

Genetic Studies on Advance Lines of Brinjal

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In

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By

DEEPA KULESH
160114002

**Department of Horticulture
College of Agriculture, Jabalpur 482004
Jawaharlal Nehru Krishi Vishwa Vidyalaya
Jabalpur, Madhya Pradesh**

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All the assistance and help received during the course of the investigation have been acknowledged by him.

Place: Jabalpur

Date:

Dr. A. K. Naidu
(Chairman of the Advisory Committee)

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Committee	Name	Signature
Chairman	Dr. A.K. Naidu	_____
Member	Dr. B.R. Pandey	_____
Member	Dr. A.K. Mehta	_____
Member	Dr. R.B. Singh	_____

Thesis is approved by _____

The Professor and Head
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Place: Jabalpur

Date:

Dr. A.K. Naidu
Chairman of the Advisory Committee)

MEMBERS OF THE ADVISORY COMMITTEE

Committee	Name	Signature
Chairman	Dr. A.K. Naidu	_____
Member	Dr.B.R. Pandey	_____
Member	Dr. A.K. Mehta	_____
Member	Dr. R.B. Singh	_____

Head of the Department **Dr. A.K. Naidu** _____

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The matter embodied in the thesis has not been submitted for the award of any other degree/diploma. Due credit has been made to all the assistance and help.

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Place: Jabalpur

Date:

**Dr. A.K. Naidu
(Major Advisor)**

**Deepa Kulesh
(Student)**

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Place: Jabalpur
Date:

(Deepa Kulesh)

CONTENTS

CHAPTER No.	TITLE	PAGE No.
1.	Introduction	1 - 2
2.	Review of Literature	3 - 18
3.	Material and Methods	19 - 37
4.	Results	38 - 67
5.	Discussion	68 - 81
6.	Summary, Conclusion and Suggestions for further work	82 - 89
6.1	Summary	82-86
6.2	Conclusion	87-88
6.3	Suggestions for further work	89
	References	90 - 95
	Appendices	I

LIST OF TABLES

Table No.	Title	Page No.
3.1	Meteorological information (week wise) during entire crop season of the year 2017-18 at Jabalpur.	21
3.2	Details of Genotypes used in study.	23
3.3	Arrangement of data from Randomized Complete Block Design	29
3.4	ANOVA for Randomized Completely Block Design	30
4.1	Analysis of variance for different characters in Brinjal (mean sum of squares)	39
4.2a	Mean performance of morphological characters of brinjal	41
4.2b	Mean performance of phenological characters of brinjal	42
4.2c	Mean performance of yield characters of brinjal	44
4.2d	Mean performance of yield characters of brinjal	46
4.3	Estimates of genetic parameters of variations for various characters in Brinjal	49
4.4	Estimates of genotypic and phenotypic correlation coefficients among fruit yield and its attributing traits in brinjal	53
4.5	Genotypic path coefficients showing direct and indirect effects of different characters on fruit yield plant ⁻¹ (g) in brinjal	57
4.6	Phenotypic path coefficients showing direct and indirect effects of different characters on fruit yield plant ⁻¹ (g) in brinjal	58
4.7	Clustering pattern of forty one genotypes of brinjal on the basis of genetic divergence	60

Table No.	Title	Page No.
4.8	Average intra (diagonal) and inter-cluster D ² values among forty one genotypes of brinjal	61
4.9	Characters means of different clusters in brinjal	62
4.10	Contribution of various characters towards total divergence	63
4.11	Qualitative characters of brinjal genotypes	66
4.12	Mean performance of incidence of shoot borer (%) in brinjal	67

LIST OF FIGURE

Figure No.	Title	Page No. (in between)
1	Meteorological information (week wise) during entire crop season of the year 2017-18 at Jabalpur.	23 - 24
2	Layout plan of the experimental field	23 - 24
3	Clustering pattern of 41 genotypes of brinjal	60 - 61

LIST OF PLATE

Plate No.	Title	Page No. (in between)
1	Genotype of brinjal showing fruits shapes, colour and size	66 - 67

LIST OF SYMBOLS

ABBREVIATION	Stand for
@	At the rate
ANOVA	Analysis of Variance
Cm	Centimeter
C.D	Critical difference
D.F	Degree of Freedom
DAT	Days after Transplanting
et.al	Et al (And other co-worker)
M	Meter
Fig.	Figure
GA	Genetic Advance
GCV	Genotypic coefficient of
variation	
G	Gram
Ha	Hectare
Kg	Kilogram
Max.	Maximum
Min.	Minimum
M.S.S	Mean Sum of Square
No.	Number
PCV	Phenotypic coefficient of
variation	
S.Em.±	Standard Error of Mean
%	Percentage
Viz.	(Videlicet) Namely

INTRODUCTION

Brinjal (*Solanum melongena* L.), belonging to family Solanaceae, is one of the most common, popular and principal vegetable crops grown in India and other parts of the world. Solanum is a very large genus and among the 22 Indian species of brinjal all are diploid with somatic chromosome number $2n = 2x = 24$. It is highly productive and usually referred as the poor man's crop.

India is the major producer of brinjal in the world and it is grown in an area of 711 thousand hectare with a productivity of 19.1 metric tonnes hectare⁻¹ and produces 13558 thousand metric tonnes in India. In Madhya Pradesh the annual production is 1068.7 thousand metric tonnes in an area of 42.7 thousand hectare with a productivity of 26.0 metric tonnes hectare⁻¹ (Anonymous, 2014). Major producing states are Orissa, Bihar, Karnataka, West Bengal, Andhra Pradesh, Maharashtra and Uttar Pradesh.

Brinjal has been a staple vegetable in many tropical countries since ancient times. It ranks fair in nutritional value (carbohydrates, proteins and fibre). It contains vitamin A 124 IU, vitamin C 12 mg, calcium 18 mg, phosphorous 47 mg, iron 0.9 mg, protein 1.3 mg, carbohydrates 6.4%, water 91.5% per 100g of fresh weight (Aykroyd, 1966). White brinjal is said to be good for diabetic patients.

Brinjal is usually self pollinated crop but the extent of cross pollination has been reported as high as 29 per cent due to heterostyly condition and hence it is classified as often cross pollinated crop or facultative cross pollinated crop. Being primary centre of origin, India has wide range of variability in this crop in plant type, stem colour, leaf size, leaf tip, midrib colour, fruit size, shape, colour, yield, fruit quality, cooking quality, tolerance to pest and diseases etc. Further, the varietal preference for brinjal is strictly location specific and even in a location the acceptance differs from place to place. So, there is a need to develop preferable varieties to a particular location.

The success of breeding programme for high yield and quality depends on the nature and magnitude of variation available in the genotypes. Greater the variability in a population more will be chance for effective selection for desirable traits (Vavilov, 1951). Evaluation of the brinjal genotypes is necessary to know the performance in terms of yield and other yield attributing characters and the promising genotypes needs to be identified. The genotypes performing well can be released as a variety or it can be put to further use in the breeding programme as a breeding line by the breeder.

Selection from quantitative characters is less efficient, if it is based on phenotypic expression. Hence, it is necessary to assess the relative extent of genetic and non-genetic variability exhibited by individual characters. So partitioning of overall variability is necessary into heritable and non-heritable components by calculating genetic parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) (Chadha and Sindhu, 1983 and Singh and Singh, 1994). Heritability in conjunction with genetic advance is more effective and reliable in predicting the result and the effect of selection.

This crop is having a greater genetic variation with regard to fruit yield and its components. In any crop improvement programme, genetic diversity plays a very important role as it helps in selecting the suitable parents for hybridization programme resulting is superior hybrids and desirable recombinants (Rathi *et al.* 2011). Genetic diversity can be worked out with the help of D^2 analysis which has given by Mahalanobis (1936). It is a very potent technique of measuring genetic divergence.

In view of the above facts, the present studies in brinjal entitled “Genetic studies on advance lines of Brinjal” have been carried out with the following objectives:

1. To estimate the parameters of genetic variability in Brinjal
2. To find out the association analysis among yield and its attributes
3. To assess the genetic divergence in Brinjal

REVIEW OF LITERATURE

Brinjal is one among the vegetables which is having a high potential for exploitation. The phenotype of quantitative trait is the joint product of genotype and environment. Hence, the estimates of variability and its heritable components for the yield contributing characters in the available germplasm are pre-requisite for a breeding programme for high yield.

It is necessary to understand the genetic architecture of the various characters of importance and interrelationship among them. In the present investigation an attempt has been made to study genetic variability, heritability, genetic advance, correlation coefficient analysis, path coefficient analysis and genetic divergence in brinjal. A brief review of available literature pertaining to the investigation has been presented in this chapter under the following headings:

- 2.1 Genetic variability
- 2.2 Heritability and genetic advance
- 2.3 Correlation coefficient analysis
- 2.4 Path coefficient analysis
- 2.5 Genetic divergence

2.1 Genetic variability

For the development of new superior varieties which are far better than the existing ones, we should choose the material that possesses genetic variability having high GCV along with high mean.

Sherly and Shanthi (2008) evaluated twenty four brinjal genotypes for variability, they observed high phenotypic and genotypic coefficients of variation for fruit length, number of fruits plant⁻¹ and fruit weight and fruit yield plant⁻¹.

Nair and Mehta (2009) reported that the phenotypic coefficient of variation was greater than genotypic coefficient of variation for all the

characters. Both phenotypic coefficient of variation as well as genotypic coefficient of variation was high for seed pulp ratio, weight of fruit and number of fruits plant⁻¹.

Prabhu *et al.* (2009) reported that genotypic coefficient of variation was lower than that of phenotypic coefficient of variation for all observed characters. Among the various characters studied, fruit borer infestation showed high genotypic coefficient of variation and phenotypic coefficient of variation.

Gangopadhyay *et al.* (2010) revealed that the large variability for growth habit, leaf blade lobing, calyx colour, fruit shape, size and colour and colour distribution. The objective of this study was to develop a core set of brinjal germplasm to facilitate access, conservation and utilization.

Muniappan *et al.* (2010) carried out a study to assess the variability for eight morphological characters in thirty four eggplant genotypes. They recorded high PCV and GCV by the character viz., number of branches plant⁻¹, fruit breadth, number of fruits plant⁻¹, average fruit weight and fruit yield plant⁻¹.

Ansari *et al.* (2011) concluded that the moderate estimates of genotypic coefficient of variation and phenotypic coefficient of variation were observed for number of fruits cluster⁻¹, average fruit weight, total number of fruits plant⁻¹, fruit length. Maximum genotypic coefficient of variation & phenotypic coefficient of variation were observed for number of flowers inflorescence⁻¹, number of fruits picking⁻¹ and fruit girth.

Indiresh and Santhosha (2011) revealed that the analysis of variance showed the prevalence of sufficient genetic variation among the genotypes from all the characters studied. The high phenotypic coefficient of variation and genotypic coefficient of variation were observed for fruit volume, fruit weight, fruit length, leaf area index, number of fruits plant⁻¹, fruit borer incidence, fruit diameter and number of fruits cluster⁻¹.

Kumar *et al.* (2011) revealed that the phenotypic coefficient of variation was higher than their corresponding genotypic coefficient of variation for days

to 50% flowering, number of flowers cluster⁻¹, number of long and medium styled flowers cluster⁻¹, number of short styled flowers cluster⁻¹, days to first fruit set, plant height, number of primary branches plant⁻¹, number of fruits cluster⁻¹, fruit length, fruit diameter, fruit weight and total yield plant⁻¹. The highest GCV and PCV were recorded for total yield plant⁻¹ and lowest for days to 50% flowering.

Thangavel *et al.* (2011) reported that the magnitude of phenotypic coefficient variation was observed higher than genotypic coefficient of variation, indicating the greater influence of environment. Wider variation was observed for fruit length and number of fruits plant⁻¹, while, it was low for days to first flowering and number of branches plant⁻¹.

Chourasia and Sangeeta (2012) revealed that highest range of variation was reported for fruit weight (g) followed by fruit length (cm), number of fruits cluster⁻¹ and number of fruits plant⁻¹. The highest PCV and GCV were estimated for number of fruits cluster⁻¹ in all the four seasons indicating its widest range of variability in all the situations under study.

Kumar *et al.* (2012) revealed that high estimates of genotypic coefficient of variation and phenotypic coefficient of variation were observed for number of primary branches plant⁻¹, internodal length, average fruit weight, number of fruits plant⁻¹ and fruit yield plant⁻¹ indicating that selection can be predicted to improve the brinjal genotypes for these characters.

Balaji *et al.* (2013) concluded that high PCV and GCV values were seen for plant height, plant spread, number of branches plant⁻¹, number of fruits cluster⁻¹, average fruit diameter, average fruit weight, shoot and fruit borer incidence on shoot and fruit and fruit yield plant⁻¹ indicating high variability in the germplasm.

Chaudhary *et al.* (2013) studied genetic variability in terms of yield plants⁻¹ and its attributing traits in 16 Brinjal germplasm. Values of higher GCV was observed by fruit weight, number of leaves plant⁻¹, number of fruits plant⁻¹. Values of higher PCV were observed by plant height, fruit length, fruit diameter.

Nayak and Nagre (2013) revealed that high PCV and GCV values were seen for average fruit weight whereas, low PCV and GCV were observed for all the characters. High heritability coupled with high genetic advance was seen for fruit width.

Chaudhary and Kumar (2014) studied the genetic variability in brinjal under Lucknow condition. The high PCV and GCV were observed for number of flowers plant⁻¹, fruit yield plant⁻¹, yield plot⁻¹, yield hectare⁻¹ and average weight of fruits.

Gavade and Ghadage (2015) concluded that high PCV and GCV were seen for fruit yield plant⁻¹, width of fruit, weight of fruit and length of fruit whereas number of branches plant⁻¹ recorded least phenotypic and genotypic variance. High heritability values and high per cent of genetic advance were recorded in case of fruit yield plant⁻¹, weight of fruit, length of fruit and width of fruit.

Shende *et al.* (2015) concluded that high PCV and GCV were noticed in number of fruits cluster⁻¹, number of fruits plant⁻¹, average fruit weight and fruit yield plant⁻¹. High heritability and high genetic advance noted in fruit yield plant⁻¹.

Koundinya *et al.* (2017) concluded that higher phenotypic and genotypic co-efficient of variation values were number of fruits plant⁻¹, fruit weight, harvest index, fruit yield plant⁻¹ indicating that a greater amount of genetic variability was present for these characters which provide greater scope for selection.

Patel *et al.* (2017) studied genetic variability for yield and related traits in 72 eggplant genotypes. The highest GCV was recorded in fruit shape, followed by average fruit weight.

2.2 Heritability and genetic advance

It is well known that right selection of the material is one of the important causes for the success of any improvement programme. The proper selection will depend on the knowledge of heritability. Estimate of genetic advance is an important parameter to evaluate effectiveness of selection.

Dhameliya and Dobariya (2007) reported that the estimates of heritability and genetic advance were high for number of fruits plant⁻¹, plant height, days to 1st picking and fruit yield plant⁻¹. The simple selection involving these traits would be effective in genetic improvement of fruit yield in brinjal.

Golany *et al.* (2007) studied 23 genotypes of brinjal to determine the genetic variability and genetic diversity for fruit yield and its contributing characters like plant height, plant spread, fruit length, fruit girth and fruit weight. The GCV, heritability and genetic advance as percentage of mean were high for fruit length, fruit girth and fruit weight indicating that the role of additive gene action.

Ram *et al.* (2007) carried out an experiment, studied the variability and selection parameters was under taken during kharif 2003-2004 in Uttar Pradesh, India. High heritability coupled with high genetic advance indicating additive gene action was exhibited by plant height, days to marketable maturity, plant spread, and yield plant⁻¹ and fruit weight.

Mishra *et al.* (2008) reported that the heritability estimates were highest for fruit shape index. High level of genetic advance was registered for fruit shape index and average weight of fruits. Plant height, plant spread, girth of fruit and number of fruits plant⁻¹ exhibited high levels of heritability and genetic advance, indicating the importance of additive gene effect for these traits. Thus, simple selection will be effective for these traits.

Sherly and Shanthi (2008) revealed that high heritability coupled with high genetic advance was registered for fruit length, number of fruits plant⁻¹, fruit weight and fruit yield plant⁻¹. These characters can be effectively improved through selection.

Nair and Mehta (2009) reported that the high heritability accompanied by high genetic advance was observed for weight of fruit. High heritability and moderate genetic advance were observed for plant height, fruiting span and number of fruits plant⁻¹ suggesting that selection based on phenotypic performance of these traits is possible.

Sao and Mehta (2009) showed that high degree of genetic variability was observed for the characters such as average fruit weight, fruit length, fruit girth, number of flowers inflorescence⁻¹, number of fruits cluster⁻¹, total number of fruits plant⁻¹ and total fruit yield plant⁻¹ accompanied with high heritability and genetic advance. Some characters like days to 1st flowering, days to 1st fruiting, plant height, number of primary branches plant⁻¹, total soluble solids and rind thickness showed low to moderate variability coupled with high heritability and low to moderate genetic advance in the present material.

Naik *et al.* (2010) conducted experiment using 61 genotypes with randomized block design. High heritability values and high percentage of genetic advance were recorded in fruit length, no. of fruits plant⁻¹ and yield plant⁻¹. This indicated yield could be improved by selection.

Ansari *et al.* (2011) revealed that the highest estimates of heritability coupled with high genetic advance estimated for the average fruit weight and number of fruits plant⁻¹ showed effectiveness of simple selection for improvement of these characters.

Indiresh and Santhosha (2011) revealed that the high heritability coupled with high genetic advance were observed for fruit volume, fruit weight, leaf area index, fruit length, fruit diameter and number of fruits plant⁻¹, indicating these characters are governed by additive gene action. Hence, direct selection may be followed for the improvement of brinjal for these characters.

Kumar *et al.* (2011) showed that the heritability estimates were highest for fruit weight, plant height, days to 1st fruit set, total yield plant⁻¹, fruit length, days to 50% flowering, number of flowers cluster⁻¹, long styled flowers cluster⁻¹, number of short styled flowers cluster⁻¹, number of medium styled flowers cluster⁻¹, number of primary branches plant⁻¹ and number of fruits cluster⁻¹.

Thangavel *et al.* (2011) reported that the low heritability was observed for fruit girth and yield plant⁻¹. High heritability coupled with high genetic advance was observed for days to 1st flowering and number of branches plant⁻¹.

¹ indicating the involvement of additive gene action in the inheritance of these traits.

Dhaka and Soni (2012) revealed that high heritability was observed for number of fruits plant⁻¹ and average fruit weight. High heritability coupled with high genetic advance was seen for fruit yield plant⁻¹, number of fruits plant⁻¹ and average fruit weight.

Shekhar *et al.* (2012) concluded that high heritability coupled with high genetic advance were observed for number of branches plant⁻¹, number of fruits plant⁻¹, fruit length, fruit width, fruit yield plant⁻¹ and fruit yield plot⁻¹ indicating these characters are governed by additive gene action.

Ambade *et al.* (2013) revealed that high heritability estimates was recorded for average fruit weight, followed by fruit yield plant⁻¹, fruit girth, number of long style flower inflorescence⁻¹, plant height, total number of fruits plant⁻¹, fruit length, number of fruits cluster⁻¹, number of primary branches plant⁻¹, number of flowers cluster⁻¹, days to 1st fruiting and days to 1st flowering.

