5.51	86.35	58.14	34.24

4.6.2 Juice pH

The range of juice pH of the selected genotypes varied from 3.74 to 3.95 and maximum juice pH was observed in genotypes SJJS-18 and SJJS-26 while genotype SJJS-16 showed minimum juice pH (Table 5).

4.6.3 Total soluble solids (^{o}B)

The results of the genotypes studied with respect to TSS are presented in Table 5. The observation of results showed that TSS ranged from 10.00 to 17.37 ^{o}Brix. The lowest value of T.S.S. was recorded for SJJS-8 followed by SJJS-7 with 12.00 whereas highest value was found in genotype SJJS-29 followed by genotype SJJS-13 and SJJS-14 with 16.87.and 16.67 ^{o}Brix respectively.

4.6.4 Titratable Acidity

The range of titratable acidity varied between 0.47 and 0.94 per cent with maximum value in genotype SJJS-16 followed by SJJS-28 with 0.87 per cent whereas the minimum value was observed in genotype SJJS-18 (Table 5).

4.6.5 TSS: acidity ratio

The range of TSS: acidity ratio varied from 13.89 to 32.75 with minimum value in genotype SJJS-16 and maximum value in genotype SJJS-29 (Table 5).

4.6.5 Ascorbic acid

The perusal of data related to ascorbic acid presented in Table 5 showed that its range varied from 22.71 to 45.93 mg per 100 g fruit. The maximum ascorbic acid content was recorded in genotype SJJS-12 followed by SJJS-4 with 41.55 mg per 100 g fruit while minimum ascorbic acid was recorded in genotype SJJS-33.

4.6.6 Sugars

The results with respect to total, reducing and non-reducing sugars are presented in Table 5.

4.6.6.1 Reducing sugars

Reducing sugar content was found highest with 10.00 in SJJS-29 followed by SJJS-28 to 9.90 per cent while lowest reducing sugar content with 4.34 per cent was observed in genotype SJJS-8.

4.6.6.2 Total Sugars

The results revealed that total sugars ranged from 5.84 to 10.69 per cent. Highest total sugar content in genotype SJJS-29 followed by SJJS-28 with 10.24 per cent whereas lowest total sugars was observed in genotype SJJS-8 followed by SJJS-31 with 6.10 per cent.

4.6.6.3 Non-reducing sugars

The perusal of Table 5 revealed that highest non-reducing sugar content of 3.02 per cent was observed in genotype SJJS-27 followed by SJJS-13 with 1.65 per cent non-reducing sugar content whereas lowest values were observed in genotype SJJS-34 with 0.20 per cent.

4.6.7 Total anthocyanin content

The perusal of data related to total anthocyanin content revealed that the maximum anthocyanins content of 7.50 mg per 100 g was present in SJJS-10 and SJJS-27 genotypess followed by genotype SJJS-9 with 7.48 mg per 100 g while minimum anthocyanins content of 6.80 mg per 100 g was found in SJJS-36 followed by SJJS-24 with 6.81 mg per 100 g (Table 6).

4.6.8 Total tannins

The results for total tannin content of selected forty genotypes are presented Table 6. As per the observations, maximum total tannin content of 1.90 mg per 100 g fresh weight was recorded in genotype SJJS-27 followed by SJJS-9 and SJJS-10 with 1.89 mg per 100 g fresh weight whereas genotype SJJS-3, SJJS-25 and SJJS-31 with 1.70 mg per 100 g fresh weight.

4.6.9 Antioxidant activity

The perusal of results obtained for antioxidant activity showed that the antioxidant activity measured as DPPH per cent inhibition was found to be maximum in SJJS-27 with a value of 96.55 whereas minimum value of 61.45 was noted in SJJS-36 (Table 6).

4.6.10 Organoleptic evaluation

The selected jamun genotypes were categorized on the basis of the 9 point hedonic scale for organoleptic evaluation and the data is presented in Table 6. The perusal of data revealed that, with a score of 8.20, genotype SJJS-29 was liked very much as well as genotypes SJJS-13, SJJS-14 and SJJS-28 with score of 8.00. The genotypes SJJS-1, SJJS-2, SJJS-4, SJJS-5, SJJS-10, SJJS-15, SJJS-16, SJJS-17, SJJS-18, SJJS-19, SJJS-20, SJJS-21, SJJS-25, SJJS-26, SJJS-27, SJJS-30, SJJS-31, SJJS-32, SJJS-33 and SJJS-40 were categorized as liked moderately whereas the genotypes SJJS-34, SJJS-35, SJJS-36, SJJS-37, SJJS-38 and SJJS-39 were categorized as slightly liked by the panellists.

4.7 Range and means

The magnitude of variability present in various quantitative traits is presented in Table 7. Wide range of variability was recorded among all the traits studied. Perusal of

Table 5: Fruit chemical characteristics of jamun genotypes-I

S. No.	Genotype	Juice pH	TSS (°Brix)	Titratable acidity (%)	TSS: acidity ratio	Ascorbic acid (mg/100 g)	Total Sugars (%)	Reducing Sugars (%)	Non-reducing sugars (%)
1	SJJS-1	3.79	13.33	0.64	20.89	29.18	8.37	6.96	1.41
2	SJJS-2	3.81	14.03	0.67	21.25	29.86	7.81	6.94	0.87
3	SJJS-3	3.79	11.43	0.64	17.91	34.34	7.21	6.01	1.20
4	SJJS-4	3.89	13.80	0.67	20.96	41.55	7.9	6.8	1.10
5	SJJS-5	3.80	13.60	0.63	21.85	30.84	7.26	5.91	1.35
6	SJJS-6	3.80	12.43	0.64	19.77	28.17	7.25	6.15	1.10
7	SJJS-7	3.80	12.00	0.64	18.78	27.06	7.41	6.09	1.32
8	SJJS-8	3.80	10.00	0.64	15.68	24.74	5.84	4.34	1.50
9	SJJS-9	3.86	15.60	0.59	26.74	31.88	9.75	8.62	1.13
10	SJJS-10	3.75	12.57	0.81	15.62	30.43	7.20	6.25	0.95
11	SJJS-11	3.81	12.87	0.65	19.96	29.76	7.23	6.10	1.13
12	SJJS-12	3.82	13.73	0.69	20.14	45.93	7.81	6.75	1.06
13	SJJS-13	3.85	16.87	0.58	29.50	29.18	8.06	6.41	1.65
14	SJJS-14	3.78	16.67	0.76	22.30	40.24	7.96	6.33	1.63
15	SJJS-15	3.88	13.63	0.59	23.55	24.74	7.28	6.80	0.48
16	SJJS-16	3.74	12.93	0.94	13.89	36.77	7.66	6.50	1.16
17	SJJS-17	3.78	15.60	0.64	24.52	30.43	6.90	5.81	1.09
18	SJJS-18	3.95	15.00	0.47	31.69	29.86	8.35	7.35	1.00
19	SJJS-19	3.90	15.07	0.60	25.14	29.39	8.40	7.41	0.99

20	SJJS-20	3.86	14.20	0.58	24.70	29.45	7.39	6.57	0.82
21	SJJS-21	3.90	15.03	0.58	25.98	30.53	8.36	7.37	0.99
22	SJJS-22	3.89	14.27	0.59	24.56	27.06	7.48	6.80	0.68
23	SJJS-23	3.80	12.97	0.63	20.82	29.86	7.29	6.20	1.09
24	SJJS-24	3.91	16.23	0.53	31.01	25.41	9.93	9.40	0.53
25	SJJS-25	3.75	14.73	0.76	19.82	27.43	7.72	6.94	0.78
26	SJJS-26	3.95	14.47	0.54	26.98	26.76	7.45	6.70	0.75
27	SJJS-27	3.78	15.80	0.76	20.62	28.71	8.39	5.37	3.02
28	SJJS-28	3.75	16.50	0.87	19.22	27.43	10.24	9.90	0.34
29	SJJS-29	3.90	17.37	0.53	32.75	27.43	10.69	10.00	0.69
30	SJJS-30	3.90	15.13	0.53	28.53	26.96	8.40	7.30	1.10
31	SJJS-31	3.88	15.53	0.57	27.81	39.06	6.10	5.82	0.28
32	SJJS-32	3.87	14.53	0.61	24.05	25.31	7.62	6.84	0.78
33	SJJS-33	3.80	14.50	0.58	25.05	22.71	7.50	6.79	0.71
34	SJJS-34	3.80	15.87	0.64	24.98	26.45	7.80	7.60	0.20
35	SJJS-35	3.75	12.37	0.76	16.31	35.25	7.50	6.30	1.20
36	SJJS-36	3.85	12.07	0.59	20.70	24.43	7.30	6.01	1.29
37	SJJS-37	3.80	15.03	0.66	23.38	29.18	8.21	7.32	0.89
38	SJJS-38	3.80	12.10	0.66	18.64	29.45	7.40	6.09	1.31
39	SJJS-39	3.86	12.97	0.59	22.51	27.43	7.20	6.10	1.10
40	SJJS-40	3.85	14.80	0.59	25.60	26.66	7.77	6.99	0.78

Table 6: Fruit chemical characteristics of jamun genotypes

S. No.	Genotype	Total Anthocyanin content (mg/100 g)	Total Tannins (mg/100 g)	Antioxidant Activity (DPPH % inhibition)	Organoleptic Evaluation (average score)
1	SJJS-1	7.34	1.82	87.31	7.00
2	SJJS-2	7.39	1.88	94.30	7.40
3	SJJS-3	7.25	1.70	78.60	6.40
4	SJJS-4	7.33	1.80	89.91	7.20
5	SJJS-5	7.21	1.74	75.58	7.00
6	SJJS-6	6.89	1.74	69.10	6.60
7	SJJS-7	7.30	1.81	82.33	6.60
8	SJJS-8	6.89	1.74	66.98	6.00
9	SJJS-9	7.48	1.89	93.40	7.60
10	SJJS-10	7.50	1.89	95.50	7.00
11	SJJS-11	7.42	1.87	91.81	6.60
12	SJJS-12	7.32	1.87	92.10	6.40
13	SJJS-13	7.39	1.84	87.50	8.00
14	SJJS-14	7.39	1.84	89.93	8.00
15	SJJS-15	6.97	1.73	69.78	7.00
16	SJJS-16	7.34	1.84	88.50	6.20
17	SJJS-17	7.34	1.81	85.56	7.40
18	SJJS-18	7.30	1.82	84.50	7.40
19	SJJS-19	6.91	1.75	67.90	7.20
20	SJJS-20	7.35	1.84	85.91	7.00
21	SJJS-21	7.39	1.84	86.73	7.60
22	SJJS-22	7.25	1.80	77.90	7.40
23	SJJS-23	7.37	1.81	83.12	6.40
24	SJJS-24	6.81	1.73	62.00	7.80
25	SJJS-25	7.12	1.70	73.30	7.20
26	SJJS-26	7.40	1.87	94.10	7.00
27	SJJS-27	7.50	1.90	96.55	7.80
28	SJJS-28	7.41	1.88	95.31	8.00
29	SJJS-29	7.13	1.82	81.67	8.20
30	SJJS-30	6.89	1.77	72.40	7.80
31	SJJS-31	7.20	1.70	75.50	7.60
32	SJJS-32	6.84	1.73	62.56	7.40

33	SJJS-33	7.29	1.77	78.40	7.40
34	SJJS-34	7.31	1.79	79.30	6.60
35	SJJS-35	7.40	1.85	88.40	6.60
36	SJJS-36	6.80	1.73	61.45	6.20
37	SJJS-37	7.39	1.85	87.60	6.20
38	SJJS-38	6.92	1.75	70.66	6.60
39	SJJS-39	7.36	1.85	86.40	6.80
40	SJJS-40	7.30	1.85	85.50	7.00

Table 7 : Range and mean of various traits in jamun genotypes

Characters	Range	Means
Fruit weight (g)	8.30 - 11.47	10.04± 0.34
Fruit size (cm^2)	416.85 – 629.62	537 ± 34.67
Specific gravity	0.94 – 1.18	1.05 ± 0.06
Pulp: stone ratio	4.75 – 7.71	5.89 ± 0.61
T.S.S (^oBrix)	10.00 –17.35	14.19 ± 1.01
Acidity (%)	0.47 – 0.94	0.64 ± 0.04
Ascorbic acid (mg/100g)	22.71 – 45.93	29.93 ± 1.83
Yield efficiency	0.19 – 0.26	0.21 ± 0.02

data revealed that the fruit weight, fruit size, specific gravity, pulp: stone ratio, T.S.S., titratable acidity, ascorbic acid and yield efficiency ranged between 8.30 to 11.47 g, 416.85 to 629.62 cm^2, 0.94 to 1.18, 4.75 to 7.71, 10.00 to17.35 ^oBrix, 0.47 to 0.94 per cent, 22.71 to 45.93 mg per100 g and 0.19 to 0.26, respectively with a mean of 10.04± 0.34 g, 537 ± 34.67cm^2 , 1.05 ± 0.06, 5.89 ± 0.61, 14.19 ± 1.01 ^oBrix, 0.64 ± 0.01 per cent, 29.93 ± 1.83 mg per 100 g and 0.21 ± 0.02, respectively.

