EVALUATION OF BRINJAL GERMPLASM FOR WINTER SEASON

A THESIS

SUBMITTED TO THE

UTTAR BANGA KRISHI VISWAVIDYALAYA

IN PARTIAL FULFILLMENT OF THE REQUIREMENTS FOR THE DEGREE OF

MASTER OF SCIENCE (HORTICULTURE)

In

VEGETABLE AND SPICE CROPS

By

SANJAY K R

Registration No.H-2016-09-M

DEPARTMENT OF VEGETABLE AND SPICE CROPS

FACULTY OF HORTICULTURE

UTTAR BANGA KRISHI VISWAVIDYALAYA

PUNDIBARI, COOCH BEHAR, WEST BENGAL, INDIA

2018


I dedicate this
thesis to my parents,
Ramareddy K. P and
Sugunamma,
brother Sagar K. R
and Miss. Navya Shree C M
for their love, support and
encouragement

DEPARTMENT OF VEGETABLE AND SPICE CROPS
UTTAR BANGA KRISHI VISWAVIDYALAYA
FACULTY OF HORTICULTURE
Pundibari, Cooch Behar, West Bengal – 736165, India.

Dr. Subhamoy Sikder
Assistant Professor

Mobile : +91 8436956667
Email : Subhamoy.sms@gmail.com

CERTIFICATE I

This is to certify that the thesis entitled, **"Evaluation of brinjal germplasm for winter season"** submitted for the degree of M. Sc. in the subject of *Vegetable and Spice Crops* of the **Uttar Banga Krishi Viswavidyalaya**, Pundibari, is a bonafide research work carried out by **Mr. Sanjay K R (Registration No. : H-2016-09-M)** under my supervision and that no part of this thesis has been submitted for any other degree.

The assistance and help received during the course of investigation have been fully acknowledged.

Date : 20.06.2018
Place: UBKV, Pundibari

Dr. Subhamoy Sikder
Chairman
Advisory Committee

DEPARTMENT OF VEGETABLE AND SPICE CROPS
UTTAR BANGA KRISHI VISWAVIDYALAYA
FACULTY OF HORTICULTURE
Pundibari, Cooch Behar, West Bengal – 736165, India.

CERTIFICATE II

This is to certify that the thesis entitled, **"Evaluation of brinjal germplasm for winter season"** submitted by **Mr. Sanjay K R (Registration No – H-2016-09-M)** to the Uttar Banga Krishi Viswavidyalaya, Pundibari, in partial fulfillment of the requirements for the degree of M. Sc. in the subject of ***Vegetable and Spice Crops*** has been approved by the Student's Advisory Committee after an Oral Examination on the same, in collaboration with an External Examiner.

1.	Dr. Laxuman Sharma SIKKIM UNIVERSITY	20/6/18 **External Examiner**
2.	**Chairman, Advisory Committee,** **Dr. Subhamoy Sikder** (Assistant Professor, Department of Vegetable and Spice Crops)	21/06/18
	Members, Advisory Committee	
3.	**Dr.R. Chatterjee** (Professor and HOD Department of Vegetable and Spice Crops)	20/06/18
4.	**Dr.Suchand Datta** (Professor, Department of Vegetable and Spice Crops)	20/6/18
5.	**Dr. Lakshmi Hijam** (Assistant Professor, Department of GPB)	20/6/18
	20/06/18 **Dr. Ranjit Chatterjee** **Head of the Department**	20/6/18 **Prof. S. C. Sarker** **Dean PG Studies** **Faculty of**

Acknowledgement

The consanguineous flagging but edulcorative phase is now over and at this stage of metamorphosis, in respect, I feel indebted to all those who helped me.

It is of immense pleasure to me to express my deepest sense of gratitude with overwhelming joy and glory to the chairman of my advisory committee, Dr. Subhamoy Sikder, Assistant professor, Department of Vegetable and Spice Crops, Faculty of Horticulture, Uttar Banga Krishi Viswavidyalaya, Pundibari, Coochbehar, West Bengal, for his noble supervision, sagacious guidance, valuable suggestions, and ever encouraging inspirations. He is a man of erudition and always been my inspiration for higher studies. His close monitoring and encouragement made the work complete in time and with perfection. I feel proud being a scholar under the guidance of such a learned person.

I render my heartfelt thanks and obligation to Mr. Sibnath Basfore, Assistant professor, Dept. of Vegetable and Spice Crops, Faculty of Horticulture, U.B.K.V for his inexplicable support. I am indebted to him for his sound technical guidance for my thesis and seminars this For his noble supervision, sagacious guidance, valuable suggestions, and ever encouraging inspirations. He is a man of erudition and always been my inspiration for higher studies. His close monitoring and encouragement made the work complete in time and with perfection. I am thankful to his support.

I am highly grateful to Prof. Jagadish Chandra Jana, Dean, Faculty of Horticulture and Dr. Ranjit Chatterjee, Head, department of Vegetable and Spice Crops for his support and encouragement.

With a profound and unfading sense of obligation I express my heartfelt thanks to the member of my advisory committee, Dr. Suchand Datta, Dept. of Vegetable and Spice Crops and Dr. Lakshmi Hijam, Dept. of GPB, Faculty of Agriculture, Uttar Banga Krishi Viswavidyalaya, for their help throughout course of this investigation. Their humble behavior, prudency and endless support made them my inspiration.

I am highly grateful to all others teachers of Faculty of Horiculture and Agriculture , Uttar Banga Krishi Viswavidyalaya for their endless support and inspiration thoughout the journey of my M.Sc. course work and thesis work.

I feel my pleasure to breathe my deepest respect and gratitude to my Friend, Well wisher, Supporter, Mr. Ragupathi B. prodigious inspirations, moral support, spontaneous love and affection and silent blessing at every step of my life.

I shall be failing in my duty if I do not express my obligation to my seniors, Rakesh da, Ravi da, Reman da, Yougendr da, Pranali di, Aradhana di, Vijay da, Adarsh da, Somshekhar da, Susmita di, Khoni de, Mumtak Di, with their expertise from the time of initiation of the thesis work.

I will be happy to mention the support and cooperation received from my dear friends Ramesh E, Subha Laxmi, Ujoyl Roy, Dinesh, Ranga, Dev, Ponnu, Supriya, Santhu, Sindhu, who have always been beside me whenever I needed them and also I would like to thank them for being a part of my life.

I reiterate to my juniors Manju, Yathish, Vinodh, Sangoy, who helped me a lot during my course of study.

Words are not sufficient to thank Field Assistant Bola Da, Ms. Sapna Rava, Farm Assistant Monoranjan da and the Field Labours Sajal da, Biswajit da, Avijit da and all other staffs of the farm section for assisting me in Laboratory works as well as in the field works to carry out my thesis work successfully.

I feel my pleasure to breathe my deepest respect and gratitude to my parents for their continuous sacrifice, prodigious inspirations, moral support, spontaneous love and affection and silent blessing at every step of my life.

I am indebted to so many people that a complete acknowledgement would be an encyclopedia and hence is not possible in this short circumstances but none has been forgotten.

Lastly, I want to thank Lord Sri Ganapathi for blessing me.

Uttar Banga Krishi Viswavidyalaya

Department of Vegetable and Spice Crops

Faculty of Horticulture
Pundibari, Coochbehar, West Bengal

Title of the Thesis	:	Evaluation of brinjal germplasm for winter season.
Name of the student	:	Mr. Sanjay K R.
Registration Number	:	H-2016-09-M
Name of the Chairman	:	Dr. Subhamoy Sikder
Degree to be awarded	:	Master of Science (Horticulture) in Vegetable & Spice Crops
Department	:	Vegetable and Spice Crops
Year of submission	:	2018

ABSTRACT

The present investigation "Evaluation of brinjal germplasm for winter season" was conducted on 32 genotypes for total of 22 characters *i.e.*, 7 morphological characters, 11 quantitative characters 4 qualitative characters under the department of Vegetable and Spice Crops, Faculty of Horticulture, Pundibari, Cooch Behar, West Bengal, India 2016-17 and 2017-18 following the standard cultivation practices with the objectives to collect, record and documentation of the different genotypes of brinjal from different parts of North Bengal; to study the genetic variability, heritability, genetic advance, character association, effect and genetic diversity among the collected germplasm.

Based on average mean performance the genotypes UBB 3, UBB 5, UBB 8, UBB 12, UBB 14, UBB 21, UBB 23, UBB 27 and UBB 32 showed highest estimates for most of the qualitative and yield parameters. The magnitude of PCV and GCV indicated wide range of variability for all the characters and less affected by environment in contributing final expression. The high estimate of PCV and GCV for the ccharacters viz., fruit diameter, fruit length, fruit weight, number of fruit per plant, phenol content indicated prevalence of high genetic variation among the genotypes under study for these characters. Low estimates of the same for fruiting span, ascorbic acid, total soluble solid and days to fruit maturity was the evident of very less variability. However, plant height, number of primary branch, calyx length, days to fruit maturity, fruit diameter, fruit length, fruit weight, number of fruit per plant, phenol content and anthocyanin content showed high heritability coupled with high genetic advance of mean as percentage which suggested that these characters might possibly be improved through selection, specifically recurrent selection method. Study for character association and path analysis revealed that for number of fruit per plant, fruit weight, fruit diameter, calyx length, plant height would likely to be effective in increasing fruit yield per plant. In the present investigation residual effect indicated 61.50 % contribution of selected characters for yield.

Through diversity D^2 analysis whole genotypes were categorized under seven groups with no evidence for geographical diversity as necessarily cause of genetic diversity. However, highest genetic diversity was recorded in cluster I and V argued for their utilization to develop transgressive segregate lines. Genotypes under cluster VI and VII found to be effective for the improvement of yield related attributes. The cross combinations between cluster VI and V, cluster VI and II, cluster VI and VI, cluster VI and I, cluster VI and III, cluster VI and cluster VII could be effectively utilized to develop improved heterotic population or recombinant.

Keywords: Brinjal, Germplasm, Variability, Heritability, Genetic advance, Correlation, Genetic divergence

CONTENTS

LIST OF TABLES

LIST OF PLATES

1. Introduction

Introduction

Brinjal (*Solanum melongena* L.), the name brinjal is more popular in Indian subcontinents and it's derived from Sanskrit and Arabic and it is also known as garden egg, melanzana, patlican, aubergine, (in France and England) eggplant due to the some varieties having round shape with white colour which resembles like chicken eggs. Brinjal belongs to the family Solanaceae with diploid chromosome number 2n=24. It is a versatile crop adopted and grown in different agro-climatic regions and can be cultivate throughout the country. Brinjal have different shapes (oval or egg shaped to long club-shaped), colour (white, yellow, green and purple) and size. Being a primary center of origin India have a many advanced cultivars and local landraces which can be grown in all parts of the nation throughout the year for its young, tender fruits which are consumed fresh, dried or pickled (Karihaloo and Gottileb, 1995). It's also known as poor man's vegetable (Yadav *et al*., 2016). It's a good source of income for to small and marginal farmers. Brinjal is a warm, perennial plant but commercially grown as annual vegetable crop in tropical and sub tropical regions of the world.

China is in leading position in area and production followed by India and Egypt. China is having highest productivity followed by Japan and Turkey. In India, West Bengal having highest area and production followed by Odhisa, Gujarath, Bihar and Madhya Pradesh, where Uttar Pradesh followed by Karnataka, Andhra Pradesh, Himachal Pradesh leads in productivity respectively. In India Brinjal is cultivated in 662.54 thousand Ha with 12515.19 thousand MT. West Bengal is first in both area and production with 162.93 thousand Ha 3019.00 MT respectively. Murshidabad, Nadia, Maldah, Bankura, 24 Paraganas South etc. are the main districts of brinjal production. Peak harvesting season is January, February, November, December in Odisha, January to April, October to December in Gujarat, September to October in Madhya Pradesh, November to December in Bihar where as in West Bengal its throughout the year (Horti update 2017).

Autumn-winter and summer-rainy seasons are the main two distinct seasons in West Bengal for brinjal production, in this two seasons autumn-winter is the most popular season and lies between August to February; and the summer-rainy season lies between February to August. Several high yielding and improved varieties are available for autumn-winter season brinjal production which performance better due to low incidence of insect pests and suitable climatic conditions like low moderate night temperature along with no heavy showers during

first couple of days after anthesis during winter months (Pandit *et al.*, 2010). During spring summer season the vegetative phage was favored and earlier flowering took place and in autumn winter season the reproductive phase was favored. The quantitative characters like plant height and number of branches per plant were high and took less number of days for flowering in spring summer and yield components like fruit weight, fruit yield per plant, number of fruits per plant and harvesting index were high during autumn winter season (Koundinya *et al*., 2017).

Brinjal is a stable vegetable in our diet since ancient times. It's prepared by both poor and rich; it is compared with tomato for its nutritive value. The tender unripe brinjal fruit is primarily prepared for cooking various dishes around the world. And it's got a much potential in pickle and dehydration industries. Brinjal has also got high demand for its high nutritional and medicinal values like de cholestrolizing property primarily due to presence lenoleic and lenolenic fatty acids which are present abundant in flesh and seeds (Hanchinmani and Imamsaheb, 2015) and fruits are rich source of minerals like Ca, Mg, P and fatty acids. It has medicinal use like curing diabetics, asthma, cholera, bronchitis, diarrhea and liver complaints (Santhosha *et al.,* 2017). It contains1.4 g of protein, 4 g of carbohydrates, 92.7 g of moisture and 124 IU of vitamin A, 12 mg of vitamin C, 18 mg of calcium, 47 mg of phosphorous, 0.9 mg of iron, per 100g of edible portion. Bitterness is due to glycoalkolide solasodine in brinjal.

Brinjal is a good source protein, dietary fiber, and minerals like potassium, manganese, magnesium, and copper. It also contains good quantities of vitamin B1 (thiamine), vitamin B3 complex (niacin), vitamin B6 (pyridoxine), folate. Phytonutrients composition of brinjal has good quantities of nasunin and chlorogenic acid and phytonutrients have a power to neutralize the levels of free radicals and other toxins attributed to their antioxidant property. Brinjal is devoid of cholesterol and it has been used in treatments of hypercholesterolemia. And nasunin is good antioxidant and scavenger of free radical it protects cell membranes damage. It is helpful in preserving fats and other lipids inside the brain cell membranes from getting oxidized. Antimicrobial, antimutagenic, anti viral and anti-LDL properties of chlorogenic acid is highly helpful. And in brinjal oblong fruited variety have high Total Solibale Solids (TSS), long fruited cultivars have high content of free reducing sugars, anthocyanin, phenols, glycoalkaloids (such as solasodine), dry matter, and amide proteins. In Indian commercial varieties the glycoalkaloid content is varies between 0.37mg to 4.83mg per 100 g of fresh weight, if it reaches higher concentration like 20 mg per 100 g of fresh

weight it will leads to bitter taste and off flavor. Brinjal is used in the improvement of cardiovascular and liver health. (Patel *et al.*, 2013)

Evaluation of brinjal genotypes helps in recommending particular genotype in terms of yield, quality and resistance to major pest and diseases. And it also helps in developing in variety with high yield, colour, size, shape, weight, quality parameters and resistance to major pest and diseases.

In *melongena* species three main botanical varieties are there namely var. *esculentum* (the common brinjal) which is large, round or egg shaped fruit forms, var. *serpentinum* which are the long, slender types and var *depressum* which is the dwarf brinjal plants. A large indigenous biodiversity exists in eggplant with variation in plant type, stem color, leaf size, leaf tip, midrib color, fruit size, fruit shape, fruit color, fruit yield, fruit quality, cooking quality, and tolerance to pests and diseases (Ullah *et al.,* 2014). India is being primary centre of origin shows greater extent of variability and greater the variability in a population, greater is the chance for effective selection for desirable types (Vavilov, 1951).

And the varietal acceptance of brinjal is region specific and even in particular region itself demands for colour, shape, size, weight and flavor varies. Still there is demand and scope for developing varieties for particular region. Hence, there is a need to develop varieties preferable and suitable to a particular location. Genetic architecture and the mode of inheritance of characters are important considerations to determine the breeding procedures. The existence of variability in a particular trait is an important prerequisite for its heritable improvement.

Evaluation of the genotypes is needed to know the performance of the genotypes in terms of yield and other yield attributing characters. Based on evaluation, good genotypes can be exploited and upon breeding program they can be released as a variety or used in breeding program for developing variety as a breeding line. To create any high yielding, resistant, good quality variety, the nature and magnitude of variation in the genotypes are the key factors. In any plants yield and its components are complex and they are controlled by polygenes in their mode of inheritance. And they are highly influenced by the environment (Kumar *et al.,* 2012).

Further, the varietal preference for brinjal is strictly location specific and even within a location the acceptance differs from place to place. For improving the yield potential of

varieties and hybrids the decision should be made about the choice of right type of parents for hybridization. Therefore, induction of variability in brinjal is urgently needed for ultimate use in any crop improvement programme. It has been found that the progenies derived from crossing between divergent parents give divergent and useful trait.

The qualification of genetic diversity has made it possible to choose genetically diverse parents for a successful hybridization program. Knowledge on genetic diversity, its nature and degree is useful for selecting desirable parents from a germplasm for the successful breeding programme. Earlier, eggplant breeding was relied both on mass selection and pureline selection from the land races for the development of improved varieties. It is a fact that selection of parents on the basis of their performance does not necessarily lead to desired results. In breeding for high yielding crop plants through hybridization, the breeders are often faced with the problem of selecting genitors and crosses. The performance of genotypes is not always a good index of their superior combining ability. Certain cross combinations nick well to provide superior hybrids where as others involving equally promising genitors produce disappointing progeny (Reddy *et al.*, 2013). Hence, there is a constant need to screen germplasm to isolate potential combining lines and desirable cross combinations, either to exploit heterosis or to obtain new recombinants. The combining ability analysis helps breeders in choosing suitable genotypes as parents for hybridization and superior cross combinations through gca and sca studies, respectively. At the same time, it also elucidates the nature and magnitude of different types of gene action involved, which is essential for an effective breeding programme.

Genetic analysis provides a guideline for the assessment of relative breeding potential of the genitors or identifies best combiners (Devi *et al.*, 2005). Hence, the present investigation was undertaken to study 32 brinjal genotypes from northern part of West Bengal to ascertain the nature and magnitude of genetic diversity and to elucidate information on combining ability of several eggplant genotypes in order to obtain superior hybrids, of excellent high yields, and in addition, to identify hybrid combinations valuable for commercial exploitation.

OBJECTIVES

Keeping all this information in the purview, the present investigation employing thirty two diverse genotypes of tomato was outlined with the following objectives

1. Collection of different genotypes of brinjal from different parts of North Bengal.
2. To record and documentation of morphological variation throughout the collected genotypes.
3. To assess the amount of genetic variability, heritability and genetic advance for different qualitative and quantitative characters present in a population of different brinjal genotype.
4. To study the character association and, direct and indirect effect of different qualitative and quantitative characters influencing fruit yield.
5. To obtain information on genetic diversity present among the brinjal genotype based on qualitative and quantitative characters respectively.

2. Review of Literature

Review of Literature

Being a centre of origin India exhibits huge amount of genetic variability in brinjal and have a high potential for exploitation. The phenotypic expression is controlled by both genotype and environment. Hence, the existence of genetic variability in population is most important primary thing for any crop improvement programme.

It is important to known the genetic architecture for the various characters of importance and interrelationship within them. In the present study an attempt has been made to study genetic variability, heritability, genetic advance, character association, path coefficient analysis and genetic divergence, and pest and disease relation in brinjal. A brief review of available literature related to the present study has been presented in this chapter under the following headings.

2.1 Variability, heritability and genetic advance

2.2 Character association

2.3 Path coefficient analysis

2.4 Genetic divergence

2.1 Variability, Heritability and Genetic advance

The amount of genetic variability present in the population greatly contributes to the genetic improvement. Phenotypic variance is sum of genotypic variance (heritable) and environment variance (non-heritable). Genetic variability is a measure of variation in population which is due to the genotype that can be study by genetic parameters like GCV (genotypic coefficient of variation), Heritability, GA (genetic advance), etc. Selections which are made based on genetic variability are effective and reliable as it is heritable. It is important to known the relative extent of genetic and non-genetic variability exhibited by individual characters. Partitioning of overall variability is necessary into heritable and non-heritable components by calculating genetic parameters such as GCV (genotypic coefficient of variation) and PCV (phenotypic coefficient of variation) Chadha and Sindhu, 1983 and Singh and Singh, 1994).

Heritability is the transmissibility of characteristics from parents to progeny. Heritability in a broad sense is the ratio of genotypic variance to total or phenotypic variance in percentage where as in narrow sense it is the ratio of additive genetic variance to phenotypic *i.e.*, total variance. Higher the heritable variation greater will be the possibility of fixing the characters by selection methods. However, it explained that heritability and genetic advance are important selection parameters. Heritability estimates along with genetic advance are usually more effective in predicting the gain under selection than heritability estimates alone.

Genetic advance denotes the improvement in the genotype value of the new population when compared to the parental (original) population and measures genetic gain under selection. So, for the effective breeding program knowledge of genetic advance is to be expected by applying selection pressure to a segregating and variable population. Genetic advance is the improvement in the mean genotypic value of selected plants over the parental population. It is the measure of genetic gain under selection. The success of genetic advance under selection depends upon genetic variability, heritability, and selection intensity. The genetic advance is higher for the characters having high heritability.

The nature and extent of variation, heritability, genetic advance and GAM for different characters of brinjal and other solanaceous crops as reported by different workers is summarized as follows.

2.1.1 Plant height

Crop	Materials used for the study	Variation		Heritability	GA	GAM	Reference
		PCV	GCV				
Brinjal	16 genotypes	Low 4.7	Low 1.33	Low 8.01	Low 0.95	Low 1.2	Isalam and Uddin (2009)
	40 genotypes	Moderate 12.04	Moderate 11.63	High 93.0	Moderate 16.91		Das *et al.* (2010)
	34 genotypes	Moderate 18.89	Moderate 18.72	High 98.92	High 33.69	High 38.24	Muniappan *et al.* (2010)
	7 Parents & 21 hybrids	Moderate 15.58	Moderate 16.13	Moderate 34.19		31.02	Ansari *et al.* (2011)
	33 local types	Low 9.75	Low 9.61	High 97.23		Moderate 19.53	Kumar *et al.* (2012)
	70 genotypes	Moderate 16.53	Moderate 14.30	High 74.9	Moderate 18.34	Moderate 25.49	Karak *et al.* (2012)
	60 genotypes	High 24.75	High 24.31	High 96.49		High 49.20	Lokesh *et al.* (2013)

	14 genotypes	Moderate 13.93	Moderate 10.21	Moderate 53.74		Moderate 15.42	Kumar *et al.* (2013)
	40 genotypes	Moderate 19.4	Moderate 18.3	High 88.7	High 35.4	High 35.4	Yadav *et al.* (2016)
	55 genotypes	Moderate 12.51	Moderate 12.42	High 98		Moderate 25.37	Pujer *et al.* (2017)
	36 genotypes	Moderate 12.68	Moderate 18.51	Moderate 47	Moderate 17.94	Moderate 17.88	Rani *et al.* (2017)
	25 accessions	Low 8.52	Low 8.43	High 97.90	Moderate 16.29	Moderate 17.18	Ravali *et al.* (2017)
	60 genotypes	Moderate 18.96	Moderate 18.73	High 93.57		High 58.93	Samlindsujin *et al.* (2017)

2.1.2 Number of Primary branches

Crop	Materials used for the study	Variation		Heritability	GA	GAM	Reference
		PCV	GCV				
Brinjal	7 parents and 21 hybrids	Moderate 16.60	Moderate 15.36	Moderate 24.07		High 29.34	Ansari *et al.* (2011)
	70 genotypes	Moderate 18.53	Moderate 16.12	High 75.7	Low 3.92	Low 28.91	Karak *et al.* (2012)
	33 local types	High 26.45	High 26.05	High 97.23		High 52.85	Kumar *et al.* (2012)
	36 genotypes	High 21.44	Moderate 15.15	Moderate 75.7	Moderate 50	Low 22.07	Rani *et al.* (2012)
	14 parents	Moderate 14.05	Moderate 10.03	Moderate 51.01		Moderate 14.76	Kumar *et al.* (2013)
	40 genotypes	High 21.3	High 15.8	Low 55.6	Low 1.5	Low 24.4	Yadav *et al.* (2016)
	60 genotypes	High 30.57	High 29.57	High 93.57		High 58.93	Samlindsujin *et al.* (2017)

2.1.3 Calyx Length

Crop	Materials used for the study	Variation		Heritability	GA	GAM	Reference
		PCV	GCV				
Brinjal	14 parents	High 34.37	High 33.68	High 96.00		High 67.98	Kumar *et al.* (2013)

2.1.4 Days to First Flowering

Crop	Materials used for the study	Variation		Heritability	GA	GAM	Reference
		PCV	GCV				
Brinjal	16 genotypes	Low 5.2	Low 4.18	High 62.7	Low 5.5	Low 7.8	Islam and Uddin (2009)
	F2 generation	Low 5.54	Low 4.10	Moderate 54.74	Low 6.57	Low 6.25	Thangavel *et al.* (2011)
	33 Local types	Low 3.35	Low 3.06	83.19		5.75	Kumar *et al.* (2012)

	10 accessions	Moderate 9.6	Moderate 10.5	High 83.5			Danquah *et al.* (2012)
	14 parents	Low 5.70	Low 5.18	High 81.46		Low 9.64	Kumar *et al.* (2013)
	36 genotypes	Moderate 12.89	Moderate 13.90	High 86	10.83	High 24.64	Rani *et al.* (2017)
	25 accessions	Moderate 14.72	Moderate 14.59	High 98.23	12.72	High 29.80	Ravali *et al.* (2017)
	60 genotypes	Moderate 12.36	Moderate 12.04	High 94.96		High 24.17	Samlindsujin *et al.* (2017)
Chilli	65 genotypes	High 21.88	High 21.51	High 96.7	High 27.84		Data and Jana (2010)
	55 genotypes	Moderate 14.09	Moderate 13.98	High 99		Moderate 23.17	Pujer *et al.* (2017)

2.1.5 Fruit Diameter

Crop	Materials used for the study	Variation		Heritability	GA	GAM	Reference
		PCV	GCV				
Brinjal	40 genotypes	High 39.1	High 35.5	High 82.7	Moderate 32.3	Moderate 66.6	Yadav *et al.* (2016)
	55 genotypes	High 20.55	High 20.44	High 99		Moderate 41.81	Pujer *et al.* (2017)
	36 genotypes	Moderate 13.48	High 21.81	High 38	0.85	Moderate 17.16	Rani *et al.* (2017)

2.1.6 Fruit Length

Crop	Materials used for the study	Variation		Heritability	GA	GAM	Reference
		PCV	GCV				
Brinjal	7 parents and 21 hybrids	High 41.35	High 41.30	Moderate 32.47		High 85.19	Ansari *et al.* (2011)
	33 local types	Moderate 20.99	Moderate 17.95	High 73.14		High 31.62	Kumar *et al.* (2012)
	10 accessions	High 22.7	High 23.4	High 94.7			Danquah *et al.* (2012)
	14 parents	High 21.2	High 20.61	High 96.11		High 41.63	Kumar *et al.* (2013)
	60 genotypes	High 20.64	High 20.43	High 97.55		High 41.56	Lokesh *et al.* (2013)
	9 cultivars	High 109.28	High 118.25	High 85.40	7.96		Rad *et al.* (2015)
	40 genotypes	High 31.7	High 29.9	High 89.4	High 6.3	High 58.4	Yadav *et al.* (2016)

2.1.7 Fruit Weight

Crop	Materials used for the study	Variation		Heritability	GA	GAM	Reference
		PCV	GCV				
Brinjal	16 genotypes	High 62.0	High 61.6	High 99.0	High 75.8	High 126.0	Islam and Uddin (2009)
	34 genotypes	High 26.78	High 26.88	High 99.28	Moderate 10.83	High 54.77	Muniappan *et al.* (2010)
	10 accessions	High 15.4	High 17.7	High 76.0			Danquah *et al.* (2012)
	33 local types	High 35.68	High 35.54	High 99.27		High 72.96	Kumar *et al.* (2012)
	14 parents	Moderate 15.93	Moderate 15.51	High 94.74		High 31.10	Kumar *et al.* (2013)
	21 genotypes	High 59.42	High 59.42	High 99.8	High 108.91		Madhavi *et al.* (2015)
	9 cultivars	High 407.3	High 452.05	High 81.18	106.19		Rad *et al.* (2015)
	40 genotypes	High 63.3	High 62.5	High 97.6	High 65.6	High 127.2	Yadav *et al.* (2016)
	55genotypes	High 50.58	High 50.57	High 100		High 104.14	Pujer *et al.* (2017)
	60 genotypes	High 50.70	High 50.41	High 98.87		High 103.27	Samlindsujin *et al.* (2017)