Patel *et al.* (2013) conducted an experiment with 68 accessions of brinjal at IIVR, Vanarasi. High heritability and high genetic advance were found among the characters except days to 50% flowering. All the traits contain highly significant mean squares due to genotypes. In this case it could be inferred that simple selection will be effective for improving this traits as the characters were mostly controlled by additive genes.

Kumar *et al.* (2014) observed that high heritability coupled with high genetic advance was seen for all the characters except days to 50 per cent flowering.

Singh *et al.* (2014) concluded that high heritability estimates in narrow sense were observed for length of fruit, width of fruit and weight fruit⁻¹, whereas, high genetic advance was observed in weight fruit⁻¹ and plant height.

Vidhya and Kumar (2015) revealed that the genotypic and phenotypic coefficients of variations were highest for fruit girth followed by number of

fruits plant⁻¹. The high heritability and high genetic advance has been observed for fruit girth, number of fruits plant⁻¹, single fruit weight and marketable yield plant⁻¹.

Koundinya *et al.* (2017) observed that high heritability coupled with high genetic advance as percent of mean was seen for the characters like plant height, days to 1st flowering, days to 50% flowering, number of fruits plant⁻¹, fruit weight, harvest index and fruit yield plant⁻¹ depicting that these traits were under the strong influence of additive gene action and hence simple selection based on phenotypic performance of these traits would be more effective.

2.3 Correlation coefficient analysis

Correlation refers to the degree and direction of association between two or more variables. Correlation analysis measures the mutual relationship between various plant characters and determines the component characters on which selection can be based for genetic improvement of yield.

Kamani and Monpara (2006) reported that the fruits plant⁻¹ exhibited positive correlation with fruit yield plant⁻¹, fruit weight and fruit girth and negative association with fruit length only in one cross, whereas association between fruit weight and fruit yield was significantly positive in both the crosses. Thus, fruit weight seemed to be a major component of fruit yield and due consideration on this character should be given for improvement in fruit yield.

Naliyadhara *et al.* (2007) revealed that the genotypic correlation coefficients were higher than corresponding phenotypic coefficient for most characters reflecting predominant role of heritable factors. Fruit yield displayed significant and positive genotypic and phenotypic correlations with fruit weight.

Nair and Mehta (2007) revealed that the correlation coefficient at the phenotypic level of yield plant⁻¹ was significant and positive with number of fruits plant⁻¹ and plant height. These traits should be considered highly dependable and reliable during selection to improve the yield. Negative and

significant correlation was observed with days to flower initiation, number of branches plant⁻¹, days to 1st picking, number of fruits cluster⁻¹ and days to last picking.

Prabhu and Natarajan (2008) found that marketable yield plant⁻¹ recorded positive correlation with plant height, branches plant⁻¹, mean fruit weight, fruit length and fruit number plant⁻¹.

Prabhu *et al.* (2008) revealed that the marketable yield plant⁻¹ showed positive significant correlation with plant height, number of branches plant⁻¹ and mean fruit weight.

Dharwad *et al.* (2009) indicated strong correlation of number of branches plant⁻¹, fruit weight and flowers inflorescence⁻¹ with fruit yield. However, it exhibited weak association with days to flowering and fruits cluster⁻¹.

Sing *et al.* (2010) carried out an experiment containing 99 genotypes of Brinjal to assess the character association and contribution of quantitative trait towards yield. Yield hectare⁻¹ was positively correlated with number of flowers plant⁻¹, number of fruits plant⁻¹, fruit length, fruit weight, fruit volume, number of fruit picking, plant height and plant girth.

Ansari *et al.* (2011) studied the association analysis of total fruit yield plant⁻¹ in brinjal and reported positive and significant correlation with marketable fruit yield plant⁻¹, number of primary branches plant⁻¹, number of fruit picking⁻¹ and total number of fruits plant⁻¹ in both the seasons, number of fruits cluster⁻¹ in rainy season only. Whereas, they found negative significant correlation with days to 1st picking, days to flowering, days to 1st fruiting in both the seasons.

Dubey (2012) conducted correlation studies on twelve F₁ hybrids and one open pollinated variety of brinjal at Raipur. He reported that total fruit yield showed significant and positive correlation with number of fruits plant⁻¹. Plant height showed significant and positive correlation with days to 1st flowering and days to 1st picking at phenotypic level. Pericarp thickness showed

significant and positive correlation with fruit length and fruit weight while it showed negative correlation with number of flowers cluster⁻¹.

Thangamani and Jhansirani (2012) conducted correlation studies with twenty five F₁ hybrids in brinjal which revealed that yield plant⁻¹ showed positive correlation with number of branches plant⁻¹, percentage of long styled flowers and number of fruits plant⁻¹. A significant negative correlation of yield was observed with days to 1st flowering.

Ahmed *et al.* (2013) stated about an experiment containing 35 genotypes of brinjal. This experiment revealed that phenotypic and genotypic association of fruit yield was significantly positive with number of fruits plant⁻¹, fruit weight, fruit width whereas, plant height, plant spread, number of primary branches and fruit length was insignificantly negatively correlated.

Rekha *et al.* (2012) stated that correlation provides information on the nature and extent of relationship among all pair characters. They conducted an experiment containing 27 accessions. This revealed that yield plant⁻¹ provided positive correlation with percent of long and medium styled flowers, number of primary branches, fruit length, number of secondary branches, plant height, canopy spread and fruits plant⁻¹. It exhibited negative correlation with fruit infestation.

Lakshmi *et al.* (2014) revealed that the correlation coefficient analysis in 84 varieties of brinjal for number of flowers cluster⁻¹, number of fruit cluster⁻¹, average fruit length and number of fruits plant⁻¹ with fruit yield among themselves was positive and highly significant and these traits were identified as yield components.

Shende *et al.* (2014) reported that association of fruit yield plant⁻¹ with number of fruits cluster⁻¹ and number of fruits plant⁻¹ was found positive and highly significant at genotype level.

Patel *et al.* (2015) observed that fruit yield displayed highly significant and positive correlation with number of flowers cluster⁻¹, number of flowers plant⁻¹, number of fruits cluster⁻¹, number of fruits plant⁻¹ and number of branches plant⁻¹ at genotypic level.

Koundaniya *et al.* (2017) observed that fruit yield plant⁻¹ showed highly positive significant correlation with number of primary branches plant⁻¹, number of fruits plant⁻¹ and harvest index and significant negative correlation with days to 1st flowering.

2.4 Path coefficient analysis

This method illustrate as a means of analyzing correlation coefficient. A path coefficient is simply standardized partial-regression coefficient and as such measures the direct influence of one variable upon another and permits the separation of the correlation coefficients into components of direct and indirect effects.

Kushwah and Bandhyopadhy (2007) revealed that the fruits plant and fruit diameter had direct positive effect on fruit yield, while, the days to 1st picking exhibited negative direct effect on yield. The residual effect of both path analysis suggested that more number of characters should be incorporated to account the entire variability of brinjal crop in cold climatic condition.

Naliyadhara *et al.* (2007) exhibited an experiment with 21 genotypes of brinjal. Path coefficient analysis showed that fruit length, fruit weight and plant spread exerted positive direct effect on fruit yield suggesting giving emphases on such fruit weight.

Nair and Mehta (2007) showed that weight of fruit, number of fruits plant⁻¹, days to flower initiation, seed weight fruit⁻¹, number of fruits cluster⁻¹, days to 1st picking, length of fruits and number of branches plant⁻¹ exerted direct positive effect on yield plant⁻¹. Hence, emphasis should be given for such traits when imposing selection to improve aubergine yield.

Lohakare *et al.* (2008) found that in 23 genotypes of green fruited brinjal revealed positive direct effect on yield plant⁻¹ through number of fruits plant⁻¹, average fruit weight, fruit index, days to 1st fruit harvest, number of primary branches and plant spread. Hence, these characters may be given consideration while making selection for the improvement of brinjal.

Prabhu *et al.* (2008) revealed that the number of branches plant⁻¹, mean fruit weight, fruit length and number of fruits plant⁻¹ exhibited positive direct effect on marketable yield.

Jadhao *et al.* (2009) revealed that plant height, number of branches plant⁻¹, days to initiation of flowering, days to 1st picking, days to last picking, fruit length and fruit weight showed positive direct effect on fruit yield plant⁻¹ indicating these characters had direct relation with yield.

Sing *et al.* (2010) carried out an experiment containing 99 genotypes of brinjal to assess the character association and contribution of quantitative trait towards yield. The path analysis revealed that fruit weight and fruit plant⁻¹ had high direct effect on fruit yield. However, indirect effect of fruit diameter, leaf area and plant spread were appreciable to affect fruit yield in brinjal.

Chattopadhyay *et al.* (2011) showed that among the eleven yield component traits, fruit weight and number of marketable fruits plant⁻¹ showed highly positive direct effect on marketable fruit yield plant⁻¹. Attention should be paid on selection based on marketable fruit weight and number of marketable fruits plant⁻¹ for marketable yield improvement of brinjal.

Ahmed *et al.* (2013) carried out an experiment with 35 brinjal genotype. This research revealed direct effect of fruit weight, number of fruits plant⁻¹, plant spread, fruit weight and number of primary branches whereas, plant height had indirect effect on fruit yield.

Patel *et al.* (2013) conducted an experiment with 68 accessions of brinjal at IIVR, Vanarasi. Path analysis showed average fruit weight and number of fruits plant⁻¹ were the major factors to determine fruit yield plant⁻¹ and had high direct effects. Hence, in this research work, it was evident that number of branches, average fruit weight and number of fruits plant⁻¹ indicated direct contribution on yield of fruits.

Verma (2013) conducted experiment with 16 genotypes of eggplant. Over all observation of path coefficient analysis showed that direct contribution of fruit yield plant⁻¹, fruit yield hectare⁻¹, fruit weight, number of

fruits plant⁻¹ and number of flowers plant⁻¹ was of higher magnitude on fruit yield.

Lakshmi *et al.* (2014) evaluated path coefficient analysis in brinjal and revealed that characters viz., fruit set percentage, fruit weight, number of fruits plant⁻¹, relative style length, number of flowers cluster⁻¹ had high direct and correlation values.

Shande *et al.* (2014) studied path coefficient analysis and revealed that length of fruit, number of fruits cluster⁻¹, plant height, days to last picking, average weight of fruit and number of fruits plant⁻¹ would be selection criteria for yield improvement in brinjal.

Gupta *et al.* (2017) observed that high magnitude of positive direct effect on fruit yield was exerted by marketable fruit yield plant⁻¹ followed by fruit weight and fruits plant⁻¹. The negative direct effects on yield was showed by fruit circumference and plant height but were substantially low. Marketable fruit yield plant⁻¹ was found to have substantial positive indirect effect for fruit weight, fruit circumference and fruits plant⁻¹.

2.5 Genetic divergence

Genetic diversity refers to the total amount of genetic variation present in a germplasm or population or species or variety of genes and genotypes found in a particular crop species. Study of genetic divergence in existing germplasm in for hybridization is more realistic selecting the parents. The genetic diversity is represented in terms of statistical distance is called D² statistic. It measures the distance for a number of traits between two populations.

Sharma and Maurya (2004) assessed forty genotypes of aubergine for genetic divergence. The genotypes were grouped into seven clusters. The characters like number of fruits plant⁻¹, 1000 seed weight and average width of fruit had the maximum contribution toward genetic divergence. Inter-cluster distance was maximum between cluster V and VII. They also found that there was no relationship between genetic divergence and geographic distribution.

Singh *et al.* (2005) studied thirty five genotypes of brinjal for genetic diversity at Ludhiana and are grouped into eleven clusters. The clustering was irrespective of geographic distribution. Three genotypes viz., Punjab Sadabahar, Punjab Jamunigola and HP-14 exhibited maximum diversity from other genotypes and thus can effectively be used as one of the parents in hybrid breeding programme to exploit heterotic expressions for fruit yield and other economic characters.

At Karnataka, Naik (2006) studied sixty one genotypes of brinjal and is grouped into eight clusters. The cluster III showed maximum intra cluster distance and maximum inter-cluster distance observed between clusters III and VIII. Among sixteen characters, fruit length contributed maximum to genetic diversity followed by number of primary branches, plant height and number of fruits cluster⁻¹.

Bansal and Mehta (2007) reported that Mahalanobis D² statistics was used to study genetic divergence for 23 characters in a collection of 26 brinjal genotypes which were grouped into six clusters. The maximum inter cluster distance was observed between cluster III and VI, while minimum distance was recorded between cluster III and IV.

Kumar *et al.* (2007) assessed genetic diversity in 57 genotypes of brinjal using Mahalanobis D² statistics. They were grouped into eight clusters. Intra-cluster distance was quite high in cluster VIII, VII, and III inferring that variability within these clusters can be crossed to get some improvements. The inter-cluster distance was maximum between cluster VIII and VII. The characters such as fruit length, fruit weight and fruit yield plant⁻¹ contributed maximum to genetic divergence indicating that diversity in brinjal has resulted mostly from fruit characters.

Sherly and Shanthi (2007) studied 24 genotypes of brinjal for genetic diversity. The maximum inter cluster distance was observed between cluster II and cluster IV (43.45), while minimum distance was recorded between cluster I and III (24.39). The contribution of characters towards genetic divergence was noticed more in fruit yield plant⁻¹.

Genetic diversity was assessed in 75 aubergine genotypes by Vandana Yadav (2008) cultivars IC-1, IC-7, IGB-1, IGB-4 and IC-19 showed higher values for yield and yield contributing characters and were placed in different clusters.

Mehta and Sahu (2009) studied genetic divergence in 14 aubergine genotypes using Mahalanobis D^2 statistics for fruit yield and fruit characters. These genotypes were grouped into 5 different clusters. The highest inter-cluster distance was observed between clusters I and II, followed by cluster III and IV, suggesting wide diversity among these groups. Considering cluster mean and the genetic distances, the crossing between genotypes of cluster I and cluster II with IV were likely to recombine the genes for high fruit yield.

Genetic divergence among 19 eggplant genotypes was estimated using Mahalanobis's D^2 statistic by Quamruzzaman *et al.* (2009). Altogether five clusters were formed. The highest inter-cluster distance was observed between cluster IV and V (10.748). Therefore, more emphasis should be given on cluster V for selecting genotypes as parents for crossing with the genotypes of cluster II which may produce new recombinants with desired traits.

Genetic divergence among 11 eggplant genotypes was estimated using Mahalanobis D^2 statistics by Islam *et al.* (2011). The 11 genotypes were grouped into four distinct clusters. The highest and the lowest intra cluster distance were observed in cluster II and cluster IV respectively. The highest inter cluster distance was between clusters I and III (8.757), while, it was the lowest between clusters I and II (2.203). Fruit weight, fruit length, fruit breadth, plant height and yield plant⁻¹ had the highest contribution towards total divergence.

Rathi *et al.* (2011) studied 30 genotypes of brinjal for genetic diversity. The 30 genotypes were grouped into five distinct clusters. The maximum inter cluster distance was observed between cluster I and cluster IV (5.78), while, minimum distance was recorded between cluster I and II (2.78).

Caguiat and Hautea (2014) conducted an experiment for genetic diversity sessment of 64 Philippine eggplant germplasm. The morphological trait and SSR data were analyzed as separate and combined data sets using principal component analysis (PCA) and unweighted pair-group method with arithmetic averages (UPGMA) cluster analysis. This study provided significant information for the need to increase the present eggplant collection and to widen the genetic diversity of currently cultivated eggplant varieties in the Philippines.

Madhavi *et al.* (2015) studied genetic diversity in 21 genotypes of egg plant using Mahalanobis's D^2 statistics. Maximum inter-cluster genetic distance was between cluster V and cluster VI (3041.06), while it was the minimum between cluster II and cluster III (778.03). 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 plant⁻¹ (31.82), number of pickings (6.00) and fruit yield plant⁻¹ (1.57 kg).

Karim *et al.* (2016) conducted an experiment and multivariate analysis of twenty six genotypes of eggplant were done to estimate the genetic diversity and to select the potential parents for a successful hybridization program. As per Principle Component Analysis, D^2 and cluster analysis, the genotypes were grouped into five clusters. The highest inter-cluster distance was between Cluster II and Cluster III (37.82) and the lowest between Cluster I and Cluster III (4.39). Cluster III showed the maximum intra-cluster distance (1.58), whereas Cluster II showed the lowest intra-cluster distance (0.48).

Kumar *et al.* (2016) 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. Intermating between genotypes of clusters I and IX would produce more desirable transgressive segregants for breeding.

Ravali *et al.* (2017) studies 35 genotypes for 19 characters for genetic divergence. The maximum intra cluster distance was exhibited by cluster II followed by cluster V and cluster X. The maximum inter-cluster D^2 value was observed between VIII and IX. Maximum contribution towards the total

divergence was exhibited by fruit yield plant⁻¹ (30.57%) followed by average fruit weight (29.90%) and ascorbic acid content (15.51%).

MATERIAL AND METHODS

The materials used and methods employed during the course of investigation on “Genetic studies on advance lines of Brinjal” are as follows:

3.1 Experimental site

The present investigation was conducted at Horticulture complex, Department of Horticulture, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur (M.P.) during the year 2017-18.

3.1.1 Soil

The soil of the experimental field was medium black with good drainage, uniform texture and medium NPK status.

3.1.2 Climate and Weather

Jabalpur is situated in “Kymore Plateau and Satpura Hills” agro climatic region of M.P. It falls in 23.9⁰ N latitude and 79.58⁰E longitudes with an altitude of 411.8 m above the mean sea level. Jabalpur is situated in the semi-arid region having sub-tropical climate with hot dry summer, and cold winter. The average rainfall is about 1375 mm, which is mainly distributed from mid June to September. The average maximum and minimum temperature ranges between 46.6⁰C and 21⁰C. The mean relative humidity reaches up to 78% during winter (November- February) with occasional frost.

The data related to weekly maximum and minimum temperature, relative humidity rainfall (mm), sunshine hours and wind velocity (km/hr) recorded at Meteorological Observatory Krishi Nagar, J.N.K.V.V, Jabalpur are presented in the Table 3.1.

3.2 Experimental material

The experimental material includes 39 genotypes and two check of the brinjal collected from different states of India. Genotypes are presented in Table 3.2.

3.3 Experimental details

3.3.1 Design of experiment

The experiment was laid out in Randomized Complete Block Design with three replications and each replication consisted of forty one genotypes. All the genotypes were randomized separately in each replication. The plan of layout is given in Fig.2 and other details are given as below:-

S. No.	Particulars	Details
1.	Crop	Brinjal (<i>Solanum melongena</i> L.)
2.	Design of experiment	Randomized Complete Block Design
3.	Number of replication	3
4.	Number of genotypes	41
5.	Total number of plots	123
6.	Plot size	4.50 x 1.4m
7.	Spacing	70cm x 45cm
8.	Total number of plants per	20
9.	Gross experimental area	210.7m ²
10.	Net experimental area	774.9m ²
11.	Date of nursery sowing	14/08/2017
12.	Date of transplanting	14/09/2017
13.	Season	Rabi

3.4 Agronomical Operations

3.4.1 Raising of seedlings

The nursery beds were dug and prepared thoroughly. After sowing seeds were covered with a thin layer of sieved FYM. Sprinkling of water was done immediately to make the beds well moisturized till the germination. Seeds of different genotypes were treated with Thiram @ 2g/kg of seeds before sowing and were sown on 14 August 2017 in Separate bed uniformly at a depth of 2-3 cm.