4.8 Variance and coefficient of variation

Phenotypic and genotypic variances and phenotypic and genotypic coefficient of variation for various traits are presented in Table 8. The data revealed that the estimates of phenotypic variance were higher than the corresponding estimates of genotypic variance. The magnitude of phenotypic and genotypic coefficient of variation was low (less than 10 %) for fruit weight and specific gravity whereas it was moderate (10-30 %) for fruit size, pulp: seed ratio, T.S.S., titratable acidity, ascorbic acid and it was high (more than 30 %) for yield efficiency.

4.9 Heritability and genetic gain

The broad sense heritability estimates and per cent genetic gain have been presented in Table 8. Heritability was grouped in three classes wherein less than 10 per cent hertability was classified as low, 10-30 per cent as medium and 30-60 per cent as high heritability. Highest heritability of 67.7 per cent was recorded in pulp: seed ratio followed by ascorbic acid (67.3 %), fruit weight (61.4 %), fruit size (58.2 %), yield efficiency (57.1 %), T.S.S. (56.4 %), titratable acidity (53.8 %) and specific gravity (28.6 %).

Genetic gain was grouped into three distinct classes wherein less than 20 per cent genetic gain was classified as low, 20-40 per cent as medium and greater than 40 per cent as high genetic gain. The results revealed that genetic gain was low for fruit weight (12.17 %), fruit size (15.86 %), specific gravity (4.70 %), T.S.S. (17.81 %) and acidity (19.73 %) whereas the genetic gain was medium for pulp: seed ratio (26.08 %), ascorbic acid (25.76 %) and high for yield efficiency (46.89 %).

4.10 Correlation

Correlation coefficients of eight quantitative characters were estimated at genotypic and phenotypic level and the results are presented in Table 9. The results revealed that fruit weight showed a positive correlation with fruit size, specific gravity,

pulp: seed ratio, T.S.S. and yield efficiency at both genotypic and phenotypic levels. However, the correlations with ascorbic acid and titratable acidity were negative at both genotypic and phenotypic levels. Fruit size exhibited positive correlation with fruit weight, specific gravity, pulp: seed ratio, T.S.S. and yield efficiency at both genotypic and phenotypic level but negative correlation with ascorbic acid and titratable acidity at both genotypic and phenotypic levels. Specific gravity showed positive correlation with pulp: seed ratio, T.S.S. and yield efficiency at both genotypic and phenotypic levels but negative correlation with ascorbic acid and acidity at both levels. T.S.S. exhibited negative correlation with acidity at both genotypic and phenotypic levels but positive correlation with yield efficiency at both the levels. Acidity and ascorbic acid both showed negative correlation to yield efficiency at both genotypic and phenotypic levels.

4.11 Path Analysis

Direct and indirect contribution of seven different quantitative traits including fruit weight, fruit size, specific gravity, pulp: seed ratio, TSS, acidity and ascorbic acid towards yield efficiency were estimated through partitioning of their genotypic correlation coefficient analysis. The results obtained are presented in Table 10. Fruit size with 0.3515 recorded the maximum positive direct effect on yield efficiency followed by pulp: seed ratio (0.3196) while as titratable acidity had the maximum negative effect (-0.2633) on yield efficiency. Highest positive indirect effect on yield efficiency came from fruit size through pulp: seed ratio. Highest negative indirect effect came from acidity through fruit size. In addition to direct and indirect contribution of various traits towards yield efficiency, path analysis revealed a residual variance of 18.09 indicating thereby that 89.01 per cent of variance was accounted by path analysis.

4.12 Divergence and Clustering

Based on the performance of various genotypes, forty genotypes were grouped into seven clusters as presented in Table 11. Cluster-IV comprised of maximum 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

Table 8: Estimates of components of variance and coefficient of variation for various traits in jamun genotypes

Characters	Components of Variance		Components of coefficient of variation		Heritability	Genetic gain
	$\sigma^2 g$	$\sigma^2 p$	GCV	PCV	(Broad sense)	(per cent of mean)
Fruit weight	0.5720	0.9312	7.5374	9.6172	0.6143	12.1694
Fruit size	2938.4760	5046.0410	10.0884	13.2202	0.5823	15.8590
Specific gravity	0.0020	0.0070	4.2714	7.9910	0.2857	4.7033
Pulp: seed ratio	0.8200	1.2100	15.3794	18.6821	0.6777	26.0808
T.S.S	2.6670	4.7250	11.5081	15.3177	0.5644	17.8108
Acidity	0.0070	0.0130	13.0524	17.7874	0.5385	19.7304
Ascorbic acid	20.9460	31.1010	15.2387	18.5689	0.6735	25.7620
Yield efficiency	0.0040	0.0070	30.1169	39.8410	0.5714	46.8985

Table 9: Genotypic and phenotypic correlation coefficients for various traits in jamun genotypes

Characters	Correlation	Fruit weight	Fruit size	Specific gravity	Pulp: seed ratio	T.S.S	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

* = significance at 5%

Table 10: Path analysis at genotypic level showing direct (diagonal) and indirect (off diagonal) effects of various traits on yield efficiency in jamun genotypes

Characters	Fruit weight	Fruit size	Specific Gravity	Pulp: seed ratio	T.S.S	Acidity	Ascorbic acid	Genetic correlation of yield efficiency
Fruit weight	**0.2437**	0.1475	0.1104	0.1778	0.2012	-0.0189	-0.0175	**0.698**
Fruit size	0.1222	**0.3515**	0.1022	0.2615	0.1202	-0.0011	-0.0007	**0.749**
Specific gravity	0.2182	0.2902	**0.1028**	-0.0004	0.0340	-0.0003	0.0001	**0.533**
Pulp: seed ratio	0.1522	0.1431	0.3841	**0.3196**	-0.0083	-0.0016	0.0066	**0.599**
T.S.S	0.1653	0.1215	-0.0574	-0.0915	**0.2685**	-0.0309	0.0015	**0.662**
Acidity	-0.1138	-0.1959	-0.0971	0.0287	0.0483	**-0.2633**	-0.0749	**-0.377**
Ascorbic acid	-0.0898	-0.1088	-0.0124	-0.097	-0.002	-0.0638	**-0.2233**	**-0.308**

Residual effect:18.09

Table 11: Distribution of different jamun genotypes into clusters based on D^2 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

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.

Mean intra and inter cluster distance (D^2) values are presented in Table 12. The perusal of the results revealed that Cluster-III had the maximum intra cluster distance (3.56) followed by Cluster-V (2.99). Maximum inter cluster distance was found between Cluster-V and Cluster-VI (200.92) followed by Cluster-II and Cluster-VI (188.62), Cluster-III and Cluster-VI (155.65), Cluster-II and Cluster-V (135.00) and Cluster-V and Cluster-VII (130.30).

Perusal of data on cluster means for various quantitative traits presented in Table 13 reveals that Cluster-I had a fruit weight of 10.16 g, fruit size of 551.24 cm^2, specific gravity of 1.05, pulp: seed ratio of 6.71, T.S.S of 14.36 ^oBrix, titratable acidity of 0.64 per cent, ascorbic acid 42.18 mg per 100 g and yield efficiency of 0.19. Cluster-II had a fruit weight of 11.36 g, fruit size of 620.71 cm^2, specific gravity of 1.03, pulp: seed ratio of 6.02, T.S.S of 14.95 ^oBrix, titratable acidity of 0.81 per cent, ascorbic acid 28.86 mg per 100 g and yield efficiency of 0.19. Cluster-III had a fruit weight of 9.09 g, fruit size of 496.79 cm^2, specific gravity of 1.05, pulp: seed ratio of 5.82, T.S.S of 13.23 ^oBrix, titratable acidity of 0.61 per cent, ascorbic acid 27.22 mg per 100 g and yield efficiency of 0.20. Cluster-IV had a fruit weight of 10.26 g, fruit size of 535.85 cm^2, specific gravity of 1.06, pulp: seed ratio of 5.68, T.S.S of 13.9 ^oBrix, titratable acidity of 0.61 per cent, ascorbic acid 29.83 mg per 100 g and yield efficiency of 0.21. Cluster-V had a fruit weight of 9.96 g, fruit size of 540.00 cm^2, specific gravity of 1.05, pulp: seed ratio of 5.83, T.S.S of 15.04 ^oBrix, titratable acidity of 0.62 per cent, ascorbic acid 26.76 mg per 100 g and yield efficiency of 0.23. Cluster-VI had a fruit weight of 8.52 g, fruit size of 440.60 cm^2, specific gravity of 1.04, pulp: seed ratio of 6.24, T.S.S of 14.28 ^oBrix, titratable acidity of 0.58 per cent, ascorbic acid 25.05 mg per 100 g and yield efficiency of 0.21. Cluster-VII had a fruit weight of 10.79 g, fruit size of 576.29 cm^2, specific gravity of 1.04, pulp: seed ratio of 5.78, T.S.S of 14.44 ^oBrix, titratable acidity of 0.70 per cent, ascorbic acid 32.85 mg per 100 g and yield efficiency of 0.19.

Per cent contribution of traits towards total divergence has been presented in Table 14. The perusal of the data presented revealed that ascorbic acid was the main contributor of divergence (32.69 per cent), followed by fruit weight (20.00 per cent), yield efficiency (13.59 per cent), acidity (11.41 per cent), specific gravity (8.85 per

cent), TSS (8.33 per cent) and fruit size (2.69 per cent). Least contribution towards divergence came from pulp: seed ratio (2.44 per cent).

Table 12: Average inter-cluster (above diagonal) and intra-cluster (diagonal) 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 13: Cluster means for various traits in different clusters of jamun genotypes

Clusters	Fruit weight	Fruit size	Specific Gravity	Pulp: seed ratio	T.S.S	Acidity	Ascorbic acid	Yield efficiency
I	10.159	551.24	1.055	6.713	14.356	0.642	42.181	0.199
II	11.36	620.71	1.024	6.018	14.956	0.813	28.858	0.199
III	9.085	496.79	1.049	5.820	13.233	0.606	27.215	0.203
IV	10.261	535.85	1.058	5.675	13.900	0.605	29.825	0.208
V	9.962	540.00	1.047	5.832	15.039	0.623	26.758	0.232
VI	8.519	440.6	1.039	6.244	14.278	0.577	25.050	0.212
VII	10.788	576.29	1.04	5.777	14.443	0.702	32.848	0.197

Table 14: Per cent contribution of individual traits towards total divergence in jamun genotypes

Traits	Number of times appearing first in ranking	Per cent 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

Discussion

CHAPTER-5

DISCUSSION

The present investigations entitled "Characterization and evaluation of genetic diversity of jamun (*Syzygium cumini* L.) for horticultural traits" were undertaken during 2013 and 2014 in the jamun growing areas of Jammu district in order to survey the available germplasm of seedling origin jamun to obtain the quantitative measures of the degree of variability of various morphological and horticultural traits, predict heritability and genetic advance and estimate possible association among morphological and phenological traits in jamun germplasm.

For the success of a breeding programme and selection to be effective, variability at genetic level must be present in the breeding material. Thus, choosing the breeding stocks that have sufficient genetic variability is of vital importance. It is necessary to assess the relative magnitude of variability in order to use such information, together with other selection parameters, for the improvement of fruit yield and quality of any fruit crop through adoption of effective breeding methods (William, 1964; Briggs and Knowels, 1967). Fisher (1919) was the first to divide total variability into genetic and environmental components. He further divided the genetic component into additive, dominance and epistatsis effects. Phenotypic differences among the plants are correlated in lesser or larger extent with the corresponding genotypic difference among them. Selection on the basis of phenotypic characteristics in an individual is actually indirectly selecting the genotype responsible for it. In other words, objective is to search and select the genotype, which in combination of environmental effects imposed on it during the process of selection, provides the desirable phenotypes that is observed and selected deliberately for selecting the underlying genotype. The extent of genetic variability indicates the potential of exercising selection of a particular genotype whereas heritability (h^2) along with genetic advance (per cent of mean) is more useful in predicting the resultant effect of selection of best genotype. Knowledge of the extent of genetic variation and diversity in fruit phenology, quality, maturity and yield component traits in locally available genotypes and subsequent identification of adapted superior genotypes/cultivars as potential donors for yield and quality improvement is therefore essential. Potent variability is the result of prolonged natural and artificial selection, which is heritable and accumulation of significant magnitude of variability for economic

traits leads to the genetic diversity, which is important for creation of new genetic variability through hybridization and reorganization of new gene constellation. Being highly cross pollinated, each seedling raised plant is therefore a distinct genotype due to its heterozygous nature. The magnitude of cross pollination together with diversity at allelic level for most of the genes results in formation of new gene groups and constellation in the resultant seed. Thus tremendous genetic variability is created which on the outer play of environmental conditions produces some excellent genotypes (possessing many desirable traits in a single plant). In view of the importance of the diversity of jamun genotypes, it is important to survey these populations and identify the superior genotypes for their use in the future breeding programmes through *in-situ* or *ex-situ* conservation. The present study was therefore taken up to survey the available gene pool in Jammu district and identify the superior and promising genotypes for use in future improvement programmes of this fruit crop. The experimental material for the study consisted of selected ninty jamun genotypes identified during the survey in different areas of Jammu district. Out of these genotypes, only forty were evaluated on the basis of various quantitative and qualitative traits and the results obtained are discussed in this chapter.