2.1.8 Number of fruits for plant

Crop	Materials used for the study	Variation		Heritability	GA	GAM	Reference
		PCV	GCV				
Brinjal	16 genotypes	High 72.0	High 70.7	High 96.0	High 26.9		Islam and Uddin (2009)
	34 genotypes	High 50.42	High 43.73	High 75.19	Moderate 10.82	High 78.12	Muniappan *et al.* (2010)
	F2 generation	Low 17.89	Low 5.28	Low 8.72	Low 0.28	Low 3.12	Thangaval *et al.* (2011)
	33 local types	High 29.66	High 28.46	High 92.08		High 56.27	Kumar *et al.* (2012)
	60 genotypes	Moderate 18.00	Moderate 17.65	High 96.23		High 35.68	Lokesh *et al.* (2013)
	14 parents	High 22.52	High 21.88	High 94.39		High 43.79	Kumar *et al.* (2013)
	21 genotypes	High 65.21	High 65.62	High 98.0	High 23.04		Madhavi *et al.* (2015)
	40 genotypes	High 27.5	High 24.9	High 81.9	High 3.4	High 46.4	Yadav *et al.* (2016)

	60 genotypes	High 29.99	High 29.79	98.58		60.92	Samlindsujin *et al.* (2017)
	55 genotypes	High 37.55	High 36.06	High 92		High 71.34	Pujer *et al.* (2017)

2.1.9 Fruit yield per Plant

Crop	Materials used for the study	Variation		Heritability	GA	GAM	Reference
		PCV	GCV				
Brinjal	16 genotypes	High 70.0	High 69.0	High 96.5		High 141.0	Islam and Uddian (2009)
	34 genotypes	High 53.43	High 45.39	High 72.18	Low 2.38	High 79.44	Muniappan *et al.* (2010)
	33 local types	High 22.91	High 21.99	High 92.13	High 43.48	High 65.5	Kumar *et al.* (2012)
	60 genotypes	High 37.26	High 37.07	High 99.01	Low 1.11	High 75.98	Lokesh *et al.* (2013)
	14 parents	High 26.61	High 25.84	High 94.26		High 51.68	Kumar *et al.* (2013)
	21 genotypes	High 55.36	High 56.10	High 97.4	1.13		Madhavi *et al.* (2015)
	40 genotypes	High 30.7	High 30.5	High 98.9	High 233.1		Yadav *et al.* (2016)
	60 genotypes	High 67.94	High 67.27	High 98.05		High 137.21	Samlindsujin *et al.* (2017)
	55 genotypes	High 32.35	High 31.69	High 100		High 63.93	Pujer *et al.* (2017)

2.1.10 Ascorbic Acid

Crop	Materials used for the study	Variation		Heritability	GA	GAM	Reference
		PCV	GCV				
Brinjal	33 local types	Moderate 14.66	Moderate 14.65	High 99.98	High 30.18	High 29.95	Kumar *et al.* (2012)
	14 parents & 40 hybrids	Moderate 15.13	Moderate 14.83	High 96.07	High 29.95		Kumar *et al.* (2013)
	55 genotypes	High 32.07	High 28.57	High 79		High 52.22	Pujer *et al.* (2017)
	55 genotypes	High 23.49	High 27.33	High 74	1.75	High 41.59	Rani *et al.* (2017)
	25 accessions	High 22.79	High 22.66	High 98.91	Low 2.92	High 46.44	Ravali *et al.* (2017)
	18 genotypes	Moderate 18.86	Moderate 16.03	High 72.27	1.71	27.33	Tirkey *et al.* (2018)

2.1.11 Total soluble solid

Crop	Materials used for the study	Variation		Heritability	GA	GAM	Reference
		PCV	GCV				
Brinjal	7 parents & 21 hybrids	Moderate 16.97	Moderate 11.04	Low 14.89		14.75	Ansari *et al.* (2011)
	18 genotypes	Moderate 18.86	Moderate 16.03	High 72.27	1.54	28.08	Tirkey *et al.* (2018)

2.1.12 Anthocyanin

Crop	Materials used for the study	Variation		Heritability	GA	GAM	Reference
		PCV	GCV				
Brinjal	36 genotypes	High 68.32	High 68.16	High 160	Low 1.75	High 140.07	Rani *et al.*(2017)

2.1.13 Phenol content

Crop	Materials used for the study	Variation		Heritability	GA	GAM	Reference
		PCV	GCV				
	70 genotypes	High 33.33	High 32.54	High 95.3		High 61.40	Karak *et al.* (2012)
Brinjal	14 parents	High 23.21	High 23.05	High 98.67		High 47.18	Kumar *et al.* (2013)
	36 genotypes	High 60.07	High 61.23	High 96.24	High 150.09	High 121.40	Rashmika *et al.* (2015)
	55 genotypes	High 29.81	High 29.58	High 98		High 60.44	Pujer *et al.* (2017)
	36 genotypes	High 32.75	High 31.63	High 93	15.95		Rani *et al.* (2012)
	25 accessions	High 30.34	High 28.98	High 91.24	26.71	High 57.30	Ravali *et al.* (2017)

2.1.14 Yield per hectare

Crop	Materials used for the study	Variation		Heritability	GA	GAM	Reference
		PCV	GCV				
Brinjal	36 genotypes	High 61.23	High 60.07	High	Low 1.75	High 140.07	Rasmika *et al.* (2017)
Tomato	60 genotypes	High 32.29	High 24.21	High 96.24	High 150.09	High 121.40	Dar and Sharma (2011)

2.2 Character association

Correlation studies give the information on the nature and extent of association between any pairs of traits and help to bring the genetic up gradation in one trait by selecting other traits. Yield is the most important trait and polygenic in nature, influenced by several traits. Correlation among these traits gives an idea about the extent of association existing between yield and yield components. Basically there are three types of correlations i.e., phenotypic correlation, genotypic correlation and environmental correlation. Phenotypic correlation is the observable correlation between two variables and combination of both genotypic and environmental effects. And genotypic correlation is interrelationship between characters which may be derived from genetic linkage, from pleiotrophy, or from developmentally induced relationships between components that are indirectly the consequence of gene action.

Association among different characters of brinjal as reported by many reporters is discussed in bellow tables.

Character	Association	Correlated character	Reference
Plant height	Negative	Number of fruit per plant, fruit length, fruit weight, fruit yield per plant	Nair and Mehta (2007)
	Positive	Fruit yield per plant, Number of fruits per plant	
	Positive	Fruit yield per plant, Fruit length, Fruit weight	Muniappan *et al.* (2010)
	Negative	Fruit yield per plant	Chattopadhyay *et al.* (2011)
	Positive	Fruit diameter	Shekar *et al.* (2014)
	Positive	Yield per plant	Shende *et al.* (2014)
	Positive	Fruit yield	Ullah *et al.* (2014)
	Positive	Fruit weight and Fruit girth	Prabakaran *et al.* (2015)
	Negative	Number of primary branches	Kumar *et al.* (2016)
Number of primary branches per plant	Negative	Fruit yield per plant	Chattopadhyay *et al.* (2011)
	Positive	Total number of harvest, Number of fruit per plant, and Ascorbic acid content	Prabakaran *et al.* (2015)
	Negative	Primary branches per plant	Guptha *et al.* (2017)
	Negative	Fruit weight, Fruit girth	Tripathy *et al.* (2018)
	Positive	Yield per plant	
Calyx length	Positive	Fruit weight	Prabakaran (2015)
	Positive	Fruit weight	Kumar *et al.* (2016)
Days to first flower	Negative	Fruit yield per plant	Chattopadhyay *et al.* (2011)

	Positive	Fruit length	Danquah and Ofori (2012)
	Positive	Fruit length	Shekar *et al.* (2014)
	Positive	Fruit diameter, Fruit girth, Fruit length, Fruit weight, Phenol content	Prabakaran *et al.* (2015)
	Negative	Fruit yield per plant	
	Negative	Yield per plant	Samlindsujin *et al.* (2016)
Fruit diameter	Positive	Fruit yield	Ullah *et al.* (2014)
	Positive	Fruit girth, Fruit weight, Fruit yield per plant, phenol content	Prabakaran (2015)
	Positive	Yield per plant, Fruit girth, Fruit weight, total phenol content	Kumar *et al.* (2016)
	Negative	Fruit diameter	Nair and Mehta (2007)
	Positive	Fruit weight	
	Negative	Number of fruits per plant	
Fruit length	Positive	Mean fruit weight, Plant height	Muniappan *et al.* (2010)
	Positive	Fruit yield per plant	Chattopadhyay *et al.* (2011)
	Positive	Fruit weight	Shekar *et al.* (2014)
	Negative	Total number of harvest	Ullah *et al.* (2014)
	Negative	Fruit yield and Fruit diameter	
	Positive	Plant yield per plant	Prabakaran (2015)
	Positive	Yield per plant	Tripathy *et al.* (2018)
Fruit weight	Positive	Fruit yield per plant	Dharwad *et al.* (2009)
	Positive	Fruit yield per plant	Islam and Uddin (2009)
	Positive	Fruit yield per plant, Fruit length , Fruit diameter, Plant height	Muniappan *et al.* (2010)
	Positive	Fruit yield per plant	Chattopadhyay *et al.* (2011)
	Positive	Ascorbic acid content	Praneetha *et al.* (2011)
	Positive	Fruit diameter and Fruit length	Danquah and Ofori (2012)
	Negative	Number of fruit per plant	Tangamani and Jansirani (2012)
	Positive	Yield per ha and yield per plant	Reza *et al.* (2015)
	Positive	Fruit yield per plant	Shekar *et al.* (2014)
	Positive	Yield per plant	Shende *et al.* (2014)
	Positive	Fruit yield per plant, phenol content	Prabakaran (2015)
	Negative	Total number of harvest, Ascorbic acid content	
	Positive	Yield per plant and phenol content	Kumar *et al.* (2016)
	Negative	Ascorbic acid content	
	Positive	Yield per plant	Sujin *et al.* (2016)
	Positive	Fruit girth, Plant height	Guptha *et al.* (2017)
	Negative	Number of fruit per plant	
	Positive	Yield per plant	Samlindsujin *et al.* (2017)
	Positive	Yield per plant	Tripathy *et al.* (2018)
	Negative	Number of fruit per plant	
Number of fruit	Positive	yield per plant	Nair and Mehta (2007)

per plant	Positive	Fruit yield per plant	Islam and Uddin (2009)
	Positive	Fruit yield per plant	Muniappan *et al.* (2010)
	Positive	Fruit yield per plant	Chattopadhyay *et al.* (2011)
	Positive	Ascorbic acid content	Praneetha *et al.* (2011)
	Negative	Fruit weight	Karak *et al.* (2012)
	Positive	Fruit yield per plant, Fruit girth	Tangamani and Jansirani (2012)
	Positive	Total number of harvest and fruit yield per plant	Shekar *et al.* (2014)
	Positive	Yield per plant	Shende *et al.* (2014)
	Positive	Fruit yield per plant	Prabakaran (2015)
	Positive	Yield per plant	Sujin *et al.* (2016)
	Negative	Fruit weight	Kumar *et al.* (2016)
	Positive	Yield per plant	Sujin *et al.* (2017)
	Positive	Yield per plant	Tripathy *et al.* (2018)
	Positive	Number of fruits per plant, plant height Days to first harvest	Nair and Mehta (2007)
	Negative	Fruit weight, Number of fruits per plant	Dharwad *et al.* (2009)
	Positive	Plant height, Fruit girth, Calyx length, Number of fruit per plant, Fruit weight, Ascorbic acid And phenol content Fruit borer	Praneetha *et al.* (2011)
	Positive	Number of fruit per plant, Ascorbic acid content	Tangamani and Jansirani (2012)
	Negative	Fruit girth, Fruit weight, Days to first flowering	
	Positive	Number of fruit per plant, fruit weight, total number of harvest	Shekar *et al.* (2014)
	Negative	Ascorbic acid content	Prabakaran (2015)
	Negative	Phenol content	Rashmika *et al.* (2015)
	Positive	Yield per ha	
	Positive	Fruit girth, Fruit weight, Number of fruit per plant	Gupta *et al.* (2017)
Ascorbic acid	Negative	Fruit bore infestation	Praneetha *et al.* (2011)
	Positive	Fruit yield	Tangamani and Jansirani (2012)
	Positive	Total number of harvest	Prabakaran (2015)
	Negative	Fruit yield per plant	
	Negative	Fruit yield per plant	Kumar *et al.* (2016)
Total soluble solid	Positive	Yield per plant	Tripathy *et al.* (2018)
Phenol	Negative	Fruit borer infestation	Praneetha *et al.* (2011)
	Positive	Fruit yield per plant	Prabakaran (2015)
	Positive	Fruit yield per plant	Kumar *et al.* (2016)

2.3 Path coefficient analysis

Correlation and path coefficient analysis are most important biometrical technique used to determine the yield components and the characters which are positively correlated with yield are considerably important in selection during plant breeding program. Correlation coefficient shows the nature of association among the different traits but path analysis divides the correlation coefficient into measure of direct and indirect effects and it will gives the understanding of direct and indirect contribution of each characters towards the good breeding program for yield and other parameters.

The correlation co-efficient between yield and a particular yield component was the net result of direct effect of that attribute and indirect effect through other yield contributing traits and the total correlation between yield and component trait may be sometimes misleads because of over or under estimation. So direct selection based on character association may not be effective and it is necessary to partition the total correlation coefficient into direct effect and indirect effect. The path coefficient analysis was originally developed by Wright (1921), but the technique was first used in plant breeding by Dewey and Lu (1959).

Path coefficient analysis is a most important tool for partitioning the correlation coefficient into direct and indirect effects of independent variables on a dependent variable with the inclusion of more variables in correlation study. Their indirect association becomes more complex. Two characters may exhibit correlation just because they are correlated with the common third one, in such causes path coefficient gives an effective means of a critical examination and measure the relative importance of each factor. A detailed discussion of different earlier research works about the different traits and their effect on yield components were given hereunder

2.3.1 Plant height

Nair and Mehta (2007) studied on 20 brinjal genotypes and found that plant height had maximum negative and direct effect on yield per plant. Thangamani and Jansirani (2012) worked on 25 F1 hybrids and reported that plant height had a negative direct effect on yield. Shekar *et al.* (2014) were evaluated on 31 brinjal genotypes and found that plant height had a high negligible and negative effect on fruit yield per plant. Shende *et al.* (2014) were evaluated 15 F2 and 8 parents of brinjal and reported plant height to last harvest had a positive direct effect on fruit yield per plant. Ullah *et al.* (2014) studied on 15 brinjal

genotypes and reported that plant height had a direct negative effect on fruit yield. Prabakaran *et al.* (2015) were studied on 33 brinjal genotypes and found that plant height had a positive direct effect on fruit yield per plant. Samlindsujin *et al.* (2016) were studied on 60 genotypes of brinjal and reported that plant height had negative direct effect on yield. Reza *et al.* (2015) were evaluated 9 advanced cultivars of brinjal and found that plant height had a positive direct effect on total yield.

2.3.2 Number of primary branches per plant

Datta and Jana (2010) studied on 65 chilli genotypes and found that number of primary branches per plant had a positive direct effect on yield. Prabakaran *et al.* (2015) were studied on 33 brinjal genotypes and found that number of primary branches per plant had a positive direct effect on fruit yield per plant.

2.3.3 Calyx length

Thangamani and Jansirani (2012) studied on 25 brinjal genotypes and found that calyx length had a negative direct effect on yield.

2.3.4 Days to first flowering

Nair and Mehta (2007) studied on 20 brinjal genotypes and reported that Days to first flowering had direct and positive effect on yield per plant. Thangamani and Jansirani (2012) worked on 25 F1 hybrids of brinjal and reported that days to first flowering had negative direct effect on yield through number of fruit per plant. Shekar *et al.* (2014) were evaluated on 31 brinjal genotypes and found that days to first flowering recorded moderate negative and direct effect on fruit yield per plant.

2.3.5 Fruit diameter

Shekar *et al*. (2014) were evaluated on 31 brinjal genotypes and reported that fruit diameter had a positive direct effect on fruit yield per plant. Ullah *et al*. (2014) studied on 15 brinjal genotypes and reported that fruit diameter had a positive direct effect on fruit yield.

2.3.6 Fruit length

Nair and Mehta (2007) assessed 20 diverse genotypes of brinjal and found that fruit length had a direct and positive effect on yield per plant. Thangamani and Jansirani (2012) studied on 25 F1 hybrids and reviled that fruit length had a positive and direct effect on yield,

negative through number of fruits per plant and positive through number of branches per plant. Shekar *et al.* (2014) were studied on 31 brinjal genotypes and found that fruit length had a positive direct effect on fruit yield per plant. Shende *et al.* (2014) were assed 15 F2 and 8 parents of brinjal and reported that fruit length had a positive direct effect on fruit yield per plant. Ullah *et al.* (2014) studied on 15 brinjal genotypes and reported that fruit length had a positive direct effect on fruit yield. Prabakaran *et al.* (2015) were studied on 33 brinjal genotypes and reported that fruit length had a positive direct effect on fruit yield per plant. Tripathy *et al.* (2018) were evaluated 18 brinjal genotypes and found that fruit length exhibited high positive direct effect on plant height, primary branches per plant, number of fruits per cluster and TSS.

2.3.7 Fruit weight

Nair and Mehta (2007) assed 20 diverse brinjal genotypes and reported that fruit weight exhibited direct positive effect on yield per plant. Muniappan *et al.* (2010) studied on 34 brinjal genotypes and found that average fruit weight had high positive and direct effect on fruit yield per plant. Chattopadhyay *et al.* (2011) were studied on 35 brinjal genotypes and reported that fruit weight had a positive and direct effect on fruit yield per plant. Thangamani and Jansirani (2012) studied on 25 F1 brinjal hybrids and reported that fruit weight had negative direct effect on yield through number of fruits per plant. Shekar *et al.* (2014) were studied on 31 brinjal genotypes and found that average fruit weight had a high positive and direct effect on fruit yield per plant. Shende *et al.* (2014) were evaluated 15 F2 and 8 parents of brinjal and reported that fruit weight had a positive direct effect on fruit yield per plant. Prabakaran *et al.* (2015) were studied on 33 brinjal genotypes and found that fruit weight had a positive direct effect on fruit yield per plant. Reza *et al.* (2015) were evaluated 9 advanced cultivars of brinjal and found that plant height had a positive direct effect on total yield. Sujin *et al.* (2017) were evaluated on 60 genotypes of brinjal and reported that fruit weight had positive direct effect on yield.

2.3.8 Number of fruits per plant

Muniappan *et al.* (2010) evaluated 34 brinjal genotypes and reported that number of fruits per plant had a high positive effect on yield per plant. Chattopadhyay *et al.* (2011) studied on 35 brinjal genotypes and reported that number of fruits per plant had a highly positive and direct effect on fruit yield per plant. Thangamani And Jansirani (2012) assed 25 F1 brinjal genotypes and noticed that number of fruits per plant had high positive direct effect

on yield and which is indirectly influenced by number of branches per plant and fruit weight. Shekar *et al.* (2014) were studied on 31 brinjal genotypes and reported that number fruits per plant had a high positive and direct effect on fruit yield per plant. Shende *et al.* (2014) were evaluated 15 F2 and 8 parents of brinjal and found that number of fruits per plant had a positive direct effect on fruit yield per plant. Prabakaran *et al.* (2015) were evaluated on 33 brinjal genotypes and reported that number of fruits per plant had a positive direct effect on fruit yield per plant. Samlindsujin *et al.* (2017) were studied on 60 genotypes of brinjal and reported that number of fruits per plant had positive direct effect on yield. Guptha *et al.* (2017) were studied on 32 brinjal genotypes and reported that fruit yield per plant had positive direct effect on fruit weight and fruits per plant, and negative direct effect on fruit girth and plant height.

2.3.9 Ascorbic acid content

Thangamani and Jansirani (2012) studied on 25 F1 brinjal genotypes and reported that ascorbic acid content had a positive and direct effect on yield indirectly by number of fruit per plant.

2.3.10 Total soluble solid

Tripathy *et al*. (2018) studied on 18 brinjal genotypes and reported that Total soluble solid content had a positive and direct effect on fruit yield per plant.

2.3.11 Phenol content

Thangamani and Jansirani (2012) assed on 25 F1 brinjal genotypes and reported that phenol content had a negative and direct effect on yield. Karak *et al.* (2012) assed on 70 brinjal genotypes and reported that phenol content had a negative and direct effect on yield.

2.4 Genetic divergence

Genetic diversity arises mainly by geographical separation or by genetic crossing barriers. Variability and diversity differs like observable phenotypic difference and later may or may not have such expressions. To estimate the genetic diversity D^2 static proposed by mahalanobis (it is based on multivariant analysis) is found to be best. Important information on evaluation of genetic diversity is must to get know the source of genes for the particular traits among the available germplasm and the multivariant analysis will helps to quantify the degree of divergence between the biological populations at genotypic level and to assess the

relative contribution of different components to total divergence at both intra and inter cluster levels. Higher the inter cluster distance indicated grater genetic divergence between the genotypes of the cluster and lower inter cluster indicates genotypes of the cluster not much genetically diverse from each other and cluster means for different traits proves considerable difference between the clusters. Selection of one or two genotypes from the clusters which are having maximum statistical distance for yield, earliness, resistance and quality parameters will give fruitful results. Genetic diversity and variability act as a best tool for improving genetic makeup of any crop and it is a one of the criteria of selection of parents for crossing and for isolation of transgressive sergeants from hybrids in further filial generations. Some earlier research findings with extract were represented hereunder.

Quamruzzaman *et al.* (2009) were studied genetic divergence among 19 brinjal genotypes (divided into 5 clusters) using Mahalanobis's D^2 statistic. Cluster I had a highest number of genotypes (7) and cluster IV and V had the lowest (2). The highest intra-cluster distance was found in cluster V (1.067) and the lowest in cluster III (0.916). Inter-cluster distance was highest between cluster IV and V (10.748). Cluster V recorded the highest mean for plant height at last harvest (cm), leaf blade length (cm), leaf blade diameter (cm), leaf pedicel length (cm), fruit pedicel length (cm), prickle on calyx. Whereas, number of branches per plant, fruit diametre (cm), individual fruit weight (g), fruit yield (t/ha) and prickle on fruit pedicel were in cluster II.

Begum *et al.* (2013) were studied morphological diversity in 92 brinjal genotypes (divided into 10 clusters) for 21 characters using Mahalanobis's D^2 statistics. And they found that cluster VIII contains 7 genotypes with highest intra-cluster distance (2.13), and the lowest intra-cluster distance (1.18) was observed in cluster IV which had 4 genotypes in it. Highest number of genotypes was in cluster X (17), cluster II and III had minimum number (3) of genotypes. The highest inter-cluster distance was found between cluster II and VIII (30.86), where lowest inter-cluster distance was between the clusters V and X (3.72). Cluster II constitute 3 genotypes and produced the highest mean value for number of flowers per inflorescence (4.67) and yield per plant (812.33) and the lowest mean value days to 1st flowering (108.22). Cluster IV constitute 3 genotypes namely EP-080, EP-081, EP-089 and produced fruits for longer duration (82.33). Cluster VIII constitute 7 genotypes and showed the lowest mean value for number of infected shoots per plant (1.57). Cluster X established with 17 genotypes produced the lowest mean value for number of infected fruit per plant (8.26).

Das and Das (2013) were studied on 26 brinjal genotypes for 8 characters and they are grouped into 11 clusters based on D^2 values. Cluster I and V had maximum genotypes (4). And all other Cluster had 2 genotypes except cluster XI had 1genotype respectively. The inter cluster distances were higher than the average intra cluster distances, which indicated wide genetic diversity among the genotypes of different groups than those of same cluster. On the basis of the cluster means the important cluster was cluster IV for fruit circumstances, average fruit weight, marketable yield plot-1 and total yield plot-1.

Kumar *et al.* (2013) were studied genetic divergence in 14 brinjal genotypes using Mahalanobis's D^2 statistic, and divided into six clusters. And they found that cluster III had a maximum number of genotypes (5) with intra cluster distance of 2 597.79. Cluster II and cluster V had a maximum inter cluster distance between them. The characters of yield per plant, fruit circumference, little leaf incidence and total phenols content contributed more for genetic divergence.

Shekar *et al.* (2014) were conducted experiment on 31 brinjal genotypes in kharif season to evaluate yield and its component characters and all the thirty one genotypes of brinjal were grouped in to six clusters using Ward's method by adopting Mahalanobis D^2 (1936) analysis concept. The maximum contribution towards total genetic divergence was from average fruit length. Intra cluster distance was maximum between cluster I and V. Intra cluster distance was maximum between III and V.

Ullah *et al*. (2014) were studied on brinjal to determine the genetic variability existed for six yield contributed traits. Cluster analysis grouped genotypes in three clusters; selection from the genotypes belong to cluster 1 showed high genetic diversity for leaf length, leaf width and fruit diameter. PC3 showed maximum diversity for fruit yield.

Gupta *et al.* (2015) were studied genetic divergence among the 46 genotypes of brinjal (divided into seven different non over lapping clusters) was carried out using Mahalanobis D^2 statistics. Cluster III had highest number of genotypes (26) followed by cluster I (11), cluster II (5) while, rest of the four clusters were monogenotypic. The intra cluster D^2 values ranged from 0.00 (monogenotypic clusters IV, V, VI, VII) to 119.78 (cluster I). The maximum inter-cluster distance (178.89) was observed between clusters (NDB-51) to VII (NDB 36).The inter cluster values between cluster II and cluster VII (156.95), cluster IV to VII (125.00), cluster I to VII (108.47), cluster II to V (96.22), cluster III to VI (93.20) were also very high. Cluster IV showed maximum mean values for the flower per inflorescence and earliest mean values

for days to 50% flowering, cluster V showed maximum mean values for the fruit weight, fruit circumference, fruit per plant, marketable fruit yield per plant, unmarketable fruit yield per plant and total fruit yield per plant. Cluster VI showed maximum mean values for the plant height and primary branch. Cluster VII exhibited maximum mean values for the polar length of fruit. Among the eleven quantitative traits fruit circumference (cm) contributed maximum (34.59%) towards total genetic divergence in the genotypes.

Madhavi *et al.* (2015) reported that genetic divergence among 21 genotypes of egg plant (*Solanum melongena L.*) estimated using Mahalanobis's D^2 statistics. Cluster V (Punjab Nagini, Pusa Shyamal and Azad B-3) exhibited highest cluster mean for plant height at 50% flowering (51.67 cm), fruit length (20.33 cm), number of fruits per plant (31.82), number of pickings (6.00) and fruit yield per plant (1.57 kg). Fruit weight (31.90%), number of pickings and fruit yield per plant (14.29%), leaf area and fruit volume (12.86%), number of fruits per plant (4.76%), plant height at last picking (4.29%) and dry matter content (1.90%) had the highest contribution towards total divergence.

Prabakaran *et al*. (2015) were conducted experiment on 33 land races of brinjal (*Solanum melongena L.*) and they grouped it into 3 clusters. The maximum inter-cluster distance was between clusters I and cluster III. The Fruit yield per plant, total phenol content, fruit width, ascorbic acid content, fruit circumference, number of long styled flowers per plant and days to first flowering contributed most of the genetic divergence. Local genotypes EP 11, EP 17, EP 20, EP 23, EP 27, EP 29, and EP 30 were found superior on the basis of inter-cluster distance and cluster mean values.

Sadarunnisa *et al*. (2015) Were studied genetic divergence in 27 round fruited brinjal type for various biometric characters based on D^2 values, and they were grouped into five clusters. Cluster I had the maximum number of accessions (20) followed by cluster IV (3). Cluster III had 3 accessions while clusters II and V had only 1 accession each. Between clusters II and V had a maximum inter cluster distance (D=5911.80). Maximum intra cluster distance was found in cluster IV (D = 1266.45).