Table 3.1: Meteorological information (week wise) during entire crop season of the year 2017-18 at Jabalpur

Month	No. of weeks	Temperature		Sun shine	Rainfall (mm)	Relative		Rainy days
		Max.	Min.			Morn.	Even.	
Aug.	34	23.9	31.6	5.9	72.4	90	67	3
	35	23.7	31.3	3.9	22	90	65	3
Sept.	36	24	32.5	7.1	1.5	88	65	0
	37	23.3	32.8	5.4	87.8	91	64	2
	38	22.4	30.7	3	98.3	90	73	3
	39	21.9	32.9	9.3	0	89	52	0
Oct	40	20.3	33.4	8.9	7.4	90	51	1
	41	21.7	32.6	8.4	9.2	92	56	1
	42	17.9	33.6	8.8	0	87	40	0
	43	15.9	33.1	8.9	0	81	26	0
	44	12.2	31.1	8.4	0	87	29	0
Nov	45	10.2	30	8.8	0	86	27	0
	46	11.9	28.9	7.2	0	87	42	0
	47	10.1	27.6	5.9	0	86	31	0
	48	5.1	28.1	8.6	0	82	21	0
Dec	49	8.1	26.7	6.7	0	80	30	0
	50	9	27.5	6.6	0	88	35	0
	51	5.5	24.8	4.2	0	88	32	0
	52	3.9	25.2	7.3	0	86	28	0
Jan	1	9.7	28.8	7.8	0	87	30	0
	2	12.6	24.7	9.1	0	88	29	0
	3	10.5	28.4	9.3	0	88	30	0
	4	12.7	31	9.2	0	86	25	0
	5	6.8	26.7	9.8	0	85	28	0
Feb	6	12.4	26.6	5.4	0	81	52	0
	7	11.5	25.2	6.4	18	91	45	3
	8	12.5	31.2	9.8	0	80	28	0
	9	14	32.4	8.9	15	79	26	1
March	10	14.1	30.9	6.9	1	75	33	0
	11	15.4	33.3	7.4	0.8	74	30	0
	12	14.7	34.4	8.4	17	64	20	1
	13	13.5	37	9.1	8.7	54	18	0
April	14	18.1	38	11.4	10.8	56	22	0
	15	20.6	37	15.3	17.9	67	40	0

Source: Department of Physics and Agro-meteorology, College of Agricultural Engineering, J.N.K.V.V., Jabalpur (M.P)

Table 3.2 Details of genotypes and checks used in the study

S. No.	Genotypes	Source
1.	2015/BRLVAR-1	IIVR, Varanasi
2.	2015/BRLVAR-2	IIVR, Varanasi
3.	2015/BRLVAR-3	IIVR, Varanasi
4.	2015/BRLVAR-4	IIVR, Varanasi
5.	2015/BRLVAR-5	IIVR, Varanasi
6.	2016/BRLVAR-1	IIVR, Varanasi
7.	2016/BRLVAR-2	IIVR, Varanasi
8.	2016/BRLVAR-3	IIVR, Varanasi
9.	2016/BRLVAR-4	IIVR, Varanasi
10.	2016/BRLVAR-5	IIVR, Varanasi
11.	2016/BRLVAR-6	IIVR, Varanasi
12.	2016/BRLVAR-7	IIVR, Varanasi
13.	2016/BRLVAR-8	IIVR, Varanasi
14.	2016/BRLVAR-9	IIVR, Varanasi
15.	2017/BRLVAR-1	IIVR, Varanasi
16.	2017/BRLVAR-2	IIVR, Varanasi
17.	2017/BRLVAR-3	IIVR, Varanasi
18.	2017/BRLVAR-4	IIVR, Varanasi
19.	2017/BRLVAR-5	IIVR, Varanasi
20.	2017/BRLVAR-6	IIVR, Varanasi
21.	2017/BRLVAR-7	IIVR, Varanasi
22.	2017/BRLVAR-8	IIVR, Varanasi
23.	2017/BRLVAR-9	IIVR, Varanasi
24.	2017/BRRVAR-1	IIVR, Varanasi
25.	2017/BRRVAR-2	IIVR, Varanasi
26.	2017/BRRVAR-3	IIVR, Varanasi
27.	2017/BRRVAR-4	IIVR, Varanasi
28.	2017/BRRVAR-5	IIVR, Varanasi
29.	2017/BRRVAR-8	IIVR, Varanasi
30.	2017/BRRVAR-10	IIVR, Varanasi
31.	2017/BRRVAR-11	IIVR, Varanasi
32.	2017/BRRVAR-12	IIVR, Varanasi
33.	2016/BRRVAR-1	IIVR, Varanasi
34.	2016/BRRVAR-2	IIVR, Varanasi
35.	2016/BRRVAR-4	IIVR, Varanasi
36.	2016/BRRVAR-5	IIVR, Varanasi
37.	2016/BRRVAR-7	IIVR, Varanasi
38.	2016/BRRVAR-8	IIVR, Varanasi
39.	2016/BRRVAR-9	IIVR, Varanasi
40.	Punjab Sadabahar (C)	PAU,
41.	Kashi Taru (C)	IIVR, Varanasi

3.4.2 Land preparation and transplanting

The experimental area was ploughed and harrowed in order to bring the soil in well-pulverized condition. Plots were made according to the layout plan after preparing raised beds (15 cm) covered with silver black plastic mulch with drip irrigation. Seedlings were uprooted from the nursery bed and transplanted in the plots at a spacing of 70cm row to row and 45cm plant to plant. Light irrigation was given before uprooting seedlings from the nursery beds so that minimum damage may occurs to roots of the seedling. A week after transplanting gap filling was done.

3.4.3 Irrigation.

A light irrigation was applied for establishment of the seedlings after transplanting. Subsequent irrigations were provided as and when required for growth and development of plants. The regular irrigation was given through drip at 3.0 hrs.

3.4.4 Intercultural operations

The experimental plots were kept weed free. Three hand weeding were done.

3.4.5 Manures and fertilizers

Well rotted FYM was applied @ 20 t/ha before second harrowing while preparing the field. Nitrogen, Phosphorus and Potash were applied @ 150, 80, and 100 kg/ha in the form of Urea, Di ammonium phosphate (DAP) and Murate of potash (MOP), respectively. Half of the nitrogen and full amount of the phosphorus and potash were given as basal dose before mulching, while the remaining half quantity of nitrogen was applied in two equal split at 25 and 45 days after transplanting by drip.

3.4.6 Plant protection measures

The crop was sprayed with imidachlorprid 0.005% or thiomethoxan 0.025% for control of Aphids and Jassid, alternate to keep the crop free from pest during crop growth period.

3.5 Sampling

Sampling was done at 30 days up to till harvest for growth analysis. Five plants were randomly selected from each genotype and replication for the study.

3.6 Observation recorded

The data recorded on various parameters were subdivided into four categories during the period of experimentation. The data were recorded as per standard procedure.

(A) Morphological Parameters

3.6.1 Plant height (cm):

The height of the main stem from the ground level to the apical bud (leaf apex) was measured with the meter scale at 30 days interval (i.e. 30, 60, 90 DAT and at final harvest).

3.6.2 Number of branches plant⁻¹

The numbers of primary branches arising from the main stem of each tagged plant was counted at the final picking (i.e. 150 DAT) stage.

(B) Phenological Parameters (flower characters)

3.6.3 Days to 1st flowering

Number of days taken from the transplanting to the appearance of 1st flower on the five randomly selected plants in each plot was noted and average was calculated.

3.6.4 Days to 50% flowering

Number of days from the date of transplanting to 50 percent of the plants flowered in a plot was recorded.

3.6.5 Days to 1st picking

The number of days from transplanting to the day when 1st picking (fruits attained proper size and colour) was counted for each genotype.

3.6.6 Fruiting span

The number of days from 1st fruit harvest till the final picking was counted as the duration of the fruiting or fruiting span.

3.6.7 Number of flowers cluster⁻¹

One flower clusters from each of the tagged plants were selected and distinctly labeled. Number of flowers were counted from each cluster and recorded.

(C) Yield Parameters

3.6.8 Number of fruits cluster⁻¹

One flower clusters from each of the tagged plants were selected and distinctly labeled for number of fruits was counted from each cluster.

3.6.9 Number of fruits plant⁻¹

The number of fruits was counted in each picking in five randomly tagged plants from each genotype and it was calculated by dividing the total number of fruits harvested in all the pickings with five.

3.6.10 Fruit length (cm)

The length of fruits from joint of calyx to the apex was measured in centimeter for five randomly selected fruits from each plot, at peak fruiting stage.

3.6.11 Fruit width (cm)

The width of fruit was measured with the help of Vernier caliper and then average was recorded.

3.6.12 Average fruit weight (g)

The weight of five fruits was recorded separately with the help of weighing balance and average was worked out for each genotype.

3.6.13 Fruit yield plant⁻¹ (kg)

The weight of the fruits of the tagged plants was recorded at each picking and the average weight of the fruits plant⁻¹ was calculated in kg.

3.6.14 Fruit yield plot⁻¹ (kg)

Weight of fresh marketable fruits from each plot throughout the harvesting period was noted and average fruit yield plot⁻¹ was worked out for each genotype.

3.6.15 Fruit yield hectare⁻¹ (q/ha)

Total fruit yield (kg) plot⁻¹ was converted in quintal⁻¹ hectare by multiplying with factor.

(D) Other Parameters

3.6.16 Flower colour

The colour of flower of different genotypes was recorded on the basis of visual observation.

- White
- Purple
- Light purple
- Dark purple

3.6.17 Leaf colour

The colour of leaves of different genotypes was recorded on the basis of visual observation.

- Light green
- Dark green
- Green

3.6.18 Fruit shape

Shape of five randomly selected fruits were observed visually and were categorized as

- Long
- Oblong
- Round

3.6.19 Fruit colour

Colour of five randomly selected fruits at marketable stage was observed visually as

- Dark purple
- Light purple
- Purple
- Green
- White

3.6.20 Colour of calyx

Colour of calyx of five randomly selected fruits was observed visually.

- Green
- Dark Green
- Light Green
- Dark Purple
- Light Purple

3.6.21 Incidence of shoot and fruit borer:

Incidences of pest like shoot and fruit borer was recorded at every picking.

$$\text{Percentage of fruit borer incidence} = \frac{\text{Number of fruit borer infested fruit}}{\text{Total number of fruit}} \times 100$$

3.6.22 Incidence of Phomopsis blight, Little leaf and Bacterial wilt

Incidences of diseases like phomopsis blight, little leaf and bacterial wilt was recorded at ten days interval. The incidence of above mentioned diseases was calculated as follows:

$$\text{Percentage disease incidence} = \frac{\text{Number of disease \& affected plants}}{\text{Total number of plants per plot}} \times 100$$

3.7 Statistical methodology

The data obtained in respect of all the characters has been subjected to the following statistical analyses.

Table 3.3: Arrangement of data from Randomized Complete Block Design

Treatment	1	2	3		R	
1	Y_{11}	Y_{12}	Y_{13}	-	Y_{1r}	T_1
2	Y_{21}	Y_{22}	Y_{23}	-	Y_{2r}	T_2
3	Y_{31}	Y_{32}	Y_{33}	-	Y_{3r}	T_3
.	.	.		-	.	.
.	.	.		-	.	.
.	.	.		-	.	.
T	Y_{t1}	Y_{t2}	Y_{t3}	-	Y_{tr}	T_t
Total	R_1	R_2	R_3	-	R_r	G.T.

$$\text{Model : } Y_{ij} = \mu + t_i + r_j + e_{ij}$$

Where,

Y_{ij} = Performance of i^{th} genotype in j^{th} block

μ = General mean

t_i = i^{th} treatment effect

r_j = J^{th} replication effect

e_{ij} = The environmental effect

For working out the standard error for comparison of the means, an ANOVA table is prepared for randomized complete block design.

3.7.1 Analysis of variance

The data based on the mean of individual plants selected for observation were statistically analysed to find out overall total variability present in the material under study for each character and for all the

populations. The first and foremost step is to carry out analysis of variance to test the significance of differences among the populations. The analysis of variance was carried out as per methods suggested by Panse and Sukhatme (1967). The skeleton of analysis of variance used was as follows:

Table 3.4: ANOVA for Randomized Completely Block Design

Source of	d.f.	Sum of	Mean sum	F	F _t 5% or 1%
Replication	r-1	RSS	RMS	RMS/EMS	-
Genotypes	g-1	GSS	GMS	GMS/EMS	-
Error	(r-1)(g-1)	ESS	EMS	-	-
Total	rg-1	TSS	-	-	-

Where,

r = Number of replications

g = Number of genotypes

d.f. = Degree of freedom

RSS = Replication sum of square

GSS = Genotype sum of square

ESS = Error sum of square

TSS = Total sum of square

RMS = Replication mean sum of square

GMS = Genotype mean sum of square

EMS = Error mean sum of square

A significant value of F test indicates that the test entries differ significantly among themselves, which requires computing C.D.

$$C.V. = \sqrt{\frac{EMS}{GM}} \times 100$$

$$SEm \pm = \sqrt{\frac{EMS}{r}}$$

$$SE_{diff} = \sqrt{\frac{2EMS}{r}}$$

CD at 5% prob. Level = SE diff x t_{5%} table value

Where,

C.V. %	=	Coefficient of variation
SE _m ±	=	Standard error of means
S E diff	=	Standard error of difference
GM	=	Grand mean
C.D.	=	Critical difference
t 5%	=	t, table value 5% probability level at error d.f.

3.7.2 Estimation of mean, components of variance, phenotypic, genotypic and environmental coefficient of variation, heritability, genetic advance and genetic advance as percentage of mean:

The mean of different characters were calculated by conventional method:

$$Mean = \frac{\sum xi}{n}$$

Where,

$\sum xi$	=	The sum of all the observation for i th character.
n	=	Number of observations.

Range was recorded by observing the lowest and the highest mean values for each character.

The component of variance was calculated as follows:

S. No.	Source	M.S.S.	Expected M.S.S.
1.	Replications	-	-
2.	Genotypes	M_i	$\sigma^2 e_i + r. \sigma^2 g_i$
3.	Error	E_i	$\sigma^2 e_i$

$$\sigma^2 g_i = M_i - E_i$$

$$\sigma^2 e_i = E_i$$

$$\sigma^2 p_i = \sigma^2 g_i + \sigma^2 e_i$$

Where,

$\sigma^2 g_i$ = Genotypic variance for i^{th} character.

$\sigma^2 e_i$ = Environmental variance for i^{th} character.

$\sigma^2 p_i$ = Phenotypic variance for i^{th} character.

Phenotypic and genotypic coefficient of variation (expressed in %) were calculated by using the formula given by Burton (1952). Genotypic coefficient of variation (GCV) was calculated as below:

$$\text{GCV}\% = \frac{\sqrt{\sigma^2 g_i}}{\bar{X}_i} \times 100$$

Phenotypic coefficient of variation (PCV)

$$\text{PCV}\% = \frac{\sqrt{\sigma^2 p_i}}{\bar{X}_i} \times 100$$

Where,

$\bar{x}_i$ = General mean of the i^{th} character under consideration.

$\sigma^2 g_i$ and $\sigma^2 p_i$ = Genotypic and phenotypic standard deviation of the i^{th} character respectively.

3.7.3 Heritability and genetic advance

Heritability (broad sense) which is ratio of genotypic variance to the total phenotypic variance is symbolized as h^2 (BS) and expressed in percentage. Estimation of heritability was done as per the formula given by Hanson *et al.* (1956).

$$h^2 \text{ (BS)} = \frac{\sigma^2 g_i}{\sigma^2 p_i} \times 100$$

or

$$= \frac{\text{Genotypic variance of the } i^{\text{th}} \text{ character}}{\text{Phenotypic variance of the } i^{\text{th}} \text{ character}}$$

Expected genetic advance was calculated by using the method suggested by Johnson *et al.* (1955) at 5% selection intensity.

$$\text{Genetic advance (GA)} = K \cdot P_i \cdot h_i^2$$

Genetic advance as percentage of mean was calculated as follows:

$$\frac{\text{Genetic advance}}{\bar{X}_i}$$

Where,

K= Selection intensity its value at 5% selection level is 2.06.

P_i = Phenotypic standard deviation of the i^{th} character.

h_i^2 = Broad sense heritability (fraction) of the i^{th} character.

$\bar{X}_i$ = General mean of the i^{th} character under consideration.

3.7.4 Correlation coefficients

Correlation coefficients were calculated in all possible combinations taking all the characters in to consideration at genotypic, phenotypic and environmental levels by using the formula as proposed by Miller *et al.* (1958).

$$r = \frac{\sum xy - \frac{\sum x \sum y}{n}}{\sqrt{\left(\sum x^2 - \frac{(\sum x)^2}{n}\right)\left(\sum y^2 - \frac{(\sum y)^2}{n}\right)}}$$

Where,

- r = Correlation coefficient
n = Number of treatments
X and Y = Character under study

Genotypic, phenotypic and environmental correlations were computed by substituting corresponding variance and covariance in the above formula, e.g.

$$r_G (X_i X_j) = \frac{G \text{ Cov } (X_i X_j)}{\sqrt{V_G (X_i) \cdot V_G (X_j)}}$$

$$r_P (X_i X_j) = \frac{P \text{ Cov } (X_i X_j)}{\sqrt{V_P (X_i) \cdot V_P (X_j)}}$$

$$r_E (X_i X_j) = \frac{E \text{ Cov } (X_i X_j)}{\sqrt{V_E (X_i) \cdot V_E (X_j)}}$$

3.7.5 Testing of correlations:

The phenotypic correlations are tested for their significance by following formula based on “t” test:

$$T_e = \frac{r}{\sqrt{\frac{n-2}{1-R^2}}} \quad \text{at } (n-2) \text{ d.f.}$$

Where,

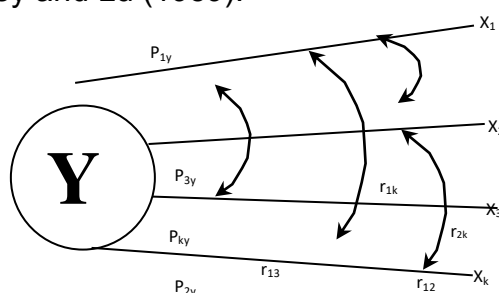
N= Number of treatments

R= phenotypic correlations coefficient

The calculated value of “t” is compared with table of “t” at (n-2) d.f. If the calculated value is equal to or greater than table value, it is significant at given probability level. If $t_c < t_T$, it is non significant.