5.1 Vegetative characters

5.1.1 Tree characters

Tree characteristics showed substantial amount of variability among various genotypes as evident by the data presented in table 1. Out of forty genotypes, maximum tree height was recorded in SJJS-12 and SJJS-15 as 16.5 m in each genotype followed by SJJS-38, SJJS-11 and SJJS-7 with tree height of 16.4 m, 15.5 m and 15.4 m respectively. Minimum tree height was noted in genotype SJJS-34 as 6.55 m, preceded by SJJS-21 with 7.4 m. Tree spread was found to be maximum in genotype SJJS-2 followed closely by genotypes SJJS-12 and SJJS-40, respectively whereas minimum tree spread was recorded in genotype SJJS-28 followed by SJJS-29.The high range of variation of in case of tree characteristics such as tree habit, tree height and tree spread have been reported by Wani *et al*., (2010) in quince population of seedling origin in Kashmir, India and they attributed it to the genetic contitution of individual seedling tree, variation in soil condition, age of the plant and environmental conditions. The canopy volume was found to maximum (4905.13 m^3) in genotype SJJS-12 followed by

SJJS-38 whereas minimum canopy volume (305.59 m^3) was recorded in genotype SJJS-34. Sanou *et al.* (2006) studied variability of agromorphological traits of shea trees in Mali and revealed that the range of plant height, crown diameter, width, petiole length, fruit length, fruit width, nut weight and pulp weight was 6-25 m, 2-22.5 m, 5.4-21.3 cm, 2.2-6.8 cm, 3.7-17.0 mm, 2.1-6.5 cm, respectively.

5.1.2 Leaf characters

Leaf characteristics of all the forty genotypes studied showed wide variation in the characters observed. The leaf shape of the studied genotypes was either elliptic or broadly ovate. Wani *et al*. (2010) reported variation in leaf shape in thirty three seedling origin quince genotypes and found ovate oblong leaf shape in thirty two genotypes and oblate in one of them and further they attributed the variations arising due to genetic constitution of the individual seedling tree, variation in soil condition, age and environmental conditions under which plants were growing. Leaf colour did not show variation as all forty genotypes studied had dark green leaf colour.On the other hand, Sharma *et al*. (2010) while studying leaf variability in guava genotypes reported that Allahabad Safeda and Smooth Green had green shade of foliage whereas Nasik and Apple Colour showed pale green shade and Spear Acid and Lucknow-49 exhibited dark green foliage. Leaf length showed wide variations among genotypes studied. Longest leaf length of 20.2 cm was recorded in genotype SJJS-19 and SJJS-32 followed by genotype SJJS-21, SJJS-20 and SJJS-29. Shortest leaf length of 12.5 cm was found in genotype SJJS-7 and 13.5 cm in SJJS-5. Leaf breadth varied between 6.4 to 10.7 cm with minimum leaf breadth in genotype SJJS-7 and maximum in SJJS-13 followed by SJJS-31. Lone and Wafai (1995) reported that cherries show remarkable diversity in leaf size and divided the varieties into two groups i.e. small and large leaved on this basis. Sanou *et al.* (2006) studied variability of agromorphological traits of shea trees in Mali and revealed that the range of leaf width and petiole length was 2.2-6.8 cm and 3.7-17.0 mm respectively.

The maximum leaf area of 70.30 cm^2 was recorded in genotype SJJS-13 followed by genotype SJJS-31, SJJS-12 and SJJS-19. Bianco *et al.* (2013) characterized 25 Sicilian olive genotypes on morphological characteristics and recorded considerable variation range in leaf area of these genotypes which ranged between 2.79 to 6.73 cm^2. Petiole length was found maximum (3.0 cm) in SJJS-34 followed by petiole length in

genotypes SJJS-25, SJJS-36 and SJJS-37. Minimum petiole length was observed in SJJS-10 and SJJS-26 as 1.4 cm in each preceded by 1.5 cm in SJJS-16 and SJJS-32 each. Leaf length: petiole length ratio varied between 6.4 to 13.3. The genotype SJJS-32 recorded maximum leaf length: petiole length ratio with 13.3 followed by SJJS-10 with 12.8. Minimum leaf length: petiole length ratio of 6.4 was observed in genotype SJJS-34 preceded by 6.7 in SJJS-1 and SJJS-2 in each genotype. Prabhuraj *et al*. (2002) sampled 55 jamun trees in Gokak taluk of Belgaum district for variability studies and reported that each tree was distinct for different morphological leaf traits which included leaf length, breadth and petiole length. Ayyanar and Subash-Babu (2012) reviewed various characteristics of jamun and found that leaves show variations as leathery, oblong, ovate to elliptic or obovate elliptic with 6 to 12 cm length and the leaf tip being broad and acuminate. Lone and Wafai (1995) reported that cherries show remarkable diversity in leaf size and divided the varieties into two groups, small and large leaved. Sanou *et al.* (2006) studied variability of agromorphological traits of shea trees in Mali and reported wide range of variability in leaf length, leaf width and petiole length. Wani *et al*. (2010) studied variation in leaf shape in thirty three seedling origin quince genotypes and found ovate oblong leaf shape in thirty two genotypes and oblate in one of them.

5.2 Floral characters

5.2.1 Full bloom time

The results revealed that full bloom time in jamun genotypes studied under Jammu region varied from 20th April-12th May. SJJS-29 and SJJS-30 were the genotypes to show earliest full bloom on 20-22nd April while in the genotypes SJJS-18 and SJJS-20 the time of full bloom was 10th -12th of May. In genotypes SJJS-26, SJJS-24, SJJS-28, SJJS-17, SJJS-27, SJJS-33 and SJJS-34 full bloom time was recorded in 4th week of April. Orwa *et al.* (2009) reported that generally jamun flower panicles appear from March to May, however, Chaudhary and Mukhopadhyay, (2012) found that jamun flowers in February-March and fruits in May to July. The variation in time of flowering may be attributed to the climate of the place and genetic make of the plant. Singh and Singh (2012) studied flowering in sixteen jamun genotypes and revealed wide variation in flowering among them and the earliest flowering took place in mid February. Devi *et al*. (2016) studied the variability on flowering characters of six jamun genotypes and found considerable differences among the genotypes for the characters studied wherein

month of flower initiation among the selected genotypes ranged from last week of February to mid-April. Genotype AJG-58 and AJG-45 showed early initiation of flowering (Late February) and minimum flowering duration, whereas, AJG-85, T.C-85 and Konkan Bahadoli revealed late flower initiation in mid April.

5.3 Fruit characters

The physico-chemical characteristics of fruit decide the suitability and acceptability fruit crop cultivar. Many workers have stressed the importance of fruit characters in different crops like jamun (Inamdar *et al.*, 2002, Prabhuraj, 2002, Patel *et al.*, 2005, Singh *et al.*, 2007, Ghojage *et al.*, 2011 and Shahnawaz and Sheikh, 2011), ber (Meena *et al.*, 2009) and aonla (Rao and Subramanym, 2009 and Patel *et al.*, 2010).

Physical components of fruits refer to those, whose chemical procedure determination is not almost needed. According to variety and growth conditions, Jamun fruits vary in shape, size and weight and other parameters. Devi *et al.* (2002) collected ripe fruits from 18 selected jamun trees, analyzed for physico-chemical traits and found wide range of variation in traits like fruit weight, length, width, pulp and seed content, pulp: seed ratio, TSS (°B), titratable acidity and total sugars and reducing sugars. In the present investigations, it is apparent from the results regarding fruit characteristics of jamun genotypes that wide variation is present in horticultural traits such as fruit weight, fruit size, fruit volume, specific gravity, percent consumable and non-consumable matter, seed weight, seed length, seed breadth, pulp: seed ratio, moisture content of fruit and seed, juice content, juice pH, T.S.S., titratable acidity, TSS: acidity ratio, ascorbic acid, total sugars, non-reducing sugars and reducing sugars, total anthocyanin content, antioxidant activity, total tannins and organoleptic evaluation. Singh *et al*. (2015) reported enormous variability with respect to morphology and physico-chemical attributes due to pre-dominance of seed propagation in jamun trees. studied variability in respect to physico-chemical and phytochemical characteristics of jamun such as fruit weight, fruit size, length breadth ratio, pulp weight, pulp content, seed weight, seed length and breadth, pulp: seed ratio, TSS, titrable acidity, TSS: acid ratio, total sugar content, reducing sugars, non reducing sugar, sugar: acid ratio and ascorbic acid.

Duration of fruiting of a genotype determines the earliness, lateness and period of availability of fruits in market. It also affects the price of fruits in market. A close observation of the results pertaining to duration of fruiting in selected genotypes

disclosed that the duration of fruiting starts earliest from 3rd June in genotype SJJS-29 and it concluded on 2nd of August in genotypes SJJS-18 and SJJS-20. The earliest fruiting genotype recorded the ending of fruiting on 20th July. The other early bearing genotypes were SJJS-24, SJJS-26, SJJS-30 and SJJS-36 while the late bearing genotypes were SJJS-9, SJJS-10, SJJS-13, SJJS-14, SJJS-15, SJJS-16 and SJJS-39. Srivastava *et al*. (2010) studied the physico-chemical characteristics of fruits from 25 genotypes of jamun grown in Varanasi and Pantnagar harvested during June to July 2006. Singh and Singh (2012) reported wide variations among fruiting period of sixteen jamun genotypes. The fruiting period found to be earliest during first week of May in genotypes GJ-3, GJ-2, GJ-10 and GJ-14 while genotypes GJ-16 and GJ-13 ripened at last during last week of June month.

Under the present study fruit shape varied from ellipsoid to oval. Among the forty genotypes, eighteen genotypes *viz*., SJJS-1, SJJS-2, SJJS-3, SJJS-7, SJJS-8, SJJS-11, SJJS-14, SJJS-16, SJJS-20, SJJS-22, SJJS-25, SJJS-29, SJJS-30, SJJS-33, SJJS-34, SJJS-35 and SJJS-39 had ellipsoid fruit shape whereas twenty two genotypes *viz*., SJJS-4, SJJS-5, SJJS-6, SJJS-9, SJJS-10, SJJS-12, SJJS-13, SJJS-15, SJJS-17, SJJS-18, SJJS-19, SJJS-21, SJJS-23, SJJS-24, SJJS-26, SJJS-27, SJJS-28, SJJS-31, SJJS-32, SJJS-36, SJJS-37, SJJS-38 and SJJS-40 had oval shape. Srivastava *et al*. (2010) studied 25 genotypes of jamun fruits grown in Uttar Pradesh, and Uttarakhand from June to July and found variability in fruit shape. They reported that genotype PJ-25 had cylindrical fruits, whereas genotypes PJ-24 and VJ-19 had round fruits.

Higher fruit weight is a preferred as a character for selecting superior genotypes. Maximum fruit weight was recorded as 11.40 g in SJJS-27 followed by 11.21 g and 11.14 g in SJJS-28 and SJJS-2 respectively. Minimum fruit weight was noted in SJJS-32 preceded SJJS-19 and SJJS-24. Fruit weight is a dependent character which is governed by many factors, *viz*. fruit length, breadth, volume, size, pulp weight, pulp per cent, pulp thickness, pulp to seed ratio, seed length, breadth, volume, size, weight and seed per cent (Devi *et al.*, 2016). The characters which govern the fruit weight too had shown different degrees of variability in these characters and were reported by Inamdar *et al*. (2002) and Prabhuraj (2002) in jamun. Agrawal *et al*. (2017) studied the genetic resources of Jamun in Madhya Pradesh and revealed that all the characters studied indicated sufficient diversity among the genotypes. The range of variation was very broad for character fruit weight (14.40 g in JJ-1 to 55.40 g in JJ-5). The genotype JJ-5

was found to be superior to JJ-13 and JJ-11 with 49.50 g and 36.15 g fruit weight respectively. In jamun genotypes grown in North India fruit weight was reported 16.5 g, however, among thirty selected jamun genotypes fruit weight was found to be 13.45 g (Ghojage *et al.,* 2011).