Sadarunnisa *et al.* (2015) were studied on genetic divergence in 50 brinjal genotypes for 16 characters using Mahalanobis D^2 statistic, and the genotypes were divided into eight clusters on the basis of relative magnitude of D^2 values. And they found that among the 8 clusters, cluster IV was the largest with 17 genotypes. Cluster VI and cluster I had a maximum and minimum intra cluster distance respectively. Maximum inter cluster D^2 values

were between the cluster VI and VII while the minimum inter cluster distance was found between cluster I and II. Cluster VII had the highest mean values for most of the traits. The characters like average fruit weight, days to last harvest and bacterial wilt incidence contributed maximum to genetic divergence.

Bashar *et al,* (2016) were studied genetic divergence among 21 brinjal genotypes was assessed for a number of agro-morphological traits. Based on D^2 statistics these genotypes were grouped into 5 distinct clusters. Genotype belongs to cluster I and cluster V had a highest inter-cluster distance (72.15). Genotypes of cluster V had a highest intra-cluster distance (4.97). Highest cluster mean for different yield and yield contributing traits was found in cluster I which contains a solitary genotype (Sada Begun) followed by cluster IV. As important contributor towards genetic divergence the character yield/plant (g) (48.10%), fruit stalk length (cm) (11.90%), fruit length (cm) (11.43%), harvesting period (10.95%), fruit circumference (cm) (10.00%), fresh weight/fruit (g) (4.76%) and fruits/plant (2.86 %), can be considered as authentic as well as desirable traits.

Kumar *et al*. (2016) were studied on Genetic divergence of 33 brinjal genotypes which were divided into 10 clusters. And they found that cluster I contained the most genotypes (15) followed by cluster IX (5) and the minimum number of genotypes were in clusters II, V, VII and X. Inter mating between genotypes of clusters I and IX would produce more desirable transgressive segregates for breeding.

Mangi *et al.* (2016) were studied genetic divergence among 60 brinjal genotypes (grouped into 7 clusters) using Mahalanobis D^2 statistic. The maximum number of genotypes (36) was found in cluster I with intra-cluster distance of 20.79 and the maximum inter-cluster distance was observed in between cluster III and cluster VII. The characters of average fruit weight (52.32%), number of fruits per cluster (14.52%), plant spread at 60 DAT (13.90%) and plant height at 60 DAT (10.62%) contributed more for genetic divergence.

Samlindsujin and Karuppaiah (2016) were studied genetic divergence with 60 brinjal genotypes for 16 characters. And these genotypes were grouped into five clusters irrespective of geographic divergence, indicating no parallelism between geographic and genetic diversity. Cluster V was the largest cluster comprised of 43 genotypes followed by cluster I which consisted of eleven genotypes. Cluster II, III and IV consisted of two genotypes each. As regard to cluster means, cluster V and II performed better in most of the biometric characters studied. The maximum inter-cluster distance was observed in cluster III and V.

The intra cluster distance was the maximum in cluster V followed by cluster I and cluster IV. Cluster II had the least intra cluster distance

Ravali, *et al.* (2017) were studied Genetic divergence among 35 genotypes (divided into 10 clusters) of brinjal for 19 characters by using Mahalanobis D^2 statistics. And they found that the cluster V had maximum number of genotypes (10), followed by II and IV having 6 and 4 genotypes respectively. The intra-cluster D2 value ranged from 21.71 to 52.61 while, inter cluster D^2 value ranged from 39.09 to 103.59. Intra cluster distance was maximum in cluster II followed by cluster V and cluster X. The maximum inter-cluster D2 value was observed between VIII and IX. Maximum contribution towards the total divergence was exhibited by fruit yield per plant (30.57%) followed by average fruit weight (29.90%) and ascorbic acid content (15.51%). Noteworthy is that cluster VIII and X reflected high cluster means for fruit yield per plant, average fruit weight, number of fruits per plant.

Yadav *et al.* (2017) were studied on genetic divergence in 40 brinjal (*Solanum melongena L.*) genotypes to study the diversity based on qualitative and quantitative characters. Using D^2 values, the accessions were divided into seven clusters. And they found that cluster II showed a minimum intra-cluster value of 3.793, while the cluster I showed maximum intra-cluster D^2 value (4.681). The minimum inter-cluster D^2 value was observed between cluster III and IV (4.657), the maximum inter-cluster value was observed between cluster V and II (7.174).

Nand *et al.* (2018) studied on genetic divergence in 30 brinjal genotypes using Mahalanobis D^2 Statistics. Intra-cluster distance was highest in cluster I (1250.024) followed by cluster II (1217.052) lowest in cluster-V (389.277). Inter-cluster distance was highest between cluster IV and V (6815.521) and lowest between cluster III and IV (1149.46). The highest contribution in manifestation of genetic divergence was exhibited by days to first flowering; followed by days to 50 % flowering, fruit set percentage and fruit girth. Except number of primary branches cluster III shows moderate mean values for all the characters. For number of primary branches and fruit set percentage cluster II had a highest mean values. For number of fruits per plant Cluster I showed higher mean values, for plant height and fruit yield per plant Cluster IV showed higher mean values, for fruit length, petiole length and test weight Cluster V showed higher mean values, for fruit weight, plant spread, days to first flowering, days to 50 % flowering, fruit girth, days to first harvest cluster VI had higher mean values.

3. Materials and Methods

Materials and Methods

The present study on "Evaluation of brinjal germplasm for winter season" was undertaken to study the genetic divergence, variability and potentiality of the 32 brinjal genotypes collected from different locations of North Bengal region. The details of the materials used and methods adopted during the course of investigations are discussed here under.

3.1 Location of the experiment

Two experiments were conducted at the Experimental Farm of Uttar Banga Krishi Viswavidyalaya, Pundibari, Cooch Behar, West Bengal, India during 2016-17 and 2017-18. Geographically the farm is situated at 26 ^{0}19'86" N latitude and 89^{0} 23'53" E longitude, at an elevation of 43 meter above mean sea level. The area lies under the terai agro climatic zone of West Bengal.

3.1.1 Soil characteristics

The topography of the experimental site was medium high in situation. The soil is sandy loam in nature, coarse in texture, poor in water holding capacity with low pH (5.5). In both years the composite soil samples from the entire experimental field were collected and analyzed before transplanting the crop. The average physicochemical properties of the experimental soil (0-15 cm depth) are presented in Table 1.

Table 1: Physico-chemical properties of experimental soil.

Particulars	**1st year**	**2nd year**
Sand (%)	64.25	65.71
Sand (%)	20.15	19.48
Clay (%)	15.60	14.81
pH	5.65	5.55
Organic carbon (%)	0.914	0.925
Available nitrogen (kg per ha)	135.25	132.57
Available phosphorus (kg per ha)	45.72	43.57
Available potassium (kg per ha)	56.87	60.05

3.1.2 Agro-climatic conditions

The climatic condition of terai zone is sub-tropical humid in nature characterized by high rainfall, high relative humidity, moderate temperature, prolonged winter with high residual soil moisture. The meteorological data recorded during the course of study have been presented in Table 2.

Table 2: Meteorological parameters during the period of field experiment

Month	Year	Rainfall (mm)	Temperature (°C)		Relative humidity (%)	
			Maximum	Minimum	Maximum	Minimum
November	2016	0.0	31.33	16.52	75.00	69.00
December	2016	0.0	28.32	12.30	80.00	70.00
January	2017	0.0	26.28	9.66	97.00	47.00
February	2017	0.0	27.70	12.10	97.00	49.00
March	2017	67.70	28.40	15.30	93.00	53.00
April	2017	10.80	21.68	80.47	73.66	10.80
November	2017	0.0	29.51	15.69	94.83	55.41
December	2017	0.0	26.94	12.78	97.25	55.42
January	2018	0.0	21.84	9.25	94.94	60.42
February	2018	0.14	26.18	12.57	84.11	52.79
March	2018	0.29	30.04	16.09	72.05	47.09
April	2018	177.70	20.00	90.00	90.00	65.00
Y_1: 2016-17, Y_2: 2017-18						
Source: GKMS Project, AMFU-Pundibari, UBKV						

3.2 Experimental details

3.2.1 Experimental material

The experimental material consisted of 32 genotypes of brinjal considering the variety Pusa Purple Long (released from IARI, New Delhi and collected from local reputed distributor) as check. The collected germplasm and their sources have been given hereunder in table 3.

Table 3. Different collected brinjal germplasm and their sources

Sl No	Accession	Variety/cultivar	Collection area/Source
1	UBB 1	Long and thick brinjal	Pundibari
2	UBB 2	Kabra Gol	Maldha
3	UBB 3	Phasidewa local 2	Pundibari
4	UBB 4	Ashpuri Ghia Brinjal	Malda
5	UBB 5	Long Brinjal	Pundibari
6	UBB 6	Chanda Tara Brinjal	Malda
7	UBB 7	Long Golden Brinjal	Dinhata
8	UBB 8	Mukhta Brinjal Green	Malda
9	UBB 9	Aspuri Changa Brinjal	Malda
10	UBB 10	Panjipara Local	Khoribari
11	UBB 11	Phasidewa local 1	Malda
12	UBB 12	Muktakeshi	Nadia
13	UBB 13	Jhosna Brinjal	Malda
14	UBB 14	Long Black	Pundibari
15	UBB 15	Hajipur Bhasta Brinjal	Malda
16	UBB 16	Debjhuri Hajari	Malda
17	UBB 17	Black Beauty	Nadia
18	UBB 18	Kokila	Alipurduar
19	UBB 19	Pusa Purple Long	IARI, New Delhi
20	UBB 20	Ram Begun	Malda
21	UBB 21	Nababganj	North 24 Pargana
22	UBB 22	Pundibari 2	Pundibari
23	UBB 23	Jhuri Begun	Pundibari
24	UBB 24	Thick Brinjal	Pundibari
25	UBB 25	Tufanganj 1	Tufanganj
26	UBB 26	Special Mukra	Nadia
27	UBB 27	Shitali	Jateswar
28	UBB 28	White Brinjal	Pudibari
29	UBB 29	Swarna Mani	Dept. VSC, UBKV
30	UBB 30	Pusa Kranthi	Dept. VSC, UBKV
31	UBB 31	Punjab Sadabahar	Dept. VSC, UBKV
32	UBB 32	KasiTaru	Dept. VSC, UBKV

3.2.2 Layout of the experiment

The entire germplasm of brinjal was laid out in a Randomized Block Design with 3 replications. Randomization was followed in each replication.

3.2.3 Details of Layout

Crop	: Brinjal
Title	: Evaluation of Brinjal germplasm for winter season
Crop period	: Rabi season
Number of treatments	: 32 Brinjal genotypes
Experimental design	: RCBD
Replications	: 3
Spacing	: 75 x 75 cm
Plot size	: 3m x 3m
Sampling	: 5 randomly selected plant from per replication
Year of Study	: 2016-2017 & 2017-18
Location	: Horticultural research farm, UBKV, Pundibari

3.3 Cultural practices

Generally all the 32 brinjal genotypes were grown in the main field maintaining the replication and package of practice followed for the cultivation is given hereunder

3.3.1 Characteristics of the soil

The soil of the experimental field was from Teesta alluvial plain group which is sandy loam in texture with poor water holding capacity and moderate fertility status. The pH value was acidic in nature.

3.3.2 Nursery raising

Brinjal seedlings were raise on raised nursery beds of 10 m x 1 m x 15 cm with 15 kg of well decomposed farmyard manure (FYM) and 500 g of 10:20:20 NPK complex fertilizer, well mixed thoroughly in each bed. The seeds of the 32 brinjal genotypes were sown in rows spaced at 15 cm apart.

3.4.3 Land preparation

The soil was ploughed and harrowed to fine tilth. The experimental area was divided into plots of 3 m x 3 m size. Soil was mixed with well decomposed farmyard manure @ 25 t ha-1 uniformly as basal application. Standard cultural practices were followed during the entire crop period.

3.4.4 Planting

Seedlings of 40 days old were transplanted at a spacing of 75 cm x 75 cm on sides of the ridges in each replication. At the time of planting spacing of 30 cm was left from the borders of the plot. A light irrigation was given immediately after planting.

3.3.5 Manures and Fertilizers

A recommended dosage of N, P and K at 120: 90: 80 kg/ha was applied in the form of urea, single super phosphate and murate of potash to each plot respectively. The entire dose of phosphorus, potash and 1/3 rd of nitrogen were applied at the time of planting as basal dose. DAP (Diammonium phosphate) was applied as split dose at 30 days after transplanting. Vermicompost was also applied along with DAP at 30 days after planting. The remaining 2/3 rd nitrogen was applied in two split doses at 30 and 60 days after planting.

3.3.6 Weeding and Irrigation

The experimental site was kept free from weeds by periodical hand weeding. Irrigation was given at regular interval of 7-8 days depending on the soil moisture condition.

3.3.7 Plant protection

Timely and need based plant protection measures were taken up to protect the plants free from incidence of pest and diseases. For the control shoot and fruit bore incidence application of Carbaryl 50% @ 0.3 per cent and Chlorantraniliprole 18.5% w/w @ 0.05 per cent sprays were taken up. Spray formulation of COC (Copper Oxy Chloride) 50% WP @ 0.3 per cent was applied to control wilt and Phomopsis blight.

PLATE 1: Field operations and quality analysis conducted during the experiment.

3.4 Observations recorded

The following observations on various characters were recorded for each genotype from five randomly selected plants in each replication leaving the border plants and the average of the five values from per replication was computed for analysis.

3.4.1 Morphological characters

The description regarding growth habit, leaf blade spinyness, calyx colour, fruit calyx spinyness and surface colour was given according to descriptors of IBPGR, Rome while fruit shape was described as per NBPGR and are presented in Appendix.

3.4.1.1Plant growth habit

The plant growth of the genotype was noted as upright, intermediate, and prostrate.

3.4.1.2 Leaf blade spinyness

The leaf blade spinyness of genotypes was noted as 0-none, 1-very few (1-2), 3-few (3-5), 5-intermediate (6-10), 7-many (11-20) and 9-very many (>20).

3.4.1.3 Bearing habit

Bearing habit of genotypes was noted as Cluster bearing or solitary bearing

3.4.1.4 Calyx colour

Calyx colour of the genotypes was noted as 1-light green, 3-dark green, 5-light purple and 7-dark purple.

3.4.1.5 Fruit shape

Fruit shape of the genotypes was noted as round, oblong, oval and long.

3.4.1.6 Fruit calyx spinyness

The fruit calyx spinyness of genotypes was noted as 0-none, 1-very few (<3), 3-few (5), 5-intermediate (10), 7-many (20) and 9-very many (>30).

3.4.1.7 Fruit colour

Fruit colour of the genotypes was noted as 1 green, 2-milkkwhite, 3-deep yellow, 4-fire red, 5-scarlet red, 6-lilac grey, 7-purple, 8-purple black and 9-black.

3.4.2 QUANTITATIVE PARAMETERS

3.4.2.1 Plant height (cm)

Plant height was measured from collar region to the emerging leaf at the main stem at the time of the last harvest and expressed in centimeter (cm).

3.4.2.2 Number of primary branches

The number of branches arising from the main stem above the ground level at final harvest was counted and expressed as number.

3.4.2.3 Calyx length (cm)

Calyx length was measured individually with the help of a measuring tape from the base of calyx to tip of calyx of five fruits and average was recorded in centimetres (cm).

3.4.2.4 Days to first flowering

The number of days taken for the flower opening was recorded from the date of transplanting to the first flower opening.

3.4.2.5 Days to fruit maturity

The number of days required to obtain harvestable maturity from the anthesis was recorded.

3.4.2.6 Fruiting span

The number of days taken for the first flowering to final harvest was calculated.

3.4.2.7 Fruit diameter (cm)

Fruit diameter was measured from the matured full sized fruit and data were collected after cutting horizontally into half and expressed in centimeter (cm).

3.4.2.8 Fruit length (cm)

Length of the fruit at horticultural maturity was measured individually with the help of a measuring scale from the base to the tip of five fruits and the average was recorded in centimetres (cm).

3.4.2.9 Fruit weight (g)

Five mature and healthy fruits were randomly taken from selected plants for each treatment and weighed individually and average was recorded in grams (g).

3.4.2.10 Number of fruits per plant

The number of fruits harvested per plant for each treatment during the harvesting period was recorded and average was worked out.

3.4.2.11 Yield per ha (t/ha)

The estimated average yield per ha was recorded throughout the harvesting period based on the yield and expressed in tonnes per hectare.

3.4.3 Qualitative characters

Different pigments and proximate compositions were estimated in the PG laboratory of the Department of Vegetable and Spice Crops, Faculty of Horticulture, Uttar Banga Krishi Viswavidyalaya, Pundibari, Coochbehar.

3.4.3.1 Anthocyanin content (mg/100g)

Composite pulp of 10 randomly sampled ripe fruits per replication from both parental lines were used to estimate total anthocyanin content in the fresh fruits following standard biochemical methods (Rangana, 1997).

Reagents required

- Methanol
- Carbinol 85%
- 15 % conc. HCL

Procedure:

1 g sample + 10 ml reagent.

⬇

Dipped for one day under cover

⬇

If need for further dilution sample + 4 ml reagent

⬇

Reading from spectrophotometer (535 nm)

Calculation:

Formula:

Total OD/100g = (OD x volume made up x 100/wt of sample) x dilution factor

Anthocyanin content content in sample (mg/100g) = (Total OD/100g)/98.2

Dilution factor = 10/1 x 5/1

3.4.3.2 Ascorbic acid content (mg/100 g)

Composite pulp of 10 randomly sampled ripe fruits per replication from both parental lines were used to estimate ascorbic acid content in the fresh fruits following standard biochemical methods (AOAC, 1990)

Materials

- Metaphosphoric acid 3% (30g/l of distilled water)
- Dye solution: 42 mg Sodium bicarbonate was taken into a small volume of distilled water and 52 mg of 2, 6-dichlorophenol indophenol was dissolved in it. Volume was made upto 200 ml with distilled water.
- Stock standard solution : 100 mg ascorbic acid was dissolved in 100 ml of 3% metaphosphoric acid solution in a standard flask (1mg/ml)
- Working Standard: 10 ml of the stock solution was diluted to 100 ml with 3% metaphosphoric acid.

Procedure

- 5 ml of the working standard solution was pipetted out into a 100 ml conical flask.
- 10 ml metaphosphoric acid was added in it and titrated against the dye solution (V_1ml). End point was the appearance of pink colour which persists for a few minutes. The amount of the dye consumed was equivalent to the amount of ascorbic acid.
- 5g of fruit sample was crushed and extracted in 3% metaphosphoric acid. Volume was made upto 100ml and centrifuged for 20 minutes
- 5 ml of this supernatant was pipetted out and added into the 10 ml of 3% metaphosphoric acid.
- It was titrated against the dye (V_2 ml)

Calculation

$$\text{Amount of ascorbic acid mg/100 g sample} = \frac{0.5 \text{ mg}}{V_1 \text{ ml}} \times \frac{V_2}{5 \text{ ml}} \times \frac{100 \text{ ml}}{\text{Weight of the Sample}} \times 100$$

3.4.3.3 Total soluble solids (^{0} brix)

Mettler Toledo RE50 refractometer was used for the determination of the refractive index of of brinjal fruit samples based on total reflection method. Then data was converted to ^{0}brix from refractive index using the values provided by user manual (Anonymous, 2003) for better understanding of the results.

3.4.3.4 Phenol content (mg/100 g of fruit)

The concentration of total phenol content in plant extracts was determined spectrophotometrically (Singleton *et al.*, 1999).

Materials

i. 80% Ethanol
ii. Folin-Ciocalteau Reagent
iii. Na_2CO_3, 20%
iv. Gallic acid

Preparation of standard curve

- 1000 mg of gallic acid was mixed in 1L of distilled water to prepare the 1000ppm gallic acid stock solution.
- 0, 2, 4, 6, 8, 10ml from the stock gallic acid solution was taken and volume made up to 100ml with the distilled water to make the solution of 0, 20, 40, 60, 80, 100 ppm.
- 1ml from each was taken separately and added 2.9mldistilled water, 1ml of Folin-Ciocalteau reagent, 1ml 20% Na_2CO_3 and volume made up to 10 ml with the distilled water.
- The strength of the prepared solution became 0, 2, 4, 6, 8, 10 ppm.
- After colour development, the reading was taken in spectrophotometer at 760nm against the solution had strength of 0 ppm as reference.
- The value of spectrophotometer reading was plotted against the concentration to prepare a curve.

Concentration (ppm)	Absorbance (nm)
2	0.116
4	0.231
6	0.347
8	0.463
10	0.578

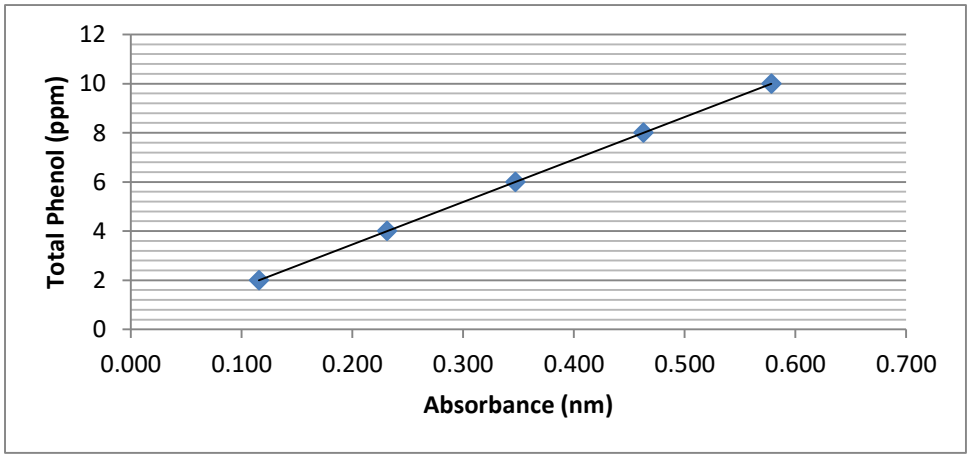


Figure 1. Standard curve for estimation of total phenol

Sample reading

- Weight exactly 2g of sample and grind it with a pastle and morter in 10 times volume of 80% Ethanol.
- Take 100 µl of sample and mix 2.9 ml of distilled water, 0.5 ml of Folin-Ciocalteau reagent and 20% Na_2CO_3.
- The mixture was then allowed to stand for 90min and absorption was measured against the reagent blank in UV-VIS spectrophotometer at 760nm.
- **Calculation**

Total phenol content was calculated by using standard curve and expressed as mg per 100g.

3.5 Statistical methodology

The data obtained in respect of all the characters have been subjected to the following statistical analysis.

3.5.1 Analysis of variance

Analysis of variance was carried out as per the procedure given by Panse and Sukhatme (1967) using the mean values of random plants in each replication from all treatments to find out the significance of treatment effects.

The analysis of variance for each character was carried out as indicated below:

Sources of variation	Df	SS	MSS	F ratio
Replications	r-1	RSS	RMSS	RMSS/EMSS
Treatments	t-1	trSS	TrMSS	TrMSS/EMSS
Error	(r-1) (t-1)	ESS	EMSS	
Total	(rt-1)	TSS		

Where,

r = Number of replications

t = Number of genotypes or treatments

df = degrees of freedom

SS = sum of squares

MSS = Mean sum of squares

RSS = Replication Sum of squares

TrSS = Treatment sum of squares

ESS = Error sum of squares

TSS = Total sum of squares

RMSS = Mean sum of squares due to replications

TrMSS = Mean sum of squares due to treatments

EMSS = Mean sum of squares due to error

The test of significance was carried out by 'F' table values given by Fisher and Yates (1963).

3.5.2 Estimation of genetic parameters

The genetic parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense and genetic advance for different characters were worked out by following the standard procedures for all the genotypes under study.

3.5.2.1 Phenotypic and genotypic coefficient of variation

Genotypic and phenotypic coefficients of variance were estimated according to Burton and Devane (1953) based on estimate of genotypic and phenotypic variance.

$$\text{Genotypic coefficient of variance (GCV)} = \frac{\sqrt{\sigma_g^2}}{\bar{X}} x100$$

$$\text{Phenotypic coefficient of variance (PCV)} = \frac{\sqrt{\sigma_p^2}}{\bar{X}} x100$$

$$\text{Environmental coefficient of variance (ECV)} = \frac{\sqrt{\sigma_e^2}}{\bar{X}} x100$$

Where

$\overline{X}$ = General mean of the character

σ_g^2 = Genotypic variance $= \frac{\text{Treatment MSS - Error MSS}}{\text{r}}$

σ_e^2 = Environmental variance = Error mean sum of squares

σ_p^2 = Phenotypic variance $= \sigma_g^2 + \sigma_e^2$

Where, 'r' is number of replications.

Estimates of coefficient of variation has been classified as high (>20%), moderate (10-20%) and low (10%) as described by Nadarajan and Gunasekaran (2008).

3.5.2.2 Heritability

Heritability in broad sense was calculated as per formula given by Burton and Devane (1953) and Allard (1960).

Heritability (h^2) = $\frac{\sigma_g^2}{\sigma_p^2} \times 100$

Where

σ_g^2 = Genotypic variance

σ_p^2 = Phenotypic variance

Estimates of heritability has been classified into high (>60%), moderate (30-60%) and low (30%) as suggested by Nadarajan and Gunasekaran (2008).

3.5.2.3 Expected genetic advance

Expected genetic advance (GA) was worked out as suggested by Burton and Devane (1953) and Johnson *et al.* (1955).

Expected genetic advance (GA) = $h^2 \times \sigma_p \times K$

Where,

K = Selection intensity, the value of which is 2.06 at 5 % individual selection.

h^2 = Heritability in broad sense

σ_p = Phenotypic standard deviation

Genetic advance mean (GAM) in percent was worked out as

$$GAM = \frac{GA}{\bar{x}} \times 100$$

Where,

$\bar{x}$ = mean of the character.

The range of genetic advance as percent of mean was classified as high (>20%), moderate (10-20%) and low (10%) as mentioned by Nadarajan and Gunasekaran (2008).

3.5.3 Genotypic and phenotypic correlation coefficients

It is estimated to determine the association between various character pairs. Phenotypic (r_p) and genotypic (r_g) correlation coefficients of important quantitative traits were estimated as suggested by Al-Jibourie *et al*. (1958).

$$\text{Phenotypic correlation} = r_{xy}(p) = \frac{Cov_{xy}(P)}{\sqrt{V_x(P) \times V_y(P)}}$$

$$\text{Genotypic correlation} = r_{xy}(g) = \frac{Cov_{xy}(G)}{\sqrt{V_x(G) \times V_y(G)}}$$

Where,

$Cov_{xy}(G)$ = Genotypic covariance between x and y

$Cov_{xy}(P)$ = Phenotypic covariance between x and y

$V_x(G)$ = Genotypic variance of character ‘x’

$V_x(P)$ = Phenotypic variance of character ‘x’

$V_y(G)$ = Genotypic variance of character ‘y’

$V_y(P)$ = Phenotypic variance of character ‘y’

Test of significance

Significance of correlation coefficients was tested by comparing phenotypic correlation coefficients with the table values (Fisher and Yates, 1963) at (n-2) degrees of freedom at 5 % and 1 % level where 'n' denotes the total number of pairs of observations used in the calculation.

3.5.4 Path coefficient analysis

Path coefficient analysis was suggested by Wright (1921). To know the direct and indirect effects of the important quantitative traits path coefficient analysis was carried out following Dewey and Lu (1959).

$r_{1y} = P_{1y} + r_{12}P_{2y} + r_{13}P_{3y} + \text{----------} + r_1n\,P_{ny}$

$r_{2y} = P_{2y} + r_{21}P_{1y} + r_{23}P_{3y} + \text{----------} + r_2nP_{ny}$

.....

$r_{ny} = P_{ny} + r_n^1 P_{1y} + r_{n2}P_{2y} + \text{----------} + r_n(n\text{-}1)\,P_{ny}$

Where,

r_{1y} to r_{ny} = Denotes coefficient of correlation between causal factor 1 to n and dependent character Y.

r_{12} to r_n (n-1) = Denote coefficient of correlation between all possible combinations of causal factors

P_{1y} to P_{ny} = Denote effect of characters 1 to n on the characters Y.

The effect of residual factor (z) which measures the contribution of rest of the characters not considered in the casual scheme obtained as :

Where,

$$R^2 = \sum_{i=1}^{n} P_{1y} + 2\sum_{1>j}^{n} P_{ly}P_{jy}r_{ij}$$

R^2 is the coefficient of multiple determinations

The direct and indirect effects were rated according to Nadarajan and Gunasekaran (2008) as very high (>1.00), high (0.30-1.00), moderate (0.20-0.29), low (0.10-0.19) and negligible (0.00-0.09).