3.7.6 Path coefficient analysis

Path coefficients are standardized partial regression coefficients and as such these provide the means to direct influence of one character upon another character and also permit portioning of correlation coefficients into direct and indirect effect via other character. The direct indirect contributions of various independent characters on a dependent character yield were calculated through path coefficient analysis as suggested by Wright (1921) and elaborated by Dewey and Lu (1959).



The following set of simultaneous questions were formed and used for the estimation of direct and indirect effects.

$$r_{1y} = p_{1y} + r_{12} p_{2y} + r_{13} p_{3y} + \dots + r_{1y} p_{1y}$$

$$r_{2y} = r_{2y} p_{1y} + p_{2y} + r_{23y} p_{3y} + \dots + r_{21y} p_{1y}$$

$$r_{ky} = r_{ki} p_{1y} + r_{k-1} p_{2y} + r_k^3 p_{3y} + \dots + p_{ky}$$

$$r_{xky} = r_{xk1} p_{1y} + r_{xk2} p_{2y} + r_{xk3} p_{3y} + \dots + p_{xky}$$

$$r_{xky} = \text{Coefficient of correlation between independent character}$$

$$P_{1y} \text{ to } P_{3y} = \text{Direct effect of character 1 to 3 character y}$$

3.7.6a Direct Effect

The direct effects were calculated as follows

$$P_{ky} = \sum_{i=1}^K C_{kirk} Y$$

3.7.6b Indirect effect

Indirect effect of any independent traits on the dependent one (= yield) via other independent traits are computed by multiplying the direct effects (P_{ky}) of that independent variables with the corresponding correlation coefficient as follows:

$$K^{\text{th}} \text{ trait via } (n-1) = r_{k(n-1)} P_{(n-1)Y}$$

3.7.7 Residual effects

A residual effect was calculated using formula from Singh and Chaudhary (1985).

$$R = \sqrt{1 - \sum d_i \times r_{ij}}$$

Where,

- R = Residual effect.
- d_i = Direct effect of the ith character.
- r_{ij} = Correlation coefficient between the ith character and jth dependent character.

3.7.8 Genetic divergence analysis

The Mahalanobis (1936) D² statistic was used to measure the genetic divergence between the populations. The D² values were estimated on the basis of P character by the formula:

$$D^2P = \sum_{i=0}^p = \sum_{j=0}^p = (\lambda_{ij}) \lambda_i \lambda_j$$

Where,

(λ_{i, j}) is the reciprocal or (λ_{j, i}), the pooled common dispersion matrix (i.e. error matrix)

i = the difference in the mean value for the ith character

j = the difference in the mean value for the jth character

For calculating the D^2 values, the variance and covariance were calculated. The genotypes were grouped into different clusters by Tocher's method. The population was arranged in order of their relative distances from each other. For including a particular population in the clusters, a level of D^2 was fixed by taking the maximum D^2 values between any two populations in the first row of the table where D^2 values were arranged in increasing order of magnitude. The two populations having the smallest distance from each other were considered first to which a third population was added. Then nearest fourth population and soon till the stage the average D^2 of a group did not exclude the value already fixed. Similarly, all the other clusters were formed till all the populations were included into one or the other cluster.

RESULTS

The results obtained from the present investigation “Genetic studies on advance lines of Brinjal” are presented under the following heads:

- 4.1 Analysis of variance
- 4.2 Genetic Variability
 - 4.2.1 Range and Mean performance
 - 4.2.2 Coefficient of variation
 - 4.2.3 Heritability
 - 4.2.4 Genetic advance
- 4.3 Correlation coefficient analysis
- 4.4 Path coefficient analysis
- 4.5 Genetic divergence
- 4.6 Other qualitative parameters

4.1 Analysis of variance

The analysis of variances for all the characters studied has been presented in Table 4.1 Mean square due to genotypes were highly significant for all the characters indicating the presence of genetic diversity in the existing material.

Eight characters viz., fruit yield hectare⁻¹, average fruit weight, plant height at harvest, plant height at 90 DAT, plant height at 60 DAT, days to 1st picking, fruiting span and fruit yield plot⁻¹ exhibited the value of higher magnitude.

Table 4.1: Analysis of variance for different characters in Brinjal (mean sum of squares)

Source of variance	D.F.	Plant height (cm) at			
		30DAT	60DAT	90DAT	Final harvest
Replications	2	3.433	17.365	6.668	32.198
Genotypes	40	148.706**	247.961**	336.872**	462.422**
Error	80	9.130	7.757	9.367	16.245

Source of variance	D.F.	No. of branches plant ⁻¹ at final harvest	Days to 1 st flowering	Days to 50% flowering	No. of flower cluster ⁻¹
Replications	2	2.588	11.934	4.130	0.141
Genotypes	40	5.652**	102.190**	113.367**	2.531**
Error	80	1.924	5.376	3.113	0.117

Source of variance	D.F.	Days to 1 st picking	Fruiting span	No. of fruits plant ⁻¹	No. of fruits cluster ⁻¹
Replications	2	22.853	22.373	2.021	0.129
Genotypes	40	240.235**	197.816**	47.510**	0.869**
Error	80	24.428	26.015	1.850	0.061

Source of variance	D.F.	Fruit length (cm)	Fruit width (cm)	Av. fruit weight (g)	Fruit yield plant ⁻¹
Replications	2	3.416	0.419	21.029	0.014
Genotypes	40	39.901**	6.695**	2777.893**	0.403**
Error	80	1.444	0.427	72.983	0.011

Source of variance	D.F.	Fruit yield plot ⁻¹	Fruit yield hectare ⁻¹	Incidence of fruit and shoot borer (%)
Replications	2	5.875	1480.018	52.073
Genotypes	40	161.359**	40639.415**	194.200
Error	80	4.657	1172.953	169.858

4.2 Genetic Variability

4.2.1 Range and mean performance of the genotypes

Range (maximum and minimum) and mean performance of the forty one genotypes of brinjal for all the eighteen characters are presented in Table 4.2 a, b, c and d.

4.2.1.1 Plant height (cm)

Plant height varied from 28.70 to 62.77 cm, 33.97 to 75.93 cm, 36.83 cm to 84.73 cm and 42.20 to 103.66 cm with an overall mean performance of 53.10, 63.10, 71.97 and 80.45 cm at 30, 60, 90 DAT and at final harvest respectively. Genotype 2015/BRLVAR-5 recorded the maximum plant height 103.66 cm and genotype 2017/BRRVAR-10 exhibited the minimum 42.20 cm plant height at final harvest.

4.2.1.2 Number of branches plant⁻¹

Number of branches plant⁻¹ ranged from 9.83 to 15.93 with an average performance of 12.41. The maximum branches plant⁻¹ (15.93) was recorded in genotype 2016/BRRVAR-7, while it was recorded minimum in 2017/BRRVAR-10 (9.83).

4.2.1.3 Days to 1st flowering

Days to 1st flowering varied from 21.66 to 47.33 days with an average being 36.10. Early flowering was observed in genotype 2015/BRLVAR-4 (21.66 days) followed by 2015/BRLVAR-1 (21.67 days), while, the genotype 2017/BRRVAR-4 (47.33 days) recorded the late days to 1st flowering.

4.2.1.4 Days to 50 per cent flowering

Early 50 per cent flowering was recorded in genotype 2015/BRLVAR-4 (28.00 days) followed by 2015/BRLVAR-1 (29.00 days), while, the genotype 2017/BRRVAR-5 (54.33 days) was recorded the late 50 per cent flowering. The average days for 50 per cent flowering were 42.91 days and it ranged from 28.00 to 54.33 days.

Table 4.2a: Mean performance of morphological characters of brinjal.

Genotypes	Plant height (cm) at				Branches plant ⁻¹
	30DAT	60DAT	90DAT	Final harvest	
.	52.87	65.70	70.33	89.37	12.03
2015/BRLVAR-2	47.67	58.47	62.57	74.57	12.40
2015/BRLVAR-3	52.90	64.70	67.50	79.77	11.83
2015/BRLVAR-4	58.53	73.47	80.23	82.50	12.77
2015/BRLVAR-5	62.77	75.93	84.73	103.66	13.67
2016/BRLVAR-1	58.70	65.83	76.30	85.03	14.00
2016/BRLVAR-2	51.63	55.73	69.03	82.80	12.80
2016/BRLVAR-3	49.67	67.77	75.30	85.00	12.67
2016/BRLVAR-4	58.20	69.50	84.67	92.47	12.60
2016/BRLVAR-5	53.77	56.93	68.30	81.90	13.67
2016/BRLVAR-6	54.05	65.40	83.03	88.43	13.27
2016/BRLVAR-7	60.83	74.63	82.17	94.87	12.40
2016/BRLVAR-8	58.37	61.57	69.37	86.40	10.93
2016/BRLVAR-9	58.27	72.80	70.50	80.10	13.00
2016/BRRVAR-1	56.77	63.90	70.05	87.92	11.70
2016/BRRVAR-2	61.13	65.75	82.01	93.08	12.48
2016/BRRVAR-4	49.77	56.70	64.40	70.80	10.80
2016/BRRVAR-5	47.70	57.97	61.17	68.07	13.23
2016/BRRVAR-7	55.77	62.60	83.15	96.25	15.93
2016/BRRVAR-8	48.03	60.77	66.47	78.27	13.17
2016/BRRVAR-9	62.17	74.83	82.87	89.67	12.62
2017/BRLVAR-1	56.17	60.70	63.37	68.25	14.80
2017/BRLVAR-2	52.63	58.77	79.13	88.07	15.90
2017/BRLVAR-3	57.67	60.90	72.16	80.40	10.90
2017/BRLVAR-4	54.13	58.10	73.72	81.85	10.50
2017/BRLVAR-5	53.77	70.43	79.67	82.08	11.80
2017/BRLVAR-6	52.97	66.80	72.67	89.70	11.90
2017/BRLVAR-7	52.32	62.40	68.11	69.75	10.73
2017/BRLVAR-8	57.10	75.47	82.83	90.60	12.10
2017/BRLVAR-9	47.61	56.97	61.73	67.72	14.03
2017/BRRVAR-1	58.63	65.20	74.57	82.67	10.73
2017/BRRVAR-2	50.50	62.00	76.44	70.78	11.80
2017/BRRVAR-3	45.13	51.40	67.73	75.67	10.83
2017/BRRVAR-4	56.43	63.93	72.83	77.07	11.83
2017/BRRVAR-5	55.73	64.53	73.30	62.58	10.57
2017/BRRVAR-8	56.50	72.83	82.03	93.97	12.13
2017/BRRVAR-10	28.70	33.97	36.83	42.20	9.83
2017/BRRVAR-11	29.57	34.10	39.10	44.27	12.47
2017/BRRVAR-12	47.57	56.87	60.53	71.07	12.07
Punjab Sadabahar (C)	55.23	70.23	80.77	84.50	12.20
Kashi Taru (C)	49.03	70.53	79.10	84.67	13.98
S.Em±	1.74	1.60	1.76	2.32	0.79
C.D.5% level	4.93	4.54	4.99	6.58	2.25

Table 4.2b: Mean performance of phenological characters of brinjal.

Genotypes	Days to 1 st flowering	Days to 50% flowering	No. of flower cluster ⁻¹	Days to 1 st picking	Fruiting span
2015/BRLVAR-1	21.67	29.00	4.77	56.33	141.33
2015/BRLVAR-2	38.33	43.33	4.37	56.33	140.67
2015/BRLVAR-3	24.67	28.67	3.67	70.00	150.00
2015/BRLVAR-4	21.66	28.00	3.77	47.00	128.00
2015/BRLVAR-5	33.33	38.00	4.73	53.33	143.00
2016/BRLVAR-1	32.67	38.33	4.43	61.33	137.33
2016/BRLVAR-2	33.00	41.33	4.18	61.00	136.67
2016/BRLVAR-3	37.67	45.67	4.13	58.33	134.67
2016/BRLVAR-4	34.67	37.33	4.40	59.33	135.33
2016/BRLVAR-5	32.67	38.33	3.67	59.00	135.00
2016/BRLVAR-6	34.33	43.33	4.72	62.00	138.00
2016/BRLVAR-7	33.67	44.67	4.57	61.33	137.33
2016/BRLVAR-8	35.33	40.33	3.57	55.00	141.67
2016/BRLVAR-9	39.67	48.33	4.27	60.33	136.33
2016/BRRVAR-1	40.67	51.00	3.48	61.33	137.33
2016/BRRVAR-2	41.67	51.33	2.57	60.33	136.33
2016/BRRVAR-4	36.33	45.00	4.17	60.33	136.33
2016/BRRVAR-5	31.67	39.67	2.53	61.00	137.00
2016/BRRVAR-7	38.33	42.33	4.57	61.67	137.67
2016/BRRVAR-8	34.33	42.33	5.27	61.67	137.67
2016/BRRVAR-9	35.00	42.33	3.53	61.33	137.33
2017/BRLVAR-1	46.33	49.67	2.13	60.67	136.67
2017/BRLVAR-2	40.00	48.67	4.13	60.33	136.33
2017/BRLVAR-3	34.33	42.33	4.13	60.67	136.67
2017/BRLVAR-4	37.00	45.33	4.43	61.33	137.33
2017/BRLVAR-5	38.00	46.67	2.47	62.00	138.00
2017/BRLVAR-6	40.67	45.00	3.33	60.33	136.33
2017/BRLVAR-7	42.33	47.00	3.70	60.33	137.33
2017/BRLVAR-8	35.33	41.67	3.27	61.67	137.33
2017/BRLVAR-9	43.33	50.00	3.67	61.00	137.00
2017/BRRVAR-1	35.00	38.33	3.97	60.00	136.00
2017/BRRVAR-2	42.33	48.00	5.00	74.67	124.33
2017/BRRVAR-3	45.67	52.67	5.17	75.67	119.33
2017/BRRVAR-4	47.33	54.33	5.07	85.33	118.67
2017/BRRVAR-5	40.67	48.67	5.90	84.67	114.67
2017/BRRVAR-8	35.33	43.67	2.37	72.00	128.33
2017/BRRVAR-10	36.00	43.33	6.17	84.00	115.00
2017/BRRVAR-11	35.00	40.00	5.27	81.67	116.33
2017/BRRVAR-12	34.67	40.00	5.00	62.00	138.00
Punjab Sadabahar (C)	24.33	33.00	4.57	47.00	149.33
Kashi Taru (C)	35.33	42.33	3.83	52.33	141.33
S.Em±	1.32	1.01	0.19	2.81	2.90
C.D.5% level	3.76	2.86	0.56	8.03	8.28

4.2.1.5 Number of flowers cluster⁻¹

The number of flowers cluster⁻¹ varied from 2.13 to 6.17 with a mean value of 4.12. Genotype 2017/BRRVAR-10 produced considerably more (6.17) flowers cluster⁻¹. Whereas, genotype 2017/BRLVAR-1 recorded minimum flowers cluster⁻¹ (2.13).

4.2.1.6 Days to 1st picking

Days to 1st picking ranged from 47.00 to 85.33 days. Genotype 2015/BRLVAR-4 (47.00 days) was earliest for days to 1st picking, while 2017/BRRVAR-4 (85.33 days) was late for the same. The mean was calculated to be 62.82 days.

4.2.1.7 Fruiting span

The mean for fruiting span was 134.86 days and it ranged from 114.66 to 150.00 days. Maximum length of fruiting period was observed in genotype 2015/BRLVAR-3 (150.00 days) and minimum for genotype 2017/BRRVAR-5 (114.66 days).

4.2.1.8 Number of fruits plant⁻¹

The maximum number of fruits plant⁻¹ was observed in 2015/BRLVAR-1 (20.40), while it was least in genotype 2017/BRRVAR-11 (2.20). The average number of fruits plant⁻¹ was 8.76 and it ranged from 2.20 to 20.40.

4.2.1.9 Number of fruits cluster⁻¹

Maximum number of fruits cluster⁻¹ was observed in genotype 2016/BRR VAR-8 (3.73), while, it was least (1.27) in genotype 2016/BRLVAR-2, 2016/BRLVAR-4 and Punjab Sadabahar. The average number of fruits cluster⁻¹ was 1.91 and it ranged between 1.27 to 3.73 fruits per cluster.

4.2.1.10 Fruit length (cm)

The fruit length varied from 6.77 to 18.99 cm with a mean value of 11.62 cm. Genotype 2016/BRLVAR-4 produced considerably long fruit (18.99 cm), while, genotype 2017/BRRVAR-11 (6.77 cm) produced small fruit.

Table 4.2c: Mean performance of yield characters of brinjal

Genotypes	No. of fruits plant ⁻¹	No. of fruits cluster ⁻¹	Fruit length (cm)	Fruit width (cm)	Av. fruit weight (g)
2015/BRLVAR-1	20.40	2.37	15.63	3.85	77.20
2015/BRLVAR-2	10.47	2.27	8.74	4.83	90.33
2015/BRLVAR-3	13.83	2.07	17.27	3.47	63.67
2015/BRLVAR-4	18.53	2.93	10.58	4.46	77.77
2015/BRLVAR-5	17.07	2.13	17.18	3.57	85.00
2016/BRLVAR-1	8.60	1.67	15.59	5.63	86.30
2016/BRLVAR-2	7.10	1.27	12.75	4.07	86.90
2016/BRLVAR-3	10.47	2.53	14.12	4.00	73.23
2016/BRLVAR-4	6.85	1.27	18.99	6.07	110.33
2016/BRLVAR-5	11.10	1.43	17.75	3.49	71.57
2016/BRLVAR-6	6.80	1.53	17.05	3.97	193.97
2016/BRLVAR-7	12.50	2.67	17.79	4.29	68.50
2016/BRLVAR-8	8.47	2.53	12.38	4.03	73.67
2016/BRLVAR-9	13.13	2.13	8.30	4.25	104.27
2016/BRRVAR-1	8.03	1.73	14.28	3.67	73.13
2016/BRRVAR-2	8.37	1.30	10.14	4.97	123.39
2016/BRRVAR-4	7.80	1.53	12.29	3.48	72.00
2016/BRRVAR-5	8.00	1.60	10.94	3.59	48.73
2016/BRRVAR-7	8.67	1.70	11.39	4.05	72.30
2016/BRRVAR-8	12.97	3.73	11.43	3.39	48.83
2016/BRRVAR-9	8.67	2.60	10.80	3.43	71.27
2017/BRLVAR-1	3.20	1.80	10.61	4.47	58.09
2017/BRLVAR-2	9.03	1.60	14.81	3.46	69.97
2017/BRLVAR-3	4.03	1.67	9.91	7.90	107.47
2017/BRLVAR-4	7.68	1.63	8.97	8.49	141.97
2017/BRLVAR-5	4.47	1.63	10.08	8.66	141.23
2017/BRLVAR-6	5.87	1.47	7.76	6.09	165.40
2017/BRLVAR-7	6.07	2.23	8.05	5.17	101.53
2017/BRLVAR-8	5.97	2.53	9.56	6.83	107.17
2017/BRLVAR-9	8.40	1.47	9.05	6.37	88.70
2017/BRRVAR-1	5.73	1.77	9.11	7.69	108.80
2017/BRRVAR-2	8.62	2.27	8.29	5.18	65.03
2017/BRRVAR-3	7.20	1.50	7.33	4.48	76.20
2017/BRRVAR-4	10.27	2.67	8.25	5.39	96.87
2017/BRRVAR-5	3.33	1.63	7.11	6.30	107.00
2017/BRRVAR-8	7.10	1.63	8.45	5.01	85.57
2017/BRRVAR-10	2.73	1.67	7.80	7.11	129.47
2017/BRRVAR-11	2.20	1.87	6.77	3.65	88.90
2017/BRRVAR-12	8.29	1.70	7.79	5.97	103.47
Punjab Sadabahar (C)	9.40	1.27	13.51	4.21	56.50
Kashi Taru (C)	12.00	1.43	18.17	3.51	92.20
S.Em±	0.77	0.14	0.68	0.37	4.87
C.D.5% level	2.21	0.40	1.95	1.06	13.88

4.2.1.11 Fruit width (cm)

Fruit width ranged from 3.39 to 8.66 cm and the average was calculated in 4.93 cm. Fruit width was recorded maximum in 2017/BRLVAR-5 (8.66 cm) and least was recorded in genotype 2016/BRRVAR-8 (3.39 cm).