The data pertaining to fruit size revealed that it was recorded maximum in genotype SJJS-2 with 629.62 mm^2 followed by genotypes SJJS-27 and SJJS-28, whereas, minimum fruit size was recorded in genotype SJJS-21 preceded by genotype SJJS-36. The probable reason behind such variation in fruit size may be climatic variation like frequency of rainfall as well as genetic constitution of the tree. Rakesh and Shivanna (2015) surveyed different taluks in Uttar Kannada and found variations in important fruit and seed traits of jamun. Fruit length showed wide variations among the different seed sources. Significantly higher fruit length was recorded from Mundgod (21.26 mm) followed by Yellapur (20.31 mm) as compared to the other seed sources. Maximum fruit diameter and higher fruit test weight were recorded in fruits collected from Mundgod, followed by Yellapur. According to Agrawal *et al*. (2017), among the 16 genotypes studied minimum fruit length (18.26 mm) was recorded in JJ-1 while it was maximum (27.78 mm) in genotype JJ-5 which was statistically at par with JJ-7 (27.53 mm) and JJ-8 (27.51 mm), whereas fruit width ranged from 22.71 mm in JJ-13 to 15.25 mm in JJ-1. It was noted that JJ-13 had significantly more fruit width than JJ-5 (22.01 mm) and JJ-8 (21.14mm). Similar results were reported by Srimathi *et al.* (2001) in jamun for the characters of fruit length (2.10 cm) and fruit breadth (1.30 cm). Srivastava *et al*. (2010) reported that, out of 25 genotypes of jamun fruits grown in Uttar Pradesh, and Uttarakhand from June to July the fruit weight ranged from 2.24 (VJ-1 5) to 7.05 g (PJ-24), fruit length was greatest for PJ-22 (2.66 cm) and lowest for VJ-4 (1.97 cm), whereas fruit breadth was greatest for PJ-24 (2.07 cm) and lowest for PJ-25 (1.26 cm).

Volume of fruit is also a very important character for its acceptability in the market. Maximum fruit volume was recorded in genotypes SJJS-10 and SJJS-27 and minimum in genotype SJJS-32. The maximum value of specific gravity was observed as 1.19 in SJJS-39 whereas minimum value was recorded in SJJS-25. Significant variation in relation to volume of fruit was observed in jamun as reported by Agrawal *et al*. (2017). Highest fruit volume of 1.01cc was recorded in JJ-1 which was significantly superior to other genotypes. It was followed by JJ-15 with 1.65 cc, whereas it was lowest in genotype JJ-2 (1.01 cc) against mean value of 1.32cc. Garnayak *et al*. (2008) also

reported that volume of fruit is another important factor like that of its weight in determining fruit quality. In the market, the consumers have a preference to select the large sized fruits and accordingly the price of those fruits goes higher with size.

Higher pulp percentage is a desirable character for table purpose jamun and for breeding quality fruits. Under the present study, fruits of genotype SJJS-36 had maximum consumable content (pulp) and minimum non-edible matter (seed) with 88.38 per cent and 11.62 per cent followed by SJJS-4. However, minimum value of consumable matter and maximum non-edible matter was observed in SJJS- 21 with 82.15 per cent and 17.85 per cent respectively followed by SJJS-38. Similar variability was also reported by Srivastava *et al.* (2010) in jamun genotypes collected from Uttar Pradesh and Uttarakhand. As reported by Agrawal *et al*. (2017), the seed percent in 16 jamun genotypes varied from 19.36 in JJ-9 to 34.07 in JJ-1 with maximum (85.28%) in genotype JJ-16 and minimum (57.60%) in genotype JJ-5. Maximum per cent seed content was recorded in genotype JJ-1 (34.07) which was at par with JJ-14 (33.49) and JJ-16 (30.94) whereas, it was minimum in JJ-9 with 19.36%. Variation in pulp per cent was also revealed among the genotypes as per the results obtained by Kumar *et al.* (2013) in aonla but it was non significant. The seed per cent fully depends on fruit weight and pulp content. If pulp content is more, definitely seed per cent will be less and *vice-versa*. Srivastava *et al*. (2010) reported that, out of 25 genotypes of jamun fruits grown in Uttar Pradesh, and Uttarakhand from June to July the pulp weight was greatest for PJ-23 (5.82 g), PJ-24 (5.54 g) and PJ-2 1 (5.32 g). Pulp content varied from 47.76 to 83.5% (PJ-23). The lowest percentage of seeds was recorded for PJ-23 (16.5%).

The minimum seed weight of 0.96 g was recorded in SJJS- 36 preceded by 1.19 g and 1.22 g in genotypes SJJS-15 and SJJS-4 respectively whereas maximum seed weight of 1.93 g was recorded in genotype SJJS-26 followed by 1.91 g in genotype SJJS-21. Srimathi *et al.* (2001) concluded that good and viable seeds are always having higher sinks. Hence, seed weight can be used as one of the useful criteria for early selection of superior genotypes. The minimum seed length was observed in genotype SJJS-8 followed by SJJS-36 and SJJS-19 whereas maximum seed length of 20.83 mm was observed in genotype SJJS-5 followed by SJJS-26 and SJJS-16. Seed breadth ranged from 9.52 to 12.57 mm. Minimum seed weight was observed in SJJS-8 followed by SJJS-36 and SJJS-24 whereas maximum seed weight was noted in SJJS-21 followed by SJJS-26. This variation in seed traits among the different genotypes may be due to fact

that this species grown over a wide range of climatic condition rainfall, temperature and soil type.

Rakesh and Shivanna (2015) reported that the lower seed length (12.16 mm) was recorded in the seeds collected from Sirsi area. Higher test seed weight (32.85 g) was recorded in Mundgod and least seed weight was recorded in Sirsi seed source. Similarly, higher seed diameter (8.42 mm) and seed length (15.20 mm) were recorded in Mundgod. Lower seed length and diameter was recorded in the seeds collected from Sirsi area. Agrawal *et al*. (2017) concluded that seed sources with higher seed length and width possessed higher seed weight. They reported highest seed length (25.10 mm) in genotype JJ-5 which was significantly superior to JJ-8 with 21.55 mm and lowest seed length in JJ-1 (12.99 mm). Seed width ranged from 15.43 mm in JJ-5 to 8.01mm in JJ-4. Genotype JJ-5 recorded the maximum width (15.43 mm) which was followed by JJ-14 with 11.96 mm width. Genotypes JJ-4 (8.01 mm), JJ-15 (8.57 mm) and JJ-6 with 8.95 mm were small seeded which is a desirable character for jamun. The pulp: stone ratio is an important aspect for selection of superior genotype by breeder. Under the present study pulp: seed ratio varied between 4.75 and 7.71. Minimum pulp: seed ratio was noted in SJJS-21 followed by SJJS-38 and maximum pulp: seed ratio was observed in SJJS-36. Similar results were also reported by Garanade *et al.* (1998). Malik *et al*. (2010) reported that total of 20 diverse jamun accessions collected by NBPGR from Haryana and Uttar Pradesh revealed tremendous variability for seed characters.

Agrawal *et al.* (2017) reported that pulp: seed ratio of jamun fruits varied considerably. JJ-9 genotype had the maximum ratio of 4.05 whereas JJ-14 reported the lowest pulp: seed ratio of 1.81against the mean value of 2.73. Higher pulp:seed ratio is a necessary character for table purpose in jamun, hence, parents should be selected as a genotype having high fruit pulp:seed ratio. These results obtained in the present study are also in consonance with that reported by Patel *et al.* (2005) for genotypes collected from Uttar Pradesh and Jharkhand.

The per cent moisture content of fruit was found maximum in genotype SJJS-25 (92.04 per cent) followed by genotype SJJS-15 whereas minimum moisture content was noted genotype SJJS-30 followed by genotype SJJS-15. Moisture content of seed ranged between 53.41 to 62.79 per cent with minimum in genotype SJJS-21 followed by SJJS-1 (53.85 per cent) and maximum in genotype SJJS-36 followed by SJJS-33. Raza *et al*.

(2015) reported that jamun fruit proximately contains moisture percentage of 82.19±2.46 per cent and jamun seeds contains moisture percentage of 16.34±0.49 per cent. These results are in accordance with earlier reported by Shahnawaz and Sheikh (2011) for improved jamun fruit cultivar wherein moisture content was noted as 81.32±0.203 per cent whereas for indigenous, it was 80.14±0.087 per cent. In the seed, moisture content for improved was noted as 13.31±0.262 per cent whereas 12.34±0.021 per cent for indigenous.

Minimum juice content was found in SJJS-14 followed by SJJS-30 whereas maximum juice content was observed in genotype SJJS-36 (37.47 per centAccording to Shahnawaz and Sheikh (2011) for elliptical improved Jamun fruit, juice yield was 32% whereas in indigenous it was 38%. Juice pH of the genotypes studied ranged from 3.74 to 3.95 with SJJS-16 having minimum and SJJS-26 and SJJS-18 having maximum pH repectively. Shahnawaz and Sheikh (2011) compared improved and indigenous varieties of jamun and found that improved had a pH of 3.87±0.010 while indigenous had a pH of 3.77±0.010.

The TSS of genotypes studied ranged from 10.00 to 17.37^{o}B wherein the lowest value of TSS was recorded for SJJS-8 followed by SJJS-7 whereas highest value was found in genotype SJJS-29 followed by SJJS-13 and SJJS-14. Titratable acidity ranged between 0.47 to 0.94% with minimum value in genotype SJJS-18 and maximum value in genotype SJJS-16 followed by SJJS-28. TSS: acidity ratio ranged from 13.89 to 32.75 with minimum value in genotype SJJS-16 and maximum value in genotype SJJS-29. Total solids are measure of the amount of material dissolved in cell sap. This material can include carbonate, bicarbonate, chloride, sulfate, phosphate, nitrate, calcium, magnesium, sodium, organic ions, and other ions. Present results are in consonance with those observed by Srivastava *et al.* (2010) who reported maximum acidity in VJ-20 (1.14%) whereas, minimum in genotype VJ-5 (0.37%) while total soluble solids (TSS) content varied from 14.3% (VJ-12) to 26.2% (VJ-14). The TSS: acid ratio ranged from 14.50 (PJ-25) to 43.78 (VJ-5). Agrawal *et al*. (2017) reported that genotype JJ-4 was recorded to be the sweetest with TSS value 21.25°B while it was lowest in JJ-13 (7.70°B). Even though JJ-4 fruits were the sweetest but fruit size was small with 17.42 mm fruit width. Acidity ranged from 0.30% in JJ-11 to 0.53% JJ-9 which was followed by 0.47% in genotype JJ-9. The genotypes with higher TSS *i.e.* JJ-4 and JJ-3 recorded low acidity as 0.36% and 0.39% respectively. This is a fact in many fruits that if total

soluble solids increases then definitely acidity decreases, these findings are partially supplemented by Devi *et al.* (2002) and Kumar *et al.* (2013). Wide variation of physico-chemical composition in thirty three seedling origin quince genotypes from Budgam district of Jammu and Kashmir has been reported by Wani *et al*., (2010) with respect to fruit weight, TSS, acidity, ascorbic acid and TSS/acidity ratio.

The perusal of results related to ascorbic acid showed that it ranged from 22.71 to 45.93 mg per 100 g fruit with minimum ascorbic acid in genotype SJJS-33 followed by SJJS-36. Maximum ascorbic acid content was recorded in genotype SJJS-12 followed by SJJS-4. Shahnawaz and Sheikh (2011) reported that fresh extract of Jamun fruit is highly acidic and may be responsible for astringency in taste. Noomrio and Dahot (1996) authenticated the same view point on acidity of Jamun fruit. Acidity recorded significant differences among the 15 genotypes. Significantly higher acidity was recorded in the genotype KJS-65 (1.03%) and minimum in the genotype KJS-20-D (0.51%). Srivastava *et al*. (2010) reported that the ascorbic acid content of jamun fruits from grown in Uttar Pradesh, and Uttarakhand varied from 30.0 (VJ-10) to 45.3/100 g pulp (PJ-23). Agrawal *et al*. (2017) reported values of ascorbic acid in 16 jamun genotypes which ranged from 21.75 mg/100 g in JJ-10 to 42.30 mg/100 g in JJ-15 which was followed by 38.10 (mg/100 g) in JJ-14.

Data pertaining to sugar content of the selected forty jamun genotypes indicated variation among the genotypes. The minimum value of total sugars was observed in genotype SJJS-8 followed by SJJS-31 whereas maximum total sugar content (10.69%) in genotype SJJS-29 followed by SJJS-28. This is maybe due to its high TSS content and genetic constitution of the genotype (Shahnawaz and Sheikh, 2011). The reducing sugar content was found maximum (10.00) in SJJS-29 followed by SJJS-28 whereas minimum reducing sugar content of 4.34 per cent was observed in genotype SJJS-8. The values of non-reducing sugar content was observed to be highest in genotype SJJS-27 with 3.02 per cent followed by genotype SJJS-13 and lowest in genotype SJJS-34 with 0.20 per cent preceded by SJJS-31. This may be due to the variability in the genetic makeup of the genotypes (Shahnawaz and Sheikh, 2011). Similar results were reported by Patel *et al.* (2005) in jamun. Srivastava *et al*. (2010) reported that, out of 25 genotypes of jamun fruits grown in Uttar Pradesh, and Uttarakhand from June to July the total sugar content was lowest (9.94%) for VJ-12 and highest (25.46%) for VJ-14. The reducing sugar content was highest (20.54%) for VJ-14 and lowest (8.14%) for VJ-12.