3.5.5 Genetic divergence

Mahalanobis (1936) D^2 statistics was used for assessing the genetic divergence between brinjal genotypes. The original correlated un standardised character mean values were transformed into standardised uncorrelated values to simplify the computational procedure. The D^2 values were obtained as the sum of squares of the differences between the pairs of corresponding uncorrelated (Ys) values of any two genotypes (Rao, 1952). A total of $\frac{n(n-1)}{2}$ D^2 values were calculated.

Where n = number of genotypes.

3.5.5.1 Clustering of genotypes

Using all D^2 values, the genotypes were grouped into clusters using Tocher's method as described by Rao (1952).

3.5.5.2 Inter and intra cluster distances

The intra- and inter-cluster distances were calculated by the formula given by Singh and Chaudhary (1985).

$$\text{Inter-cluster distance} = \sqrt{\frac{D_{ij}^2}{n_i n_j}}$$

Where D_{ij}^2 is the sum of distances between all possible combinations ($n_i n_j$) of the genotypes included in the clusters 'i' and 'j'.

n_i = number of genotypes in cluster 'i'

n_j = number of genotypes in cluster 'j'.

$$\text{Intra-cluster distance} = \sqrt{\frac{D_i^2}{n}}$$

Where D_i^2 is the sum of D^2 values between all possible combinations of the genotypes included in cluster 'i'.

Testing the significance of D^2 values

The D^2 value obtained for a pair of population was taken as calculated value of x2 and was tested against the tabulated value of x2 for P (15) degrees of freedom where P (15) is the number of characters considered.

Intra cluster distance

The average intra cluster distances were calculated by the formula given by Singh and Chaudhary (1977).

Square of intra cluster distance = $\sum D^2 i / n$

Where,

$\sum D^2 i$ = sum of distance between all possible combinations.

n = Number of all possible combinations

Inter cluster distance

The average inter cluster distances were calculated by the formula described by Singh and Chaudhary (1977).

Square of inter cluster distance = $\sum D^2 i / n_i\, n_j$

Where,

$\sum D^2 i$ = sum of distances between all possible combinations ($n_i\, n_j$) of the entries included in the cluster study.

N_i = Number of entries in cluster i

N_j = Number of entries in cluster j

3.5.5.6 Contribution of individual characters towards genetic divergence

The character contribution towards genetic divergence was computed using the method given by Singh and Chaudhary (1977). In all the combinations, each character was ranked on the basis of $di = y_i^j - y_i^k$ values.

Where,

D_i = mean deviation

y_i^j = mean value of the j^{th} genotype for the i^{th} character and

y_i^k = mean value of the k^{th} genotype for the i^{th} character.

Rank 'I' is given to the highest mean difference and rank 'P' is given to the lowest mean difference

Where, P is the total number of characters.

Finally, the number of times that each character appeared in the first rank was computed and per cent contribution of characters towards divergence was estimated using the formula Percent contribution of character $x = \frac{N \times 100}{M}$

N = Number of genotype combinations where the character was ranked first.

M = All possible combinations of number of genotypes considered.

3.5.5.7 Grouping of genotypes into various clusters by cluster analysis

Cluster analysis classifies a set of observations into two or more mutually exclusive unknown groups based on combinations of interval variables. In this agglomerative hierarchical clustering technique was followed. The method is agglomerative and hierarchical because the strategy starts from all the individuals as single member groups and forms a complete hierarchy joining single pairs of groups till the process is completed with all members in one group. It is the incremental sum of squares as the strategy fuses the pair of groups at each level of the hierarchy that increases the within group sum of squares the least.

4. Results and Discussion

Results and Discussion

A study entitled “Evaluation of brinjal germplasm for winter season” was carried out in 31 genotypes and one check variety of brinjal for total of 22 characters *i.e.,* 7 morphological characters, 11 quantitative characters 4 qualitative characters. The data was subjected to statistical analysis to get information on mean performance, variability, heritability, genetic advance as per cent of mean, correlation coefficient, path coefficient analysis, diversity. Results are presented under the following subheads and discussed appropriately in the light of recent literature.

4.1 Analysis of variance

4.2 Morphological characters of brinjal genotypes

4.3 Mean performance of genotypes

4.4 Variability, heritability and genetic advance

4.5 Character association analysis

4.6 Path coefficient analysis

4.7 Genetic divergence

4.1 Analysis of variance

The mean sum of squares for fifteen (15) characters in thirty one (31) genotypes and one check variety of brinjal was presented in table 4. Highly significant differences were observed among the genotypes for all the characters indicating presence of sufficient amount of variability in all the characters studied.

4.2 Morphological characters of brinjal genotypes

Morphological characters like plant growth habit, bearing habit, leaf blade spinyness, calyx colour, fruit shape, fruit calyx spinyness and fruit colour of all thirty two (32) accessions were represented in the table 5.

Table 4: Analysis of variance of pooled data (2016-17 and 2017-18) for different characters of Brinjal

Character	Mean sum of squares (d.f)		
	Genotypes (31)	Replication (2)	Error (62)
Plant height (cm)	775.471**	35.781	0.044
Number of primary branches	3.601**	0.065	0.0001
Calyx length (cm)	1.797**	0.078	0.0002
Days to first flower	114.906**	21.609	0.0333
Days to fruit maturity	93.432**	10.406	0.0073
Fruiting span	108.313**	11.531	0.0252
Fruit diameter (cm)	19.262**	1.787	0.0014
Fruit length(cm)	179.299**	1.578	0.0102
Fruit weight (g)	88432.53**	143.000	0.246
Number of fruit per plant	383.201**	6.497	0.0349
Ascorbic acid (mg/100g)	2.660**	0.076	0.0001
TSS (°B)	0.158**	0.043	0.0002
Phenol (mg/100g)	0.093**	0.039	0.0001
Anthocyanin (mg/100g)	7432.872**	17.594	0.1721
Yield ha^{-1} (t/ha)	244.439**	5.477	0.0071

**= Significant at 1% level, *= Significant at 5% level

4.2.1 Plant growth habit

All 32 genotypes of brinjal were categorized into three group viz., upright, intermediate and prostrate. Maximum genotypes (25) had intermediate growth habit which included UBB 1, UBB 4,UBB 5, UBB 6, UBB 7, UBB 8, UBB 9, UBB 10, UBB 11, UBB 12, UBB 13, UBB 14, UBB 15, UBB 16, UBB 17, UBB 18, UBB 19, UBB 20, UBB 21, UBB 22, UBB 23, UBB 28, UBB 29, UBB 30, UBB 31. Total six (6) genotype viz., UBB 2, UBB 3, UBB 24, UBB 25, UBB 27 and UBB 32 showed upright growth habit. The only genotype UBB 26 showed prostrate growth habit.

4.2.2 Leaf blade spinyness

The genotypes were categorized into two classes of which twenty nine (29) genotypes were noted as non spiny leaved genotypes viz., UBB 1, UBB2, UBB3, UBB 4,UBB 5, UBB 6, UBB 7, UBB 8, UBB 9, UBB 10, UBB 11, UBB 12, UBB 13, UBB 14, UBB 15, UBB 18, UBB 19, UBB 20, UBB 21, UBB 22, UBB 23, UBB 24, UBB 25, UBB26, UBB 27, UBB 29, UBB 30, UBB 31, UBB 32. Further, three genotypes viz., UBB 16, UBB 17 and UBB 28 had few spines on the leaves.

4.2.3 Fruit calyx spinyness

Data on fruit calyx spinyness was collected based on fruit calyx spinyness. Genotypes were classified into two groups where maximum genotypes i.e., twenty six (26) numbers of genotype had no spines on fruit calyx UBB 1, UBB2, UBB3, UBB 4, UBB 6, UBB 9, UBB 11, UBB 13, UBB 14, UBB 15, UBB16, UBB 18, UBB 19, UBB 20, UBB 21, UBB 22, UBB 23, UBB 24, UBB 25, UBB26, UBB 27, UBB28, UBB 29, UBB 30, UBB 31, UBB 32. Whereas, six genotypes viz., UBB 5, UBB 7, UBB 8, UBB10, UBB 12, UBB 17exhibited few spines on calyx.

4.2.4 Fruit shape

All 32 genotypes of brinjal were grouped into four groups depending on fruit shape. Maximum number of genotypes (15) produced Long shaped fruits that included UBB 1, UBB2, UBB3, UBB 5, UBB 7, UBB16, UBB 17,UBB 18, UBB 19, UBB 23, UBB 24, UBB 25, UBB 27, UBB 31, UBB 32. Total 8 number genotype exhibited by oblong fruits that constituted UBB 10, UBB 11, UBB 12, UBB 14, UBB 20, UBB 21, UBB 22, UBB 30. Round shaped fruit was recorded in six genotypes viz., UBB 4, UBB 6, UBB 9, UBB 13,

UBB 15, UBB 28. While, oval fruits were observed in three genotypes viz., UBB 8, UBB 26, UBB 29.

4.2.5 Fruit colour

Fruit colour was recorded based on fruit colour at commercial ripeness. Genotypes were classified into total four groups. Among all genotypes, twelve genotypes were purple in colour that constituted UBB 1, UBB2, UBB3, UBB 5, UBB 7, UBB10, UBB 16, UBB 18, UBB 23, UBB 24, UBB 25, and UBB 30. Eleven genotype were green fruited which include UBB 4, UBB 6, UBB 8, UBB 9, UBB 11, UBB 13, UBB 14, UBB 15, UBB 20, UBB 21, UBB 26. Purple black colour fruits were observed in seven genotypes viz., UBB 12, UBB 17, UBB 19, UBB 22, UBB 27, UBB 29, UBB 31, UBB 32 and one genotype registered Milk white colour fruits i.e. UBB 28.

4.2.6 Calyx colour

Maximum genotypes (31) had fruits with light green colour calyx which included UBB 1, UBB 2, UBB 3, UBB 4, UBB 5, UBB 6, UBB 7, UBB 8, UBB 9, UBB 10, UBB 11, UBB 12, UBB 13, UBB 14, UBB 15, UBB 16, UBB 17, UBB 18, UBB 19, UBB 20, UBB 21, UBB 22, UBB 23, UBB 24, UBB 25, UBB 26, UBB 27, UBB 28, UBB 30, UBB 31, UBB 32. Only one genotype i.e., UBB 29 showed light purple colour calyx.

4.2.7 Bearing Habit

Maximum genotypes had solitary bearing habit and the number of genotype was thirty (30) viz., UBB 1, UBB 2, UBB 3, UBB 4, UBB 5, UBB 6, UBB 7, UBB 8, UBB 9, UBB 10, UBB 11, UBB 12, UBB 13, UBB 14, UBB 15, UBB 17, UBB 18, UBB 19, UBB 20, UBB 21, UBB 22, UBB 24, UBB 25, UBB 26, UBB 27, UBB 28, UBB 29,UBB 30, UBB 31, UBB 32. Only two genotype i.e., UBB 16 and UBB 23 exhibited cluster bearing habit genotype.

Wide variation in morphological characters was observed in all the genotypes under study. Maximum genotypes had no spines on leaves (29 numbers of genotype) and fruit calyx (26numbers of genotype). 25 numbers of genotype were intermediate in growth habit. Maximum genotypes produced long type (15 numbers of genotype) and oblong type (8 numbers of genotype) fruit. In most genotype the fruit colour was purple (12 numbers of

Table 5: Morphological characters of thirty two genotypes

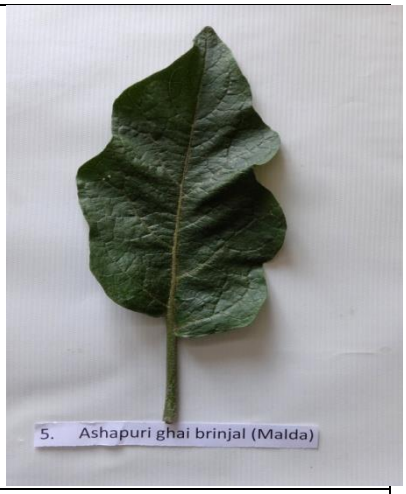
Genotype	Plant growth habit	Leaf blade spinyness	Fruit calyx spinyness	Fruit shape	Fruit colour	Calyx colour	Bearing habit
UBB 1	Intermediate	Absent	Absent	long	Purple	Green	Solitary
UBB 2	Upright	Absent	Absent	long	Purple	Green	Solitary
UBB 3	Upright	Absent	Absent	long	Purple	Green	Solitary
UBB 4	Intermediate	Absent	Absent	Round	Green	Green	Solitary
UBB 5	Intermediate	Absent	Low	long	Purple	Green	Solitary
UBB 6	Intermediate	Absent	Absent	Round	Green	Green	Solitary
UBB 7	Intermediate	Absent	Low	long	Purple	Green	Solitary
UBB8	Intermediate	Absent	Low	Oval	Green	Green	Solitary
UBB 9	Intermediate	Absent	Absent	Round	Green	Green	Solitary
UBB 10	Intermediate	Absent	Low	Oblong	Purple	Green	Solitary
UBB 11	Intermediate	Absent	Absent	Oblong	Green	Green	Solitary
UBB 12	Intermediate	Absent	Low	Oblong	Purple black	Green	Solitary
UBB 13	Intermediate	Absent	Absent	Round	Green	Green	Solitary
UBB 14	Intermediate	Absent	Absent	Oblong	Green	Green	Solitary
UBB 15	Intermediate	Absent	Absent	Round	Green	Green	Solitary
UBB 16	Intermediate	Low	Absent	long	Purple	Green	Cluster
UBB 17	Intermediate	Low	Low	long	Purple black	Green	Solitary
UBB 18	Intermediate	Absent	Absent	long	Purple	Green	Solitary
UBB 19	Intermediate	Absent	Absent	long	Purple black	Green	Solitary
UBB 20	Intermediate	Absent	Absent	Oblong	Green	Green	Solitary
UBB 21	Intermediate	Absent	Absent	Oblong	Green	Green	Solitary
UBB 22	Intermediate	Absent	Absent	Oblong	Purple black	Green	Solitary
UBB 23	Intermediate	Absent	Absent	long	Purple	Green	Cluster
UBB 24	Upright	Absent	Absent	long	Purple	Green	Solitary
UBB 25	Upright	Absent	Absent	long	Purple	Green	Solitary
UBB 26	Prostrate	Absent	Absent	Oval	Green	Green	Solitary
UBB 27	Upright	Absent	Absent	long	Purple black	Green	Solitary
UBB 28	Intermediate	Low	Absent	Round	Milk white	Green	Solitary
UBB 29	Intermediate	Absent	Absent	Oval	Purple black	Light purple	Solitary
UBB 30	Intermediate	Absent	Absent	Oblong	Purple	Green	Solitary
UBB 31	Intermediate	Absent	Absent	long	Purple black	Green	Solitary
UBB 32	Upright	Absent	Absent	long	Purple black	Green	Solitary


UBB 1


UBB 2


UBB 3

PLATE 2: Growth habit, fruit type and leaf shape of UBB 1, UBB 2 & UBB 3.

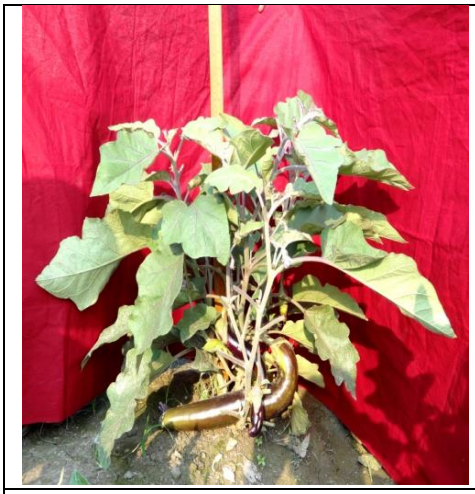


UBB 4

UBB 5

UBB 6

PLATE 3: Growth habit, fruit type and leaf shape of UBB 4, UBB 5 & UBB 6.

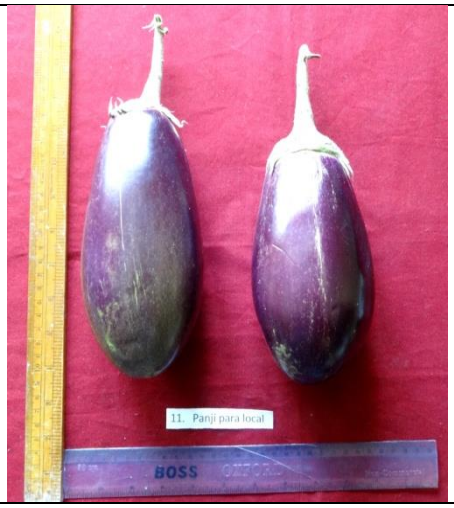



UBB 7


UBB 8

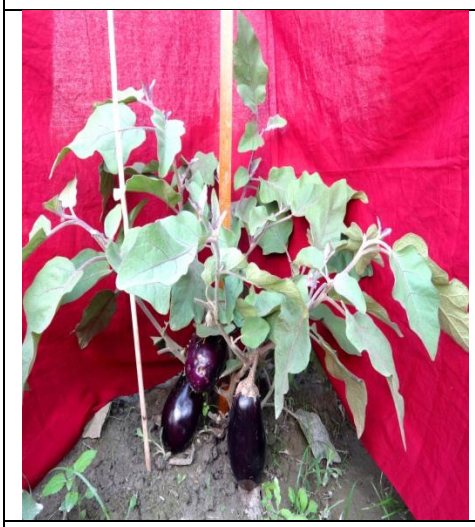

UBB 9

PLATE 4: Growth habit, fruit type and leaf shape of UBB 7, UBB 8 & UBB 9.

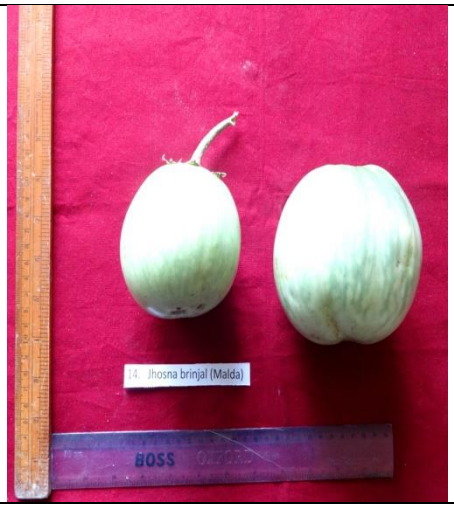
UBB 10


UBB 11

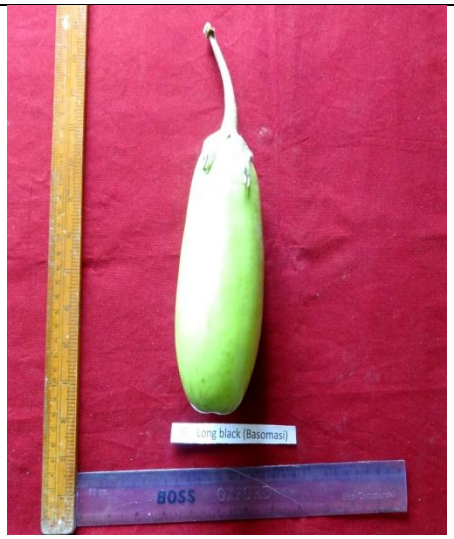


UBB 12

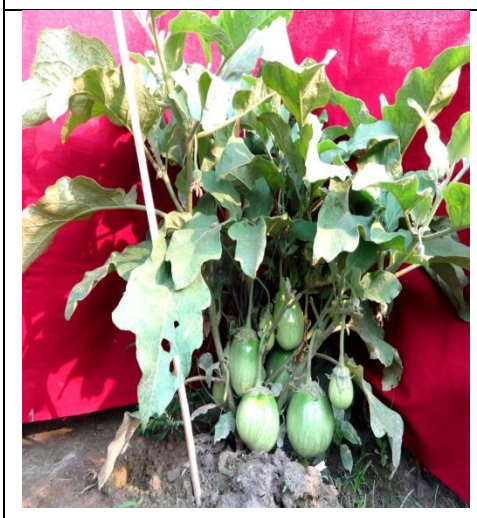
PLATE 5: Growth habit, fruit type and leaf shape of UBB 10, UBB 11 & UBB 12.

UBB 13

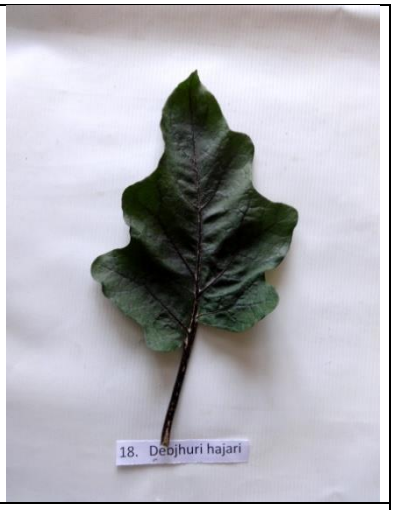



UBB 14




UBB 15

PLATE 6: Growth habit, fruit type and leaf shape of UBB 13, UBB 14 & UBB 15.

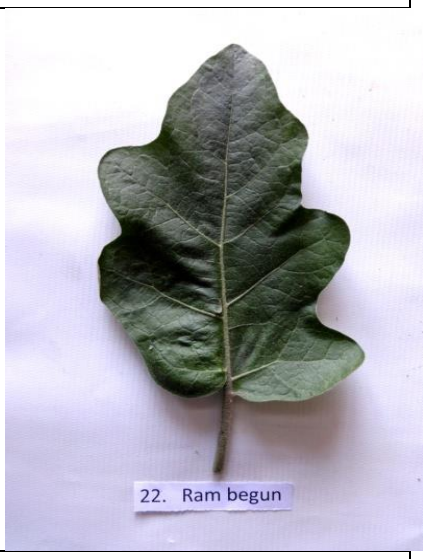
UBB 16


UBB 17


UBB 18

PLATE 7: Growth habit, fruit type and leaf shape of UBB 16, UBB 17 & UBB 18.

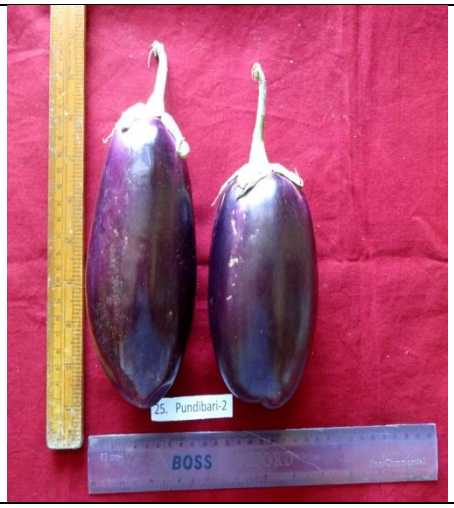

UBB 19

UBB 20


UBB 21

PLATE 8: Growth habit, fruit type and leaf shape of UBB 19, UBB 20 & UBB 21.

UBB 22


UBB 23


UBB 24

PLATE 9: Growth habit, fruit type and leaf shape of UBB 22, UBB 23 & UBB 24.


UBB 25


UBB 26


UBB 27

PLATE 10: Growth habit, fruit type and leaf shape of UBB 25, UBB 26 & UBB 27.

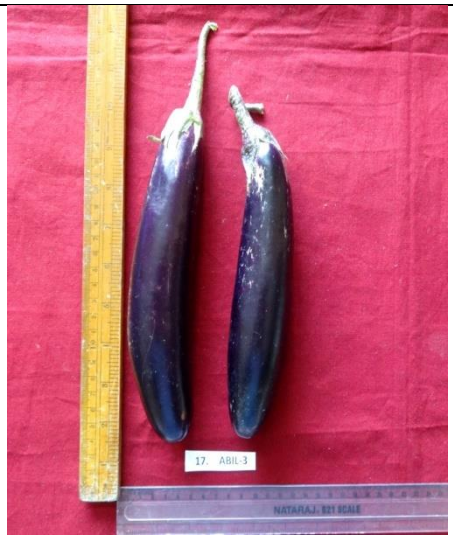

UBB 28


UBB 29


UBB 30

PLATE 11: Growth habit, fruit type and leaf shape of UBB 28, UBB 29 & UBB 30.


UBB 31

UBB 32

PLATE 12: Growth habit, fruit type and leaf shape of UBB 31 & UBB 32.

genotype) with light green colour calyx (31 numbers of genotype). All these morphological manifestation in majority cases are most preferable in the local areas of North Bengal.

4.3 Mean performance of genotypes

The data on the mean performance of genotypes for qualitative and quantitative characters were presented in table 6 and 7.

4.3.1 Plant height

Significant variation was observed with respect to plant height (Table 6) which ranged from 58.49 to 123.57 cm. The genotype UBB 2 recorded the maximum height of 123.57 cm followed by UBB 21 (115.94 cm), while UBB 23 recorded the minimum height of 58.46 cm.

4.3.2 Number of primary branches

Significant variation was observed with respect to number of primary branches per plant (Table 6) that ranged from 4.15 to 8.14. Maximum number of primary branches were observed in UBB 22 (8.14) followed by UBB 17 (7.44), while UBB 11 had minimum number of primary branches 4.15**.**

4.3.3 Calyx length

Significant variation was observed with respect to calyx length (Table 6) which ranged from 2.47 to 6.18 cm. Maximum calyx length was noticed in the genotype UBB 24 (6.18 cm) followed by UBB 27 (5.54cm), while the genotype UBB 29 had minimum length of 2.47 cm .

4.3.4 Days to first flowering

Significant variation was recorded in genotypes in relation to days to first flowering (Table 6) which ranged from 51.97 to 82.86 days. The genotype UBB 2 was observed as earliest to flower (51.97 days) followed by UBB 12 (53.00 days), while the genotype UBB 28 took maximum days to flower (82.86 days).

4.3.5 Days to fruit maturity

Significant variation was noticed with respect to days to fruit maturity (Table 6) which ranged from 49.21 to 23.71 days. The genotype, UBB 12 had maximum number of days to

fruit maturity (49.21 days) followed by UBB 21 (47.10 days). And genotype UBB 1 had minimum days to fruit maturity (23.71 days).

4.3.6 Fruiting span

Significant variation was noticed with respect to Fruiting span (Table 6) which ranged from 87.28 to 110.14 days. The genotype UBB 17 had maximum days of fruiting span (110.14 days) followed by UBB 2 (107.53 days). And genotype UBB 1 had minimum days of fruiting span (87.28 days).

4.3.7 Fruit diameter

Significant variation was found among the genotypes with respect to fruit diameter (Table 6) which ranged from 2.41 to 13.22 cm. Highest fruit diameter was recorded in the genotype UBB 21 (13.22 cm) followed by UBB 32 (12.48cm), while the genotype UBB 23 recorded the least fruit diameter (2.41 cm).

4.3.8 Fruit length

Significant variation was found among the genotypes with respect to fruit length (Table 6) which ranged from 5.86 to 40.36 cm. Maximum fruit length was observed in the genotype UBB 5 (40.36 cm) followed by UBB 27 (32.09 cm), whereas the genotype UBB 28 had the minimum fruit length (5.86 cm).

4.3.9 Fruit weight

There was a high, significant variation among the genotypes with respect to fruit weight (Table 7) which ranged from 41.24 to 899.27 g. highest individual mean fruit weight was observed in the genotype UBB 21 (899.27 g) followed by UBB 8 (538.98 g), whereas the genotype UBB 23 recorded the least weight (41.24 g).

4.3.10 Number of fruits per plant

There was significant variation with respect to number of fruits per plant (Table 7) which ranged from 2.30 to 61.03. Genotype UBB 23 was found to produce the highest number of fruits per plant (61.03) followed by UBB 16 (33.62), whereas the genotype UBB 21 had the least number of fruits per plant (2.30).

4.3.11 Ascorbic acid

Significant variation was noticed with respect to ascorbic acid (Table 7) which ranged from 7.74 to 12.20 mg/100g. Highest ascorbic acid was recorded in the genotype UBB 23 (12.20 mg/100g) followed by UBB 20 (11.19 mg/100g), while lowest ascorbic acid observed in genotype UBB 2 (7.74mg/100g).

4.3.12 Total soluble solid

Significant variation was noticed with respect to total soluble solid (Table 7) which ranged from 6.25 to 5.33 ^{0}brix. Highest total soluble solid was recorded in the genotype UBB 14 (6.25 ^{0}brix) followed by UBB 23 (6.24 ^{0}brix), while least total soluble solid 5.33^{0}brix of genotype UBB 24.