4.2.1.12 Average fruit weight (g)

The heaviest fruits were observed in genotype 2016/BRLVAR-6 (193.96 g) and were lightest in 2016/BRRVAR-5 (48.73 g). The weight of fruit lied between 48.73 g to 193.96 g with an average of fruit was 91.80 g.

4.2.1.13 Fruit yield plant⁻¹ (kg)

Maximum fruit yield plant⁻¹ was recorded in genotype 2016/BRRVAR-2 (2.103 kg) followed by 2016/BRRVAR-7 (1.820 kg), 2016/BRRVAR-9 (1.563 kg) and 2017/BRLVAR-7 (1.545 kg) as compared to other genotypes. Genotype 2017/BRRVAR-2 (0.526 kg) was poor yielder. The average yield plant⁻¹ was 1.158 kg and it ranged from 0.526 kg to 2.103 kg.

4.2.1.14 Fruit yield plot⁻¹ (Kg)

Maximum fruit yield plot⁻¹ was recorded in genotype 2016/BRRVAR-2 (42.067 Kg) followed by 2016/BRRVAR-7 (36.383 Kg). Genotype 2017/BRRVAR-2 (10.510 kg) was poor yielder. The average yield plant⁻¹ was 28.147 Kg and it ranged from 10.510 Kg to 42.067 Kg.

4.2.1.15 Fruit yield hectare⁻¹ (q)

Fruit yield in quintal hectare⁻¹ varied from 166.79 to 667.59 qha⁻¹ with an average yield of 367.35 qha⁻¹. The maximum fruit yield was recorded in genotype 2016/BRRVAR-2 (667.59 qha⁻¹). However, it was found least in 2017/BRRVAR- 2 (166.79qha⁻¹).

Table 4.2d: Mean performance of yield characters of brinjal

Genotypes	Fruit yield plant⁻¹	Fruit yield plot⁻¹	Fruit yield hectare⁻¹
2015/BRLVAR-1	1.353	27.057	429.39
2015/BRLVAR-2	1.325	26.473	420.13
2015/BRLVAR-3	1.172	23.400	371.36
2015/BRLVAR-4	0.708	14.150	224.56
2015/BRLVAR-5	0.740	14.783	234.61
2016/BRLVAR-1	1.173	23.450	372.15
2016/BRLVAR-2	1.012	20.233	321.10
2016/BRLVAR-3	1.650	32.983	523.45
2016/BRLVAR-4	1.277	25.483	404.42
2016/BRLVAR-5	1.330	26.567	421.61
2016/BRLVAR-6	1.245	24.883	394.90
2016/BRLVAR-7	1.072	21.417	339.88
2016/BRLVAR-8	0.625	12.500	198.38
2016/BRLVAR-9	0.733	14.667	232.76
2016/BRRVAR-1	1.452	29.000	460.23
2016/BRRVAR-2	2.103	42.067	667.60
2016/BRRVAR-4	1.187	23.717	376.38
2016/BRRVAR-5	0.530	10.583	167.96
2016/BRRVAR-7	1.820	36.383	577.40
2016/BRRVAR-8	1.538	30.750	488.00
2016/BRRVAR-9	1.563	31.233	495.67
2017/BRLVAR-1	0.700	13.983	221.92
2017/BRLVAR-2	1.372	27.417	435.10
2017/BRLVAR-3	1.370	27.400	434.84
2017/BRLVAR-4	1.078	21.567	342.26
2017/BRLVAR-5	1.257	25.130	398.81
2017/BRLVAR-6	1.360	27.183	431.40
2017/BRLVAR-7	1.545	30.867	489.86
2017/BRLVAR-8	1.333	26.650	422.94
2017/BRLVAR-9	0.918	18.367	291.48
2017/BRRVAR-1	0.870	17.383	275.87
2017/BRRVAR-2	0.526	10.510	166.79
2017/BRRVAR-3	1.247	24.933	395.70
2017/BRRVAR-4	1.332	26.633	422.67
2017/BRRVAR-5	0.773	15.450	245.19
2017/BRRVAR-8	1.115	22.300	353.90
2017/BRRVAR-10	0.615	12.283	194.94
2017/BRR VAR-11	1.173	23.450	372.15
2017/BRR VAR-12	0.577	11.440	181.55
Punjab Sadabahar (C)	1.510	30.183	479.01
Kashi Taru (C)	1.208	24.133	382.99
S.Em±	0.06	1.24	19.77
C.D.5% level	0.17	3.52	55.92

4.2.2 Coefficient of variations

Estimation of genetic parameters for yield and its attributes exhibited a wide range of variation for the characters studied (Table 4.3). Result indicated that the value of phenotypic coefficient of variations were higher in magnitude than that of genotypic coefficient of variation for all the characters showing that the environment had an important role in influencing the expression of the characters.

4.2.2.1 Phenotypic coefficient of variations

The phenotypic coefficient of variation ranged from 6.77% for fruiting span to 47.13 % for number of fruit plant⁻¹. The phenotypic coefficient of variation was highest for characters viz., number of fruits plant⁻¹ (47.13%), average fruit weight (34.01%), fruit yield plot⁻¹ (32.59%), fruit yield hectare⁻¹ (32.59%), fruit yield plant⁻¹ (32.55%), fruit length (32.48%) and fruit width (32.13%). However, it exhibited low for characters like fruiting span (6.77%), plant height at 30 DAT (14.05%), number of branches plant⁻¹ at final harvest (14.33%), days to 50% flowering (14.71%), plant height at 60 DAT (14.85%), plant height at 90 DAT (15.13%), days to 1st picking (15.62%), plant height at final harvest (15.96%) and days to 1st flowering (16.99%). Number of flower cluster⁻¹ (23.31%) and number of fruits cluster⁻¹ (30.07%) exhibited moderate phenotypic coefficient of variation.

4.2.2.2 Genotypic coefficient of variation

It is revealed from the Table 4.3 that GCV varied from 5.61% for fruiting span to 44.50% for number of fruits plant⁻¹.

High genotypic coefficient of variation was noted for number of fruits plant⁻¹ (44.50%) followed by average fruit weight (32.71%), fruit yield plot⁻¹ (31.22%), fruit yield hectare⁻¹ (31.22%), fruit yield plant⁻¹ (31.19%), fruit length (30.79%) and fruit width (29.27%). Fruiting span (5.61%) and number of branches plant⁻¹ (8.98%) showed lowest GCV. While, it was moderate for plant height at 30 DAT (12.85%), days to 1st picking (13.50%), days to 50% flowering (14.13%), plant height at 60 DAT (14.18%), plant height at 90 DAT (14.52%), plant height at final harvest (15.16%), days to 1st flowering (15.73%), number of flower cluster⁻¹ (21.77%) and number of fruit cluster⁻¹ (27.13%).

4.2.3 Heritability

The heritability (BS) was computed for each of the characters by the variance components for estimating their relative magnitudes of genotypic and phenotypic variability contributed through environmental factors. The estimates of heritability (BS) for all the characters have been discussed as follows (Table 4.3). It was partitioned as very high (above 90%), high (70 to 90%), medium (50-70%) and low (less than 50%). Heritability ranged between 39.24% for number of branches per plant at final harvest to 92.51% for average fruit weight.

Result indicated that the heritability estimates were very high for average fruit weight (92.51%) followed by days to 50% flowering (92.19%), plant height at 90 DAT (92.10%), fruit yield plant⁻¹ (91.83%), fruit yield plot⁻¹ (91.81%), fruit yield hectare⁻¹ (91.81%), plant height at 60 DAT (91.17%) and plant height at final harvest (90.15%). However, it was recorded high for fruit length (89.87%), number of fruit plant⁻¹ (89.16%), number of flower cluster⁻¹ (87.22%), days to 1st flowering (85.72%), plant height at 30 DAT (83.59%), fruit width (83.01%), number of fruit cluster⁻¹ (81.40%) and days to 1st picking (74.65%).

Low estimation of heritability was recorded for number of branches plant⁻¹ at final harvest (39.24%). Whereas, moderate heritability was found in fruiting span (68.76%).

4.2.4 Genetic advance

Based on the estimate of heritability (BS), expected genetic advance was computed on the hypothetical selection at 5 per cent best individual ($K=2.06$). Due to masking influence of environment upon characters concerned, values of genetic advance exhibited high fluctuations. Therefore to attain relative comparison of the characters in relation to environment, genetic advance as percentage of mean was calculated to predict the genetic gain (Table 4.3).

Table 4.3: Estimates of genetic parameters of variations for various characters in Brinjal

Characters		Grand Mean	Range		Coefficient of variations		Heritability % (BS)	Genetic Advance	GA as % of mean
			Min.	Max.	Phenotypic	Genotypic			
Plant height (cm) at	30DAT	53.10	28.70	62.77	14.05	12.85	83.59	12.85	24.19
	60DAT	63.10	33.97	75.93	14.85	14.18	91.17	17.60	27.89
	90DAT	71.97	36.83	84.73	15.13	14.52	92.10	20.66	28.70
	Final harvest	80.45	42.20	103.66	15.96	15.16	90.15	23.85	29.65
No. of Branches plant ⁻¹		12.41	9.83	15.93	14.33	8.98	39.24	1.44	11.59
Days to 1 st flowering		36.10	21.66	47.33	16.99	15.73	85.72	10.83	30.01
Days to 50% flowering		42.91	28.00	54.33	14.71	14.13	92.19	11.99	27.94
No. of flower cluster ⁻¹		4.12	2.13	6.17	23.31	21.77	87.22	1.73	41.88
Days to 1 st picking		62.82	47.00	85.33	15.62	13.50	74.65	15.10	24.03
Fruiting span		134.86	114.66	150.00	6.77	5.61	68.76	12.93	9.59
No. of fruits plant ⁻¹		8.76	2.20	20.40	47.13	44.50	89.16	7.59	86.63
No. of fruits cluster ⁻¹		1.91	1.27	3.73	30.07	27.13	81.40	0.96	50.50
Fruit length (cm)		11.62	6.77	18.99	32.48	30.79	89.87	6.99	60.17
Fruit width (cm)		4.93	3.39	8.66	32.13	29.27	83.01	2.71	55.02
Av. fruit weight (g)		91.80	48.73	193.96	34.01	32.71	92.51	59.50	64.81
Fruit yield plant ⁻¹		1.158	0.526	2.103	32.55	31.19	91.83	0.71	61.58
Fruit yield plot ⁻¹		23.147	10.510	42.067	32.59	31.22	91.81	14.27	61.63
Fruit yield hectare ⁻¹		367.35	166.79	667.59	32.59	31.22	91.81	226.40	61.63

Genetic advance as percentage of mean ranged between 9.59% for fruiting span to 86.63% for number of fruits plant⁻¹. The highest estimate of genetic advance as percentage of mean was recorded for number of fruits plant⁻¹ (86.63%), average fruit weight (64.81%), fruit yield plot⁻¹ (61.63%), fruit yield hectare⁻¹ (61.63%), fruit yield plant⁻¹ (61.58%) and fruit length (60.17%). Fruit width (55.02%), number of fruits cluster⁻¹ (50.50%), number of flower cluster⁻¹ (41.88%) and days to 1st flowering (30.01%) showed moderate value of genetic advance as percentage of mean. Whereas low estimate were observed for fruiting span (9.59%), number of branches plant⁻¹ (11.59%), days to 1st picking (24.03%), plant height at 30 DAT (24.19%), plant height at 90 DAT (28.89%), days to 50% flowering (27.94%), plant height at 90 DAT (28.70%) and plant height at final harvest (29.65%).

4.3 Correlation coefficient

Correlation coefficients were worked out at phenotypic, genotypic and environmental levels for all possible combination of thirteen characters (Table 4.4). Results indicated that genotypic correlation coefficient in general were of higher magnitude than the corresponding phenotypic correlation coefficient for all the characters.

The results of phenotypic correlation coefficients have been discussed only as the genotypic and environmental correlation were mostly influenced by the environmental conditions, hence phenotypic correlation will give the correct idea about the association between two variables.

4.3.1 Plant height (cm) at final harvest

Plant height at final harvest showed highly significant and positive correlation with fruit length (0.482) followed by fruiting span (0.474), fruit yield plant⁻¹ (0.420), number of fruits plant⁻¹ (0.363) and number of branches plant⁻¹ (0.255). Significant and negative association of this character was observed with days to 1st flowering (-0.196), number of flower cluster⁻¹ (-0.319) and days to 1st picking (-0.485).

4.3.2 Number of branches plant⁻¹

Number of branches plant⁻¹ showed highly significant and positive correlation with fruit length (0.314), fruiting span (0.231) and number of fruits plant⁻¹ (0.178), while it was found highly significant and negative association with fruit width (-0.394), average fruit weight (-0.207) and days to 1st picking (-0.230).

4.3.3 Days to 1st flowering

Days to 1st flowering recorded highly significant and positive association with days to 50 per cent flowering (0.859), days to 1st picking (0.358) and average fruit weight (0.185), while it was found highly significant and negative with number of fruits plant⁻¹ (-0.484), fruit length (-0.432) and fruiting span (-0.363).

4.3.4 Days to 50 per cent flowering

Days to 50 per cent flowering recorded highly significant and positive association with days to first picking (0.387) and average fruit weight (0.199). However, it was exhibited highly significant and negative with number of fruits plant⁻¹ (-0.414), fruiting span (-0.398) and fruit length (-0.384).

4.3.5 Number of flowers cluster⁻¹

Number of flowers cluster⁻¹ showed highly significant and positive association with days to 1st picking (0.367), whereas highly significant and negative association with fruiting span (-0.360).

4.3.6 Days to 1st picking

Highly significant and positive association of days to 1st picking was observed with fruit width (0.194) whereas highly significant and negative association with fruiting span (-0.964), fruit length (-0.512) and number of fruits plant⁻¹ (-0.365).

4.3.7 Fruiting span

Association of fruiting span was recorded highly significant and positive with fruit length (0.470), number of fruits plant⁻¹ (0.341) and fruit yield plant⁻¹ (0.203).

4.3.8 Number of fruits plant⁻¹

Number of fruits cluster⁻¹ expressed highly significant and positive correlation with number of fruits cluster⁻¹ (0.436), fruit length (0.435) and fruit yield plant⁻¹ (0.332) while highly significant and negative association was with fruit width (-0.449) and average fruit weight (-0.334).

4.3.9 Number of fruits cluster⁻¹

Number of fruits cluster⁻¹ showed highly significant and negative association with fruit width (-0.184) and average fruit weight (-0.317).

4.3.10 Fruit length

Fruit length recorded positive and significant with fruit yield plant⁻¹ (0.276) and negative association was with fruit width (-0.405).

4.3.11 Fruit width

Fruit width recorded positive and highly significant association with average fruit weight (0.535), while it was recorded negative and significant with fruit yield plant⁻¹ (-0.324).

4.3.12 Average fruit weight

Average fruit weight was exhibited positive and significant with fruit yield plant⁻¹ (0.461).

4.3.13 Fruit yield plant⁻¹ (g)

Fruit yield plant⁻¹ was recorded highly significant and positive association with average fruit weight (0.461), plant height at final harvest (0.420), number of fruits plant⁻¹ (0.332) fruit length (0.276) and fruiting span (0.203). However, it exhibited highly significant and negative association with fruit width (-0.324) and days to 1st picking (-0.208).

Table 4.4: Estimates of genotypic and phenotypic correlation coefficients among fruit yield and its attributing traits in brinjal

Characters		No. of Branches plant ⁻¹	Days to 1 st flowering	Days to 50% flowering	No. of flower cluster ⁻¹	Days to 1 st picking	Fruiting span	No. of fruits plant ⁻¹	No. of fruits cluster ⁻¹	Fruit length (cm)	Fruit width (cm)	Av. fruit weight (g)	Fruit yield plant ⁻¹
Plant height (cm) at Final harvest	G	0.423	-0.210	-0.157	-0.385	-0.597	0.608	0.397	0.043	0.539	-0.114	0.022	0.459
	P	0.255**	-0.196*	-0.136	-0.319**	-0.485**	0.474**	0.363**	0.017	0.482**	-0.095	0.021	0.420**
No. of Branches plant ⁻¹	G		0.007	-0.053	-0.304	-0.370	0.385	0.345	-0.025	0.504	-0.542	-0.367	0.206
	P		-0.002	-0.018	-0.156	-0.230*	0.231*	0.178*	-0.069	0.314**	-0.394**	-0.207*	0.128
Days to 1 st flowering	G			0.981	-0.044	0.397	-0.437	-0.553	-0.142	-0.475	0.229	0.195	0.064
	P			0.859**	-0.055	0.358**	-0.363**	-0.484**	-0.123	-0.432**	0.185*	0.162	0.071
Days to 50% flowering	G				-0.038	0.417	-0.433	-0.445	-0.097	-0.424	0.183	0.199	0.122
	P				-0.046	0.387**	-0.398**	-0.414**	-0.094	-0.384**	0.147	0.199*	0.116
No. of flower cluster ⁻¹	G					0.471	-0.491	0.071	0.170	-0.066	0.000	0.058	-0.145
	P					0.367**	-0.360**	0.066	0.140	-0.060	0.004	0.042	-0.125
Days to 1 st picking	G						-0.991	-0.441	0.062	-0.639	0.253	0.173	-0.267
	P						-0.964**	-0.365**	0.053	-0.512**	0.194*	0.131	-0.208*
Fruiting span	G							0.427	-0.020	0.598	-0.230	-0.145	0.255
	P							0.341**	-0.010	0.470**	-0.161	-0.106	0.203*
No. of fruits plant ⁻¹	G								0.482	0.492	-0.501	-0.370	0.422
	P								0.436**	0.435**	-0.449**	-0.334**	0.332**
No. of fruits cluster ⁻¹	G									-0.073	-0.236	-0.341	-0.013
	P									-0.043	-0.184*	-0.317**	-0.009
Fruit length (cm)	G										-0.473	-0.185	0.284
	P										-0.405**	-0.171	0.276**
Fruit width (cm)	G											0.605	-0.353
	P											0.535**	-0.324**
Av. fruit weight (g)	G												0.463
	P												0.461**

Significant at 5% level = *

Significant at 1% level = **

4.4 Path coefficient analysis

To measure the direct as well as indirect association of one variable (cause) through another on the end product (effect), path coefficient was calculated at genotypic and phenotypic levels for all the yield attributing traits. The observed correlation coefficients of fruit yield with its contributing traits were partitioned into direct and indirect effects. In the present investigation, important characters viz., fruit yield plant⁻¹ is been used as dependable variable. Since the values of genotypic path are more reliable in predicting the correct idea about the direct and indirect effects of the component traits, only this has been discussed below.