It was observed that the maximum content of anthocyanins was present in genotype SJJS-10 and SJJS-27 with 7.50 mg per 100 g in each followed by genotype SJJS-9 (7.48 mg per 100 g). Minimum content of anthocyanins was found in SJJS-36 preceded by SJJS-24. Antioxidant activity measured as DPPH per cent inhibition was found to be maximum in SJJS-27 with a value of 96.55 whereas minimum value of 61.45 was noted in SJJS-36. Rai *et al* (2011) found that jamun at harvest contains 55.48 mg ascorbic acid, 1175.17 mg phenol, 115.11 mg flavinoid, 7.25 mg anthocyanin per 100 g fresh weight respectively. They also found 61.56 per cent DPPH inhibition as antioxidant activity.

Total tannin content of 1.90 g per 100 g fresh weight was observed to be maximum in genotype SJJS-27 followed by SJJS-9 and SJJS-10 whereas genotype SJJS-25 and SJJS-31 with 1.70 g per 100 g fresh weight each. Singh *et al* (2015) reported that high tannins content in pulp of semi ripe and ripe fruits of the jamun accessions J–37, J–40, J–42 and J–49 with ferric chloride ($FeCl_3$) test, however, The lead acetate method did not show considerable variation with respect to tannins content in all stages of pulp of all the accessions except J–37, J–49 and J–42 in which recorded higher tannins content in the pulp of semi-ripe and ripe pulp of jamun.

5.4 Organoleptic evaluation

The organoleptic evaluation of selected jamun genotypes, categorized on the basis of the 9 point hedonic scale, varied between liked-slightly to liked-very much with a score range of 6 to 8.20. The genotype SJJS-29 (8.20) was liked very much as well as genotypes SJJS-13, SJJS-14 and SJJS-28 with score of 8.00. Thirty genotypes were categorized as liked moderately whereas six genotypes were categorized as slightly liked by the panellists. Nisar *et al*. (2015) studied sensory evaluation of *Prunus domestica* fruits on the basis of aroma, consistency and flavor, fruit excellence was assessed by a team of judges and revealed that Fruits of the genotypes DR3 and DR4 scored the maximum value of ranking (9.33) followed by those of LY4 (9.27), SY2 (8.83) and RB1 (8.07). The minimum score were achieved by the fruits of RB2 (2.43), LY1 (2.83) and LY3 (3.20). They noted that the genotypes with higher sugar content (reducing and/or non-reducing) had the higher organoleptic score compared with those with lower sugar content. Swami *et al.* (2017) reported that results on organoleptic evaluation of fifteen elite jamun genotypes showed no significant differences among the genotypes with respect to colour and taste. The overall acceptance showed significant difference among

the genotypes. Significantly high score for overall acceptability was recorded in the genotype KJS- 45 (4.17) and lowest score of 2.90 was recorded in KJS-84 and KJS-20a. They attributed it to the comparatively bigger size of the fruit with higher pulp content, higher TSS and moderate acidity in the genotype KJS-45 when compared to other genotypes.

5.5 Yield efficiency

The results pertaining to yield efficiency showed variation among the studied genotypes. The variability in respect to yield characteristic have also been reported in jamun under various climatic conditions (Keskar *et al*., 1989, Kundu *et al*., 2001, Prabhuraj *et al*., 2002 and Singh and Singh, 2012). Kaushal and Sharma (2004) also reported yield variation in seedling origin tree of pecan nut. According to Lombard *et al*. (1998) potential yield increases with tree size, although not linearly since bigger trees are less efficient. Singh and Singh (2012) studied variability in sixteen jamun genotypes and revealed that maximum yield was recorded in GJ-2 (152.00 kg/plant) and minimum in GJ-4 (90.00 kg/plant). Baba (2015) studied variability in yield efficiency of 45 cherry genotypes in Kashmir region. He reported that yield efficiency ranged from 0.21 to 1.44 with lowest yield efficiency (0.21) in three genotypes CHR-SGR-009, CHR- BLA-020 and CHR-BLA-023 whereas highest yield efficiency of 1.44 was observed in CHR-SHP-038, followed by 1.35, 1.28 and 1.25 in CHR-SHP-033, CHR-SHP-032 and CHR-SHP-036 respectively. Wani *et al*. (2010) reported variation in yield and yield efficiency of quince due to variation in the age of the tree and other yield attributing characteristics like tree height, tree spread, trunk girth etc. and genetic constitution of the individual.

5.7 Statistical parameters for important quantitative characters

5.7.1 Range and means

The results regarding magnitude of variability present in various quantitative traits reveals that wide variability was recorded among all the traits studied. Perusal of data revealed that the fruit weight, fruit size, specific gravity, pulp: stone ratio, TSS, titratable acidity, ascorbic acid and yield efficiency ranged between 8.30 - 11.47 g, 416.85 - 629.62 cm^2, 0.94 - 1.18, 4.75 - 7.71, 10.00 -17.35^oB, 0.47 - 0.94 per cent, 22.71 - 45.93 mg per100 g and 0.19 - 0.26 respectively with a mean of 10.04± 0.34 g, 537 ± 34.67cm^2 , 1.05 ± 0.06, 5.89 ± 0.61, 14.19 ± 1.01 ^oB, 0.64 ± 0.01 per cent, 29.93 ± 1.83 mg per

100 g and 0.21 ± 0.02 respectively. Agrawal *et al.* (2017) studied the genetic resources of jamun in Madhya Pradesh and revealed that all the characters studied indicated sufficient diversity among the genotypes. The range of variation was very broad for character fruit weight (14.40 g in JJ-1 - 55.40 g in JJ-5). Among the 16 genotypes studied minimum fruit length (18.26 mm) was recorded in JJ-1 while it was maximum (27.78 mm) in genotype JJ-5 which was statistically at par with JJ-7 (27.53 mm) and JJ-8 (27.51 mm). Fruit width ranged from 22.71mm (JJ-13) to 15.25 mm (JJ-1). It was noted that JJ-13 had significantly more fruit width than JJ-5 (22.01 mm) and JJ-8 (21.14mm). Similar results were reported by Srimathi *et al.* (2001) in jamun for the characters of fruit length (2.10 cm) and fruit breadth (1.30 cm). In jamun genotypes normally grown in North India the fruit weight was 16.5 g and among thirty selected jamun genotypes was 13.45 g (Ghojage *et al.* 2011). Shahnawaz and Sheikh (2011) recorded mean values of fruit weight (gm) specific gravity, TSS (^{o}B), titratable acidity (%) of improved cultivars as 9.55±0.685, 13.75±0.501, 1.26±0.031 and 1.26±0.120 respectively and of indigenous cultivars as 6.71±0.520, 15.82±0.505, 1.58±0.021 and 1.25±0.048 respectively.

4.8 Variance and coefficient of variation

The results related to variance and coefficients of variation have been obtained for the forty jamun genotypes during the present investigations. Usually fruit trees show continuous variation and as such they require the use of quantitative genetic analysis. Very long gestation period and requirement of wider spacing required in fruit trees for the improvement programmes pose difficulties as compared to other field crops which require less time and space. The factors including time, space and resources have been found to be the main constraints in the generation of genetic parameters and inheritance patterns in the fruit crops. The total phenotypic variance is the outcome of summation of genotypic and environmental variance. However for a breeder it is the genotypic variability which is of paramount importance. Presence of adequate amount of genetic variability in the base population is indispensable for right and effective selection. Genetic improvement of a crop through direct improvement of traits in which breeder is interested for indirect improvement through component characters can be performed effectively on the basis of sound genetic information generated from magnitude and nature of variability (Bisati, 2012). The aim of the present investigation was to collect information which could assist to throw light on the strategy to be adopted for genetic

improvement of jamun in Jammu. Since the existence of genetic variability is of prime importance for an effective improvement programme, thus comprehensive survey to study genetic variability is essential for planning and evaluating breeding programme.

All the characteristics under study *viz*., fruit weight, fruit size, specific gravity, pulp: seed ratio, T.S.S., titratable acidity, ascorbic acid and yield efficiency showed positive phenotypic and genotypic variances. The results revealed that the estimates of phenotypic variance were higher than the corresponding estimates of genotypic variance in all the characteristics. Similar findings have been found by Bisati (2012) and Srivastava *et al*. (2014) for different characters. The estimates of variances alone do not provide the nature of genetic variability hence phenotypic, genotypic and environmental coefficients of variation were also estimated. A better idea can be gained by comparing the relative magnitude of phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) and environmental coefficient of variation (ECV) for the actual strength of variability. The estimates of phenotypic coefficient were observed to be higher in magnitude than their corresponding estimates of genotypic coefficient of variations for all the traits, which indicates the influence of additive effect of the environment on the expression of these traits. The magnitude of phenotypic and genotypic coefficient of variation was low (less than 10 per cent) for fruit weight and specific gravity whereas it was moderate (10-30 per cent) for fruit size, pulp: seed ratio, TSS, titratable acidity, ascorbic acid and it was high (more than 30 per cent) for and yield efficiency. The estimates of PCV and GCV indicated the presence of fairly high degree of variability for yield efficiency. The results are in conformity with the findings of Al-Aysh *et al*. (2012).

The phenotypic coefficient of variation followed same trend indicating that the scope for improvement of these traits during selection could be based on phenotypic variability. These findings are in line with those of Barua and Sharma (2002) wherein significant differences between genotypes of apple for various traits have been observed and PCV and GCV were highest for yield per plant. PCV was found higher than GCV for all the characters studied, which signifies the presence of environmental influence to some degree in the phenotypic expression of characters. High GCV, along with high heritability and high GA, provides better information than single parameters alone (Baye *et al*., 2005). PCV and GCV with higher value specified that the genotypes show evidence of much variation among themselves with respect to morphological and

biochemical characters. Lowest values of PCV and GCV indicate that the genotypes do not show much variation among themselves with respect to these morphological and biochemical characters. Similar findings were reported by Singh *et al*. (2008) and Punetha *et al*. (2011) in different fruit crops. The variation in different characters studied indicates the presence of environmental influence. Hancock and Bringhurst (1988) determined sufficient variation for fruit size in different strawberry cultivars.

4.9 Heritability and genetic gain

The amount of heritable portion of variation cannot be predicted with the help of PCV and GCV alone, but by estimating heritability along with genetic advance which in turn helps in predicting the resultant effect of selection on phenotypic expression. Heritability is the measure of the degree to which parents transfer heritable characteristics to their offspring (Jansson, 2005). The differences in the degree of transfer of these characteristics result in variation in genotypes among the offspring. This variation is usually referred to as genetic variance (additive and non-additive variance) and that of the environment as environmental variance (Suzuki *et al*., 1986). Additive genetic variance is responsible for the similarities between relatives and the population in response to selection (Lavi *et al*., 1993) and mostly transmissible by seed (Wright, 1976). According to Abengmeneng *et al*. (2015) heritability is useful, among other things, in predicting genetic gain from selection and in selecting superior phenotypes on the basis of the phenotypic performance of quantitative characters. Heritability was grouped in three classes wherein less than 10 per cent hertability was classified as low, 10-30 per cent as medium and 30-60 per cent as high heritability (Robinson, 1966). Highest heritability of 67.7 per cent was recorded in pulp: seed ratio followed by ascorbic acid (67.3 per cent), fruit weight (61.4), fruit size (58.2 per cent), yield efficiency (57.1 per cent), T.S.S. (56.4per cent), titratable acidity (53.8 per cent) and specific gravity (28.6 per cent). Abengmeneng *et al*. (2015) and Swarup and Chaugale (1962) suggested that it is not necessary that high heritability is always coupled with high genetic advance. Heritable variation is useful for permanent genetic improvement (Singh, 2000). The most important function of heritability in the genetic study of quantitative characters is its predictive role to indicate the reliability of the phenotypic value as a guide to breeding value (Dabholkar, 1992; Falconer and Mackay, 1996). The GCV, along with heritability estimates, provides reliable estimates of the amount of GA to be expected through phenotypic selection (Burton, 1952). Genetic gain

being the function of heritability, selection intensity and phenotypic standard deduction, indicated that magnitude of improvement in desired direction that can be expected in a particular trait by selecting a certain portion of the population.