4.3.13 Phenol

Significant variation was noticed with respect to phenol content of fruit (Table 7). It ranged from 0.69 to 1.50mg/100g. Highest phenol was recorded in the genotype UBB 32 (1.50 mg/100g), while least phenol 0.69 mg/100g found in UBB 1.

4.3.14 Anthocyanin

Significant variation was noticed with respect to anthocyanin (Table 7) which ranged from 7.84 to 133.55 mg/100g. Highest Anthocyanin was recorded in the genotype UBB 12 (133.55 mg/100g) followed by UBB 29 (144.34 mg/100g), while least Anthocyanin of 7.84 mg/100g was recorded in UBB 2.

4.3.15 Yield per ha

Significant variation was observed with respect to yield per ha (Table 7) which ranged from 28.62 to 64.45 t/ha. Highest yield per ha was observed in the genotype UBB 8 (64.45 t/ha) followed by UBB 3 (59.57 t/ha), while least yield found in UBB 14 (28.62 t/ha).

Table 6: Pooled (2016-17 and 2017-18) mean of different quantitative characters of Brinjal

Genotypes	Plant Height (cm)	Primary Branch	Calyx Length (cm)	Days to 1st flower	Days to Fruit maturity	Fruiting span	Fruit diameter (cm)	Fruit Length (cm)
UBB 1	86.79	4.30	3.53	69.22	23.71	87.28	7.11	26.89
UBB 2	123.57	5.24	3.17	51.97	47.40	107.53	7.70	21.21
UBB 3	101.12	4.31	3.37	63.84	38.09	105.66	5.83	17.50
UBB 4	69.71	4.46	3.80	64.19	28.21	90.81	10.25	11.48
UBB 5	93.25	5.39	3.42	64.71	37.83	94.79	6.70	40.36
UBB 6	70.68	5.26	3.45	73.89	32.81	91.61	9.60	11.10
UBB 7	115.29	7.35	3.83	64.22	37.16	97.28	4.78	24.09
UBB8	112.48	5.44	5.09	71.80	33.41	87.70	11.14	17.29
UBB 9	92.95	5.39	3.49	65.87	37.78	99.13	9.58	11.42
UBB 10	96.25	5.55	4.74	54.45	46.37	107.05	10.15	20.37
UBB 11	90.19	4.15	4.52	65.76	36.68	89.74	8.78	19.60
UBB 12	97.69	4.47	4.77	53.00	49.21	106.50	9.34	21.02
UBB 13	107.01	6.17	3.72	69.58	35.09	91.92	11.22	12.16
UBB 14	80.77	4.33	4.72	64.37	37.12	96.13	8.15	19.25
UBB 15	96.29	4.21	3.58	66.26	37.13	95.24	8.83	9.07
UBB 16	103.68	4.25	3.82	62.82	42.27	101.18	5.76	23.23
UBB 17	114.52	7.44	4.53	53.36	47.98	110.14	5.55	28.54
UBB 18	113.98	5.24	4.13	62.81	38.38	98.69	6.30	23.98
UBB 19	112.52	6.25	4.20	62.16	42.43	103.34	3.91	23.16
UBB 20	115.07	5.30	4.18	66.09	39.30	100.41	9.71	12.03
UBB 21	115.94	6.29	3.99	70.86	48.10	101.14	13.22	17.93
UBB 22	82.49	8.14	4.32	63.36	39.85	100.14	8.52	13.57
UBB 23	58.46	5.19	3.79	61.49	43.41	106.01	2.41	21.38
UBB 24	92.22	4.20	6.18	62.86	44.37	105.64	6.29	26.53
UBB 25	115.94	6.28	4.49	65.86	43.63	103.64	5.76	30.93
UBB 26	107.65	7.15	4.12	70.35	37.36	95.15	10.73	12.53
UBB 27	94.83	6.32	5.54	69.36	36.57	103.14	5.28	32.09
UBB 28	80.34	6.23	4.49	82.86	38.64	100.14	7.11	5.86
UBB 29	105.93	6.21	2.47	64.39	39.83	97.11	7.42	9.06
UBB 30	98.14	5.19	4.28	65.94	40.53	97.56	7.09	12.04
UBB 31	78.61	5.15	2.80	64.77	43.25	98.73	10.49	17.85
UBB 32	114.67	7.18	5.15	68.93	41.02	101.57	12.48	17.94
Mean	98.10	5.56	4.12	65.04	39.53	99.13	8.04	19.11
SED	0.171	0.01	0.011	0.149	0.07	0.13	0.03	0.083
CD(0.5%)	0.342	0.02	0.021	0.298	0.14	0.259	0.06	0.165

Table 7: Pooled (2016-17 and 2017-18) mean of different quantitative and qualitative characters of Brinjal

Genotypes	Fruit weight (cm)	Fruit/plant	Ascorbic acid (mg/100g)	TSS (°B)	Phenol (mg/ 100g)	Anthocyanin (mg/100g)	Yield/ha (t/ha)
UBB 1	379.30	8.68	9.22	5.62	0.69	86.22	44.52
UBB 2	296.49	11.84	7.74	5.54	0.98	87.43	47.79
UBB 3	314.72	17.89	8.76	5.44	1.13	79.98	59.57
UBB 4	290.15	14.55	9.04	5.34	1.06	16.41	58.05
UBB 5	455.75	4.68	8.81	5.63	1.17	83.51	41.44
UBB 6	248.74	11.94	8.29	5.37	1.06	17.37	44.86
UBB 7	199.74	9.98	8.89	5.72	1.24	106.71	35.64
UBB8	538.98	11.35	8.29	5.53	1.32	27.71	64.45
UBB 9	301.57	10.89	10.33	5.77	1.13	14.02	45.64
UBB 10	519.38	3.94	9.85	5.71	0.98	116.88	45.39
UBB 11	472.19	4.79	9.44	5.54	0.98	16.75	35.48
UBB 12	484.86	13.34	8.94	5.42	1.13	133.55	46.03
UBB 13	351.05	6.29	8.92	5.53	1.17	13.56	29.67
UBB 14	414.72	4.24	9.87	6.25	1.17	12.35	28.62
UBB 15	254.67	5.84	9.30	5.54	1.28	16.03	33.62
UBB 16	154.46	33.62	8.59	5.34	1.43	107.53	44.37
UBB 17	209.63	21.01	8.69	5.52	1.30	131.61	49.98
UBB 18	208.87	5.21	9.83	5.56	1.35	98.53	30.09
UBB 19	93.94	17.86	10.47	5.73	1.28	127.09	33.25
UBB 20	297.32	4.84	11.19	6.00	1.35	12.29	33.59
UBB 21	899.27	2.30	9.74	5.74	1.43	14.05	32.42
UBB 22	294.38	5.25	10.33	5.35	1.32	130.49	29.24
UBB 23	41.24	61.03	12.20	6.24	1.43	101.52	31.70
UBB 24	268.90	4.73	8.83	5.33	1.13	95.75	35.65
UBB 25	320.37	7.80	9.25	5.43	0.98	96.91	37.10
UBB 26	428.32	4.34	8.43	5.35	1.02	13.5	42.25
UBB 27	236.37	12.30	9.55	5.52	1.13	91.84	46.71
UBB 28	120.22	8.88	11.18	5.54	1.43	7.84	35.82
UBB 29	153.31	14.91	9.49	5.62	1.11	142.46	37.46
UBB 30	211.03	11.93	9.83	5.53	1.17	118.89	38.42
UBB 31	53.73	26.41	9.87	5.75	1.28	144.34	34.49
UBB 32	118.72	17.25	9.25	5.67	1.50	131.84	45.48
Mean	301.01	12.50	9.45	5.60	1.19	74.84	40.59
SED	0.405	0.153	0.007	0.011	0.007	0.339	0.069
CD(0.5%)	0.809	0.305	0.014	0.021	0.015	0.677	0.138

4.4 Variability, Heritability and Genetic advance

The population mean, range, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, genetic advance and expected genetic advance as per cent of mean (GAM) for the different characters were analyzed and were presented in table 8. From the table it was evident that there was a wide range of variability for all the characters providing an ample scope for selecting desirable types. The magnitude PCV was higher than GCV in almost all the cases. However, close estimates of GCV and PCV indicated that contribution towards final phenotypic expression of these characters mostly by genetic architecture of the genotypes rather than environmental factors. Similar findings were also recorded by Choudhury and Samadia (2004).

4.4.1 Plant height

Overall average value of plant height for all the 32 genotypes under experiment was recorded 98.10 cm with the range of 123.57 to 58.46 cm. A moderate GCV (16.19%) and PCV (16.39%) were recorded for this trait. Whereas, heritability found to be very high i.e., 94.98% coupled with high GA (31.46) and high GAM (32.07%).

This moderate estimates for GCV and PCV indicated the extent of genotypic variation within the genotype was moderate for this character. Similar finding was reported by Muniappan *et al.* (2010), Kumar *et al*. (2013), Samlindsujin *et al.* (2017) and Pujer *et al.* (2017).

However, comparatively high heritability coupled with high GAM was the indicated preponderance of additive gene action in manifestation and inheritance of this character and improvement of this character could possibly be done due to less manipulation in performance by the influence of the environment. This result was in conformity with the findings of Muniappan *et al.* (2010), Lokesh *et al.* (2013), Ansari *et al.* (2011) and Pujer *et al.* (2017).

4.4.2 Number of primary branches

Irrespective of genotypes, average number of primary branches was 5.56 per plant, where lowest number was 4.15 and highest number was 8.14. As well as, there were moderate estimates for GCV (18.69%) and PCV (19.69%). Similar result was reported by Das *et al.* (2010), Ansari *et al.* (2011) and Kumar *et al.* (2013). Genetic advance was

recorded 2.03. Heritability for this trait was high i.e., 89.99% along with high GAM (36.51%). Present finding was also reported by several authors (Das *et al.,* 2010; Kumar *et al.*, 2012; Samlindsujin *et al.*, 2017)

Result indicated that presence of moderate variation for the present character with in the genotypes. Also, character could be improved through effective selection.

4.4.3 Calyx length

Among the 32 genotypes, estimate for calyx length was ranged from 6.18 cm to 2.28 cm with mean of 4.12cm. Result showed moderate estimate for GCV (16.81%), PCV (18.81%) and low genetic advance (1.42). But, heritability was high (88.97%) coupled with high GAM (34.47%).

Moderate estimates for GCV and PCV indicated extent of variability within the genotypes were moderate. But, high heritability and high GAM indicated importance of selection for the improvement of the following trait. This result was in conformity with the finding of Kumar *et al*. (2013).

4.4.4 Days to first flower

A mean value of 65.04 days coupled with range value 82.86 days to 51.97 days were recorded for days to first flower. The estimates were very low for GCV (9.51%) and PCV (9.52%) along with genetic advance i.e., 11.47. This finding was in accordance with the observation of Islam and Uddin (2009), Thangavel *et al.* (2011) and Kumar *et al.* (2012). Although the heritability was high (89.91%), but also there was moderate estimate for genetic advance of mean (17.64%). The phenomena of high heritability coupled with moderate GAM was also reported by Danquah *et al.* (2012) and Pujer *et al.* (2017).

Result indicated that there was there was very low variability for this character with in the genotypes coupled with preponderance of more non-additive gene action components and selection might not be the possible alternative for complete improvement of this trait, rather needed alternative breeding strategy.

4.4.5 Days to fruit maturity

For this character, result showed maximum value of 49.21 days and minimum value of 23.71 days coupled with an average value of 39.53 days. However, there was moderate GCV

(14.12%) and PCV (14.32%) coupled with high heritability (93.98%), moderate genetic advance (10.80) and high GAM (27.32%).

It indicated that existence of moderate variability for this character with in the genotype along with preponderance of additive gene effect and selection for this trait might be rewarding.

4.4.6 Fruiting span

A mean value of 99.13 days coupled with range value 110.14 days to 86.28 days were recorded for this trait. Low estimates were recorded for both GCV and PCV along high heritability (91.93%), moderate genetic advance (11.38) and GAM (11.48%).

There was less variability for this character with in the genotypes and selection could not found to be effective for improvement of fruiting span.

4.4.7 Fruit diameter

Irrespective of genotypes, average fruit diameter was 8.04 cm, where the lowest was 2.14cm and highest was 13.22cm. As well as, there were high estimates for GCV (30.53%) and PCV (31.53%). Genetic advance was recorded 4.80. Heritability for this trait was high i.e., 91.98% along with high GAM (59.70%). This whole finding was also reported by Patel *et al.* (2004), Babu and Patil (2005), Kushwah and Bandhyopadya (2005), Yadav *et al.* (2016) and Pujer *et al.* (2017).

High estimates for PCV and GCV indicated the presence of high variation for the present character with in the genotypes. Also, character could be improved through effective selection due existence of additive gene action and less affected by environmental influence.

4.4.8 Fruit length

For this character a wide range of variability was recorded in their performance i.e., range value of 40.36 cm to 5.86 cm. Although the mean performance of all 32 genotypes together was 19.11 cm indicated that most of the genotypes had tendency to manifest towards maximum estimates. Considerably high estimates were recorded for GCV (40.46%) and PCV (43.45%) along with moderate genetic advance i.e., 14.30. Although the heritability was high (89.78%) coupled with very high genetic advance of mean (74.83%).

Result indicated that there was very high variability for this character with in the genotypes (Ansari *et al.*, 2011; Danquah *et al.*, 2012; Kumar *et al.*, 2013; Lokesh *et al.*, 2013) coupled with preponderance of more additive gene action (Kumar *et al.*, 2012; Kumar *et al.*, 2013; Lokesh *et al.*, 2013; Yadav *et al.*, 2016) components and selection might be rewarding breeding strategy for complete improvement of this trait.

4.4.9 Fruit weight

For this character, result showed greater extent of variability in performance through different genotypes i.e., maximum value of 899.27 g and minimum value of 41.24 g coupled with an average value of 301g. However, there was very high GCV (54.04%) and PCV (57.04%) coupled with high heritability (88.47%), moderate genetic advance (312.90) and high GAM (103.95%). High phenotypic and genotypic coefficient of variance was also reported by Islam and Uddin (2009), Muniappan *et al.* (2010), Danquah *et al.* (2012), Kumar *et al.*(2012) and Yadav *et al.* (2016). High heritability coupled with high GAM was also evident by the earlier work of Islam and Uddin (2009), Muniappan *et al.* (2010), Danquah *et al.* (2012) and Samlindsujin *et al*. (2017).

It indicated that existence of very high variability for this character with in the genotype along with preponderance of additive gene effect and selection for this trait might be useful.

4.4.10 Number of fruit per plant

A mean value of 12.50 numbers fruit coupled with higher extent of range value i.e., 61.03 to 2.30 numbers of fruit per plant were recorded for this trait, indicated tendency of most of the genotypes were towards lower values. High estimates were recorded for both GCV (86.43%) and PCV (90.44%) along with high heritability (93.37%), high genetic advance (21.74) and GAM (173.92%) were observed. High phenotypic and genotypic coefficient of variance was also reported by Islam and Uddin (2009), Kumar *et al.* (2012), Madhavi *et al.* (2015) and Pujer *et al.* (2017). High heritability coupled with high GAM was also evident by the earlier work of Islam and Uddin (2009), Lokesh *et al*. (2013), Yadav *et al.* (2016) and Samlindsujin *et al*. (2017).

Indicated there was high variability for this character with in the genotypes and selection could be very much effective for improvement of number of fruit per plant.

4.4.11 Ascorbic acid

Irrespective of genotypes, average ascorbic acid content of fruit was 9.45 mg per 100g of fresh weight, where the lowest was 7.74 mg per 100g and highest was 12.20 mg per. As well as, there were low estimates for GCV and PCV coupled with low genetic advance (1.77), moderate GAM (18.73%) and high heritability (91.48).

Indicated there were variation for the present character with in the genotypes and improvement might not be effective through selection in spite of having less environmental influence. Similar kind of result was also reported by Kumar *et al*. (2013) and Tirkey *et al*.(2018).

4.4.12 Total soluble solid

For this character very less extent of range was recorded i.e., 6.25 to 5.33 °B with the mean value of 5.60 °B. Considerably low estimates were recorded for GCV (4.09%), PCV (4.10%), genetic advance (0.43) and genetic advance of mean (7.68%). But, the estimate for heritability was high (91.68%) for this character. Present finding was in accordance with the Tirkey *et al*. (2018).

Result indicated that there was there was no variability for this character among the genotypes coupled with preponderance of non-additive gene action components. Hence, selection might not be rewarding breeding strategy for complete improvement of this trait.

4.4.13 Phenol content

A mean value of 1.19 mg per 100 g of fruit (fresh weight) coupled with higher extent of range value i.e., 1.50 to 0.69 mg per 100 g of fruit (fresh weight) were recorded for this trait, indicated tendency of most of the genotypes were towards higher magnitude. High estimates were recorded for both GCV and PCV along with high heritability (90.99%), low genetic advance (0.33) and high GAM (27.73%) were observed. These high estimates for the different variability and inheritance components were supported by earlier works of Karak *et al.* (2012), Rani *et al.* (2012), Rashmika *et al.* (2015) and Ravali *et al.* (2017).

Indicated there was high variability for this character with in the genotypes and selection could be very much effective for improvement of number of fruit per plant.

4.4.14 Anthocyanin content

For this character, result showed greater extent of variability in performance through different genotypes i.e., maximum value of 144.34 mg per 100g of fruit (fresh weight) and minimum value of 7.84 mg per 100g of fruit (fresh weight) coupled with an average value of 74.84 mg per 100g of fruit (fresh weight). However, there was moderate GCV (14.80%) and PCV (14.82%) coupled with high heritability (95.73%), genetic advance (98.16) and GAM (131.16%). Similar result was reported by Rani *et al*. (2017).

It indicated that genotypes under experiment contributed almost equal proportion towards the mean estimates in spite of having wide range and there by showed moderate variability for this character with in the genotype. But, present character proved to be very much suitable for improvement through selection due to existence of additive gene effect.

4.4.15 Yield per hectare

Overall average value of yield per plant for all the 32 genotypes under experiment was recorded 40.59 t/ha with the range of 64.45 to 28.62 t/ha. A moderate GCV (18.24%) and PCV (20.24%) were recorded for this trait. Whereas, heritability found to be very high i.e., 91.97% coupled with moderate GA (17.10) and high GAM (42.13%). Present findings were supported by the earlier works of Islam and Uddian (2009), Muniappan *et al.* (2010), Lokesh *et al.* (2013) and Pujer *et al*. (2017).

These estimates for GCV and PCV indicated the extent of genotypic variation within the genotype was moderate for this character. However, comparatively high heritability coupled with high GAM was the indicated that additive gene action was predominant and selection could be feasible way for improvement of this trait.

From the above discussion it might be concluded that characters viz., fruit diameter, fruit length, fruit weight, number of fruit per plant, phenol content showed high genotypic and phenotypic coefficient of variation that indicated the prevalence of high genetic variation among the genotypes under study for these characters. Low estimates of the same were recorded for the fruiting span, ascorbic acid, total soluble solid and days to fruit maturity was the evident of very less variability among the genotype for these characters. Whereas, for rest of the characters were exhibited non-significant variation among the genotypes. However, plant height, number of primary branch, calyx length, days to fruit maturity, fruit diameter, fruit length, fruit weight, number of fruit per plant, phenol content and anthocyanin content

Table 8: Genetic variability parameters for different yield component and biochemical characters of Brinjal

Characters	Mean	Range		GCV (%)	PCV (%)	Heritability (h^2%)	Genetic Advance (GA)	Genetic Advance (% of Mean)
		Maximum	Minimum					
Plant height (cm)	98.10	123.57	58.46	16.19	16.39	94.98	31.46	32.07
Number of primary branches	5.56	8.14	4.15	18.69	19.69	89.99	2.03	36.51
Calyx length (cm)	4.12	6.18	2.28	16.81	18.81	88.97	1.42	34.47
Days to first flower	65.04	82.86	51.97	9.51	9.52	89.91	11.47	17.64
Days to fruit maturity	39.53	49.21	23.71	14.12	14.32	93.98	10.80	27.32
Fruiting span	99.13	110.14	86.28	6.06	6.06	91.93	11.38	11.48
Fruit diameter (cm)	8.04	13.22	2.14	30.53	31.53	91.98	4.80	59.70
Fruit length (cm)	19.11	40.36	5.86	40.46	43.45	89.78	14.30	74.83
Fruit weight (g)	301.01	899.27	41.24	54.04	57.04	88.47	312.90	103.95
Number of fruit per plant	12.50	61.03	2.30	86.43	90.44	93.37	21.74	173.92
Ascorbic acid (mg/100g)	9.45	12.20	7.74	9.96	9.96	91.48	1.77	18.73
TSS (°B)	5.60	6.25	5.33	4.09	4.10	91.68	0.43	7.68
Phenol (mg/100g)	1.19	1.50	0.69	66.51	66.51	90.99	0.33	27.73
Anthocyanin (mg/100g)	74.84	144.34	7.84	14.80	14.82	95.73	98.16	131.16
Yield ha^{-1} (t/ha)	40.59	64.45	28.62	18.24	20.24	91.97	17.10	42.13

showed high heritability coupled with high genetic advance of mean as percentage which suggested that these characters might possibly be improved through selection. Although, complex relationship among the genetic parameters argued for adopting recurrent selection as rewarding breeding method for improvement of most of the characters under study.

4.5 Character association analysis

Correlation denotes the degree and direction of association between two or more variables. Hence it the tool to measure extent of mutual relationship between various traits to determines the component characters, on which selection can be based for genetic improvement of dependent traits. This concept was first postulated by Galton (1889) and there after its theory was developed by Pearson (1904). Genotypic correlation reflects either the pleiotropic action of genes or linkage or more likely both. Whereas, phenotypic correlation which includes both genotypic and environmental effects, that provides information about total association between the observable characters. This does not give a true genetic picture of the relationship as it indicates the effect of both heredity as well as environmental influences. The genotypic correlation coefficients provide an estimate of an inherent association between genes controlling any two characters i.e. when two characters are invariably and linearly associated the underlined genetic mechanism causing such association may be due to complete linkage between the two characters or due to pleiotropy. Hence, genotypic correlation is of greater significance and can be effectively used in formulating an effective selection scheme. It may also help to identify the characters that prove to be of little or no importance in the selection programme. Selection for improvement of any character is more effective when it was carried out on basis of contributing characters which are highly heritable and positively correlated. Correlation coefficients among different characters of brinjal were estimated and presented in tables 9 and 10. In general, the magnitude of genotypic correlation coefficients was higher than the phenotypic correlation coefficients, which might be due to the strong inherent relationship between the variables and masking effect of environment.

From the extract of the result (table 9) it was recorded that plant height which was significantly and negatively correlated with the number of fruit per plant (Pr = -0.349, Gr = -0.351) and ascorbic acid content (Gr = -0.375, Pr = -0.378). Similar findings were obtained by Nair and Mehta 2007 in which plant height is negatively correlated with number of fruits

per plant. However, Plant height found to be significantly positive correlated with the primary branch (0.349) and days to first flower (0.348) at genotypic level only. This positive correlation among the plant height and number of primary branches was also reported by Guptha *et al*. (2017). Other than these traits, all the characters showed non-significant positive relation with the rest of the characters excepting the day to first flower (Pr = 0.205, Gr = 0.211) and total soluble solid (Pr = 0.156, Gr = 0.154) those were non-significant and negatively correlated with the plant height.

There was no significant relation obtained for the number of primary branches with the rest of the traits under the present experiment (table 9). However, non-significant but positive relation recorded with the calyx length (Pr = 0.084, Gr = 0.087) , days to first flower (Pr = 0.114, Gr = 0.117), days to fruit maturity (Pr = 0.205, Gr = 0.211), fruiting span (Pr = 0.203, Gr = 0.209), fruit diameter (Pr = 0.050, Gr = 0.044), ascorbic acid (Pr = 0.079, Gr = 0.079),anthocyanin content (Pr = 0.244, Gr = 0.251), phenol content (Pr = 0.296, Gr = 0.308). Similar result was obtained by Prabakaran*et al.* (2015) in ascorbic acid and Dharwad*et al.* (2009) in days to fruit maturity.

Again, characters viz., fruit length (Pr = -0.005, Gr = -0.005), fruit weight (Pr = -0.096, Gr = -0.096), number of fruit per plant (Pr = -0.087, Gr = -0.089), total soluble solid (Pr = -0.064, Gr = -0.067) and total yield (Pr = -0.154, Gr = -0.151) were non-significant and negetively correlated with the number of primary branch. Similar results were reported by Lohakare *et al.* (2008) in fruit length.

Calyx length also not showed any significant relation with any other characters (table 9). But, its relationship was non-significantly in positive direction for most of the traits. Only, fruit diameter (Pr = -0.005, Gr = -0.005), number of fruit per plant (Pr = -0.214, Gr = -0.214) and total soluble solid (Pr = -0.105, Gr = -0.111) content of fruit were found to be negatively correlated with the calyx length. The positive relationship among the calyx length and fruit weight was also reported by Prabakaran (2015) and Kumar *et al.* (2016).

Number of days to first flower was highly significant and negatively correlated (table 9) with days to fruit maturity (Pr = -0.548, Gr = -0.561), fruiting span (Pr = -0.572, Gr = -0.567), fruit length (Pr = -0.369, Gr = -0.373) and anthocyanin content of the fruit (Pr = -0.555, Gr = -0.566). Other than these, non-significant but negative correlation was recorded for number of fruit per plant (Pr = -0.201, Gr = -0.216), total soluble solid (Pr = -0.059, Gr = -0.056) and total yield (Pr = -0.102, Gr = -0.114). Early flowering decreases total number of

harvests by early completion of fruit bearing period. Similar results were obtained by Nair and Mehta (2007), Dhameliya and Deboriya (2008), Dharwad *et al.* (2009) and Thangamani and Jansirani (2012).

Highly significant and positive relationship for number of days to fruit maturity was recorded with fruiting span (Pr = 0.893, Gr = 0.835), anthocyanin content (Pr = 0.453, Gr = 0.458) and phenol content of the fruit (Pr = 0.360, Gr = 0.369). On consideration of the non-significant relationship data represented in the table number 9 it was observed that most of the character showed relationship in positive direction with the only exception for fruit diameter (Pr = -0.087, Gr = -0.081) and total yield (Pr = -0.198, Gr = -0.207).

The result depicted fruiting span (table 9) was highly significant and positively correlated with anthocyanin content (Pr = 0.524, Gr = -0.537) and was significant but negatively correlated with fruit diameter (Pr = -0.367, Gr = 0.364). However, non-significant but the positive relation was recorded for fruit length (Pr = 0.269, Gr = -0.279), number of fruit per plant (Pr = 0.303, Gr = 0.297), ascorbic acid content (Pr = 0.184, Gr = 0.189), total soluble solid (Pr = 0.089, Gr = 0.084) and phenol content of the fruit (Pr = 0.267, Gr = 0.279).

It was found that the diameter of the fruit was high significant and positively correlated with the fruit weight (Pr = 0.534, Gr = 0.531). Prabakaran (2015) and Kumar *et al.* (2016) also reported similar observation in their research work. Whereas, highly significant correlation towards negative direction was observed fruit length (Pr = -0.475, Gr = -0.479), number of fruit per plant (Pr = -0.452, Gr = -0.455) and anthocyanin content of the fruit (Pr = -0.419, Gr = -0.428).

Significant correlation in positive direction was recorded between the fruit length and anthocyanin content (table 9) of the fruit (Pr = 0.428, Gr = 0.437). Considering the non-significant estimates it was found that most of the characters showed relationship in positive direction excepting ascorbic acid content (Pr = -0.219, Gr = -0.216) and phenol content (Pr = -0.168, Gr = -0.175). The positive association of fruit length was also reported by Nair and Mehta (2007) and Chattopadhyay *et al*. (2011) for number of fruit per plant, Nair and Mehta (2007) and Shekar *et al.* (2014) for fruit weight, Muniappan *et al.* (2010) for plant height, Prabakaran (2015) and Tripathy *et al.* (2018) for yield per plant.

Fruit weight showed highly significant and negative correlation (table 10) with the number of fruit per plant (Pr = -0.552, Gr = -0.555) and anthocyanin content (Pr = -0.419, Gr = -0.423). Whereas, a significant relation between the fruit weight and total yield (Pr = 0.339, Gr = 0.367) in positive direction was recorded. However, characters viz., ascorbic acid (Pr = -0.279, Gr = -0.283), total soluble solid (Pr = -0.060, Gr = -0.064) and phenol content (Pr = -0.251, Gr = -0.259) were non-significantly negative correlated with the fruit weight. This positive relationship with total yield was also reported by Dharwad *et al*. (2009), Islam and Uddin (2009), Chattopadhyay *et al*. (2011), Shende *et al*. (2014) and Reza *et al*. (2015). However, negative association was also reported by Prabakaran (2015) for phenol content and ascorbic acid and Kumar *et al.* (2016) for ascorbic acid.