The estimates of path coefficient are furnished in the Table 4.5 and 4.6. In general the genotypic direct as well as indirect effects were slightly higher in magnitude as compared to corresponding phenotypic direct and indirect effects. The results obtained from genotypic direct and indirect effects are presented as under.

4.4.1 Direct effect

Path coefficient analysis of different characters contributing towards fruit yield per plant showed that average fruit weight (1.169) had highest positive direct effect followed by number of fruits plant⁻¹ (0.515), plant height at final harvest (0.298), days to 1st flowering (0.130) and days to 50% flowering (0.035). Whereas, days to 1st picking (-1.707) had the highest negative direct effect on fruit yield plant⁻¹ followed by days to fruiting span (-1.655), fruit width (-0.958), fruit length (-0.384), number of flower cluster⁻¹ (-0.171), number of branches plant⁻¹ (-0.039) and number of fruit cluster⁻¹ (-0.006).

4.4.2 Indirect effect

4.4.2.1 Plant height (cm)

Plant height at final harvest imparted highest positive indirect effect on fruit yield plant⁻¹ via days to 1st picking (1.019), number of fruits plant⁻¹ (0.204), fruit width (0.108), number of flower cluster⁻¹ (0.065) and average fruit weight (0.026). However, indirect effect was negative via fruiting span (-1.006), fruit length (-0.207), days to 1st flowering (-0.027) and number of branches plant⁻¹ (-0.016).

4.4.2.2 Number of branches plant⁻¹

Number of branches plant⁻¹ was recorded to have positive indirect effect on fruit yield plant⁻¹ through days to 1st picking (0.632), fruit width (0.519), number of fruit plant⁻¹ (0.177), plant height at final harvest (0.126) and number of flower cluster⁻¹ (0.052). However, negative indirect effect was expressed via fruiting span (-0.637), average fruit weight (-0.429) and fruit length (-0.193).

4.4.2.3 Days to 1st flowering

Days to 1st flowering revealed high values of positive indirect effect on fruit yield plant⁻¹ through fruiting span (0.723), average fruit weight (0.228), fruit length (0.182) and days to 50% flowering (0.035). However, negative indirect effect was exhibited in the characters i.e. days to 1st picking (-0.678), number of fruits plant⁻¹ (-0.284), fruit width (-0.219) and plant height at final harvest (-0.062).

4.4.2.4 Days to 50 per cent flowering

Days to 50 per cent flowering expressed a positive indirect effect on fruit yield plant⁻¹ through fruiting span (0.716), average fruit weight (0.233), fruit length (0.163) and days to 1st flowering (0.127). However, rest of the characters showed negative indirect effect viz., days to 1st picking (-0.712), number of fruits plant⁻¹ (-0.229), fruit width (-0.175) and plant height at final harvest DAT (-0.046).

4.4.2.5 Number of flowers cluster⁻¹

Number of flowers cluster⁻¹ expressed a positive indirect effect on fruit yield plant⁻¹ through fruiting span (0.812), average fruit weight (0.067), number of fruits plant⁻¹ (0.036), fruit length (0.025) and number of branches plant⁻¹ (0.012). However, high negative indirect effect exhibited via, days to 1st picking (-0.804) and plant height at final harvest (-0.115).

4.4.2.6 Days to 1st picking

Days to 1st picking revealed high values of positive indirect effect on fruit yield plant⁻¹ through fruiting span (1.640), fruit length (0.245), average fruit weight (0.202), days to 1st flowering (0.051), number of branches plant⁻¹ (0.014) and days to 50 per cent flowering (0.015). However, negative indirect

effect was shown through fruit width (-0.242), number of fruits plant⁻¹ (-0.227), plant height at final harvest (-0.178) and number of flowers cluster⁻¹ (-0.080).

4.4.2.7 Fruiting span

Fruiting span manifested highest positive indirect effect on fruit yield plant⁻¹ through days to 1st picking (1.691), fruit width (0.220), number of fruits plant⁻¹ (0.219), plant height at final harvest (0.181) and number of flowers cluster⁻¹ (0.084). However, rest of the characters showed negative indirect effect viz., fruit length (-0.229), average fruit weight (-0.170), days to 1st flowering (-0.056), days to 50 per cent flowering (-0.015) and number of branches plant⁻¹ (-0.015).

4.4.2.8 Number of fruits plant⁻¹

Number of fruits plant⁻¹ exhibited positive indirect effect via, days to 1st picking (0.753), plant height at final harvest (0.118) and fruit width (0.480). Negative indirect effect was observed through fruiting span (-0.706), average fruit weight (-0.432), fruit length (-0.189), days to 1st flowering (-0.072) and days to 50 per cent flowering (-0.016).

4.4.2.9 Number of fruits cluster⁻¹

Highest positive indirect effect of number of fruits cluster⁻¹ on fruit yield plant⁻¹ was recorded through number of fruits plant⁻¹ (0.248), fruit width (0.226), fruiting span (0.033), fruit length (0.027) and plant height at 150 DAT (0.012). However, negative indirect effect was exhibited via, average fruit weight (-0.398), days to 1st picking (-0.105), number of flowers cluster⁻¹ (-0.029) and days to 1st flowering (-0.018).

4.4.2.10 Fruit length

Fruit length revealed positive indirect effect on fruit yield plant⁻¹ through days to 1st picking (1.091), fruit width (0.453), number of fruits plant⁻¹ (0.253), plant height at final harvest (0.161) and number of flowers cluster⁻¹ (0.011). The negative indirect effect via, fruiting span (-0.989), average fruit weight (-0.216), days to 1st flowering (-0.061), number of branches plant⁻¹ (-0.020) and days to 50 per cent flowering (-0.015) was observed.

Table 4.5: Genotypic path coefficients showing direct and indirect effects of different characters on fruit yield plant⁻¹ (g) in brinjal

Characters	Plant height (cm) at final harvest	No. of Branches plant ⁻¹	Days to 1 st flowering	Days to 50% flowering	No. of flower cluster ⁻¹	Days to 1 st picking	Fruiting span	No. of fruits plant ⁻¹	No. of fruits cluster ⁻¹	Fruit length (cm)	Fruit width (cm)	Av. fruit weight (g)	"r" value fruit Yield plant ⁻¹ (g)
Plant height (cm) at final harvest	0.2985	-0.0169	-0.0274	-0.0056	0.0659	1.0193	-1.0065	0.2046	-0.0003	-0.2075	0.1088	0.0263	0.459
No. of Branches plant ⁻¹	0.1262	-0.0399	0.0010	-0.0019	0.0520	0.6323	-0.6377	0.1778	0.0002	-0.1938	0.5191	-0.4293	0.206
Days to 1 st flowering	-0.0627	-0.0003	0.1302	0.0352	0.0076	-0.6780	0.7236	-0.2849	0.0010	0.1828	-0.2191	0.2284	0.064
Days to 50% flowering	-0.0469	0.0021	0.1276	0.0359	0.0065	-0.7124	0.7167	-0.2291	0.0007	0.1630	-0.1755	0.2330	0.122
No. of flower cluster ⁻¹	-0.1150	0.0121	-0.0058	-0.0014	-0.1712	-0.8049	0.8129	0.0366	-0.0012	0.0254	-0.0003	0.0674	-0.145
Days to 1 st picking	-0.1782	0.0148	0.0517	0.0150	-0.0807	-1.7077	1.6405	-0.2272	-0.0004	0.2458	-0.2429	0.2021	-0.267
Fruiting span	0.1815	-0.0154	-0.0569	-0.0156	0.0840	1.6919	-1.6558	0.2197	0.0001	-0.2298	0.2208	-0.1700	0.255
No. of fruits plant ⁻¹	0.1186	-0.0138	-0.0720	-0.0160	-0.0122	0.7533	-0.7064	0.5151	-0.0033	-0.1894	0.4804	-0.4323	0.422
No. of fruits cluster ⁻¹	0.0128	0.0010	-0.0185	-0.0035	-0.0291	-0.1058	0.0338	0.2481	-0.0068	0.0279	0.2264	-0.3989	-0.013
Fruit length (cm)	0.1610	-0.0201	-0.0619	-0.0152	0.0113	1.0911	-0.9894	0.2536	0.0005	-0.3846	0.4535	-0.2162	0.284
Fruit width (cm)	-0.0339	0.0216	0.0298	0.0066	-0.0001	-0.4328	0.3814	-0.2582	0.0016	0.1820	-0.9585	0.7075	-0.353
Av. fruit weight (g)	0.0067	0.0146	0.0254	0.0072	-0.0099	-0.2950	0.2406	-0.1904	0.0023	0.0711	-0.5798	1.1697	0.463

Residual effect Genotypic = -0.4346

Table 4.6: Phenotypic path coefficients showing direct and indirect effects of different characters on fruit yield plant⁻¹ (g) in brinjal

[Characters	Plant height (cm) at Final harvest	No. of Branches plant ⁻¹	Days to 1 st flowering	Days to 50% flowering	No. of flower cluster ⁻¹	Days to 1 st picking	Fruiting span	No. of fruits plant ⁻¹	No. of fruits cluster ⁻¹	Fruit length (cm)	Fruit width (cm)	Av. fruit weight (g)	"r" value fruit Yield plant ⁻¹ (g)
Plant height (cm) at Final harvest	0.2311	-0.0298	-0.0676	0.0070	0.0338	-0.0524	0.0626	0.1402	0.0003	0.0093	0.0664	0.0194	0.420
No. of Branches plant ⁻¹	0.0589	-0.1168	-0.0006	0.0009	0.0165	-0.0248	0.0305	0.0689	-0.0011	0.0061	0.2767	-0.1870	0.128
Days to 1 st flowering	-0.0454	0.0002	0.3444	-0.0443	0.0058	0.0386	-0.0480	-0.1871	-0.0020	-0.0084	-0.1299	0.1468	0.071
Days to 50% flowering	-0.0313	0.0021	0.2959	-0.0516	0.0048	0.0418	-0.0526	-0.1601	-0.0016	-0.0074	-0.1031	0.1797	0.116
No. of flower cluster ⁻¹	-0.0737	0.0182	-0.0190	0.0024	-0.1060	0.0397	-0.0475	0.0254	0.0023	-0.0012	-0.0031	0.0379	-0.125
Days to 1 st picking	-0.1121	0.0269	0.1232	-0.0200	-0.0389	0.1080	-0.1273	-0.1411	0.0009	-0.0099	-0.1362	0.1183	-0.208
Fruiting span	0.1095	-0.0269	-0.1251	0.0206	0.0381	-0.1041	0.1321	0.1316	-0.0002	0.0091	0.1135	-0.0957	0.203
No. of fruits plant ⁻¹	0.0839	-0.0208	-0.1668	0.0214	-0.0070	-0.0394	0.0450	0.3864	0.0072	0.0084	0.3156	-0.3017	0.332
No. of fruits cluster ⁻¹	0.0039	0.0081	-0.0424	0.0048	-0.0148	0.0057	-0.0014	0.1685	0.0166	-0.0008	0.1297	-0.2869	-0.009
Fruit length (cm)	0.1114	-0.0367	-0.1489	0.0198	0.0064	-0.0553	0.0621	0.1680	-0.0007	0.0193	0.2850	-0.1544	0.276
Fruit width (cm)	-0.0218	0.0460	0.0637	-0.0076	-0.0005	0.0209	-0.0213	-0.1735	-0.0031	-0.0078	-0.7029	0.4836	-0.324
Av. fruit weight (g)	0.0050	0.0241	0.0559	-0.0103	-0.0044	0.0141	-0.0140	-0.1289	-0.0053	-0.0033	-0.3759	0.9043	0.461

Residual effect Phenotypic = 0.3214

4.4.2.11 Fruit width

Fruit width exhibited significant positive indirect effect via, average fruit weight (0.707), fruiting span (0.381), fruit length (0.182), days to 1st flowering (0.029) and number of branches plant⁻¹ (0.021). Negative indirect effect was observed through days to 1st picking (-0.432), number of flowers cluster⁻¹ (-0.258) and plant height at final harvest (-0.033).

4.4.2.12 Average fruit weight

Average fruit weight manifested positive indirect effect on fruit yield plant⁻¹ through fruiting span (0.240), fruit length (0.071), days to 1st flowering (0.025) and number of branches plant⁻¹ (0.014). However, rest of the characters showed negative indirect effect via, fruit width (-0.579), days to 1st picking (-0.295) and number of fruits plant⁻¹ (-0.190).

4.5 Genetic divergence (D²) analysis

The presence of genetic diversity among forty one genotypes was analyzed using Mahalanobis D² statistics and all the forty one genotypes were grouped into seven clusters.

4.5.1 Cluster analysis

Clustering pattern on the basis of D² analysis has been presented in Table 4.7.

The genotypes were grouped into seven non-overlapping clusters.

The highest number of genotypes appeared in cluster II i.e. fourteen. The cluster II had 2017/BRLVAR-1, 2017/BRLVAR-9, 2016/BRLVAR-3, 2017/BRLVAR-3, 2017/BRLVAR-7, 2017/BRLVAR-6, 2017/BRLVAR-5, 2016/BRLVAR-5, Kashi Taru, 2016/BRLVAR-7, 2016/BRLVAR-1, 2016/BRLVAR-8, 2016/BRLVAR-4 and 2015/BRLVAR-5.

Cluster I and III, which have ten numbers of genotypes are 2016/BRRVAR-2, 2016/BRRVAR-3, 2016/BRRVAR-1, 2016/BRRVAR-7, 2016/BRRVAR-9, 2016/BRRVAR-4, 2017/BRRVAR-8, 2015/BRLVAR-2, 2016/BRLVAR-2, 2016/BRRVAR-5 and 2017/BRRVAR-3, 2017/BRRVAR-4, 2016/BRRVAR-8, 2016/BRLVAR-9, 2017/BRRVAR-1, 2017/BRLVAR-8, 2017/BRRVAR-5, 2017/BRRVAR-12, 2017/BRLVAR-4 and 2017/BRRVAR-10

constituted the next highest cluster. The four genotypes viz., 2015/BRLVAR-3, Panjab sadabahar, 2015/BRLVAR-1 and 2015/BRLVAR-4 made cluster IV.

Cluster V, VI and VII constituted only one genotype i.e. 2017/BRLVAR-2, 2016/BRLVAR-6 and 2017/BRRVAR-11 which is lowest in all clusters.

Table 4.7: Clustering pattern of forty one genotypes of brinjal on the basis of genetic divergence

S. No.	Cluster	No. of genotypes	Name of genotypes
1	I	10	2016/BRRVAR-2, 2016/BRRVAR-3, 2016/BRRVAR-1, 2016/BRRVAR-7, 2016/BRRVAR-9, 2016/BRRVAR-4, 2017/BRRVAR-8, 2015/BRLVAR-2, 2016/BRLVAR-2, 2016/BRRVAR-5
2	II	14	2017/BRLVAR-1, 2017/BRLVAR-9, 2016/BRLVAR-3, 2017/BRLVAR-3, 2017/BRLVAR-7, 2017/BRLVAR-6, 2017/BRLVAR-5, 2016/BRLVAR-5, Kashi Taru, 2016/BRLVAR-7, 2016/BRLVAR-1, 2016/BRLVAR-8, 2016/BRLVAR-4, 2015/BRLVAR-5
3	III	10	2017/BRRVAR-3, 2017/BRRVAR-4, 2016/BRRVAR-8, 2016/BRLVAR-9, 2017/BRRVAR-1, 2017/BRLVAR-8, 2017/BRRVAR-5, 2017/BRRVAR-12, 2017/BRLVAR-4, 2017/BRRVAR-10
4	IV	4	2015/BRLVAR-3, Panjab sadabahar, 2015/BRLVAR-1, 2015/BRLVAR-4
5	V	1	2017/BRLVAR-2
6	VI	1	2016/BRLVAR-6
7	VII	1	2017/BRRVAR-11

Table 4.8: Average intra (diagonal) and inter-cluster D2 values among forty one genotypes of brinjal

Cluster	I	II	III	IV	V	VI	VII
I	21.439	43.905	45.297	88.080	44.707	65.146	72.231
II		27.520	63.670	63.576	56.675	87.117	104.984
III			36.639	120.737	89.466	117.075	72.056
IV				31.732	136.030	127.194	116.341
V					0.000	81.762	128.120
VI						0.000	136.858
VII							0.000

The average inter and intra-cluster distance in brinjal germplasm was presented in Table 4.8. The highest intra cluster distance was recorded in cluster III (36.369) followed by cluster IV (31.732), cluster II (27.520), cluster I (21.439) and cluster V, VI and VII (0.00) showed lowest intra cluster distance. Whereas, in case of inter-cluster distance, highest inter cluster distance were observed between cluster VI and VII (136.85), which is followed by cluster IV and V (136.03), cluster V and VII (128.12), cluster IV and VI (127.19), cluster III and IV (120.73) cluster III and VI (117.07), cluster IV and VII (116.34) and cluster II and VII (104.98). Whereas, lowest inter cluster in brinjal genotypes was recorded in between cluster I and II (43.90) followed by cluster I and V (44.70), cluster I and III (45.29) and cluster II and IV (56.67).

4.5.2 Cluster mean performance

The mean cluster value for different traits in brinjal was presented in Table 4.9. Cluster V showed highest mean for plant height at final harvest (93.08 cm), days to 1st flowering (41.67 days), days to 50% flowering (51.33 days) and fruit yield plant⁻¹ (2.10 g), cluster VI showed highest mean for number of branches plant⁻¹ (13.27), fruit length (17.05) and average fruit weight (193.97), cluster VII showed highest mean for days to 1st picking (85.33), Cluster IV showed highest mean for fruiting span (142.1 days) and number of fruits plant⁻¹ (15.54) and fruit width (6.47) was recorded highest in cluster I.

Table 4.9: Characters means of different clusters in brinjal

Characters	Plant height (cm) at final harvest	No. of Branches plant⁻¹	Days to 1st flowering	Days to 50% flowering	Days to 1st picking	Fruiting span	No. of fruits plant⁻¹	Fruit length (cm)	Fruit width (cm)	Av. fruit weight (g)	Fruit yield plant⁻¹ (g)
Cluster I	82.84	11.60	36.93	43.47	61.57	136.47	6.45	9.34	6.47	113.64	1.23
Cluster II	87.50	13.15	35.71	42.62	59.05	137.74	10.16	14.78	4.00	76.31	1.29
Cluster III	68.35	12.20	40.77	47.47	70.57	127.70	7.32	8.55	5.31	87.78	0.80
Cluster IV	84.03	12.21	23.08	29.67	55.08	142.17	15.54	14.25	4.00	68.78	1.19
Cluster V	93.08	12.48	41.67	51.33	60.33	136.33	8.37	10.14	4.97	123.39	2.10
Cluster VI	88.43	13.27	34.33	43.33	62.00	138.00	6.80	17.05	3.97	193.97	1.25
Cluster VII	44.27	12.47	35.00	40.00	85.33	116.33	2.20	6.77	3.65	88.90	1.17

4.5.3 Character contribution towards divergence

Percentage contribution of different traits towards genetic divergence was presented in Table 4.10.