Genetic gain was grouped into three distinct classes wherein less than 20 per cent genetic gain was classified as low, 20-40 per cent as medium and greater than 40 per cent as high genetic gain. In the present study, the genetic gain was low for fruit weight (12.17 per cent), fruit size (15.86 per cent), specific gravity (4.70 per cent), T.S.S. (17.81 per cent) and acidity (19.73 per cent) whereas the genetic gain was medium for pulp: seed ratio (26.08 per cent), ascorbic acid (25.76 per cent) and high for yield efficiency (46.89 per cent). High heritability coupled with high genetic gain (per cent of mean) was recorded in yield efficiency, fruit volume and fruit weight; high heritability coupled with moderate genetic gain in stone weight, fruit: stone weight and acidity and high heritability coupled with low genetic gain in T.S.S.

According to Abengmeneng *et al*. (2015), high heritability enables greater dynamism in the breeding program, allowing recombination of the best individuals in a shorter period of time. The high heritability obtained in the current study, therefore, suggests that selection of individuals based on traits having higher values for heritability have the potential to retain high productivity in future generation of the species. Likewise, genetically superior trees may appear phenotypically undesirable due to poor environmental conditions. Hence, the accessions which performed below average could possibly do well if planted in a different test environment and those which performed above the mean could possibly perform poorly if planted in another environment. It is therefore, suggested that this study be repeated in all the ecological zones and the differences in genetic gain be established. High heritability coupled with high genetic gain is usually more useful than either of these parameters taken alone in predicting the resultant effect of selecting the best genotypes (Johnson *et al*., 1955). The main drawbacks of heritability (broad sense) as obtained in the present study are non-additive and epistatic gene effects as well. Traits with high heritability together with high genetic advance are by and large controlled by additive gene effects (Panse, 1957).

High heritability estimates for the characters indicate less influence of the environment, and so there is a good scope for the improvement of these traits through direct selection (Kumar *et al*., 2012). Higher heritability (h^2) coupled with high GA was

observed for fruit yield per plant, which may be due to the additive gene action, and thus selection would be effective for this character. Similar results were also reported by Sah *et al.* (2010). Ara *et al*. (2009) reported that the high heritability (h^2) coupled with high GA for number of flowers and number of fruits in each year indicated that these characters were controlled by additive genes and effective selection could be made for these parameters. High values of GA are indicative of additive gene action, whereas low values are indicative of non-additive gene action (Singh and Narayanan, 1993). Thus, the heritability estimates will be reliable if accompanied by high GA.

4.10 Correlation

High coefficients of correlation allow indirect selection, while the existence of low coefficients does not represent lack of association between the character, but rather the lack of a cause-effect relationship (Vencovsky and Barriga 1992). The practical utility of selection of a given trait as a measure for improving another trait depends not only on the genotypic correlation but also on the phenotypic correlation and the respective variances of all the traits included in the selection procedure. Phenotypic and genotypic correlations ranged in magnitude and significance. Correlation studies are very important from breeding point of view because they reveal the magnitude of association between one or more traits and also give the indication of traits that could be useful so as to identify more important ones for a particular improvement programme. The principle assumption underlying the correlation among traits has been the pleiotropic nature of genes. Genotypic correlation between two or more traits may result from pleiotropic effects of genes governing inheritance of two or more traits (Stebbins, 1950; Adams, 1967). However, linkage has also been found to affect the correlation. Main objective of any improvement programme is yield which is the outcome of interaction of a number of inter-related or correlated traits. Hence, the correlation coefficients among different traits were worked out in all possible combination at both the phenotypic and genotypic levels. Direct selection for traits like yield efficiency is only effective when heritability of the trait selected for indirect selection is very high and the additive genetic correlation between desired trait and the trait selected for indirect selection is also very high. Hallaver and Miranda (1981) suggested that yield is an expression of fitness and any drastic change in any one of the component traits is accompanied by adjustment in other components, implying the existence of correlated changes of gene frequencies. Therefore, the most effective method for yield improvement is direct selection for yield

itself. There may be correlated changes among yield and yield components but these correlated changes will be in concert with development of most physiologically efficient genotypes for expression of genotype. The results on correlation coefficients revealed that fruit weight showed a positive correlation with fruit size, specific gravity, pulp: seed ratio, T.S.S. and yield efficiency at both genotypic and phenotypic levels. However, the correlation with ascorbic acid and titratable acidity is negative at both genotypic and phenotypic levels. Fruit size exhibited positive correlation with specific gravity, pulp: seed ratio, T.S.S. and yield efficiency at both genotypic and phenotypic level but negative correlation with ascorbic acid and titratable acidity at both genotypic and phenotypic levels. Specific gravity showed positive correlation with pulp: seed ratio, T.S.S. and yield efficiency at both genotypic and phenotypic levels but negative correlation with ascorbic acid and acidity at both levels. T.S.S. exhibited negative correlation with acidity at both genotypic and phenotypic levels but positive correlation with yield efficiency at both the levels. Acidity and ascorbic acid both showed negative correlation to yield efficiency at both genotypic and phenotypic levels. Fruit yield was significantly and positively associated with most of the characters (Biswas *et al*., 2007). Mir *et al*. (2009) also observed positive and significant correlations between yield per plant and height of plant, spread of plant, fruit weight, fruit diameter, fruit volume, and number of fruits per plant. Rai *et al*. (2001) also observed positive and significant correlations between yield/plant and fruit length, fruit girth, and fruit weight of litchi. The correlation of pulp weight and pulp to seed ratio with fruit weight was found highly significant and positive in jamun by Srivastava *et al.* 2010. In a few cases, phenotypic correlation coefficients were the same as or higher than the genotypic correlation coefficients, indicating that both environmental and genotypic correlations in these cases acted in the same direction and finally maximized their expression at the phenotypic level. Significant positive correlation was recorded between yield efficiency and its component traits fruit weight and fruit volume at both genotypic and phenotypic levels. These results are in agreement with those of Srivastava *et al.* (2014) and Adriano *et al*. (2014).

4.11 Path Correlation analysis

Correlation studies alone are not adequate to establish clear-cut associations among the traits as more variables need to be considered. Hence, the knowledge of actual contribution of individual characters towards yield per plant becomes essential. In

order to determine an efficient criterion for selection of various quantitative traits to improve the yield efficiency, it is essential to know the direct and indirect contribution of the traits towards this improvement through the study of cause and effect relationship. According to Silva *et al*. (2005) the success of this analysis is in the formulation of the cause and effect relationship between the characters studied, which depends on prior knowledge of the researcher. The application of path coefficient analysis was carried out which provides an idea of direct and indirect effects of various dependent and independent variables. Direct and indirect contribution of seven different quantitative traits including fruit weight, fruit size, specific gravity, pulp: seed ratio, T.S.S, acidity and ascorbic acid towards yield efficiency were estimated through partitioning of their genotypic correlation coefficient analysis. Fruit size recorded the maximum positive direct effect on yield efficiency followed by T.S.S. while as titratable acidity had the maximum negative effect on yield efficiency. Highest positive indirect effect on yield efficiency came from fruit size through specific gravity followed by pulp: seed ratio through fruit size. Highest negative indirect effect came from acidity through fruit size. In addition to direct and indirect contribution of various traits towards yield efficiency, path analysis revealed a residual variance of 18.09 indicating thereby that 89.01 per cent of variance was accounted by path analysis.

4.12 Divergence and Cluster analysis

The importance of genetic diversity in breeding is obvious, therefore the recognition and measurement of such diversity and its nature and magnitude are beneficial or even crucial to a breeding programme. The availability and informative value of plant germplasm are becoming more and more important for the future preservation and sustainable use of genetic resources. Evaluation and characterization as well as estimation of diversity have been performed for various sweet cherry collections. Genetic diversity, an important parameter to identify the genotypes for hybridization involving genetically diverse parents is known to provide an opportunity for bringing together gene constellations yielding desirable transgressive segregants in advanced generations. However, postulation of a rational criterion for identification of such parents is still a problem in plant breeding. Consideration of geographical diversity among parents as an index of genetic diversity has been equally acclaimed and disclaimed in numerous published reports. Genetic divergence refers to the genetic distance between species or between populations within a species. A variety of

parameters are used to measure the genetic distance. Smaller genetic distances indicate a close genetic relationship whereas large genetic distances indicate a more distant genetic relationship. Genetic distance can be used to compare the genetic dissimilarity between different species. Within a species, genetic distance can be used to measure the divergence between different sub-species or different varieties of a species. The importance of genetic diversity is evident in terms of survival and adaptability of a species. A species with high genetic diversity will tend to produce a wider variety of offspring, where some of them may become the fit variants. In contrast, a species that has little or no genetic diversity will produce offspring that are genetically similar and, therefore, will likely be susceptible to diseases or problems like those of their parent. Hence, little or lack of genetic diversity reduces biological fitness and increases the chances of species extinction (Gadekar *et al*., 1992). Genetic divergence studies have helped in designing the hybridization programmes in crop plants effectively to generate noble variants having adaptation and yielding potential far better than parental types (Sekhar *et al*., 2008). In vegetable crops like tomato, estimates of genetic divergence have been proposed to provide diverse parents for getting high yielding hybrids (Sharma *et al*., 2008).

Murty and Arunachalam (1965) hypothesized that Mahalanobis (1928) generalized distance, measure of metric distance between population centriods, could be very useful multivariate statistical tool for effective discrimination among parents on the basis of genetic diversity. Precise information about genetic divergence is critical for a productive breeding programme as genetically diverse parents are known to produce high heterotic effects increasing consequently yield desirable segregants. Almost in all crop species the procedure for identifying genetically diverse parents for hybridization is multivariate analysis proposed by Mahalanobis (1936). This method gives results based on magnitude of divergence depending on the sample size. It is most widely used method for classifying (Rao, 1952) and understanding the nature of divergence and for selecting the parents for hybridization programme (Anand and Murty, 1968).

Based on the performance of various genotypes, forty genotypes got grouped into seven clusters. Cluster-IV comprised of maximum 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. Classification of genotypes into various clusters employing D^2 statistics has also been reported by Srivastava *et al*. (2014), Lacis *et al*. (2010) and Yadav *et al*. (2010). The pattern of group constellation revealed that geographical diversity was not an essential factor for clustering of genotypes from particular origin into a specific cluster. From this it can be concluded that although geographical diversity is very important but not the only criteria in determining the genetic divergence. Thus the grouping of various genotypes from different environments into a particular cluster can be attributed to the admixture or free exchange of plant material from one place to another. At the same time many genotypes originating from the same place were scattered over different clusters. According to Murty and Arunachalam (1966) heterogeneity, genetic architecture of the populations and developmental traits are the possible reasons for the prevalence of this type of genetic diversity.

The perusal of the results on intra and inter cluster distances revealed that Cluster-III had the maximum intra cluster distance (3.56) followed by Cluster-V (2.99). Maximum inter cluster distance was found between Cluster-V and Cluster-VI (200.92) followed by Cluster-II and Cluster-VI (188.62), Cluster-III and Cluster-VI (155.65), Cluster-II and Cluster-V (135.00) and Cluster-V and Cluster-VII (130.30). From the results obtained, it is clear that the clusters have more inter-cluster distances among themselves; hence the selection of parents for hybridization from such clusters would helps to evolve novel hybrids. The parents for hybridization could be selected on the basis of their large inter-cluster distance for isolating useful recombinants in the segregating generations. Similar findings were also observed by Srivastava *et al.* (2014), Lacis *et al*. (2009), Singh *et al*. (2003), Rai and Mishra (2005), Lal *et al*. (2006) and Nagar and Fageria (2006) suggested selection of distant parents based on D^2 analysis.

The perusal of results on cluster means revealed that Cluster-I had a fruit weight of 10.16 g, fruit size of 551.24 cm^2, specific gravity of 1.05, pulp: seed ratio of 6.71, T.S.S of 14.36^oB, titratable acidity of 0.64 per cent, ascorbic acid 42.18 mg per 100 g and yield efficiency of 0.19. Cluster-II had a fruit weight of 11.36 g, fruit size of 620.71

cm^2, specific gravity of 1.03, pulp: seed ratio of 6.02, T.S.S of 14.95^oB, titratable acidity of 0.81 per cent, ascorbic acid 28.86 mg per 100 g and yield efficiency of 0.19. Cluster-III had a fruit weight of 9.09 g, fruit size of 496.79 cm^2, specific gravity of 1.05, pulp: seed ratio of 5.82, T.S.S of 13.23^oB, titratable acidity of 0.61 per cent, ascorbic acid 27.22 mg per 100 g and yield efficiency of 0.20. Cluster-IV had a fruit weight of 10.26 g, fruit size of 535.85 cm^2, specific gravity of 1.06, pulp: seed ratio of 5.68, T.S.S of 13.9^oB, titratable acidity of 0.61 per cent, ascorbic acid 29.83 mg per 100 g and yield efficiency of 0.21. Cluster-V had a fruit weight of 9.96 g, fruit size of 540.00 cm^2, specific gravity of 1.05, pulp: seed ratio of 5.83, T.S.S of 15.04^oB, titratable acidity of 0.62 per cent, ascorbic acid 26.76 mg per 100 g and yield efficiency of 0.23. Cluster-VI had a fruit weight of 8.52 g, fruit size of 440.60 cm^2, specific gravity of 1.04, pulp: seed ratio of 6.24, T.S.S of 14.28^oB, titratable acidity of 0.58 per cent, ascorbic acid 25.05 mg per 100 g and yield efficiency of 0.21. Cluster-VII had a fruit weight of 10.79 g, fruit size of 576.29 cm^2, specific gravity of 1.04, pulp: seed ratio of 5.78, T.S.S of 14.44^oB, titratable acidity of 0.70 per cent, ascorbic acid 32.85 mg per 100 g and yield efficiency of 0.19. Hence, for the improvement of any particular trait should be selected from their respective genotypes cluster showing highest cluster mean for those traits. In other words, we can say that cluster means of different clusters identify the character to be chosen for hybridization. Cluster means coupled with coefficient of variation depict the picture of genetic diversity (Sardana *et al*., 1997).