Number of fruit per plant was recorded significantly correlated in positive direction with anthocyanin content (Pr = 0.369, Gr = 0.375) and phenol content (Pr = 0.347, Gr = 0.354) of fruit. Other than these ascorbic acid, total soluble solid and total yield were non-significant positively correlated with the fruit number (table 10). Positive association of number of fruit per plant was also recorded by Praneetha *et al.* (2011) for ascorbic acid and phenol content.

Analyzed data presented in table 10 revealed that there was highly significant positive relation between ascorbic acid with total soluble solid (Pr = 0.631, Gr = 0.639) and phenol content (Pr = 0.397, Gr = 0.411). Although, total yield was highly and significantly negative correlated with the ascorbic acid content of the fruit (Pr = -0.529, Gr = -0.534).

Again there significant negative correlation was recorded between the total yield and total soluble solid content (table 10) of the fruit (Pr = -0.394, Gr = -0.408). Whereas, phenol content of fruit recorded (table 10) to be non-significant negative correlated with the total yield (Pr = -0.241, Gr = -0.247).

After summarizing all the findings it was observed that total yield is significantly correlated with the fruit weight. However, magnitude of relationship for other traits viz., plant height, calyx length, number of fruit per plant, fruit diameter and fruit length were towards positive direction with the total yield. Even all the components related to yield attributes were positively interrelated with the each other, indicated the simultaneous selection for these characters might be beneficial in getting enhanced yield attributes. But, all the qualitative parameters were negatively affected with the magnitude of yield related traits in most of the cases excepting number of fruit per plant that showed negative relationship. Present finding

Table 9: Genotypic (G) and Phenotypic (P) correlation of brinjal for quantitative and qualitative characters

Characters		1	2	3	4	5	6	7	8
Plant height (cm) (1)	G	**1.000**	0.341	0.088	-0.205	0.343	0.236	0.102	0.190
	P	**1.000**	0.349*	0.092	-0.211	0.348*	0.237	0.108	0.196
Primary branch (2)	G		**1.000**	0.084	0.114	0.205	0.203	0.050	-0.005
	P		**1.000**	0.087	0.117	0.211	0.209	0.044	-0.005
Calyx length (cm) (3)	G			**1.000**	0.031	0.171	0.227	-0.005	0.268
	P			**1.000**	0.038	0.174	0.231	-0.005	0.264
Days to 1st flower (4)	G				**1.000**	-0.548**	-0.572**	0.253	-0.369*
	P				**1.000**	-0.561**	-0.567**	0.259	-0.373*
Days to fruit maturity (5)	G					**1.000**	0.839**	-0.087	0.183
	P					**1.000**	0.835**	-0.081	0.189
Fruiting span (6)	G						**1.000**	-0.367*	0.269
	P						**1.000**	-0.364*	0.279
Fruit diameter (cm) (7)	G							**1.000**	-0.475**
	P							**1.000**	-0.479**
Fruit length (cm) (8)	G								**1.000**
	P								**1.000**
Fruit weight (g) (9)	G								
	P								
Fruit/plant (10)	G								
	P								
Ascorbic acid (mg/100g) (11)	G								
	P								
TSS (°B) (12)	G								
	P								
Anthocyanin (mg/100g) (13)	G								
	P								
Phenol (mg/100g) (14)	G								
	P								
Yield/ha (t/ha) (15)	G								
	P								

* and ** Significant at 5% level and 1% level respectively

Table 10: Genotypic (G) and Phenotypic (P) correlation of brinjal for quantitative and qualitative characters

Characters		9	10	11	12	13	14	15
Plant height (cm) (1)	G	0.216	-0.349*	-0.375*	-0.156	0.149	0.099	0.079
	P	0.219	-0.351*	-0.378*	-0.154	0.159	0.103	0.083
Primary branch (2)	G	-0.096	-0.087	0.079	-0.064	0.244	0.296	-0.154
	P	-0.091	-0.089	0.079	-0.067	0.258	0.308	-0.151
Calyx length (cm) (3)	G	0.165	-0.214	0.027	-0.105	0.008	0.133	0.051
	P	0.171	-0.217	0.024	-0.111	0.008	0.139	0.057
Days to 1st flower (4)	G	0.015	-0.201	0.169	-0.059	-0.555**	0.167	-0.102
	P	0.019	-0.216	0.173	-0.056	-0.566**	0.164	-0.114
Days to fruit maturity (5)	G	0.041	0.189	0.099	0.095	0.453**	0.360*	-0.198
	P	0.039	0.191	0.097	0.108	0.458**	0.369*	-0.207
Fruiting span (6)	G	-0.199	0.303	0.184	0.089	0.524**	0.267	-0.037
	P	-0.209	0.297	0.189	0.084	0.537**	0.279	-0.033
Fruit diameter (cm) (7)	G	0.534**	-0.452**	-0.224	-0.112	-0.419**	0.012	0.130
	P	0.531**	-0.455**	-0.231	-0.119	-0.428*	0.016	0.136
Fruit length (cm) (8)	G	0.088	0.071	-0.219	0.016	0.428*	-0.168	0.067
	P	0.086	0.078	-0.216	0.017	0.437*	-0.175	0.074
Fruit weight (g) (9)	G	**1.000**	-0.552**	-0.279	-0.060	-0.419**	-0.251	0.339*
	P	**1.000**	-0.555**	-0.283	-0.064	-0.423*	-0.259	0.367*
Fruit/plant (10)	G		**1.000**	0.312	0.295	0.369*	0.347*	0.087
	P		**1.000**	0.323	0.309	0.375*	0.354*	0.093
Ascorbic acid (mg/100g) (11)	G			**1.000**	0.631**	-0.001	0.397*	-0.529**
	P			**1.000**	0.639**	-0.001	0.411*	-0.534**
TSS (°B) (12)	G				**1.000**	-0.078	0.253	-0.394*
	P				**1.000**	-0.077	0.259	-0.408*
Anthocyanin(mg/100g) (13)	G					**1.000**	0.070	-0.014
	P					**1.000**	0.075	-0.012
Phenol (mg/100g) (14)	G						**1.000**	-0.241
	P						**1.000**	-0.247
Yield/ha (t/ha) (15)	G							**1.000**
	P							**1.000**

* and ** Significant at 5% level and 1% level respectively

argued for the implementation of different and completely separate breeding strategy for developing the line with up-regulated qualitative parameters.

4.6 Path coefficient analysis

The correlation coefficient analysis provides information about the direction and magnitude of association between pairs of variables. The correlation coefficient by itself is not sufficient to provide in depth picture of complex interaction among more than two variables and summarized strategy. In order to achieve an effective selection strategy, it is important to have knowledge of relative importance of direct and indirect influences of component traits on the dependent trait such as fruit yield per plant. The genotypic correlation coefficient of fruit yield and its components along with quantitative and qualitative traits were partitioned into direct and indirect effect on dependent variable i.e., total yield per hectare to obtain the knowledge of the relative importance of the causal factors at phenotypic level especially when more number of variables are considered in correlation. Direct and indirect effect of 15 different characters on total fruit yield per hectare is presented in table number 11.

4.6.1 Plant height

Plant height exhibited the low positive direct effect (0.1744) on total yield per hectare. Similar finding was reported by earlier works of Sharma and Swaroop (2000), Jadhao *et al.* (2009) and Reza *et al.* (2015).

Plant height showed moderate positive indirect effect on total yield per hectare through fruiting span (0.2087) and low positive indirect effect on total yield per hectare through ascorbic acid (0.1684). Whereas, negligible but positive indirect effect on total yield per hectare was recorded through calyx length (0.0113), days to first flower (0.005), fruit diameter (0.0281), fruit weight (0.0846), total soluble solid (0.0257) and phenol content (0.0141). Its indirect effect on total yield per hectare were negative through number of primary branches (-0.0333), days to fruit maturity (-0.3682), fruit length (-0.0263), number of fruit per plant (-0.2121) and anthocyanin (-0.0017). Similar results were reported by Lohakare *et al*. (2008) for plant height.

4.6.2 Number of primary branch

Number of primary branches showed negligible negative direct effect (-0.0977) on total yield per hectare.

Analysed data represented the preponderance of low positive indirect effect on total yield per hectare through fruiting span (0.1794); as well as, negligible positive indirect effect on total yield per hectare through calyx length (0.0108), plant height (0.0595), fruit diameter (0.0137), fruit length (0.0008), total soluble solid (0.0105) and phenol content (0.0231). These outcomes were in accordance with Datta and Jana (2010) in chilli.

4.6.3 Calyx length

It was recorded the low positive direct effect of calyx length (0.1281) on total yield per hectare. Madhavi *et al.* (2015) reported similar result during investigation on brinjal.

Calyx length showed moderate positive indirect effect on total yield per hectare through fruiting span (0.2005) and negligible positive indirect effect on total yield per hectare through plant height (0.0153), fruit weight (0.0647), total soluble solid (0.0173) and phenol content (0.0007). However, low negative indirect effect on total yield per hectare was recorded through number of days to fruit maturity (-0.1836) and number of fruit per plant (-0.1301).

4.6.4 Days to first flower

Days to first flower exhibited the negligible negative direct effect (-0.0242) on total yield per hectare. This negative estimate for days to first flowering was also reported by Thangamani and Jansirani (2012) and Shekar *et al.* (2014).

Days to first flower showed very high positive indirect effect on total yield per hectare through number of days to fruit maturity (0.5890). Other than this trait, negligible positive indirect effect was estimated through calyx length (0.0040), fruit diameter (0.0698), fruit length (0.0511), fruit weight (0.0058), and total soluble solid (0.0098).

Again, it was observed that rest characters under study depicted high negative indirect effect on total yield per hectare through fruiting span (-0.5065). While, for rest of the characters it was recorded to be low negative indirect effect.

4.6.5 Days to fruit maturity

Very high negative direct effect was recorded for days to fruit maturity (-1.0741) on total yield per hectare.

Again high positive indirect effect on total yield per hectare through fruiting span (0.7424) was observed for the days to fruit maturity. However, low positive indirect effect

was noted through number of fruit per plant (0.1150) and negligible positive indirect effect was noted through calyx length (0.0219), days to first flower (0.0133), fruit weight (0.0161), number of fruit per plant (0.1150) and phenol content (0.0429).

4.6.6 Fruiting span

Fruiting span exhibited high positive direct effect (0.8844) on total yield per hectare. It showed low positive indirect effect on total yield per hectare through number of fruit per plant (0.18407) and negligible positive indirect effect on total yield per hectare through plant height (0.0412), calyx length (0.0290), days to first flower (0.0139) and phenol content (0.0429). Whereas, the high negative indirect effect on total yield per hectare recorded for fruiting span through number of days to fruit maturity (-0.9016).

4.6.7 Fruit diameter

Moderate direct effect at positive direction was recorded for this character (0.2751) on total yield per hectare. As well as, it was positively correlated with the total yield.

Fruit diameter showed indirect effect on total yield per hectare moderately through fruit weight (0.2093); low through ascorbic acid (0.1005); negligible through plant height (0.0178), days to fruit maturity (0.0939), fruit length (0.0658) and total soluble solid (0.0185). Sharma *et al.* (2010) investigated in bell pepper where similar finding was reported for days to first picking. Similar finding was also reported by Datta and Jana (2010). However, high negative indirect effect was recorded for fruiting span (-0.3245).

4.6.8 Fruit length

Low estimate of the direct effect at negative direction on total yield per hectare was observed for fruit length (-0.1385).

Again moderate positive indirect effect on total yield per hectare was recorded through fruiting span (0.2380). Low but positive indirect effect was recorded through plant height (0.0331), number of primary branch (0.0005), calyx length (0.0343), days to first flower (0.0089), fruit weight (0.0346), number of fruit per plant (0.0434), ascorbic acid (0.0984), phenol content (0.0405) and anthocyanin content (0.0030). Estimate for moderate indirect effect was recorded through days to fruit maturity (-0.1961) was observed for the days to fruit maturity. These finding was in conformity with the Senapathi and Senapathi (2006) and

Prabhu and Natarajan (2008) for number of fruits per plant and Thangamani and Jansirani (2012) for calyx length.

4.6.9 Fruit weight

It was recorded the importance of high positive direct effect of fruit weight (0.3917) on total yield per hectare. As well as, significant positive relation with the total yield was recorded for fruit weight. Higher positive estimate of direct effect on total yield per hectare was reported by Nair and Mehta (2007), Muniappan *et al.* (2010), Chattopadhyay *et al.* (2011), Shekar *et al.* (2014), Prabakaran *et al.* (2015) and Reza *et al.* (2015).

Fruit weight showed low positive indirect effect on total yield per hectare through fruit diameter (0.1471) and ascorbic acid (0.1252); as well as negligible positive indirect effect through plant height (0.0377), number of primary branch (0.0093), calyx length (0.0212), total soluble solid (0.0099) and anthocyanin content (0.0044). It provided negative estimates through rest of the characters under study. Negative indirect effect through fruit diameter (Datta and Jana, 2010) and number of fruits per plant (Nair and Mehta, 2007) were also reported by earlier research work.

4.6.10 Number of fruit per plant

High and positive estimate of the direct effect on total yield per hectare was observed for number of fruit per plant (0.6078). Also, phenotypic correlation showed positive estimate for total yield. Similar finding was reported by Muniappan *et al.* (2010), Chattopadhyay *et al.* (2011) and Sujin *et al.* (2017).

Study on indirect effect revealed that most of the characters under study showed negative indirect effect on total yield per hectare except fruiting span (0.2678) which was moderate and positive; number of primary branches (0.0085), days to first flower (0.0049) and phenol content (0.0350) those were low positive effect on total yield per hectare.

4.6.11 Ascorbic acid

High estimate of the direct effect at negative direction on total yield per hectare was observed for ascorbic acid content (-0.4492) coupled with significantly negative association with total yield (-0.534).

Ascorbic acid content exhibited negative indirect for most of the characters except few viz., number of fruit per plant (0.1896) and fruiting span (0.1626) which was low positive indirect effect; calyx length (0.0034) and fruit length (0.0303) those were negligible negative effect on total yield per hectare.

4.6.12 Total soluble solid

Total soluble solid exhibited the low negative direct effect (-0.1651) on total yield per hectare. Its magnitude about correlation was significantly at negative direction total yield.

Total soluble solid showed low positive indirect effect on total yield per hectare through number of fruit per plant (0.1792). Other than this, negligible positive indirect effect was estimated through primary branch per plant (0.0062), days to first flower (0.0014) and fruiting span (0.0790).

Again, for rest of the characters negligible negative indirect effect on total yield per hectare was recorded excepting the ascorbic acid (-0.2839) that exhibited moderate negative indirect effect.

4.6.13 Phenol content

The direct effect of phenol content (0.0947) on total yield per hectare was positive but very negligible and also showed its relationship with the total yield in negative direction.

A complex and diversified relationship was recorded for this character. It showed high positive indirect effect through fruiting span (0.4635) and moderate positive indirect effect through number of fruit per plant (0.2244) on total yield per hectare. Whereas, its indirect effects were recorded to be negligibly positive through plant height (0.0260), calyx length (0.0010), days to first flower (0.0134), ascorbic acid (0.0005) and total soluble solid (0.0128). The negative indirect effects were recorded through rest of the characters at diversified ranges. Among them, high indirect effect was recorded through fruit maturity (-0.4864); low indirect effect was recorded through number of fruit diameter (-0.1153) and fruit weight (-0.1641), respectively.

4.6.14 Anthocyanin content

Anthocyanin content exhibited the negligible negative direct effect (-0.0176) on total yield per hectare. Also magnitude for the phenotypic correlation with total yield was at negative direction.

Phenol content showed moderate positive indirect effect on total yield per hectare through fruiting span (0.2367) and number of fruit per plant (0.2109). Other than these, negligible positive indirect effect was estimated through plant height (0.0173), calyx length (0.0171), fruit diameter (0.0033), fruit length (0.0233) and phenol content (0.0066).

Again, through rest of the characters under study showed negative indirect effect on total yield per hectare excepting the days to fruit maturity (-0.3874) which exhibited moderate negative indirect effect.

Overall, path analysis revealed that the direct contribution of traits under study on total yield as dependable variables were highest through fruiting span followed by number of fruit per plant, fruit weight, fruit diameter, calyx length, plant height. However, among them all the characters showed relationship with the yield component at desired direction excepting fruiting span that showed correlation at negative direction with the dependable variable due to combined negative indirect effect via fruit diameter and fruit length. Present contradictory result suggested that considering the fruit span as an important variable further thorough study should be done for better understanding the nature of relation. However, from the present investigation this could be concluded that for number of fruit per plant, fruit weight, fruit diameter, calyx length, plant height is likely to be effective in increasing fruit yield per plant. The complex relationship between coefficient of variation and inheritance component argued for recurrent selection as breeding strategy for the improvement of these characters.

In the present investigation residual effect is 0.3852 at genotypic level indicated 61.5 % contribution of selected characters for yield. Hence, some other characters need to be included as independent variables for dependent variable, yield per hectare. Also, qualitative parameters viz., ascorbic acid, total soluble solid, anthocyanin content showed negative direct effect coupled with significantly negative correlation with yield ascribed that the improvement of yield through selection would be possible by sacrificing the qualitative traits. Hence, there was need for separate breeding strategy to develop quality enriched line.

Table 11: Phenotypic path coefficient analysis for brinjal considering yield as dependent variable

Character	PH	PB	CL	DFF	DFM	FS	FD	FL	FW	FPP	VC	TSS	PHOL	ANTH	Yield/ha (Pr)
PH	**0.1744**	-0.0333	0.0113	0.0050	-0.3682	0.2087	0.0281	-0.0263	0.0846	-0.2121	0.1684	0.0257	0.0141	-0.0017	0.083
PB	0.0595	**-0.0977**	0.0108	-0.0028	-0.2200	0.1794	0.0137	0.0008	-0.0374	-0.0531	-0.0354	0.0105	0.0231	-0.0052	-0.151
CL	0.0153	-0.0082	**0.1281**	-0.0008	-0.1836	0.2005	-0.0013	-0.0371	0.0647	-0.1301	-0.0121	0.0173	0.0007	-0.0023	0.057
DFF	-0.0358	-0.0112	0.0040	**-0.0242**	0.5890	-0.5065	0.0698	0.0511	0.0058	-0.1225	-0.0761	0.0098	-0.0526	-0.0029	-0.114
DFM	0.0598	-0.0200	0.0219	0.0133	**-1.0741**	0.7424	-0.0241	-0.0253	0.0161	0.1150	-0.0444	-0.0157	0.0429	-0.0063	-0.207
FS	0.0412	-0.0198	0.0290	0.0139	-0.9016	**0.8844**	-0.1010	-0.0373	-0.0778	0.1840	-0.0826	-0.0147	0.0496	-0.0047	-0.033
FD	0.0178	-0.0049	-0.0006	-0.0061	0.0939	-0.3245	**0.2751**	0.0658	0.2093	-0.2746	0.1005	0.0185	-0.0397	-0.0002	0.136
FL	0.0331	0.0005	0.0343	0.0089	-0.1961	0.2380	-0.1307	**-0.1385**	0.0346	0.0434	0.0984	-0.0026	0.0405	0.0030	0.074
FW	0.0377	0.0093	0.0212	-0.0004	-0.0443	-0.1757	0.1471	-0.0122	**0.3917**	-0.3354	0.1252	0.0099	-0.0397	0.0044	0.367*
FPP	-0.0609	0.0085	-0.0274	0.0049	-0.2032	0.2678	-0.1243	-0.0099	-0.2161	**0.6078**	-0.1401	-0.0487	0.0350	-0.0061	0.093
VC	-0.0654	-0.0077	0.0034	-0.0041	-0.1062	0.1626	-0.0615	0.0303	-0.1092	0.1896	**-0.4492**	-0.1044	-0.0001	-0.0070	-0.534**
TSS	-0.0271	0.0062	-0.0134	0.0014	-0.1021	0.0790	-0.0308	-0.0022	-0.0234	0.1792	-0.2839	**-0.1651**	-0.0074	-0.0045	-0.408*
PHOL	0.0260	-0.0238	0.0010	0.0134	-0.4864	0.4635	-0.1153	-0.0592	-0.1641	0.2244	0.0005	0.0128	**0.0947**	-0.0012	-0.012
ANTH	0.0173	-0.0290	0.0171	-0.0040	-0.3874	0.2367	0.0033	0.0233	-0.0983	0.2109	-0.1789	-0.0419	0.0066	**-0.0176**	-0.247

Residual effect= 0.3852 ; * and ** Significant at 5% level and 1% level respectively

N.B:

PH=	Plant height (cm)	FL=	Fruit length (cm)
PB=	Number of primary branches	FW=	Fruit weight (g)
CL=	Calyx length (cm)	FPP=	Number of fruit per plant
DFF=	Days to first flower	VC=	Ascorbic acid (mg/100g)
DFM=	Days to fruit maturity	TSS=	TSS (°B)
FS=	Fruiting span	PHOL=	Phenol (mg/100g)
FD=	Fruit diameter (cm)	ANTH=	Anthocyanin (mg/100g)

4.7 Genetic divergence

For an efficient choice of parents for hybridization program information on genetic divergence among the available germplasm is of vital importance to a plant breeder. It was also found that the more diverse the parents, greater are the chances of obtaining high heterotic F1 hybrids and broad spectrum of variability in the segregating generations (Arunchalam, 1981). Hence, there is a need to quantify the degree of divergence among available germplasm.

Multivariate analysis serves as a useful tool to quantify the degree of divergence between the biological populations at genotypic level and to assess the relative contribution of different components to the total divergence both at intra and inter and cluster levels. D^2 technique of Mahalanobis based on multivariate analysis serves to be a good index for estimating genetic diversity (Gadekar *et al.*, 1992). Therefore, Genetic divergence among 32 genotypes of brinjal was assessed by adopting Mahalanobis D^2 statistic based on 15 characters.

4.7.1 Grouping of genotypes into different clusters

Result obtained from D^2 analysis presented in the table 12 showed that all the 32 genotypes under study were broadly categorized into seven different clusters. Among the entire, cluster I showed to be consisting of maximum number of genotypes viz., UBB 1, UBB 2, UBB 3, UBB 4, UBB 5, UBB 6, UBB 7, UBB 8, UBB 9, UBB 10, UBB 11, UBB 12, UBB 13, UBB 14, UBB 15, UBB 16, UBB 17, UBB 18, UBB 19, UBB 20, UBB 29, UBB 30. Other than this, total four number clusters i.e., cluster II, cluster III, cluster IV and cluster V were consisting of two genotypes in each. Rest two clusters, cluster VI and cluster VII were comprised of single genotype in each.

After evaluating the source of collection of genotypes and the pattern of cluster distribution indicated that, the geographical diversity need not necessarily be related to the genetic diversity. Among the genotypes from one geographical area, parallelism was not noticed between geographical diversity and genetic diversity. Similar finding was earlier reported by the Vanaja *et al.* (2003), Arunkumar and Biradar (2004), Sreelathakumary and Rajmony (2004) and and Senapathi *et al.* (2005).

4.7.2 Mean intra and inter cluster distance

Mean intra and inter cluster distances were presented in table 13. It was observed that average inter cluster distance was higher than the average intra cluster distance indicated wide genetic diversity among the genotypes of different groups than those of same cluster. Similar results were reported by Mahesha *et al*. 2006, Kumar *et al.* (2007), Dutta *et al.* (2009), Sekhar *et al.* (2008) and Islam *et al.* (2011) in brinjal. The intra cluster D^2 values ranged from 0.000-1932.26. Highest intra cluster distance was recorded for cluster I (1932.26) followed by cluster V (1033.35), cluster IV (734.35), cluster III (728.95), cluster IV (734.35) and cluster II (516.00). Whereas, there was no intra cluster distance observed for cluster VI and cluster VII.

In the present study, inter cluster distance found to be maximum for combination between cluster VI and cluster V (9459.58) followed by cluster VI and II (8576.57), cluster VI and cluster VI (8513.05), cluster VI and cluster I (7474.44), cluster VI and cluster III (7027.58) and cluster VI and cluster VII (5953.15). However, minimum inter cluster distance was recorded for combination between cluster IV and cluster II (636.51) followed by cluster VII and cluster III (1172.78), cluster V and cluster II (1205.75) and cluster V and cluster IV (1227.81).

However, the reason of no intra distance in the cluster VI and cluster VII in the present investigation was that both the clusters were comprises of single genotype in each case. Highest cluster distance of cluster I and cluster V indicated existence of genetic divergence among these genotypes in these each cluster and thereby could be used for improvement of yield through recombination breeding and also could be used to develop transgressive segregating lines or heterotic population due existence of high level heterogeneity (Mehta and Asati, 2008). The lowest magnitude of inter cluster distance was recorded for the combination between cluster IV and II followed by cluster VII and III indicated that there were no significant genetic diversity among the genotypes of these clusters and could not be possible to utilize in cross breeding improvement programme among them.

Again, the combinations of cluster VI and V followed by cluster VI and II, cluster VI and VI, cluster VI and I, cluster VI and III, cluster VI and cluster VII these showed greater extent of inter cluster distance which indicated on inter-cross hybridization among the genotypes under each cluster combinations might result in a wide spectrum of segregating population as genetic diversity is very distinct among the groups and there by predicted the

Table 12: Clustering pattern of 32 genotypes of Brinjal

Sl. No.	Cluster No.	Total No. of Genotypes	Name of Genotypes
1	I	22	UBB 1, UBB 2, UBB 3, UBB 4, UBB 5, UBB 6, UBB 7, UBB 8, UBB 9, UBB 10, UBB 11, UBB 12, UBB 13, UBB 14, UBB 15, UBB 16, UBB 17, UBB 18, UBB 19, UBB 20, UBB 29, UBB 30
2	II	2	UBB 23, UBB 28
3	III	2	UBB 22, UBB 25
4	IV	2	UBB 27, UBB 32
5	V	2	UBB 24, UBB 31
6	VI	1	UBB 21
7	VII	1	UBB 26

Table 13: Inter and Intra cluster (Diagonal) distance of Brinjal

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	**1932.26**	1872.88	1447.69	1822.12	2547.82	7474.44	1953.74
Cluster II		**516.00**	1674.34	636.51	1205.75	8576.57	2670.44
Cluster III			**728.95**	1590.35	2532.40	7027.58	1172.78
Cluster IV				**734.35**	1227.81	8513.05	2596.60
Cluster V					**1033.35**	9459.58	3562.85
Cluster VI						**0.00**	5953.15
Cluster VII							**0.00**

N.B: Bold values indicate inter cluster distance

Possibility of using these genotypes under each cluster to develop improved heterotic population or recombinant

4.7.3 Cluster mean of individual characters and their contribution towards diversity

The mean performance of 32 genotypes from 7 different clusters for 15 characters under study was presented in table 14. Cluster VI registered highest mean for plant height (115.94 cm) followed by cluster VII (107.65 cm) while lowest mean was noticed in cluster II (69.40 cm). Highest mean for number of primary branches was recorded in cluster III (7.21) followed by cluster VII (7.15) and lowest mean was found in cluster V (4.68). Highest mean for calyx length was recorded in cluster IV (5.35cm) followed by cluster V (4.49cm) and lowest mean was found in cluster I (3.95cm). Cluster I recorded lowest mean for days to first flowering (63.67 days) followed by cluster V (63.82 days) whereas highest mean was observed in cluster II (72.18 days). Cluster VII showed minimum mean for days to fruit maturity (37.36 days) followed by cluster I (38.58 days) while maximum mean was noticed in cluster VI (48.10 days) followed by cluster V (43.81 days). Highest mean for fruiting span was noticed in cluster II (103.08 days) followed by cluster IV (102.36 days) and lowest mean was observed in cluster VII (95.15 days) followed by cluster I (98.04 days). Cluster VI recorded maximum mean for fruit diameter (13.22 cm) followed by cluster VII (10.73 cm) and minimum mean was recorded in cluster II (4.76 cm) followed by cluster III (7.14 cm). Mean for fruit length was highest in cluster IV (25.02 cm) followed by cluster III (22.25 cm) and lowest in cluster VII (12.53 cm) followed by cluster II (13.62 cm). Cluster VI recorded maximum mean for fruit weight (899.27 g) followed by cluster VII (428.32 g) and minimum mean was recorded in cluster II (80.73 g) followed by cluster V (161.32 cm). Cluster II has shown highest mean for number of fruits per plant (34.96) followed by cluster V (15.57) while lowest mean was observed in cluster VI (2.30) followed by cluster VII (4.34). Highest mean for ascorbic acid was recorded in genotypes of cluster II (11.69 mg/100g) followed by cluster III (9.79 mg/100g) while lowest mean was shown by cluster VII (8.43 mg/100g) followed by cluster I (9.26 mg/100g). Cluster II showed highest mean for total soluble solid (5.89 °B) followed by cluster VI (5.74 °B) while lowest mean was recorded in cluster VII (5.35 °B). Highest mean for Anthocyanin (IU) was recorded in genotypes of cluster V (120.05 IU) followed by cluster III (113.70 mg/100g) while lowest mean was shown by cluster VII (13.50 mg/100g) followed by cluster VI (14.05 mg/100g). Highest mean for Phenol (mg/100g) was recorded in genotypes of cluster II & VI (1.43 mg/100g) followed by cluster IV (1.32 mg/100g) while lowest mean was shown by cluster VII (1.02 mg/100g)

followed by cluster III (1.15 mg/100g). Highest mean for Yield/ha (t/ha) was recorded in genotypes of cluster IV (46.10 t/ha) followed by cluster VII (42.25 t/ha) while lowest mean was shown by cluster VI (32.42 t/ha) followed by cluster III (33.17 t/ha).