The highest per cent contribution towards genetic divergence in brinjal was recorded in days to 50% flowering (22.67%) followed by fruit yield plant⁻¹ (21.59%), average fruit weight (16.10%), fruit length (15.12%), plant height at final harvest (11.71%) number of fruits plant⁻¹ (6.95%) and fruit width (4.39), whereas, Fruiting span (0.01%), days to 1st flowering (0.12%), number of branches plant⁻¹ (0.24%) and days to 1st picking (1.10%) showed lowest percentage contribution towards genetic divergence.

Table 4.10: Contribution of various characters towards total divergence

S No.	Characters	Time ranked first	Contribution (%)
1	Plant height (cm) Final harvest	96.000	11.71
2	No. of Branches plant ⁻¹	2.000	0.24
3	Days to 1 st flowering	1.000	0.12
4	Days to 50% flowering	186.000	22.67
5	Days to 1 st picking	9.000	1.10
6	Fruiting span	0.000	0.01
7	No. of fruits plant ⁻¹	57.000	6.95
8	Fruit length (cm)	124.000	15.12
9	Fruit width (cm)	36.000	4.39
10	Av. fruit weight (g)	132.000	16.10
11	Fruit Yield plant ⁻¹ (g)	177.000	21.59

4.6 Other qualitative parameters

Qualitative characters like leaf colour, fruit shape, fruit colour, colour of calyx, colour of flower and incidence of shoot borer.

4.6.1 Leaf colour

A wide variation was exhibited for intensity of green colour of leaf (Table 4.11). Based on intensity of green colour in leaf, brinjal genotypes were categorized into three groups i.e. dark green, green and light green. Most of the genotypes were found in light green leaf, while genotypes 2016/BRLVAR-6, 2016/BRRVAR-2, 2016/BRRVAR-8, 2017/BRLVAR-9, 2017/BRRVAR-3 and 2017/BRRVAR-5 dark green leaf. Genotypes 2015/BRLVAR-1, 2015/BRLVAR-4, 2016/BRLVAR-1, 2016/BRLVAR-2, 2016/BRLVAR-3, 2016/BRLVAR-7, 2016/BRLVAR-8 and 2016/BRLVAR-9 recorded green leaf.

4.6.2 Fruit shape

Significant variation was observed among the genotypes for shape of fruits i.e. long, oblong and round (Table 4.11). Shape of fruits was observed to be oblong in genotypes 2015/BRLVAR-2, 2015/BRLVAR-4, 2016/BRLVAR-2, 2016/BRLVAR-6, 2016/BRLVAR-9, 2016/BRRVAR-1, 2016/BRRVAR-8, 2017/BRRVAR-3, 2017/BRRVAR-10 and 2017/BRRVAR-11. Whereas genotypes 2016/BRRVAR-2, 2016/BRRVAR-4, 2016/BRRVAR-5, 2016/BRRVAR-7, 2017/BRLVAR-1 and 2016/BRRVAR-9 was produced round fruit. The remaining genotypes produced long fruit.

4.6.3 Fruit colour

Colour of fruits was observed to be dark purple, purple, light purple, white and green. Genotypes 2015/BRLVAR-4, 2015/BRLVAR-5, 2016/BRLVAR-3, 2016/BRLVAR-7, 2016/BRLVAR-9, 2016/BRRVAR-1, 2016/BRRVAR-5 and 2016/BRRVAR-7 exhibited purple fruits. Genotypes 2017/BRLVAR-5, 2017/BRLVAR-8 exhibited white fruits. However genotypes 2015/BRLVAR-2, 2016/BRLVAR-1, 2017/BRLVAR-1 and 2017/BRLVAR-3 observed green fruits. Genotypes 2016/BRLVAR-2 and 2016/BRRVAR-4 were purple. Remaining genotypes exhibited dark purple fruit. (Table 4.11).

4.6.4 Colour of calyx

Genotypes were categorized as dark green, light green, dark purple and light purple for colour of calyx (Table 4.11). Dark green colour of calyx was exhibited in genotypes 2015/BRLVAR-1, 2015/BRLVAR-2, 2016/BRLVAR-1, 2016/BRLVAR-4, 2017/BRLVAR-2 and 2017/BRLVAR-3. Genotypes

2016/BRLVAR-8, 2016/BRRVAR-2, 2016/BRRVAR-8 and 2017/BRLVAR-1 recorded dark purple calyx. Genotypes 2016/BRLVAR-9, 2016/BRLVAR-7, 2016/BRLVAR-6 and 2016/BRLVAR-3 exhibited light purple and rest of the genotypes recorded light green colour of calyx.

4.6.5 Colour of flower

The genotypes have been classified in three groups i.e. purple, light purple, dark purple and white colour flower. These groups identified by the visual observation are given in Table 4.11. Colour of flower was observed to be purple in genotypes 2015/BRLVAR-1, 2015/BRLVAR-4, 2015/BRLVAR-5, 2016/BRLVAR-6, 2016/BRLVAR-8, 2016/BRLVAR-9, 2016/BRRVAR-4 and 2016/BRRVAR-7. Genotypes 2016/BRLVAR-7, 2016/BRRVAR-8 and 2017/BRLVAR-1 were produced dark purple flowers. Whereas, genotypes 2016/BRLVAR-2 and 2017/BRRVAR-12 were produced white flowers. The remaining genotypes produced light purple flowers.

4.6.6 Incidence of Shoot borer

The result of incidence of shoot and fruit borer is depicted in the table 4.12.

Minimum 9.00% incidence of shoot borer was recorded in genotypes 2017/BRLVAR-3 followed by Punjab Sadabahar (15.65 %), 2016/BRRVAR-7 (16.13%), 2016/BRRVAR-8 (17.85%), and 2017/BRLVAR-4 (19.09). However, genotype 2017/BRRVAR-12 (48.99%) was observed highly susceptible to incidence of shoot borer under field condition.

4.6.7 Incidence of diseases

No incidence of diseases was seeing in the cropping period.

Table 4.11: Qualitative characters of brinjal genotypes

Genotypes	Leaf colour	Fruit shape	Fruit colour	Colour of calyx	Colour of flower
2015/BRLVAR-1	Green	Long	Dark purple	Dark green	Purple
2015/BRLVAR-2	Light green	Oblong	Green	Dark green	Light purple
2015/BRLVAR-3	Light green	Long	Dark purple	Green	Light purple
2015/BRLVAR-4	Green	Oblong	Purple	Light green	Purple
2015/BRLVAR-5	Light green	Long	Purple	Light green	Purple
2016/BRLVAR-1	Green	Long	Green	Dark green	Light purple
2016/BRLVAR-2	Green	Oblong	Light purple	Light green	White
2016/BRLVAR-3	Green	Long	Purple	Light purple	Light purple
2016/BRLVAR-4	Light green	Long	Dark purple	Dark green	Light purple
2016/BRLVAR-5	Light green	Long	Dark purple	Light green	Light purple
2016/BRLVAR-6	Dark green	Oblong	Dark purple	Light purple	Purple
2016/BRLVAR-7	Green	Long	Purple	Light purple	Dark purple
2016/BRLVAR-8	Green	Long	Dark purple	Dark purple	Purple
2016/BRLVAR-9	Green	Oblong	Purple	Light purple	Purple
2016/BRRVAR-1	Light green	Oblong	Purple	Green	Light purple
2016/BRRVAR-2	Dark green	Round	Dark purple	Dark purple	Light purple
2016/BRRVAR-4	Light green	Round	Light purple	Light green	Purple
2016/BRRVAR-5	Light green	Round	Purple	Light green	Light purple
2016/BRRVAR-7	Light green	Round	Purple	Light green	Purple
2016/BRRVAR-8	Dark green	Oblong	Dark purple	Dark purple	Dark purple
2016/BRRVAR-9	Light green	Round	Dark purple	Light green	Light purple
2017/BRLVAR-1	Light green	Round	Green	Dark purple	Dark purple
2017/BRLVAR-2	Light green	Long	Dark purple	Dark green	Light purple
2017/BRLVAR-3	Light green	Long	Green	Dark green	Light purple
2017/BRLVAR-4	Green	Long	Dark purple	Light green	Purple
2017/BRLVAR-5	Green	Long	White	Light green	Purple

2017/BRLVAR-6	Light green	Long	Light purple	Light green	Light purple
2017/BRLVAR-7	Green	Long	Dark purple	Green	Purple
2017/BRLVAR-8	Light green	Long	White	Light green	Light purple
2017/BRLVAR-9	Dark green	Long	Dark purple	Dark purple	Purple
2017/BRRVAR-1	Green	Long	Dark purple	Dark green	Purple
2017/BRRVAR-2	Light green	Round	Purple	Light purple	Light purple
2017/BRRVAR-3	Dark green	Oblong	Dark purple	Light purple	Dark purple
2017/BRRVAR-4	Light green	Round	Purple	Dark green	Light purple
2017/BRRVAR-5	Dark green	Round	Light purple	Light purple	Light purple
2017/BRRVAR-8	Light green	Round	Light purple	Dark green	Purple
2017/BRRVAR-10	Green	Oblong	Green	Dark green	Light purple
2017/BRRVAR-11	Light green	Oblong	Green	Dark green	Light purple
2017/BRRVAR-12	Green	Round	Light purple	Light green	White
Punjab Sadabahr	Light green	Long	Dark purple	Light green	Purple
Kashi Taru	Light green	Long	Dark purple	Light green	Purple

Table 4.12: Mean performance of incidence of shoot borer (%) in brinjal

Genotypes	Incidence of shoot borer (%)
2015/BRLVAR-1	25.46
2015/BRLVAR-2	24.46
2015/BRLVAR-3	42.62
2015/BRLVAR-4	28.89
2015/BRLVAR-5	44.56
2016/BRLVAR-1	21.31
2016/BRLVAR-2	39.38
2016/BRLVAR-3	30.29
2016/BRLVAR-4	26.76
2016/BRLVAR-5	31.85
2016/BRLVAR-6	28.09
2016/BRLVAR-7	24.50
2016/BRLVAR-8	30.28
2016/BRLVAR-9	38.78
2016/BRRVAR-1	25.92
2016/BRRVAR-2	22.90
2016/BRRVAR-4	25.69
2016/BRRVAR-5	21.35
2016/BRRVAR-7	16.13
2016/BRRVAR-8	17.85
2016/BRRVAR-9	20.21
2017/BRLVAR-1	21.93
2017/BRLVAR-2	24.92
2017/BRLVAR-3	9.00
2017/BRLVAR-4	19.09
2017/BRLVAR-5	28.05
2017/BRLVAR-6	30.95
2017/BRLVAR-7	33.23
2017/BRLVAR-8	34.95
2017/BRLVAR-9	24.65
2017/BRRVAR-1	26.70
2017/BRRVAR-2	29.96
2017/BRRVAR-3	28.73
2017/BRRVAR-4	25.38
2017/BRRVAR-5	30.46
2017/BRRVAR-8	28.61
2017/BRRVAR-10	40.77
2017/BRRVAR-11	25.01
2017/BRRVAR-12	48.99
Punjab Sadabahar (C)	15.65
Kashi Taru (C)	26.18
S.Em±	7.52
C.D.5% level	21.28

DISCUSSION

The experimental findings of the present investigation “Genetic studies on advance lines of Brinjal” have been discussed in the following heads on the basis of the available literature.

- 5.1 Analysis of variance
- 5.2 Genetic Variability
 - 5.2.1 Range and Mean Performance
 - 5.2.2 Coefficient of variation
 - 5.2.3 Heritability
 - 5.2.4 Genetic advance
- 5.3 Correlation Coefficient analysis
- 5.4 Path coefficient analysis
- 5.5 Genetic divergence
- 5.5 Other quality parameters

5.1 Analysis of variance

The estimates of mean sum of square due to genotypes were highly significant for all the characters (Table 4.1). Eight characters viz., fruit yield⁻¹ hectare, average fruit weight, plant height at final harvest, plant height at 90 DAT, plant height at 60 DAT, days to 1st picking, fruiting span and fruit yield plot⁻¹ exhibited the value of higher magnitude, indicating the presence of genetic diversity in the existing material. The findings of Sherly and Shanthi (2008), Muniappan et al. (2010), Ansari et al. (2011), Kumar et al. (2012), Balaji et al. (2013), Nayak and Nagre (2013), Chaudhary and Kumar (2014), Gavade and Ghadage (2015), Shende et al. (2015) and Patel et al. (2017) are similar to that of the present findings.

5.2 Genetic variability

5.2.1 Mean performance of the genotypes

The mean performance of the genotypes (Table 4.2 a, b, c and d) revealed a wide range of variability for all the traits. The variation was highest for fruit yield plant⁻¹ followed by fruit yield hectare⁻¹, fruiting span, average fruit weight, days to 1st picking, plant height at final harvest, plant height at 90 DAT, plant height at 60 DAT, plant height at 30 DAT and days to 50 per cent

flowering and days to 1st flowering. The findings were quite similar to as reported by Muniappan et al. (2010), Ansari et al. (2011), Kumar et al. (2011), Thangavel et al. (2011), Kumar et al. (2012), Balaji et al. (2013), Nayak and Nagre (2013), Chaudhary and Kumar (2014), Gavade and Ghadage (2015), Shende et al. (2015), Koundinya et al. (2017) and Patel et al. (2017).

5.2.2 Coefficient of variation

In the present findings phenotypic coefficient of variation were observed to be higher than the corresponding genotypic coefficient of variation for all the characters studied, however, the difference was narrow which implied their relative resistance to environmental variation. It also described that genetic factors were predominantly responsible for expression of those attributes and selection could be made effective on the basis of phenotypic performance. The findings of Nair and Mehta (2009), Kumar et al. (2011), Thangavel et al. (2011), Kumar et al. (2012), Balaji et al. (2013), Singh et al. (2014), Shende et al. (2015) and Koundinya et al. (2017) were similar to that of the present findings.

5.2.2.1 Phenotypic coefficient of variation

The phenotypic coefficient of variation ranged from 6.77% for fruiting span to 47.13% for number of fruits plant⁻¹. The phenotypic coefficient of variation was highest for characters viz., number of fruits plant⁻¹, average fruit weight, fruit yield plot⁻¹, fruit yield hectare⁻¹, fruit yield plant⁻¹, fruit length and fruit width indicating that selection of these characters can be predicted to improve the brinjal genotypes. The findings are in close harmony with those of Sherly and Shanthi (2008), Nair and Mehta (2009), Muniappan et al. (2010), Ansari et al. (2011) for fruit length, Indires and Santhosha for number of fruits plant⁻¹ (2011), Kumar et al. (2011) for fruit length, Thangavel et al. (2011), Chourasia and Sangeeta (2012), Kumar et al. (2012), Balaji et al. (2013), Chaudhary et al. (2013), Chaudhary and Kumar (2014) for fruit yield plot⁻¹ and fruit yield hectare⁻¹; Gavade and Ghadage (2015), Shende et al. (2015), Koundinya et al. (2017) and Patel et al. (2017).

However, it exhibited low for character like fruiting span, plant height at 30 DAT, number of branches plant⁻¹ at final harvest, days to 50% flowering, plant height at 60 DAT, plant height at 90 DAT, days to 1st picking, plant

height at final harvest and days to 1st flowering, which indicated that there is limited scope for improvement. The findings of Thangavel et al. (2011) and Gavade and Ghadage (2015) for number of branches plant⁻¹; Shende et al. (2015) for days to last picking; Kumar et al. (2011) for days to 50 per cent flowering are similar to present findings. The rest of the characters such as number of flowers cluster⁻¹ and number of fruits cluster⁻¹ exhibited moderate phenotypic coefficient of variation. The finding of Ansari et al. (2011) and Kumar et al. (2011) for number of flowers cluster⁻¹; Balaji et al. (2013) for number of fruits cluster⁻¹ and Shende et al. (2015) for number of fruits cluster⁻¹ are similar to the present findings.

5.2.2.2 Genotypic coefficient of variation

It is revealed from the Table 4.3 that GCV varied from 5.61% for fruiting span to 44.50% for number of fruits plant⁻¹.

High genotypic coefficient of variation was noted number of fruits per plant, average fruit weight, fruit yield plot⁻¹, fruit yield hectare⁻¹, fruit yield plant⁻¹, fruit length and fruit width. The findings are in close harmony with the results of Sherly and Shanthi (2008) for fruit length, fruit width and fruit yield plant⁻¹, Nair and Mehta (2009) number of fruits plant⁻¹, Muniappan et al. (2010) for average fruit weight, fruit length and fruit yield plant⁻¹, Ansari et al. (2011), Thangavel et al. (2011), Indires and Santhosha (2011) Kumar et al. (2011), Chourasia and Sangeeta (2012), Balaji et al. (2013), Nayak and Nagre (2013), Chaudhary and Kumar (2014) and Gavade and Ghadage (2015) for average fruit weight; Shende et al. (2015) for width of fruit, length of fruit; Patel et al. (2016), Koundinya et al. (2017) and Patel et al. (2017) are similar to the present findings. The high values of GCV suggested greater genotypic variability among the genotypes and responsiveness of the attributes for making further improvement by selection.

Fruiting span and number of branches plant⁻¹ at final harvest showed lowest genotypic coefficient of variation. The findings of Gavade and Ghadage (2015) and Shende et al. (2015) for number of branches plant⁻¹ were similar to the present finding which indicated that there is limited scope for improvement.

Plant height at 30 DAT, days to 1st picking, days to 50% flowering, plant height at 60 DAT, plant height at 90 DAT, plant height at final harvest, days to 1st flowering, number of flower cluster⁻¹ and number of fruits cluster⁻¹ recorded moderate GCV. The findings of Ansari et al. (2011) for number of fruits cluster⁻¹; Kumar et al. (2012) for fruit length and Shende et al. (2015) for width of fruit, length of fruit, plant height and days to last picking were similar to the present finding.

5.2.3 Heritability

Heritability which denotes the proportion of genetically controlled variability expressed by a programme for a particular characters or a set of character is very important biometrical tool for guiding plant breeders for adoption of appropriate breeding procedures. High heritability in broad sense is helpful in identifying appropriate character for selection and enables the breeder to select superior genotypes on the basis of phenotypic expression of quantitative characters. The estimated values of heritability in broad sense were classified as very high (more than 90%), high (70- 90%), medium (50- 70%) and low (less than 50%).