The perusal of the results presented for per cent contribution of traits towards total divergence revealed that ascorbic acid was the main contributor of divergence (32.69 per cent), followed by fruit weight (20.00 per cent), yield efficiency (13.59 per cent), acidity (11.41 per cent), specific gravity (8.85 per cent), T.S.S. (8.33 per cent) and fruit size (2.69 per cent). Least contribution towards divergence came from pulp: seed ratio (2.44 per cent).Thus, importance of these traits is emphasized as principal contributors to genetic diversity prevalent in such germplasm. According to De *et al.* (1988) traits contributing most towards divergence should be given greater emphasis for choosing the clusters for both direct selection as well as prospective hybridization scheme.

Summary and Conclusions

CHAPTER-6

SUMMARY AND CONCLUSIONS

The present investigations on characterization and evaluation of genetic diversity of jamun for horticultural traits were undertaken during 2013 and 2014 in the jamun growing areas of Jammu district in order to screen the available germplasm of seedling origin jamun to obtain the quantitative measures of the degree of variability of various morphological and horticultural traits, predict heritability and genetic advance and estimate possible association among morphological and phenological traits in the available germplasm. The observations for various parameters were recorded as per the objectives and aims of the present investigation. Survey was conducted in the subtropical areas of Jammu to locate areas of diversity for jamun during the year 2012. During the preliminary survey, ninty plants of seedling origin were identified. On the basis of expression of different characters, forty plants were selected for characterization and evaluation of genetic diversity during 2013 and 2014. The summary of the investigation are presented as under:

6.1 Vegetative and yield characteristics

6.1.1 Tree characteristics

Most of the tree characteristics showed substantial amount of variability. Maximum tree height in genotype SJJS-12 and SJJS-15 and minimum tree height was noted in genotype SJJS-34. Tree spread was found to be maximum in SJJS-2 followed closely by SJJS-12 and SJJS-40, whereas minimum tree spread was recorded in SJJS-28 followed by SJJS-29.The canopy volume was found to maximum in SJJS-12 followed by SJJS-38 whereas minimum canopy volume was recorded in SJJS-34. Highest yield efficiency of 0.26 was observed in SJJS-40 followed by SJJS-23 and SJJS-29. Lowest yield efficiency of 0.19 was recorded in SJJS-2, SJJS-8, SJJS-9, SJJS-10, SJJS-12 and SJJS-16.

6.1.2 Leaf characteristics

Leaf characteristics of all the forty genotypes studied showed wide variation in the characters studied. The leaf shaped varied between elliptic and broadly ovate. Longest leaf length of 20.2 cm was recorded in genotype SJJS-19 and SJJS-32 followed genotype SJJS-21, SJJS-20 and SJJS-30. Shortest leaf length of 12.5 cm was found in genotype SJJS-7 and 13.5 cm in SJJS-5. Leaf breadth varied between 6.4 to 10.7 cm

with minimum leaf breadth in genotype SJJS-7 and maximum in SJJS-13 followed by SJJS-31. The maximum leaf area of 70.3 cm^2 was recorded in genotype SJJS-13 followed by genotype SJJS-31, SJJS-12 and SJJS-19. Petiole length was found maximum in SJJS-34 with 3.0 cm followed by SJJS-25, SJJS-36, SJJS-37. Minimum petiole length was observed in SJJS-10 and SJJS-26 with 1.4 cm each preceded by 1.5 cm in SJJS-16 and SJJS-32 each. The genotype SJJS-32 recorded maximum leaf length: petiole length ratio with 13.3 followed by SJJS-10 with 12.8 whereas minimum leaf length: petiole length ratio of 6.4 was observed in genotype SJJS-34 preceeded by 6.7 in SJJS-1 and SJJS-2 each.

6.2 Floral characteristics

The full bloom time in jamun genotypes studied ranged from $20t^h$ April to -12^{th} May. The date of full bloom was earliest in genotypes SJJS-29 and SJJS-30 between 20-22 April while in the genotypes SJJS-18 and SJJS-20 the time of full bloom was 10-12 May. In genotypes SJJS-26, SJJS-24, SJJS-28, SJJS-17, SJJS-27, SJJS-33 and SJJS-34 full bloom time was recorded in 4^{th} week of April

6.3 Fruit characteristics

The duration of fruiting starts earliest from 3^{rd} June in genotype SJJS-29 and it concludes latest on 2^{nd} August in genotypes SJJS-18 and SJJS-20. The earliest fruiting genotype recorded the ending of fruiting on 20 July. The other early bearing genotypes were SJJS-24, SJJS-26, SJJS-30 and SJJS-36 while the late bearing genotypes were SJJS-9, SJJS-10, SJJS-13, SJJS-14, SJJS-15, SJJS-16 and SJJS-39. Fruit shape varied from ellipsoid to oval. Among the forty genotypes eighteen genotypes had ellipsoid fruit shape whereas twenty two genotypes had oval shape. Maximum fruit weight was recorded as 11.40 g in SJJS-27 followed by SJJS-28 and SJJS-2, respectively. Minimum fruit weight was noted in SJJS-32 preceded SJJS-19 and SJJS-24 respectively. Fruit size was recorded maximum in SJJS-2 with 629.62 mm^2 followed by SJJS-27 and SJJS-28. Minimum fruit size was recorded in SJJS-21 preceded by SJJS-36. Maximum fruit volume was recorded in genotype SJJS-10 and SJJS-27 and minimum in genotype SJJS-19 and SJJS-24. The maximum value of specific gravity was observed as 1.19 in SJJS-39 whereas minimum value was recorded in SJJS-25. SJJS-36 had maximum consumable and minimum non-edible matter with 88.38 per cent and 11.62 per cent followed by SJJS-4. The minimum value of consumable matter and maximum non-edible matter was observed in SJJS- 21 with 82.15 per cent and 17.85 per cent

respectively followed by SJJS-38. Minimum seed weight of 0.96 g was recorded in SJJS- 36 preceded by 1.19 g and 1.22 g in genotypes SJJS-15 and SJJS-4 respectively. Maximum seed weight of 1.93 g was recorded in genotype SJJS-26 followed by 1.91 g in genotype SJJS-21. Minimum seed length was observed in genotype SJJS-8 followed by SJJS-36 and SJJS-19. Maximum seed length of 20.83 mm was observed in genotype SJJS-5 followed by SJJS-26 and SJJS-16. Seed breadth ranged from 9.52 to 12.57 mm. Minimum seed weight was observed in SJJS-8 followed by SJJS-36 and SJJS-24 whereas maximum seed weight was noted in SJJS-21 followed by SJJS-26. Pulp: seed ratio showed a range of 4.75 to 7.71. Minimum pulp: seed ratio was noted in SJJS-21 followed by SJJS-38 and maximum pulp: seed ratio was observed in SJJS-36. Moisture content of fruit in per cent was found maximum in SJJS-25 (92.04 per cent) followed by SJJS-15. Minimum moisture content was noted in SJJS-30 followed by SJJS-15. Moisture content of seed ranged between 53.41 to 62.79 per cent with minimum in genotype SJJS-21 followed by SJJS-1 (53.85 per cent) and maximum in genotype SJJS-36 followed by SJJS-33. Minimum juice content was found in SJJS-14 followed by SJJS-30 whereas maximum juice content was observed in genotype SJJS-36 (37.47 per cent). Juice pH ranged from 3.74 to 3.95 with SJJS-16 having minimum and SJJS-26 and SJJS-18 having maximum pH. The TSS of genotypes studied ranged from 10.00 to 17.37 ^{o}Brix. The lowest value of T.S.S. was recorded for SJJS-8 followed by SJJS-7 whereas highest value was found in genotype SJJS-29 followed by SJJS-13 and SJJS-14 respectively. Titratable acidity ranged between 0.47 to 0.94 per cent with minimum value in genotype SJJS-18 and maximum value in genotype SJJS-16 followed by SJJS-28. T.S.S.: acidity ratio ranged from 13.89 to 32.75 with minimum value in genotype SJJS-16 and maximum value in genotype SJJS-29. The perusal of results related to ascorbic acid showed that it ranged from 22.71 to 45.93 mg per 100 g fruit with minimum ascorbic acid in genotype SJJS-33 followed by SJJS-36. Maximum ascorbic acid content was recorded in genotype SJJS-12 followed by SJJS-4. Minimum total sugars was observed in genotype SJJS-8 followed by SJJS-31 whereas maximum total sugar content in genotype SJJS-29 (10.69 %) followed by SJJS-28. Maximum reducing sugar content was found as 10.00 in SJJS-29 followed by SJJS-28. Minimum reducing sugar content of 4.34 per cent was observed in genotype SJJS-8. Non-reducing sugar content was observed to be highest in SJJS-27 with 3.02 per cent followed by SJJS-13 and lowest in SJJS-34 with 0.20 per cent preceded by SJJS-31. It was observed that the maximum content of anthocyanins was present in genotype SJJS-10 and SJJS-27 with

7.50 mg per 100 g each followed by genotype SJJS-9 (7.48 mg per 100 g). Minimum content of anthocyanins of was found in SJJS-36 preceded by SJJS-24. Antioxidant activity measured as DPPH per cent inhibition was found to be maximum in SJJS-27 with a value of 96.55 whereas minimum value of 61.45 was noted in SJJS-36. Total tannin content of 1.90 g per 100 g fresh weight was observed to be maximum in genotype SJJS-27 followed by SJJS-9 and SJJS-10 whereas genotypes SJJS-4, SJJS-25 and SJJS-31 with 1.70 g per 100 g fresh weight each.

6.4 Organoleptic evaluation

Organoleptic evaluation of the forty jamun genotypes revealed that, with a score of 8.20, genotype SJJS-29 was liked very much as well as genotypes SJJS-13, SJJS-14 and SJJS-28 with score of 8.00. The genotypes SJJS-1, SJJS-2, SJJS-4, SJJS-5, SJJS-10, SJJS-15, SJJS-16, SJJS-17, SJJS-18, SJJS-19, SJJS-20, SJJS-21, SJJS-25, SJJS-26, SJJS-27, SJJS-30, SJJS-31, SJJS-32, SJJS-33 and SJJS-40 were categorized as liked moderately whereas the genotypes SJJS-34, SJJS-35, SJJS-36, SJJS-37, SJJS-38 and SJJS-39 were categorized as slightly liked.

6.5 Genotypic variance

All the characteristics under study *viz*., fruit weight, fruit size, specific gravity, pulp: seed ratio, T.S.S., titratable acidity, ascorbic acid and yield efficiency showed positive phenotypic and genotpyic variances. The estimates of phenotypic variance were higher than the corresponding estimates of genotypic variance in all the characteristics. Highest coefficient of variation was recorded for yield efficiency followed by pulp: seed ratio.

6.6 Heritability and genetic gain

High heritability coupled with high genetic gain (per cent of mean) was recorded in yield efficiency, high heritability coupled with moderate genetic gain in pulp: seed ratio and ascorbic acid and high heritability coupled with low genetic gain in fruit weight, fruit size, T.S.S. and acidity.

6.7 Correlation

Fruit weight showed a positive correlation with fruit size, specific gravity, pulp: seed ratio, T.S.S., yield efficiency and negative correlation with ascorbic acid and titratable acidity at both genotypic and phenotypic levels. Fruit size exhibited positive

correlation with specific gravity, pulp: seed ratio, T.S.S., yield efficiency but negative correlation with ascorbic acid and titratable acidity at both genotypic and phenotypic levels. Acidity and ascorbic acid both showed negative correlation to yield efficiency at both genotypic and phenotypic levels

6.8 Path Analysis

Fruit size recorded the maximum positive direct effect on yield efficiency followed by T.S.S. while as titratable acidity had the maximum negative effect on yield efficiency. Highest positive indirect effect on yield efficiency came from fruit size through specific gravity followed by pulp: seed ratio through fruit size.