Contributions of the characters towards total diversity of the genotypes were represented in the table 14. It indicate that characters viz., total yield per hectare (30.04 %), number of fruit per plant (28.83) and fruit weight (20.97%) were principal contributing characters towards total divergence. However, comparatively moderate contribution was recorded for fruit diameter (8.47%), plant height (4.44%) and calyx length (3.63%). Other than these, low contributions were recorded for ascorbic acid (1.21%), total soluble solid (1.21%), anthocyanin (0.60%), fruit length (0.20%) and number of primary branch (0.20%). Whereas, for rest of the characters viz., phenol content, days to first flowers and days to fruit maturity did not showed any contribution towards the total diversity. Similar results were reported by Manju and Sreelathakumary (2002) and Senapati *et al.* (2003) in chilli and Sharma and Maurya (2004), Kumar *et al.* (2007), Dutta *et al.* (2009), Das *et al.* (2010) and Islam *et al.* (2011) in brinjal.

However, on the basis of mean of cluster performance cluster VI and VII were important for plant height, fruit diameter, primary branches, fruit weight, total soluble solid and total yield. Whereas, for the for the quality traits viz., anthocyanin, phenol and ascorbic acid as well as calyx length, number of fruit plant cluster II and cluster III could be consider as important. So, selection of the genotype from these cluster as crossing breeding parent could emerged most effective. In the other hand, total yield per hectare, number of fruit per plant and fruit weight showed maximum contribution towards the diversity followed by fruit diameter, plant height and calyx length. Result indicated that diverse genotypes can be utilized for improvement of yield productivity. The greater diversity in the present materials was due to these characters which will offer a good scope for improvement of yield through rational selection of parent's genotypes for brinjal. The genotypes of highly divergent clusters may also be utilized in a breeding programme for development of high yielding varieties with desirable attribute and can also be utilized in heterosis breeding programme for development of F1 hybrids with superior yield and quality characters.

Table 14: Cluster mean of individual characters and their percent of contribution

Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	No. of first rank	% contribution
Plant height (cm)	99.90	69.40	99.22	104.75	85.42	115.94	107.65	22	4.44
Number of primary branches	5.27	5.71	7.21	6.75	4.68	6.29	7.15	1	0.20
Calyx length (cm)	3.95	4.14	4.41	5.35	4.49	3.99	4.12	18	3.63
Days to first flower	63.67	72.18	64.61	69.15	63.82	70.86	70.35	0	0.00
Days to fruit maturity	38.58	41.03	41.74	38.80	43.81	48.10	37.36	0	0.00
Fruiting span	98.04	103.08	101.89	102.36	102.19	101.14	95.15	1	0.20
Fruit diameter (cm)	7.95	4.76	7.14	8.88	8.39	13.22	10.73	42	8.47
Fruit length (cm)	18.86	13.62	22.25	25.02	22.19	17.93	12.53	1	0.20
Fruit weight (g)	311.40	80.73	307.38	177.55	161.32	899.27	428.32	104	20.97
Number of fruit per plant	11.35	34.96	6.53	14.78	15.57	2.30	4.34	143	28.83
Ascorbic acid (mg/100g)	9.26	11.69	9.79	9.40	9.35	9.74	8.43	6	1.21
TSS (°B)	5.60	5.89	5.39	5.60	5.54	5.74	5.35	6	1.21
Phenol (mg/100g)	71.22	54.68	113.70	111.84	120.05	14.05	13.50	3	0.60
Anthocyanin (mg/100g)	1.16	1.43	1.15	1.32	1.21	1.43	1.02	0	0.00
Yield ha^{-1} (t/ha)	42.18	33.76	33.17	46.10	35.07	32.42	42.25	149	30.04

5. Summery and Conclusion

Summary and Conclusion

A study entitled “Evaluation of brinjal germplasm for winter season” was conducted on 32 genotypes for total of 22 characters *i.e.*, 7 morphological characters, 11 quantitative characters 4 qualitative characters at Experimental Farm of Uttar Banga Krishi Viswavidyalaya, Pundibari, Cooch Behar, West Bengal, India during 2016-17 and 2017-18 following the standard cultivation practices with objectives of

6. Collection of different genotypes of brinjal from different parts of North Bengal.
7. To record and documentation of morphological variation throughout the collected genotypes.
8. To assess the amount of genetic variability, heritability and genetic advance for different qualitative and quantitative characters present in a population of different brinjal genotype.
9. To study the character association and, direct and indirect effect of different qualitative and quantitative characters influencing fruit yield.
10. To obtain information on genetic diversity present among the brinjal genotype based on qualitative and quantitative characters respectively.

For this data was subjected to statistical analysis to get information on mean performance, variability, heritability, genetic advance as per cent of mean, correlation coefficient, path coefficient analysis, diversity and the results summarized and conclusions drawn are presented hereunder.

5.1 Analysis of variance

The mean sum of squares for 15 characters in 31 genotypes and one check variety of brinjal showed highly significant differences among the genotypes for all the characters indicating presence of sufficient amount of variability in all the characters studied.

5.2 Morphological characters of brinjal genotypes

Morphological characters viz., plant growth habit, bearing habit, leaf blade spinyness, calyx colour, fruit shape, fruit calyx spinyness and fruit colour of all 32 accessions were recorded. All the thirty two genotypes were categorized into three group viz., upright, intermediate and prostrate for plant growth habit. Where, total twenty five genotype exhibited intermediate growth habit, six genotype showed upright growth habit and only one genotype showed prostrate growth habit. For leaf blade spinyness genotypes were categorized into two

classes of which twenty nine genotypes were noted as non spiny leaved genotypes and three genotypes had few spines on the leaves. Data collected on fruit calyx spinyness was collected based on fruit calyx spinyness were broadly categorized into two groups. Where twenty six genotypes had no spines on fruit calyx and six genotypes exhibited few spines on calyx. All genotypes of brinjal were grouped into four groups depending on fruit shape viz., long shaped, oblong shaped, round shaped and oval shaped; the following fruit types were found in fifteen genotype, eight genotype, sex genotype and three genotype, respectively. Genotypes were classified into total four groups for mature fruit colour. Where twelve genotypes were purple, eleven genotypes were green, seven genotypes were purple black colour and single genotype registered Milk white colour fruits. Maximum genotypes (thirty one genotypes) had fruits with light green colour calyx and only one genotype showed light purple colour calyx. Most of the genotypes (thirty genotypes) had solitary bearing habit. Whereas, only two genotypes exhibited cluster bearing habit genotype.

Wide variation in morphological characters was observed in all the genotypes under study. Maximum genotypes had no spines on leaves (29 numbers of genotype) and fruit calyx (26numbers of genotype). 25 numbers of genotype were intermediate in growth habit. Maximum genotypes produced long type (15 numbers of genotype) and oblong type (8 numbers of genotype) fruit. In most genotype the fruit colour was purple (12 numbers of genotype) with light green colour calyx (31 numbers of genotype). All these morphological manifestation in majority cases are most preferable in the local areas of North Bengal.

5.3 Mean performance of genotypes

After studying the mean performance it was observed that there significant variation for plant height with range from 58.49 to 123.57 cm and the highest plant height was recorded for genotype UBB 2 (123.57 cm) followed by UBB 21 (115.94 cm). Number of primary branches per plant ranged from 4.15 to 8.14 and maximum number of primary branches were observed in UBB 22 (8.14) followed by UBB 17 (7.44). Calyx length ranged from 2.47 to 6.18 cm and highest length observed in UBB 24 (6.18 cm) followed by UBB 27 (5.54cm).

Significant variation was recorded in genotypes in relation to days to first flowering with range from 51.97 to 82.86 days. Where, the genotypes UBB 2 (51.97days) and UBB 12 (53.00 days) were earliest to flowering. Days to fruit maturity range from 49.21 to 23.71 days and maximum value obtained from UBB 12 (49.21 days) followed by UBB 21 (47.10 days). Fruiting span which ranged from 87.28 to 110.14 days, recorded maximum UBB 17 (110.14 days) followed by UBB 2 (107.53 days).

Significant variation i.e., 2.41 to 13.22 cm was found among the genotypes with respect to fruit diameter and highest was recorded in the genotype UBB 21 (13.22 cm) followed by UBB 32 (12.48cm). Fruit length ranged from 5.86 to 40.36 cm with maximum estimates in the genotype UBB 5 (40.36 cm) followed by UBB 27 (32.09 cm). There was a high, significant variation among the genotypes with respect to fruit weight (41.24 to 899.27 g) and UBB 21 (899.27 g) followed by UBB 8 (538.98 g) recorded highest fruit weight.

There was highly significant variation (2.30 to 61.03) with respect to number of fruits per plant. Genotype UBB 23 (61.03) followed by UBB 16 (33.62) exhibited highest number of fruits per plant. Ascorbic acid showed significant variation i.e., 7.74 to 12.20 mg/100g. Where, highest ascorbic acid was recorded in the genotype UBB 23 (12.20 mg/100g) followed by UBB 20 (11.19 mg/100g). Significant variation was noticed with respect to total soluble solid (6.25 to 5.33 ^{0}brix) and highest total soluble solid was recorded in the genotype UBB 14 (6.25 ^{0}brix) followed by UBB 23 (6.24 ^{0}brix). Phenol content of fruit ranged from 0.69 to 1.50mg/100g and was maximum in UBB 32 (1.50 mg/100g). Anthocyanin content ranged from 7.84 to 133.55 mg/100g with highest estimate for UBB 12 (133.55 mg/100g) followed by UBB 29 (144.34 mg/100g). Significant variation (28.62 to 64.45 t/ha) was observed with respect to yield per hectare and highest yield per ha was observed in the genotype UBB 8 (64.45 t/ha) followed by UBB 3 (59.57 t/ha).

5.4 Variability, Heritability and Genetic advance

The population mean, range, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, genetic advance and expected genetic advance as per cent of mean (GAM) for the different fifteen (15) characters of thirty two (32) genotypes were summarized hereunder.

It was evident that there was a wide range of variability for all the characters providing an ample scope for selecting desirable types. The magnitude PCV was higher than GCV in almost all the cases. However, close estimates of GCV and PCV indicated that contribution towards final phenotypic expression of these characters mostly by genetic architecture of the genotypes rather than environmental factors.

A moderate GCV (16.19%) and PCV (16.39%) were recorded for this trait. Whereas, heritability found to be very high i.e., 94.98% coupled with high GA (31.46) and high GAM (32.07%). Irrespective of genotypes, there were moderate estimates for GCV (18.69%) and PCV (19.69%) for number of primary branches. Genetic advance was recorded 2.03.

Heritability for this trait was high i.e., 89.99% along with high GAM (36.51%). In case calyx length moderate estimate for GCV (16.81%), PCV (18.81%) and low genetic advance (1.42). But, heritability was high (88.97%) coupled with high GAM (34.47%). The estimates were very low for GCV (9.51%) and PCV (9.52%) along with genetic advance i.e., 11.47 for days to first flower. Although the heritability was high (89.91%), but also there was moderate estimate for genetic advance of mean (17.64%).

For days to fruit maturity, there was moderate GCV (14.12%) and PCV (14.32%) coupled with high heritability (93.98%), moderate genetic advance (10.80) and high GAM (27.32%). Fruiting span showed low estimates for both GCV and PCV along high heritability (91.93%), moderate genetic advance (11.38) and GAM (11.48%). There were high estimates for GCV (30.53%) and PCV (31.53%) for fruit diameter. Genetic advance was recorded 4.80. Heritability for this trait was high i.e., 91.98% along with high GAM (59.70%). For fruit length, considerably high estimates were recorded for GCV (40.46%) and PCV (43.45%) along with moderate genetic advance i.e., 14.30. Although the heritability was high (89.78%) coupled with very high genetic advance of mean (74.83%). Fruit weight showed very high GCV (54.04%) and PCV (57.04%) coupled with high heritability (88.47%), moderate genetic advance (312.90) and high GAM (103.95%). High estimates of numbers of fruit per plant were recorded for both GCV (86.43%) and PCV (90.44%) along with high heritability (93.37%), high genetic advance (21.74) and GAM (173.92%) were observed. For ascorbic acid content of fruit low estimates for GCV and PCV coupled with low genetic advance (1.77), moderate GAM (18.73%) and high heritability (91.48). Considerably low estimates were recorded for GCV (4.09%), PCV (4.10%), genetic advance (0.43) and genetic advance of mean (7.68%) in case of total soluble solid. But, the estimate for heritability was high (91.68%) for this character.

High estimates were recorded for both GCV and PCV along with high heritability (90.99%), low genetic advance (0.33) and high GAM (27.73%) were observed for phenol content. For anthocyanin content, there was moderate GCV (14.80%) and PCV (14.82%) coupled with high heritability (95.73%), genetic advance (98.16) and GAM (131.16%). A moderate GCV (18.24%) and PCV (20.24%) were recorded for yield per hectare. Whereas, heritability found to be very high i.e., 91.97% coupled with moderate GA (17.10) and high GAM (42.13%).

From the above discussion it might be concluded that characters viz., fruit diameter, fruit length, fruit weight, number of fruit per plant, phenol content showed high genotypic

and phenotypic coefficient of variation that indicated the prevalence of high genetic variation among the genotypes under study for these characters. Low estimates of the same were recorded for the fruiting span, ascorbic acid, total soluble solid and days to fruit maturity was the evident of very less variability among the genotype for these characters. Whereas, for rest of the characters were exhibited non-significant variation among the genotypes. However, plant height, number of primary branch, calyx length, days to fruit maturity, fruit diameter, fruit length, fruit weight, number of fruit per plant, phenol content and anthocyanin content showed high heritability coupled with high genetic advance of mean as percentage which suggested that these characters might possibly be improved through selection. Although, complex relationship among the genetic parameters argued for adopting recurrent selection as rewarding breeding method for improvement of most of the characters under study.

5.5 Character association analysis

The magnitude of genotypic correlation coefficients was higher than the phenotypic correlation coefficients, which might be due to the strong inherent relationship between the variables and masking effect of environment.

It was recorded that plant height which was significant and negatively correlated with the number of fruit per plant (Pr = -0.349, Gr = -0.351) and ascorbic acid content (Gr = -0.375, Pr = -0.378). However, Plant height found to be significantly positive correlated with the primary branch (0.349) and days to first flower (0.348) at genotypic level only. Other than these traits, all the characters showed non-significant positive relation with the rest of the characters excepting the day to first flower and total soluble solid those were non-significant and negatively correlated with the plant height. There was no significant relation obtained for the number of primary branches with the rest of the traits under the present experiment. However, non-significant but positive relation recorded with the calyx length, days to first flower, days to fruit maturity, fruiting span, fruit diameter, ascorbic acid, anthocyanin content, phenol content.

Calyx length also not showed any significant relation with any other characters. But, its relationship was non-significantly in positive direction for most of the traits. Only, fruit diameter, number of fruit per plant and total soluble solid content of fruit were found to be negatively correlated with the calyx length. Number of days to first flower was highly significant and negatively correlated with days to fruit maturity (Pr = -0.548, Gr = -0.561), fruiting span (Pr = -0.572, Gr = -0.567), fruit length (Pr = -0.369, Gr = -0.373) and anthocyanin content of the fruit (Pr = -0.555, Gr = -0.566). Early flowering decreases total

number of harvests by early completion of fruit bearing period. Highly significant and positive relationship for number of days to fruit maturity was recorded with fruiting span (Pr = 0.893, Gr = 0.835), anthocyanin content (Pr = 0.453, Gr = 0.458) and phenol content of the fruit (Pr = 0.360, Gr = 0.369). On consideration of the non-significant relationship, it was observed that most of the character showed relationship in positive direction with the only exception for fruit diameter and total yield.

The result depicted fruiting span was highly significant and positively correlated with anthocyanin content (Pr = 0.524, Gr = -0.537) and was significant but negatively correlated with fruit diameter (Pr = -0.367, Gr = 0.364). However, non-significant but the positive relation was recorded for fruit length, number of fruit per plant, ascorbic acid content, total soluble solid and phenol content of the fruit. It was found that the diameter of the fruit was high significant and positively correlated with the fruit weight (Pr = 0.534, Gr = 0.531). Whereas, highly significant correlation towards negative direction was observed fruit length (Pr = -0.475, Gr = -0.479), number of fruit per plant (Pr = -0.452, Gr = -0.455) and anthocyanin content of the fruit (Pr = -0.419, Gr = -0.428).

Significant correlation in positive direction was recorded between the fruit length and anthocyanin content of the fruit (Pr = 0.428, Gr = 0.437). Considering the non-significant estimates it was found that most of the characters showed relationship in positive direction excepting ascorbic acid content and phenol content which was negatively correlated.

Fruit weight showed highly significant and negative correlation with the number of fruit per plant (Pr = -0.552, Gr = -0.555) and anthocyanin content (Pr = -0.419, Gr = -0.423). Whereas, a significant relation between the fruit weight and total yield (Pr = 0.339, Gr = 0.367) in positive direction was recorded. However, characters viz., ascorbic acid, total soluble solid and phenol content were non-significantly negative correlated with the fruit weight. Number of fruit per plant was recorded significantly correlated in positive direction with anthocyanin content (Pr = 0.369, Gr = 0.375) and phenol content (Pr = 0.347, Gr = 0.354) of fruit. Other than these ascorbic acid, total soluble solid and total yield were non-significant positively correlated with the fruit number. Analyzed data revealed that there was highly significant positive relation between ascorbic acid with total soluble solid (Pr = 0.631, Gr = 0.639) and phenol content (Pr = 0.397, Gr = 0.411). Although, total yield was highly and significantly negative correlated with the ascorbic acid content of the fruit (Pr = -0.529, Gr = -0.534). Again there significant negative correlation was recorded between the total

yield and total soluble solid content of the fruit (Pr = -0.394, Gr = -0.408). Whereas, phenol content of fruit recorded to be non-significant negative correlated with the total yield.

After summarizing all the findings it was observed that total yield is significantly correlated with the fruit weight. However, magnitude of relationship for other traits viz., plant height, calyx length, number of fruit per plant, fruit diameter and fruit length were towards positive direction with the total yield. Even all the components related to yield attributes were positively interrelated with the each other, indicated the simultaneous selection for these characters might be beneficial in getting enhanced yield attributes. But, all the qualitative parameters were negatively affected with the magnitude of yield related traits in most of the cases excepting number of fruit per plant that showed negative relationship. Present finding argued for the implementation of different and completely separate breeding strategy for developing the line with up-regulated qualitative parameters.

5.6 Path coefficient analysis

The genotypic correlation coefficient of fruit yield and its components along with quantitative and qualitative traits were partitioned into direct and indirect effect on dependent variable i.e., total yield per hectare to obtain the knowledge of the relative importance of the causal factors at phenotypic level especially when more number of variables are considered in correlation. The summary of direct and indirect effect of 15 different characters on total fruit yield per hectare was discussion hereunder.

Plant height exhibited the low positive direct effect (0.1744) on total yield per hectare. But, exhibited moderate positive indirect effect on total yield per hectare through fruiting span (0.2087) and low positive indirect effect on total yield per hectare through ascorbic acid (0.1684). Whereas, negligible but positive indirect effect on total yield per hectare was recorded through calyx length, days to first flower, fruit diameter, fruit weight, total soluble solid and phenol content. Number of primary branches showed negligible negative direct effect (-0.0977) on total yield per hectare and low positive indirect effect on total yield per hectare through fruiting span; as well as, negligible positive indirect effect on total yield per hectare through calyx length, plant height, fruit diameter, fruit length, total soluble solid and phenol content. It was recorded the low positive direct effect of calyx length (0.1281) on total yield per hectare. Whereas, a moderate positive indirect effect was observed through fruiting span. Days to first flower exhibited the negligible negative direct effect (-0.0242) on total yield per hectare. Days to first flower showed very high positive indirect effect on total yield per hectare through number of days to fruit maturity (0.5890).

Very high negative direct effect was recorded for days to fruit maturity (-1.0741) on total yield per hectare. Again high positive indirect effect on total yield per hectare through fruiting span (0.7424) was observed for the days to fruit maturity. However, low positive indirect effect was noted through number of fruit per plant and negligible positive indirect effect was noted through calyx length, days to first flower, fruit weight, number of fruit per plant and phenol content. Fruiting span exhibited high positive direct effect (0.8844) on total yield per hectare. It showed low positive indirect effect on total yield per hectare through number of fruit per plant and negligible positive indirect effect on total yield per hectare through plant height, calyx length, days to first flower and phenol content.

Moderate direct effect at positive direction was recorded for fruit diameter (0.2751) on total yield per hectare. As well as, it was positively correlated with the total yield. Fruit diameter showed positive indirect effect on total yield per hectare moderately through fruit weight; low through ascorbic acid; negligible through plant height, days to fruit maturity, fruit length and total soluble solid. Low estimate of the direct effect at negative direction on total yield per hectare was observed for fruit length (-0.1385). Again moderate positive indirect effect on total yield per hectare was recorded through fruiting span (0.2380). Low but positive indirect effect was recorded through plant height, number of primary branch, calyx length, days to first flower, fruit weight, numbers of fruit per plant, ascorbic acid, phenol content and anthocyanin content.

It was recorded the importance of high positive direct effect of fruit weight (0.3917) on total yield per hectare. As well as, significant positive relation with the total yield was recorded for fruit weight. Fruit weight showed positive indirect effect on total yield per hectare through fruit diameter and ascorbic acid, plant height, number of primary branch, calyx length, total soluble solid and anthocyanin content. High and positive estimate of the direct effect on total yield per hectare was observed for number of fruit per plant. Also, phenotypic correlation showed positive estimate for total yield. Study on indirect effect revealed that most of the characters under study showed negative indirect effect on total yield per hectare except fruiting span, number of primary branches, days to first flower and phenol content those were positive effect. High estimate of the direct effect at negative direction on total yield per hectare was observed for ascorbic acid content (-0.4492) coupled with significantly negative association with total yield (-0.534). It exhibited negative indirect for most of the characters.

Total soluble solid exhibited the low negative direct effect (-0.1651) on total yield per hectare. Its magnitude about correlation was significantly at negative direction total yield. It showed low positive indirect effect on total yield per hectare through number of fruit per plant (0.1792). The direct effect of phenol content (0.0947) on total yield per hectare was positive but very negligible and also showed its relationship with the total yield in negative direction. It showed high positive indirect effect through fruiting span (0.4635) and moderate positive indirect effect through number of fruit per plant (0.2244) on total yield per hectare. Whereas, it's indirect effects were recorded to be negligibly positive through plant height, calyx length, days to first flower, ascorbic acid and total soluble solid. Anthocyanin content exhibited the negligible negative direct effect (-0.0176) on total yield per hectare. Also magnitude for the phenotypic correlation with total yield was at negative direction. Phenol content showed moderate positive indirect effect on total yield per hectare through fruiting span (0.2367) and number of fruit per plant (0.2109).

Overall, path analysis revealed that the direct contribution of traits under study on total yield as dependable variables were highest through fruiting span followed by number of fruit per plant, fruit weight, fruit diameter, calyx length, plant height. However, among them all the characters showed relationship with the yield component at desired direction excepting fruiting span that showed correlation at negative direction with the dependable variable due to combined negative indirect effect via fruit diameter and fruit length. Present contradictory result suggested that considering the fruit span as an important variable further thorough study should be done for better understanding the nature of relation. However, from the present investigation this could be concluded that for number of fruit per plant, fruit weight, fruit diameter, calyx length, plant height is likely to be effective in increasing fruit yield per plant. The complex relationship between coefficient of variation and inheritance component argued for recurrent selection as breeding strategy for the improvement of these characters.

In the present investigation residual effect is 0.3852 at genotypic level indicated 61.5 % contribution of selected characters for yield. Hence, some other characters need to be included as independent variables for dependent variable, yield per hectare. Also, qualitative parameters viz., ascorbic acid, total soluble solid, anthocyanin content showed negative direct effect coupled with significantly negative correlation with yield ascribed that the improvement of yield through selection would be possible by sacrificing the qualitative traits. Hence, there was need for separate breeding strategy to develop quality enriched line.

5.7 Genetic divergence

Genetic divergence among 32 genotypes of brinjal was assessed by adopting Mahalanobis D^2 statistic based on 15 characters.

5.7.1 Grouping of genotypes into different clusters

Result obtained from D^2 analysis showed that all the 32 genotypes under study were broadly categorized into seven different clusters. Among the entire, cluster I showed to be consisting of maximum number of genotypes i.e., total twenty two genotypes. Other than this, cluster II, cluster III, cluster IV and cluster V were consisting of two genotypes in each. Rest two clusters, cluster VI and cluster VII were comprised of single genotype in each.

After evaluating the source of collection of genotypes and the pattern of cluster distribution indicated that, the geographical diversity need not necessarily be related to the genetic diversity. Among the genotypes from one geographical area, parallelism was not noticed between geographical diversity and genetic diversity.

5.7.2 Mean intra and inter cluster distance

It was observed that average inter cluster distance was higher than the average intra cluster distance indicated wide genetic diversity among the genotypes of different groups than those of same cluster. The intra cluster D^2 values ranged from 0.000 to 1932.26. Highest intra cluster distance was recorded for cluster I (1932.26) followed by cluster V (1033.35), cluster IV (734.35), cluster III (728.95), cluster IV (734.35) and cluster II (516.00). Whereas, there was no intra cluster distance observed for cluster VI and cluster VII. Whereas, inter cluster distance found to be maximum for combination between cluster VI and cluster V (9459.58) followed by cluster VI and II (8576.57), cluster VI and cluster VI (8513.05), cluster VI and cluster I (7474.44), cluster VI and cluster III (7027.58) and cluster VI and cluster VII (5953.15). However, minimum inter cluster distance was recorded for combination between cluster IV and cluster II followed by cluster VII and cluster III, cluster V and cluster II and cluster V and cluster IV. However, the reason of no intra distance in the cluster VI and cluster VII in the present investigation was that both the clusters were comprises of single genotype in each case. Highest cluster distance of cluster I and cluster V indicated existence of genetic divergence among these genotypes in these each cluster and thereby could be used for improvement of yield through recombination breeding and also could be used to develop transgressive segregating lines or heterotic population due existence

of high level heterogeneity. The lowest magnitude of inter cluster distance was recorded for the combination between cluster IV and II followed by cluster VII and III indicated that there were no significant genetic diversity among the genotypes of these clusters and could not be possible to utilize in cross breeding improvement programme among them.

Again, the combinations of cluster VI and V followed by cluster VI and II, cluster VI and VI, cluster VI and I, cluster VI and III, cluster VI and cluster VII these showed greater extent of inter cluster distance which indicated on inter-cross hybridization among the genotypes under each cluster combinations might result in a wide spectrum of segregating population as genetic diversity is very distinct among the groups and there by predicted the possibility of using these genotypes under each cluster to develop improved heterotic population or recombinant.