6.9 Divergence and Clustering

Based on the divergence of various genotypes, forty genotypes were grouped into seven clusters. Cluster-IV comprised of maximum genotypes (11) followed by Cluster-III and Cluster-VII (7 genotypes each), Cluster-V (6), Cluster-I, Cluster-II and Cluster-VI (3 genotypes each). Cluster-III had the maximum intra cluster distance (3.56) followed by Cluster-V (2.99). Maximum inter cluster distance was found between Cluster-V and Cluster-VI (200.92) followed by Cluster-II and Cluster-VI (188.62), Cluster-III and Cluster-VI (155.65), Cluster-II and Cluster-V (135.00) and Cluster-V and Cluster-VII (130.30). Cluster-I had maximum values of mean pulp: seed and ascorbic acid. Cluster-II had maximum values of mean fruit weight and fruit size. Cluster-IV had Cluster-I had maximum value specific. Cluster-V had maximum values of mean T.S.S and yield efficiency. Cluster-VI had Cluster-I had minimum value titratable acidity.

CONCLUSION

From the present studies, it is concluded that rich diversity of jamun is present in Jammu district surveyed during the investigation as indicated by the estimates of variance and coefficient of variation (genotypic and phenotypic). The high values of heritability (broad sense) and genetic gain for various horticulturally important traits indicate that the genetic diversity of jamun in Jammu can be utilized for commercial cultivation and for further improvement of existing gene pool.

On the basis of comparative evaluation, the following promising genotypes were identified for commercial cultivation and for breeding programme for further improvement:

- SJJS-10 and SJJS-27 for fruit weight and fruit size
- SJJS-4 for Pulp: seed ratio and ascorbic acid
- SJJS-29 for highest TSS
- SJJS-23 for yield efficiency

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*original not seen

Appendices

APPENDIX-I

Name of the grower/owner and location of the genotypes selected for variability studies

S. No.	Genotype	Name of the Grower/owner	Location	Block
1	SJJS-1	SKUAST- Jammu	Udheywalla	Jammu
2	SJJS-2	SKUAST- Jammu	Udheywalla	Jammu
3	SJJS-3	Chaman Lal	Flora	Marh
4	SJJS-4	Babu Ram	Kalyaanpur, Jhiri	Marh
5	SJJS-5	Babu Ram	Kalyaanpur, Jhiri	Marh
6	SJJS-6	Maharaja Hari Singh Agri Collegiate School	Nagbani	Marh
7	SJJS-7	Maharaja Hari Singh Agri Collegiate School	Nagbani	Marh
8	SJJS-8	Maharaja Hari Singh Agri Collegiate School	Nagbani School	Marh
9	SJJS-9	Tulsi Das	Kotli Bhagwana	Bishnah
10	SJJS-10	Shadi Lal	Kotli Bhagwana	Bishnah
11	SJJS-11	Tara Chand	Rakh	Bishnah
12	SJJS-12	Ujjager Singh	Kotli Bhagwana	Bishnah
13	SJJS-13	Babu Ram	Rakh	Bishnah
14	SJJS-14	Kartar Chand	Rakh	Bishnah
15	SJJS-15	Kasturi Lal	Rakh	Bishnah
16	SJJS-16	Suraj Parkash	Rakh	Bishnah
17	SJJS-17	Community Land	Shibu Chak Road	Bishnah
18	SJJS-18	Community Land	Kaku De Kothey	Bishnah
19	SJJS-19	Amar Nath	Joura	R.S.Pura
20	SJJS-20	Natharam	Joura	R.S.Pura
21	SJJS-21	Ashok Kumar	Arazi Badyal	R.S.Pura
22	SJJS-22	Sat Pal	Chakroi	R.S.Pura
23	SJJS-23	Sagar Dunni	Chakroi	R.S.Pura
24	SJJS-24	Nama Singh	Joura	R.S.Pura
25	SJJS-25	Om Lal	Morchapur	Bishnah
26	SJJS-26	Community Land	Pindi	Bishnah
27	SJJS-27	Tarsem Lal	Rakh	Bishnah

28	SJJS-28	Tarsem Lal	Rakh	Bishnah
29	SJJS-29	Sunil Kumar	Arazi Badyal	R.S.Pura
30	SJJS-30	Sunil Kumar	Arazi Badyal	R.S.Pura
31	SJJS-31	Bagaram	Chakroi	R.S.Pura
32	SJJS-32	Milkhi Ram	Chakroi	R.S.Pura
33	SJJS-33	Bagaram	Chakroi	R.S.Pura
34	SJJS-34	Girdhari Lal	Chakroi	R.S.Pura
35	SJJS-35	Sham Lal	Chakroi	R.S.Pura
36	SJJS-36	Amar Nath	Joura	R.S.Pura
37	SJJS-37	GD Goenka Public School	Gajansoo	Marh
38	SJJS-38	GD Goenka Public School	Gajansoo	Marh
39	SJJS-39	GD Goenka Public School	Gajansoo	Marh
40	SJJS-40	GD Goenka Public School	Gajansoo	Marh

APPENDIX-II

Standard week Meteorological Week data for the Year 2013 & 2014 (For the period of study)

Met. Week	Date & month	Rainfall (mm)	Rainy days	RH1 (Mor)	RH2 (After noon)	Max Temp (^{0}C)	Min Temp (^{0}C)	Mean Evaporation (mm)
1	1-7 Jan, 2013	0.0	0	94	79	10.0	5.2	0.7
2	8-14	0.6	0	91	63	17.6	4.6	1.3
3	15-21	40.8	2	90	63	17.5	5.6	1.4
4	22-28	0.0	0	86	50	19.3	2.6	1.6
5	29-4 Feb	19.8	1	88	59	20.2	7.6	1.4
6	5-11	44.4	2	92	60	20.1	4.8	2.0
7	12-18	10.8	1	91	63	19.9	7.5	1.3
8	19-25	65.8	3	93	73	19.6	8.4	0.8
9	26-4 Mar	35.8	2	86	58	23.3	8.3	2.0
10	5-11	0.0	0	78	53	27.8	10.9	2.5
11	12-18	5.7	1	89	55	25.5	11.9	2.1
12	19-25	35.7	2	80	47	27.7	13.1	2.4
13	26-1 Apr	0.0	0	89	49	28.4	12.6	2.5
14	2-8	0.0	0	83	32	30.1	13.2	3.1
15	9-15	2.2	0	79	32	32.8	14.7	3.8
16	16-22	1.2	0	72	30	32.8	16.1	3.6
17	23-29	1.2	0	68	30	33.5	16.3	4.2
18	30-6 May	0.0	0	61	21	36.5	18.1	5.1
19	7-13	0.2	0	55	20	35.7	18.7	6.2
20	14-20	0.0	0	60	22	40.1	18.9	7.6
21	21-27	9.6	1	46	23	42.5	22.6	10.2
22	28-3 Jun	12.0	1	58	27	37.9	21.5	8.0
23	4-10	0.0	0	59	32	41.1	25.0	8.7
24	11-17	95.2	3	77	55	33.9	23.3	6.2
25	18-24	2.6	1	63	41	38.3	25.8	9.6
26	25-1 July	31.6	3	74	53	34.9	24.4	7.3
27	2-8	76.2	2	84	58	35.2	25.1	7.1
28	9-15	47.2	5	89	64	33.4	23.9	7.0
29	16-22	35.4	2	84	66	33.1	25.9	6.4
30	23-29	30.6	2	85	67	33.6	26.1	6.9
31	30-5 Aug	112.5	5	88	73	33.0	24.5	6.1
32	6-12	45.2	2	91	75	31.1	25.6	5.3
33	13-19	309.4	6	96	87	28.0	23.6	1.4
34	20-26	15.6	1	85	62	34.7	25.6	5.5
35	27-2 Sep	76.4	3	87	65	33.5	23.8	6.5
36	3-9	76.1	3	84	65	32.2	23.0	6.1
37	10-16	3.2	0	83	58	32.6	23.1	5.7
38	17-23	0.0	0	86	56	33.0	21.6	6.0
39	24-30	31.1	1	84	63	32.4	22.3	5.3
40	1-7 Oct	28.2	2	84	65	31.4	21.8	4.3

41	8-14	34.6	1	89	63	30.9	22.1	3.1
42	15-21	0.0	0	89	48	31.2	17.2	3.4
43	22-28	0.0	0	90	50	29.6	16.5	3.1
44	29-4 Nov	4.4	0	93	37	27.7	12.6	2.6
45	5-11	12.2	1	92	49	23.5	11.4	1.5
46	12-18	0.0	0	93	32	25.6	7.5	1.3
47	19-25	0.0	0	94	40	25.1	7.9	1.4
48	26-2 Dec	0.0	0	94	39	25.1	7.1	1.3
49	3-9	0.0	0	94	44	23.7	7.0	1.1
50	10-16	0.0	0	95	45	22.4	6.1	1.1
51	17- 23	7.8	1	97	73	15.6	7.0	0.8
52	24-31	3.0	1	96	49	17.1	2.3	0.8
1	1-7 Jan, 2014	007.4	1	96	49	18.4	1.6	0.9
2	8-14	001.2	0	85	51	18.0	4.4	1.0
3	15-21	000.0	0	96	66	17.8	6.0	0.9
4	22-28	052.0	2	95	55	20.5	6.9	1.1
5	29-4 Feb	006.0	1	94	73	18.7	8.5	0.9
6	5-11	007.7	1	91	64	18.4	7.7	1.2
7	12-18	005.8	1	92	50	19.1	5.4	1.6
8	19-25	004.0	1	93	55	21.4	7.6	1.5
9	26-4 Mar	002.6	1	92	56	20.3	9.1	2.0
10	5-11	047.4	2	89	58	22.2	10.3	1.8
11	12-18	038.4	2	85	52	25.6	12.3	2.2
12	19-25	013.4	2	86	69	24.3	12.5	2.1
13	26-1 Apr	002.8	1	85	49	27.2	12.9	3.2
14	2-8	019.5	3	84	53	25.6	13.5	2.6
15	9-15	000.0	0	76	39	29.7	12.9	3.2
16	16-22	023.0	2	81	42	28.6	14.1	3.1
17	23-29	000.0	0	70	27	35.8	17.2	5.1
18	30-6 May	011.5	1	64	30	37.3	20.4	7.2
19	7-13	003.8	1	69	37	33.9	19.8	6.0
20	14-20	000.0	0	71	38	34.1	18.9	6.1
21	21-27	000.0	0	50	26	36.7	20.0	7.6
22	28-3 Jun	000.6	0	50	23	37.4	21.8	8.5
23	4-10	000.0	0	51	16	43.1	21.5	9.8
24	11-17	000.0	0	55	32	40.9	24.2	9.1
25	18-24	000.0	0	57	38	38.4	25.5	8.0
26	25-1 July	026.2	2	68	45	36.9	25.3	8.0
27	2-8	014.2	1	76	50	36.1	25.1	6.7
28	9-15	007.4	1	68	45	39.2	27.6	8.4
29	16-22	026.8	1	82	65	34.3	24.9	7.1
30	23-29	033.4	2	89	81	30.9	25.7	6.0
31	30-5 Aug	086.6	4	89	64	35.2	24.7	5.5
32	6-12	044.3	2	87	71	33.9	24.7	5.7
33	13-19	127.8	3	88	66	33.0	23.5	5.7
34	20-26	000.0	0	85	55	34.7	25.3	5.9

35	27-2 Sep	011.2	1	88	78	31.8	24.0	4.9
36	3-9	454.7	5	88	78	26.9	21.7	2.0
37	10-16	033.9	3	84	63	31.0	21.5	3.0
38	17-23	012.6	1	77	63	32.8	17.7	2.9
39	24-30	000.0	0	82	59	32.0	22.8	4.2
40	1-7 Oct	000.0	0	91	67	31.7	23.9	3.9
41	8-14	016.9	1	81	54	28.8	16.8	3.2
42	15-21	001.6	0	79	50	28.1	14.6	3.7
43	22-28	000.0	0	83	52	28.4	16.6	3.5
44	29-4 Nov	000.0	0	85	47	27.1	13.0	3.4
45	5-11	008.0	1	88	47	26.8	12.7	2.9
46	12-18	000.0	0	83	39	26.1	8.4	3.0
47	19-25	000.0	0	85	44	24.7	7.3	2.9
48	26-2 Dec	000.0	0	90	41	24.8	8.1	2.5
49	3-9	000.0	0	91	41	24.9	6.0	2.4
50	10-16	000.0	0	92	53	19.8	5.4	1.2
51	17- 23	000.0	0	97	78	12.9	5.1	0.3
52	24-31	000.0	0	94	67	15.8	3.3	0.6

Vita

VITA

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CERTIFICATE-IV

Certified that all necessary corrections as suggested by external examiner and the advisory committee have been duly incorporated in the thesis entitled **"Characterization and evaluation of genetic diversity of jamun (*Syzygium cumini* L.) for horticultural traits"** submitted by **Miss Madhvi Plathia,** Registration No. **J-11-D-143-A.**

17/5/18

Dr. V. K. Wali
Major Advisor

Place: Jammu
Date: 17-05-2018

17/5/2018

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