5.7.3 Cluster mean of individual characters and their contribution towards diversity

The mean performance of 32 genotypes from 7 different clusters for 15 characters under study showed that Cluster VI registered highest mean for plant height (115.94 cm) followed by cluster VII (107.65 cm). Highest mean for number of primary branches was recorded in cluster III (7.21) followed by cluster VII (7.15). Highest mean for calyx length was recorded in cluster IV (5.35cm) followed by cluster V (4.49cm). Cluster I recorded lowest mean for days to first flowering (63.67 days) followed by cluster V (63.82 days). Cluster VII showed minimum mean for days to fruit maturity (37.36 days) followed by cluster I (38.58 days). Highest mean for fruiting span was noticed in cluster II (103.08 days) followed by cluster IV (102.36 days). Cluster VI recorded maximum mean for fruit diameter (13.22 cm) followed by cluster VII (10.73 cm). Mean for fruit length was highest in cluster IV (25.02 cm) followed by cluster III (22.25 cm). Cluster VI recorded maximum mean for fruit weight (899.27 g) followed by cluster VII (428.32 g). Cluster II has shown highest mean for number of fruits per plant (34.96) followed by cluster V (15.57). Highest mean for ascorbic acid was recorded in genotypes of cluster II (11.69 mg/100g) followed by cluster III (9.79 mg/100g). Cluster II showed highest mean for total soluble solid (5.89 °B) followed by cluster VI (5.74 °B). Highest mean for anthocyanin (mg/100g) was recorded in genotypes of cluster V (120.05 mg/100g) followed by cluster III (113.70 mg/100g). Highest mean for Phenol (mg/100g) was recorded in genotypes of cluster II & VI (1.43 mg/100g) followed by cluster IV (1.32 mg/100g). Highest mean for Yield/ha (t/ha) was recorded in genotypes of cluster IV (46.10 t/ha) followed by cluster VII (42.25 t/ha).

Contribution of the characters towards total diversity of the genotypes were represented that characters viz., total yield per hectare (30.04 %), number of fruit per plant (28.83) and fruit weight (20.97%) were principal contributing characters towards total divergence. However, comparatively moderate contribution was recorded for fruit diameter, plant height and calyx lengtt. Other than these, low contributions were recorded for ascorbic acid, total soluble solid, anthocyanin, fruit length and number of primary branch. Whereas, for rest of the characters viz., phenol content, days to first flowers and days to fruit maturity did not showed any contribution towards the total diversity.

However, on the basis of mean of cluster performance cluster VI and VII were important for plant height, fruit diameter, primary branches, fruit weight, total soluble solid and total yield. Whereas, for the for the quality traits viz., anthocyanin, phenol and ascorbic acid as well as calyx length, number of fruit plant cluster II and cluster III could be consider as important. So, selection of the genotype from these cluster as crossing breeding parent could emerged most effective. In the other hand, total yield per hectare, number of fruit per plant and fruit weight showed maximum contribution towards the diversity followed by fruit diameter, plant height and calyx length. Result indicated that diverse genotypes can be utilized for improvement of yield productivity. The greater diversity in the present materials was due to these characters which will offer a good scope for improvement of yield through rational selection of parent's genotypes for brinjal. The genotypes of highly divergent clusters may also be utilized in a breeding programme for development of high yielding varieties with desirable attribute and can also be utilized in heterosis breeding programme for development of F1 hybrids with superior yield and quality characters.

It emerged conclusively from the present investigation on evaluation of brinjal germplasm for winter season that all the 32 genotypes collected from different locality of north Bengal were highly diversified and manifestation was less effected by the environment. Selection of the characters under study, specifically number of fruit per plant, fruit weight, fruit diameter, calyx length and plant height will likely to be effective in increasing fruit yield per plant due to having effect of more additive gene action and will be effective in developing heterotic population due to having more diversity. Genotypes under cluster VI and VII will be most effective for the improvement of yield related attributes. The cross combinations between cluster VI and V, cluster VI and II, cluster VI and VI, cluster VI and I, cluster VI and III, cluster VI and cluster VII can be effectively utilized to develop improved heterotic population or recombinant

Future scope of research

Future scope of research

Present investigation suggested following scope of work to be undertaken in future

- Promising genotypes should be tested in different agro-climatic zone of West Bengal and also under all three seasons (Kahrif, Rabi and pre Kharif).
- More characters related to physic-chemical properties of brinjal have to be included in further studies.
- There is need to compare the yield potential of different genotypes with number of hybrids available in the market and research station.
- There is need to screen large number of genotypes against biotic stresses (disease and insect pest) particularly little leaf and fruit borer.
- There is need to formulate breeding programme design to evaluate the performance under heterozygous condition and isolation of promising genotypes based on hybrid performance.
- The genetically divergent genotypes can be used as mapping populations to detect diversity at molecular level and also to identify molecular markers linked to desirable traits for marker assisted selection (MAS).

Bibliography

Bibliography

Ahmad, H., Hasan, M.R., Rahul, S.K., Mahbuba, S, Uddin, J.A.F.M., 2016. Growth and yield analysis of some exotic brinjal lines. *Bangladesh Research Publications Journal*, **12** (2): 112-116.

Ajjappalavara, P.S., 2013. Crop rotation in brinjal (*Solanum melongena L.)* for bacterial wilt incidence. *The Asian journal of horticulture,* **8**(2): 780-781.

Aminifard, M.H., Aroiee, H., Fatemi, H., Ameril, A., Karimpour, S., 2010. Responses of eggplant (*Solanum melongena L.)* to different rates of nitrogen under field conditions. *Journal of Central European Agriculture,* **11**(4): 453-458.

Angadi, P.K., Indiresh, K.M., Rao, M.A., 2017. Correlation studies for fruit yield and its attributing characters in brinjal (*Solanum melongena L.). International Journal of Current Microbiology and Applied Sciences,* **6**(12): 1007-1012.

Ankit, D., Gadhiya, Chaudhari, K.N., Sankhla, P.M., Viradiya, Y.A., Parekh, B., 2015. Genetic architecture of yield and its components in brinjal (*Solanum melongena L.). The Bioscan,* **10**(4): 2139-2144.

AOAC (1990). Official methods of analysis of the association of official analytical chemists, 15th edition (eds. Ed. Helrich, K.), AOAC, Inc., Arlington, Virginia, USA.

Arunkumar, B., Biradar, B.D., 2004. Genetic divergence studies in *rabi* sorghrum. Karnataka Journal of Agricultural Sciences 17: 571-573.

Assinapol, N., Praneetha, S., Rajasree, V., 2017. Performance of grafted brinjal (*Solanum melongena L.)* under different spacing and fertigation levels. *Journal of Pharmacognosy and Phytochemistry,* **6**(2): 307-311.

Ayaz, F.A., Colak, N., Topuz, M., Tarkowski, P., Jaworek, P., Seiler, G., Inceer, H., 2015. Comparison of Nutrient Content in Fruit of Commercial Cultivars of Eggplant *(Solanum melongena L.). Polish Journal of Food and Nutrition Science*, **65**(4): 251–259.

Babu, B.R., Patil, R.V., 2005. Evaluation and variability studies of brinjal genotypes. *Madras Agricultural Journal,* 92 (7-9): 578-584.

Bashar, A., Hossain, M.K., Hasan, R., Islam, S., Huque, M., A.K.M., Alam, N., 2016. Breeding potential of common eggplant (*Solanum melongena L*.) using divergence analysis. *Bangladesh Journal of Botnay*, **45**(1): 109-115.

Begum, F., AminulIslam, A.K.M., Rasul, G.M., Mian, K.M.A., Hossain, M.M., 2013. Morphological diversity of eggplant *(Solanum melongena)* in Bangladesh. *Emirates Journal of Food and Agriculture*, **25** (1):45-51.

Bhushan, A., Samnotra, R.K., 2017. Stability studies for yield and quality traits in brinjal (*Solanum melongena L.). Indian Journal of Agricultural Research*, **51**(4): 375-379.

Chaudhar, B.S., Samadia, D.K., 2004. Variability and character association in chilli landraces and genetypes under arid environment. *Indian Journal of Horticulture* **61** (2) : 132-136.

Chaudhary, A.S., Uniyal, S.P., Pandey, P., 2017. Evaluation of new genotypes of brinjal*(Solanum melongena L.)* under tarai condition of Uttarakhand, *Journal of Applied and Natural Science***, 9**(3): 1840 –1843.

Danquah, J.A., Ofori, K., 2012. Variation and correlation among agronomic traits in 10 accesssions of garden egg plant (*Solanum gilo Raddi*) in Ghana, *International Journal of Science and Nature*, **3**(2) : 373-379.

Dar, S.A., Wani, A.R., Bashir, A., Rather, Kandoo, A.A., 2017. Biochemical basis of resistance in brinjal genotypes against shoot and fruit borer (*Leucinodes Orbonalis*, *Guenee). Chemical Science Review and Letters*, **6**(23): 1931-1940.

Das, S., Mandal, A.B., Hazra, P., 2010. Genetic diversity in brinjal genotypes under eastern Indian conditions. *Indian Journal of Horticulture*. 67: 165-169.

Das, A. Das, S.S., 2013. Assessment of genetic diversity for brinjal in terai zone of West Bengal, India. *International Journal of Current Microbiology and Applied Sciences*, **6**(8): 2401-2406.

Devi, E.S., Singh, N.B., Devi, A.B., Singh, N.G. Laishram, G.M., 2005. Gene action for fruit yield and its components in tomato (*Lycopersicon esculentum* Mill.). *Indian Journal of Genetics and Plant Breeding*, 65:221-222.

Dewey, D.R. Lu, K.H., 1959. A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agronomy Journal*, **51**: 515-518.

Dhameliya, H.R., Dobariya, K.L., 2008. Assessment of genetic variability created through biparental mating and selfing in brinjal (*S. melongena* L.). *Natnl. Journal of Plant Improvement*. 10 (2): 150-153.

Dharwad, N.A., Salimath, P.M., Patil, S.A., 2009. Association and path coefficient analysis in elite germplasm lines of brinjal (*Solanum melongena* L.). *Karnataka Journal of Agricultural Sciences.* 22 (5): 965-966.

Dutta, R., Mandal, A.K., Maity, T.K., Hazra, P., 2009. Multivariate genetic divergence in brinjal (*Solanum melongena* L.). *Journal of Crop and Weed*. 5 (1): 67-70.

Galton, F., 1889. Natural inheritance. Mac Millan, London.

Gupta.S.K., Yadav, G.C., Kumar, A., Yadav, A.K., 2015. Genetic divergence in eggplant (*Solanum melongena L.). Research in Environment and Life Sciences,* **8**(4): 615-618.

Hanchinmani, C.N., Imamsaheb, S.J., 2015. Evaluation different brinjal varieties for growth, yield and economics for north eastern transition zone of Karnataka. *Life Sciences International Research Journal*, **2**: 115-118.

Horti update 2017, Source: Horticulture Statistics at a Glance 2017, published by *Indian Horticos 2018.*

Islam, M.A., Nasrin, A.I., Mian, M.A.K., Shahadat, M.K., Shahjahan, M., 2011. Genetic diversity in exotic eggplant *(Solanum melongena* L.). *Libyan Agriculture Research Center Journal Internation.* 2(1):15-19.

Isshiki, S., Okubo, H., Oda, N., Fujieda, K., 1994. Isozyme variation in eggplant (*Solanum melongena L.). Journal of Japanese Society for Horticultural Science*, **63**: 115-120.

Jadhao, S.T., Thaware, B.L., Rathod, D.R., Navhale, V.C., 2009. Correlation and path analysis studies in brinjal. *Annals of Plant Physiolog,*. 23 (2): 177-179.

Karihaloo, J.L., Gottlieb, L.D., 1995. Allozyme variation in the eggplant, *Solanum melongena L.* (Solanaceae). Theory and Applied Genetics, 90: 578-583.

Khan, R., Singh, Y.V., 2014. Germplasm characterization in eggplant (*Solanum melongena L.). The Asian journal of horticulture,* **8**(2): 356-359.

Koundinya, A.V.V., Das, A., Kumar, P.P., Pandit, M.K., 2017. Profiling of growth and yield parameters of eggplant as influenced by the cropping season. *International Journal of Current Microbiology and Applied Sciences*, **6**(5): 440-448.

Kumar, S., Singh, A.K., Sharma, J.P., Sharma, N., 2007. Genotype clustering in brinjal (*Solanum melongena* L.) using D2 statistic. *Haryana Journal of Horticultural sciences.* 68 (3): 95-96.

Kumar, R.S., Arumugam, T., 2016. Gene action in eggplant landraces and hybrids for yield and quality traits. *International Journal of Farm Sciences,* **6**(1): 79-89.

Kumar, R.S., Arumugam, T., 2013.Phenotypic evaluation of indigenous Brinjal types suitable for rainfed conditions of South India, *African Journal of Biotechnology*, **12**(27): 4338-4342.

Kumar, R.S., Arumugam, T., Anandakumar, C.R., Rajavel, D.S., 2012. Estimation of heterosis and specific combining ability for yield, quality, pest and disease incidence in eggplant (*Solanum melongena L.*), *Bulletin of Environment, Pharmacology and Life Sciences,* **2** (1):03-15.

Kumar, R.S., Arumugam, T., Anandakumar, C.R., 2013. Genetic diversity in eggplant (*Solanum melongena L.). Plant Gene and Trait,* **4**(2):4-8.

Kumar, R.S., Arumugam, T., Premalakshmi, V., 2012. Evaluation and variability studies in local types of brinjal for yield and quality (*Solanum melongena L.). Electronic Journal of Plant Breeding,* **3**(4): 977-982.

Kumar, R.S., Arumugam. T., Ulaganathan, V., 2016. Genetic diversity in eggplant germplasm by principal component analysis, *SABRAO Journal of Breeding and Genetics,* **48**(2): 162-171.

Kumar, R.S., Arumugam, T., Anandakumar, C.R., Premalakshmi, V., 2013. Genetic variability for quantitative and qualitative characters in Brinjal (*Solanum melongena L.). African Journal of Agricultural,* **8**(39): 4956-4959.

Kushwah, S., Bandhyopadhya, B.B., 2005. Variability and correlation studies in brinjal. *Indian Journal of Horticulture*, 62 (2): 210-212.

Lohakare, A.S., Dod, V.N., Peshattiwar, P.D., 2008. Correlation and path analysis studies in green fruited brinjal. *Asian Jouirnal of Horticulture*, 3(1): 173-175.

Lohakare, A.S., Dod, V.N., Peshattiwar, P.D., 2008. Genetic variability in green fruited brinjal. *Asian Journal of Horticulture*, 3(1): 114-116.

Madhavi, N., Mishra, A.C., Om Prasad, J., Bahuguna, N., 2015. Studies on variability, heritability and genetic advance in brinjal (*Solanum melongena L.), Plant Archives,* **15**(1): 277-281.

Madhavi, N., Mishra, A.C., Pushpavathi, Y., Kumari, V.L.P., 2015. Genetic diversity in brinjal (*Solanum melongena L.)* under temperate hills of Uttarakhand, India. *Plant Archives*, **15** (2):1107-1110.

Mahesha, D.K., Apte, U.B., Jadhav, B.B., 2006. Studies on genetic divergence in tomato (*Lycopersicon esculentum* Mill.). Crop Research 32(3): 401-402.

Mangi, V., Patil, H.B., Karadi, S.M., Sanganamoni, M., Jogi, M., 2016. Genetic diversity in brinjal (*Solanum melongena L.)* genotypes. *Research in Environment and Life Sciences,* **9**(8):940-942.

Manju, P.R., Sreelathakumary, I., 2002. Genetic variability, heritability and genetic advance in hot chilli (*Capsicum chinense*). *Journal of Tropical Agricultur,* 40: 4-6.

Meena, S.S., Yashishtha, B.B., Singh, R.K., 2009. Evaluation of brinjal (*Solanum melongena L*.) genotypes for horticultural traits under hot arid environment. *Annuals of Agricultural Research,* **30**(1&2): 24-25.

Mehraj, H., Shiam, I.H., Mutahera, S., Momena, K., Uddin, J.A.F.M., 2015. Performance evaluation of ten Japanese brinjal (*Solanum melongena L*.) varieties. *International Journal of Sustainable Crop Production,* **10**(1): 19-25.

Mehta, N., Asati, B.S., 2008. Genetic divergence for fruit characters in tomato (*Lycopersicon esculentum* Mill.). *Agricultural Science Digest,* 28(2): 141-142.

Nair, R., Mehta, A.K., 2007. Correlation and path coefficient analysis for some metric traits in brinjal (*Solanum melongena* L.). *Asian Journal of Horticulture* 2 (2): 164-168.

Nand, N., Adarsh, A., Kumar, A., Akhtar, S., Kumar, R., Ray, P.K., 2018. Morphological characterization of different genotype of brinjal (*Solanum melongena). International Journal of Current Microbiology and Applied Sciences,* **7**(1): 2218-2226.

Narendra, Panwar, S., Mishra, A.C., Pandey, V., Nautiyal, M., Bahuguna, A., 2013. Evaluation of brinjal (*Solanum melongena L*.) hybrids for growth and yield characters under rainfed mid hill condition of Uttarakhand. *International Journal of Forestry and Crop Improvement,* **4**(1): 32-35.

Ndereyimana, A., Praneetha, S., Pugalendhi, L., Pandian, B.J., Rukundo, P., 2013. Earliness and yield parameters of eggplant (*Solanum melongena L.)* grafts under different spacing and fertigation levels. *African Journal of Plant Science,* **7**(11): 543-547.

Pandit, M.K., Thapa, H., Akhtar, S., Hazra, P., 2010. Evaluation of brinjal genotypes for growth and reproductive characters with seasonal variation. *Journal of Crop and Weed,* **6**(2):31-34.

Patel, K.K., Sarnaik, D.A., Asati, B.S., Tirkey, T., 2004. Studies on variability, heritability and genetic advance in brinjal (*Solanum melongena* L.). *Agricultural Science Digest,* 24 (4): 256-259.

Patel. K., Patel, V.H., Subhash, Andelias, R., 2013. Antioxidant properties and oxidative DNA damage preventive activity of two eggplant (brinjal) varieties, *Journal of Cell and Tissue Research,* **13**(3): 3943-3948.

Patel, S.N., Raj, C., Popat, Patel.P.A., Vekariya, R.D., 2018. Genetic diversity analysis in brinjal (*Solanum melongena L.)* genotypes: A Principal Component Analysis Approach. *International Journal of Current Microbiology and Applied Sciences,* **7**(1): 3296-3301.

Pearson, A.K., 1904. On the generalized theory of alternative inheritance with special reference to Mendal's law. *Phil.Trass. Roy. A.*, **203**: 53-86.

Prabakaran, S., Balakrishnan, S., Kumar, R.S., Arumugam, T., Anandakumar, C.R., 2015. Genetic diversity, trait relationship and path analysis in eggplant landraces. *Electronic Journal of Plant Breeding,* **6**(3): 831-837.

Prabhu, M., Natarajan, S., 2008. Correlation and path analysis in brinjal (*Solanum melongena* L.). *Madras Agricultural Journal,* 95(1-6): 184-187.

Prabhu, M., Kumar, R.A., Ponnuswami, V., 2008. Breeding for shoot and fruit borer resistance in brinjal. *The Asian Journal of Horticulture*, **3**(2): 456-459.

Praneetha, S., 2017. Evaluation of brinjal *(Solanum melongena L.)* germplasm for yield and shoot and fruit borer resistance under drip fertigation. *Electronic Journal of Plant Breeding*, **8(**1): 356-360.

Praneetha, S., Rajashree, V., Pugalendhi, L., 2011. Association of characters on yield and shoot and fruit borer resistance in brinjal (*Solanum melongena L.*) *Electronic Journal of Plant Breeding*, **2**(4): 574-577.

Pujer, P., Jagadeesha R.C., Cholin S., 2017. Genetic variability, heritability and genetic advance for yield, yield related components of brinjal (*Solanum melongena L.*) *Genotypes, international journal of puree and applied bioscience*, **5** (5): 872-878.

Quamruzzaman, A.K.M., Rashid, M.A., Ahmad, S., Moniruzzaman, M., 2009. Genetic divergence analysis in eggplant (*Solanum melongena L.). Bangladesh Journal of Agricultural Research,* **34**(4): 705-712.

Rad, M.R.N., Poodineh, M., Ghalandarzehi, A., Abkhoo, J., 2015. Variability, heritability and association analysis in eggplant (*Solanum melongena*), *ARPN J. Agricultural and Biological Sciences.* **10**(12): 464-468.

Rangana, M., 1997. Manual of analysis of fruit and vegetable products. MacGraw, New Delhi, pp. 643.

Ravali, B., Reddy, R.K., Saidaiah, P., Shivraj, N., 2017. Genetic Diversity in Brinjal (*Solanum melongena L.). International Journal of Current Microbiology and Applied Sciences*, **6**(6): 48-54.

Reddy, M.T., Babu, K.H., Ganesh, M., Begum, H., Dilipbabu, J., Reddy, R.S.K., 2013. Gene action and combining ability of yield and its components for late kharif

season in okra (*Abelmoschus esculentus* (L.) Moench). *Chilean Journal Agricultural Research*, 73(1):9-15.

Rekha, K., Celine, V.A., 2015. Genetic divergence in round fruited brinjal (*Solanum melongena L.). Plant Archives*, **15** (2): 919-921.

Reshmika, P.K., 2015. Genetic variability, divergence and correlation studies in brinjal. *International Journal of Agricultural Science and Research,* **5**(6):103-110.

Sadarunnisa, Reddy, S., R.V.S.K., Begum, H., Reddy, T.D., Reddy, P.N., 2015. Genetic divergence in brinjal (*Solanum melongena L.). Electronic Journal of Plant Breeding*, **6**(1): 331-336.

Samlindsujin, G., Karuppaiah, P., 2016. Studies on genetic divergence in brinjal (*Solanum melongena L.)* for yield attributes and shoot and fruit borer (*Leucinodes arbonalis*) incidence. *International journal of plant sciences,* **11**(1):47-50.

Samlindsujin, G., Karuppaiah, P., Manivannan, K., 2017. Genetic variability and correlation studies in brinjal (*Solanum melongena L.). International journal of plant sciences,* **12**(1):21-27.

Samlindsujin, G., Karuppaiah, P., Manivannan, K., Saravanan, K., 2016. Correlation and path analysis for yield, yield attributes and shoot and fruit borer tolerance in brinjal (*Solanum melongena L.). International journal of plant sciences*, **11**(2):187-192.

Samlindsujin, G., Karuppaiah, P., Saravanan, K., 2017. Genetic variability and correlation studies in brinjal (*Solanum melongena L.). Indian journal of agricultural research,* **51**(2):112-119.

Santhosha, H.M., Indiresh, K.M., Lingaiah, H.B., 2017. Diallel analysis in brinjal (*Solanum melongena L.)* for fruit yield, its attributes and bacterial wilt resistance. *The Asian Journal of Horticulture*, **3**(2): 456-459.

Sekhar, L., Prakash, B.G., Salimath, P.M., Sridevi, O., Patil, A.A., 2008. Genetic diversity among some productive hybrids of tomato (*Lycopersicon esculentum* Mill.). *Karnataka Journal of Agricultural Sciences,* 21(2): 264-265.

Senapathi, A.K., Senapathi, B.K., 2006. Character association in relation to infestation by shoot and fruit borer (*Leucinodes orbonalis* L.) in brinjal (*Solanum melongena* L.). *Indian Journal of Agricultural Research,* 40(1): 68-71.

Senapati, B.K., Sarkar, G., 2005. Genetic divergence in tall indica rice (*Orya sativa* L.) under rainfed saline soil of sundarban. Oryza 42: (1) 70-72.

Senapati, B.K., Sahu, P.K., Sarkar, G., 2003. Genetic divergence in chilli. *Crop Research,* 26 (2): 314-317.

Sharma, A. and Maurya, I.B. 2004. Genetic divergence in brinjal (*Solanum melongena* L.). *Orissa Journal of Horticulture,* 32 (2): 22-25.

Sharma, V.K., Semwal, C.S., Uniyal, S.P., 2010. Genetic variability and character association analysis in bell pepper (*Capsicum annuum* L.*). Journal of Horticulture and Forestry,* 2(3): 58-65.

Shekar, C.K., Ashok, P., HariKumar,V., RaviKumar, K., 2014. Correlation, path analysis and genetic divergence in brinjal (*Solanum melongena L.). Plant Archives*, **14**(2):893-898.

Shinde, K.G., Warade, S.D., Kadam, J.H., 2009. Correlation studies in brinjal (*Solanum melongena L.). International Journal of Agricultural Sciences*, **5**(2): 507-509.

Singh, N., Mishra, A.C., Pandey, V., 2014. Evaluation of Brinjal (*Solanum melongena L.)* Hybrids for growth and yield characters under rainfedmid hill condition of Uttarakhand. *Annuals of Agri-Bio Research,* **19**(1): 144-146.

Singleton, V.L., Orthofer, R., Lamuela-Raventos, R.M., 1999. Analysis of total phenols and other oxidation substrates and antioxidants by means of Folin-Ciocalteu reagent. *Meth. Enzymol.,* **299:** 152-178.

Sreelathakumary I and Rajmony L. 2004. Genetic divergence in chilli (*Capsicum annuum* L.). *Indian Journal of Horticulture* **61**(2) : 137-139.

Swarup, V. (1995). Genetic resources and breeding of aubergine (*Solanum melongena L.*). *Acta Horiculture,* **412**: 71-79.

Swarup, V. 1995. Genetic resources and breeding of aubergine (*Solanum melongena* L.). *Acta Horiculture*. 412: 71-79.

Thangamani, C., Jansirani, P., 2012. Correlation and path coefficient analysis studies on yield and attributing characters in brinjal (*Solanum melongena* L.). *Electronic Journal of Plant Breeding*. **3**(3): 939-944.

Thangamani, C., Jansirani, P., 2012. Correlation and path coefficient analysis studies on yield and attributing characters in brinjal (*Solanum melongena L.*). *Electronic Journal of Plant Breeding,* **3**(3): 939-944.

Tripathy, B., Sharma.D., Jangde, B.P., Bairwa, P.L., 2017. Evaluation of brinjal (*Solanum melongena L.)* genotypes for growth and yield characters under Chhattisgarh condition. *The Pharma Innovation Journal,* **6**(10): 416-420.

Ullah, S., Ijaz, U., Shah, T.I., Najeebullah, M., Niaz, S., 2014. Association and genetic assessment in brinjal, *European Journal of Biotechnology and Bioscience,* **2**(5): 41-45.

Vanaja, T., Babu, L.C., Radhakrishnan, V.V., Unninthan, V.K.G., 2003 Genetic divergence in high yielding rice genotypes. Oryza, **40**(1&2): 40-42.

Vavilov, N.I., 1951. Origin, variation, immunity and breeding of cultivated plants. *Chronol. Bot.* **13**: 4-364.

Vidhya, C., Kumar, N., 2014. Genetic divergence in brinjal (*Solanum melongena* L.). *The Ecoscan,* **4**: 197-200.

Viradiya, Y.A., Chaudhari, K.N., Joshi, H.K., Ghevariya, C.B., 2016. Genetic analysis of yield and its components in egg plant in summer season (*Solanum melongena L.). International Journal of Agriculture Sciences,* **8** (48): 2038-2041.

Wright, S., 1921, Correlation and causation. *Journal of Agricultural Research,* **20**: 557-587.

Yadav, N., Dhankar, S.K., Chandanshive, A.V., Kumar, V., 2016. Studies on variability, heritability and genetic advance in brinjal (*Solanum melongena L.). The Bioscan,* **11**(4): 3001-3005.

Appendix

IBPGR Descriptors for Egg plant (1990)

Vegetative characters

Plant growth habit

3 Upright

5 Intermediate

7 Prostrate

Leaf prickles

Number of prickles on upper surface of the leaf

0 None

1 Very few (1-2)

3 Few (3-5)

5 Intermediate (6-10)

7 Many (11-20)

9 Very many (> 20)

Fruit characters

Fruit calyx spinyness

Average number of prickles per calyx

0 None

1 Very few (< 3)

3 Few (~ 5)

5 Intermediate (~ 10)

7 Many (~ 20)

9 Very many (> 30)

Fruit colour at commercial ripeness

1 Green (Methuen 27D8)

2 Milk white (Methuen 1A2)

3 Deep yellow (Methuen 3A8)

4 Fire red (Methuen 7A8)

5 Scarlet red (Methuen 9A8)

6 Lilac grey (Methuen 16C3)

7 Purple (Methuen 16D-E8)

8 Purple black (Methuen 15F5-8)

9 Black

Calyx colour

1 Light green

3 dark green

5 Light purple

7 Dark purple

Fruit shape (NBPGR)

3 Long

5 Round

7 Oblong

9 Oval