Very high estimates of heritability were obtained for the traits viz., average fruit weight followed by days to 50% flowering, plant height at 90 DAT, fruit yield plant⁻¹, fruit yield plot⁻¹, fruit yield hectare⁻¹, plant height at 60 DAT and plant height at final harvest. However, it was recorded high for fruit length, number of fruit plant⁻¹, number of flower cluster⁻¹, days to 1st flowering, plant height at 30 DAT, fruit width, number of fruit cluster⁻¹ and days to 1st picking. The results were in close proximate to that of Dhameliya and Dobariya (2007) for fruit yield plant⁻¹, number of fruits plant⁻¹, days to 1st picking; Golany et al. (2007) for plant height; Ram et al. (2007), Mishra et al. (2008), Sherly and Shanthi (2008), Nair and Mehta (2009), Sao and Mehta (2009), Naik et al. (2010) for fruit length; Ansari et al. (2011), Indires and Santhosha (2011) for fruit diameter; Kumar et al. (2011) for days to 50% flowering and number of fruits cluster⁻¹; Thangavel et al. (2011), Dhaka and Soni (2012), Ambade et al. (2013), Patel et al. (2013), Kumar et al. (2014), Singh et al. (2014), Vidhya and Kumar (2015) for number of fruits plant⁻¹; Koundinya et al. (2017). High values of broad sense heritability for the above

characters expressed that they were least influenced by environmental modification. It reflected that the phenotypes were the true representative of their genotypes and selection based on phenotypic performance would be reliable.

Low estimation of heritability was recorded for number of branches plant⁻¹ at final harvest indicated that these characters was more influenced by the environment and may not be responded to selection.

Whereas, moderate heritability was found in fruiting span which indicated that selection based on phenotypic performance would be rewarding.

5.2.4 Genetic advance

Heritability indicates only the effectiveness with which selection of a genotype can be based on phenotypic performance, but fails to indicate the genetic progress. Heritability estimates along with genetic gains are more effective and reliable in predicting the improvement through selection (Johnson et al. 1955). Estimate of genetic advance helps to predict the extent of improvement that can be achieved for improving the different characters. The estimated values of genetic advance as percent of mean were classified as high (more than 50%), moderate (20-50%) and low (less than 20%).

Genetic advance as percentage of mean ranged between 9.59% for fruiting span to 86.63% for number of fruits plant⁻¹. The highest estimate of genetic advance as percentage of mean was recorded for number of fruits plant⁻¹, average fruit weight, fruit yield plot⁻¹, fruit yield hectare⁻¹, fruit yield plant⁻¹ and fruit length. The results were in consonance with Dhameliya and Dobariya (2007) for fruit yield plant⁻¹, number of fruits plant⁻¹, days to 1st picking; Golany et al. (2007), Ram et al. (2007), Mishra et al. (2008), Sherly and Shanthi (2008), Nair and Mehta (2009), Sao and Mehta (2009), Naik et al. (2010), Ansari et al. (2011), Indiresha and Santhosha (2011) for fruit diameter; Kumar et al. (2011) number of fruits cluster⁻¹; Thangavel et al. (2011), Dhaka and Soni (2012), Ambade et al. (2013), Patel et al. (2013), Kumar et al. (2014), Singh et al. (2014), Vidhya and Kumar (2015) for number of fruits plant⁻¹; Koundinya et al. (2017).

Fruit width, number of fruits cluster⁻¹, number of flower cluster⁻¹ and days to 1st flowering showed moderate value of genetic advance as percentage of mean. The findings were in agreement to the findings of Sao and Mehta (2009), Ansari et al. (2011) for days to 1st flowering, Kumar et al. (2011) and Ambade et al. (2013) for fruit width.

Low estimates of genetic advance as percentage of mean were observed for fruiting span, number of branches plant⁻¹, days to 1st picking, plant height at 30 DAT, plant height at 90 DAT, days to 50% flowering, plant height at 60 DAT and plant height at final harvest. The findings were in agreement to Ansari et al. (2011) plant height, days to 1st picking, days to 50% flowering; Kumar et al. (2011) for plant height; Sao and Mehta (2009) for plant height and number of branches plant⁻¹; Ambade et al. (2013) and Vidhya and Kumar (2015).

High heritability coupled with high genetic advance as percentage of mean for traits like number of fruits plant⁻¹, average fruit weight, fruit yield plot⁻¹, fruit yield hectare⁻¹, fruit yield plant⁻¹ and fruit length suggested the preponderance of additive genes. It also indicated higher response for selection of high yielding genotypes as these characters are governed by additive gene actions. The findings were in agreement to the findings of Dhameliya and Dobariya (2007), Mishra et al. (2008), Sherly and Shanthi (2008), Sao and Mehta (2009), Ansari et al. (2011), Indires and Santhosha (2011), Dhaka and Soni (2012) for average fruit weight; Vidhya and Kumar (2015) and Koundinya et al. (2017) for number of fruits plant⁻¹; Koundinya et al. (2017) fruit yield plant⁻¹.

High heritability supplemented with moderate genetic advance as percentage of mean were manifested by fruit width, number of fruits cluster⁻¹, number of flower cluster⁻¹ and days to 1st flowering which might be attributed to additive gene action conditioning their expression and phenotypic selection for their amenability can be brought about. These findings were in agreement with the earlier findings of Sao and Mehta (2009), Nair and Mehta (2009), Ansari et al. (2011), shekhar et al. (2012) for number of flowers cluster⁻¹; Shende et al. (2015) and Ambade et al. (2013) for fruit width.

High heritability coupled with low genetic advance as percentage of mean was observed for plant height at 30 DAT, 60 DAT, 90 DAT and at final harvest, days to 50% flowering and days to 1st picking. This revealed the predominance of non-additive gene action in the expression of these characters. These findings corroborated the earlier findings of Ansari et al. (2011) and Dhaka and Soni (2012) for plant height.

Low estimate of heritability coupled with low genetic advance as percentage of mean were displayed by number of branches at final harvest indicated that this character was highly influenced by environmental effects and consequently its selection would be ineffective.

5.3 Correlation coefficient analysis

A wide range of variation in quantitative characters provides the basis for selection in plant breeding programme. The knowledge of association among the characters is useful to the breeder for improving the efficiency of selection. Correlation coefficient analysis measures the mutual relationship between plant characters and determines the component character on which selection can be made for genetic improvement of yield. Investigation regarding the presence of component and nature of association among themselves is essential and pre-requisite for improvement in yield. Correlation coefficient provides a clear picture of the extent of association between a pair of traits and indicates whether simultaneous improvement of the correlated traits may be possible or not. The knowledge of genetic association between yield and its component characters help in improving the efficiency of selection for yield by making proper choice and balancing one component with another.

The magnitude of phenotypic correlation was higher than the genotypic correlation for all the traits that indicated inherent association between various characters. The findings were in agreement to Naliyadhara et al. (2007), Shende et al. (2014) and Patel et al. (2015).

5.3.1 Fruit yield plant⁻¹ (g)

In the present findings significant and positive phenotypic correlation of fruit yield per plant was observed with average fruit weight, plant height at

final harvest, number of fruits plant⁻¹, fruit length and fruiting span. However, it exhibited significant and negative association with fruit width and days to 1st picking. The highest positive and significant correlation coefficient of fruit yield plant⁻¹ was noted with average fruit weight, plant height at final harvest, number of fruits plant⁻¹, fruit length and fruiting span indicating that these characters are the primary yield determinants in brinjal. These findings corroborated the earlier findings of a Shende et al. (2014) and Patel et al. (2015) for positive association with number of fruits plant⁻¹; Nair and Mehta (2007) and Singh et al. (2010) for negative association with days to 1st picking.

5.3.2 Plant height (cm)

Plant height at final harvest showed significant and positive correlation with fruit length followed by fruiting span, fruit yield plant⁻¹, number of fruits plant⁻¹ and number of branches plant⁻¹. This indicates the importance of this character in selection. Significant and negative association of these characters was observed with days to 1st flowering, number of flowers cluster⁻¹ and days to 1st picking. The positive correlation of plant height with number of branches plant⁻¹ at final harvest, fruiting span and fruit length indicates allocation and translocation of photosynthates from the source to the sink. These results are in close harmony with the findings of Nair and Mehta (2007), Prabhu and Natrajan (2008) and Thangamani and Jhansirani (2012).

5.3.3 Number of branches plant⁻¹

Number of branches plant⁻¹ showed highly significant and positive correlation with fruit length, fruiting span and number of fruits plant⁻¹, while it was found highly significant and negative association with fruit width, average fruit weight and days to 1st picking. These results are in close harmony with the findings of Thangamani and Jansirani (2012) and Koundinya et al. (2017).

5.3.4 Days to 1st flowering

Association of days to first flowering was recorded significant and positive with days to 50 per cent flowering, days to 1st picking and average fruit weight, while it was found significant and negative with number of fruits

plant⁻¹, fruit length and fruiting span. These results are in close harmony with days to 50 per cent flowering, days to 1st picking and average fruit weight. The findings of Shende et al. (2014) for days to 1st picking; Thangamani and Jansirani (2012) for positive association with average fruit weight; Thangamani and Jansirani (2012) for negative association with number of fruits plant⁻¹.

5.3.5 Days to 50 per cent flowering

Days to 50 per cent flowering recorded highly significant and positive association with days to 1st picking and average fruit weight. However, it was exhibited significant and negative association with number of fruits plant⁻¹, fruiting span and fruit length. These findings corroborated the earlier findings of Patel et al. (2015) for positive association with days to 1st picking; Patel et al. (2015) for negative association with number of fruits plant⁻¹.

5.3.6 Number of flower cluster⁻¹

Number of flower cluster⁻¹ showed significant and positive association with days to 1st picking. However it was exhibited significant and negative association with fruiting span. These findings corroborated the earlier findings of Patel et al. (2015) for positive association with number of fruits cluster⁻¹.

5.3.7 Days to 1st picking

Significant and positive association of days to picking⁻¹ was observed with fruit width. However it was exhibited significant and negative association with fruiting span, fruit length and number of fruits plant⁻¹. These findings corroborated the earlier findings of Nair and Mehta (2007), Singh et al. (2010), Patel et al. (2015) for negative association with number of fruits plant⁻¹.

5.3.8 Fruiting span

Association of fruiting span was recorded significant and positive with fruit length, number of fruits plant⁻¹ and fruit yield plant⁻¹.

5.3.9 Number of fruits plant⁻¹

Number of fruits plant⁻¹ recorded positive and significant correlation with number of fruits cluster⁻¹, fruit length and fruit yield plant⁻¹, while highly significant and negative association with fruit width and average fruit weight.

These findings corroborated the earlier finding of Dharwad et al. (2009), Thangamani and Jansirani (2012) for positive association with fruit yield plant⁻¹; Patel et al. (2015) for negative association with average fruit weight.

5.3.10 Number of fruits cluster⁻¹

Number of fruits cluster⁻¹ showed highly significant and negative association with fruit width and average fruit weight.

5.3.11 Fruit length

Fruit length recorded positive and significant with fruit yield plant⁻¹ and negative association was with fruit width.

5.3.12 Fruit width (cm)

Fruit width expressed a highly significant and positive correlation with average fruit weight, while highly significant and negative association with fruit yields plant⁻¹. These results are in close harmony with the findings of Patel et al. (2015) for average fruit weight.

5.4 Path coefficient analysis

Correlation coefficients are the indication of simple association between variables. In a biological system, however the relationship may exist in a very complex form. It is therefore, essential to study the relationship among variable in a comprehensive way. Path coefficient analysis is a power full tool, which enable portioning of the given relationships in its further components. In other words, it takes into account not only the relationship of component characters with the dependent character, but simultaneously takes care of its relationship with other component also. Thus, it helps in understanding the causal system in a better way because it enables portioning the total correlations coefficient into direct and indirect effects of various characters.

In the present investigation path coefficient analysis was carried out for characters under study using genotypic and phenotypic correlation coefficient and taking fruit yield plant⁻¹ as dependable variable, in order to see the causal factor and so as to identify the components which are responsible for producing fruit yield plant⁻¹. In general, the genotypic direct as well as indirect

effects were slightly higher in magnitude as compared to corresponding phenotypic direct and indirect effects indicating that the masking effect of the environment.

Path coefficient analysis of different characters contributing towards fruit yield plant⁻¹ showed that average fruit weight had highest positive direct effect followed by number of fruits plant⁻¹, plant height at 1st harvest, days to 1st flowering and days to 50% flowering. The results are in propinquity with Kushwah and Bandhyopadhyaya (2007), Nair and Mehta (2007), Prabhu et al. (2008), Lohakare et al. (2008), Singh et al. (2010), Chattopadhyay et al. (2011), Shende et al. (2014) for number of fruits plant⁻¹; Naliyadhara et al. (2007), Jadhao et al. (2009), Chattopadhyay et al. (2011) and Shende et al. (2014) for average fruit weight. The characters average fruit weight, number of fruits plant⁻¹, fruiting span, fruit length and number of branches plant⁻¹ and number of fruits cluster⁻¹ had correlation coefficient values positive and at par with their direct effect on fruit yield plant⁻¹. This indicates true relationships with fruit yield plant⁻¹ and direct selection for these traits would result in higher breeding efficiency for improving yield. Thus, these traits might be reckoned as the most important component traits for fruit yield plant⁻¹.

Whereas, days to 1st picking had the highest negative direct effect on fruit yield plant⁻¹ followed by days to fruiting span, fruit width, fruit length, number of flower cluster⁻¹, number of branches plant⁻¹ and number of fruit cluster⁻¹. The results are in propinquity with Patel et al. (2015) for number of fruits cluster⁻¹ and fruit length. Days to 1st picking, fruit width, number of flowers cluster⁻¹ and number of fruits cluster⁻¹ imparted a negative direct effect on fruit yield plant⁻¹, as well as they were negatively correlated to it. Under such circumstance direct selection for this character should be avoided, instead indirect selection should be followed.

Path coefficient analysis revealed that average fruit weight, number of fruits plant⁻¹, fruiting span, fruit length and number of branches plant⁻¹, number of fruits cluster⁻¹ and fruit width are the most important characters contributing towards fruit yield and hence purposeful and balanced selection based on these characters would be rewarding for improvement in brinjal.

5.5 Genetic divergence

D^2 statistic helps in the selection of genetically divergent parents for their exploitation in hybridization programmes. The technique measures the degree of diversification and determines the relative proportion of each components character to the total divergence. It measures the forces of differentiation at two levels i.e. intra cluster and inter cluster levels. It provides reliable estimates of genetic divergence and a large number of germplasm lines can be evaluated at time for genetic diversity by this technique. In the present investigation, 41 genotypes were grouped into 7 clusters using tocher methods. The intra and inter cluster distance was calculated by using D^2 values.

5.4.1 Contribution of individual characters toward divergence

The variance of cluster mean of different characters indicated that there is a significant variation for all the characters. Hence, characters like days to 50% flowering contributed maximum genetic divergence followed by fruit yield plant⁻¹, average fruit weight, fruit length, plant height at final harvest, number of fruits plant⁻¹ and fruit width. These findings corroborated with the earlier findings of Sharma and Maurya (2004) for number of fruits plant⁻¹, Naik (2006) for plant height and Kumar et al. (2007) for fruit length.

5.4.2 Grouping of genotypes in to various clusters

The maximum number of genotypes (14) was found in the cluster II followed by cluster I and III (10), cluster IV (4). While remaining cluster V, VI and cluster VII were solitary clusters. From the composition of genotypes of most of the clusters, it was found that the genotypes included in clusters are heterogeneous in terms of their origins. These results revealed that geographic diversity might not be an important factor in determining genetic divergence. These finding are in agreement with the results obtained by Sharma and Maurya (2004), Singh et al. (2005), Naik (2006), Bansal and Mehta (2007) and Kumar et al. (2007).

5.4.3 Inter and intra cluster distance

The inter cluster distances were found higher than the intra cluster distance revealing a considerable amount of genetic diversity among the genotypes studied. The highest inter cluster distance was observed between

cluster VI and VII, followed by cluster IV and V, cluster V and VII, cluster IV and VI, cluster III and IV, cluster III and VI, cluster IV and VII and cluster II and VII. The genotypes grouped in these clusters can be used in breeding programme in order to get a wide spectrum of variability and Maximum intra cluster distance was revealed in cluster III followed by cluster IV and cluster II. The minimum intra cluster distance was expressed by cluster I. The least intra cluster distance was expressed by cluster V, VI and cluster VII.

5.4.4 Cluster mean

Highest mean value for a large number of characters was exhibited in cluster V [viz. plant height at final harvest, days to 1st flowering, days to 50% flowering and fruit yield plant⁻¹] followed by cluster VI [viz. number of branches plant⁻¹, fruit length and average fruit weight], cluster IV [viz. fruiting span and number of fruits plant⁻¹], cluster VII for days to 1st picking and cluster I fruit width. The present results are in accordance with the findings of Madhavi et al. (2015).

5.4.5 Genotypes identified as parents in hybridization programme

Crossing among the genotypes in cluster V (2017/BRL VAR-2), cluster VI (2016/BRL VAR-6) and cluster VII (2017/BRR VAR-11) were identified as genetically diverse parents, which can be utilized for future crop improvement programme may lead to maximum diversity in the segregating population and develop high yielding varieties in brinjal.

5.6 Other Quality parameters

Qualitative characters like leaf colour, fruit shape, fruit colour, colour of calyx, colour of flower and incidence of shoot borer is discussed in below.

Wide variation was exhibited in leaf colour (viz., dark green and light green), fruit shape (i.e. long, oblong and round), fruit colour (viz., dark purple, purple, light purple, white and green), colour of calyx such as dark green, light green, dark purple and light purple and color of flower purple, light purple and white colour flower. The findings are in agreement with the findings of Golani et al. (2007) and Gangopadhyay et al. (2010) and Nair and Mehta (2009).

5.6.1 Incidence of Shoot borer

Significantly minimum 9.00% incidence of shoot borer was recorded in genotypes 2017/BRLVAR-3 followed by Punjab Sadabahar, 2016/BRRVAR-7, 2016/BRRVAR-8 and 2017/BRLVAR-4. However, genotype 2017/BRRVAR-12 was observed highly susceptible to incidence of shoot borer under field condition. The findings are in agreement with the findings of Prabhu et al. (2009).

5.6.2 Incidence of diseases

No incidence of diseases was seen in the cropping period.

SUMMARY, CONCLUSION AND SUGGESTIONS FOR FUTURE WORK

6.1 Summary

The present investigation “Genetic studies on advance lines of Brinjal” was carried out during the season of 2017-2018 at the Horticulture Complex, Department of Horticulture, College of Agriculture, J.N.K.V.V., Jabalpur (M.P.). The experimental material for the present investigation was comprised of forty one genotypes of brinjal. These genotypes were sown in Randomized Complete Block Design with three replications, to observed morphological, phenological, yield and other quality parameters and to estimate the genetic variability, association analysis (correlation coefficient and path coefficient analysis) and genetic divergence. Observations were recorded on the basis of five random competitive plants selected from each genotype separately for morphological, phenological, yield and other quality parameters were evaluated as per standard procedure. On the basis of results, the present investigation is summarized as follows:

The estimates of mean sum of square due to genotypes were highly significant for all the characters indicating the presence of genetic diversity in the existing material.

The mean performance of the genotypes revealed a wide range of variability for all the traits. The variation was highest for fruit yield plant⁻¹ followed by fruit yield hectare⁻¹, fruiting span, average fruit weight, days to 1st picking, plant height at final harvest, plant height at 90 DAT, plant height at 60 DAT, plant height at 30 DAT, days to 50 per cent flowering and days to 1st flowering. The present study revealed that the phenotypic coefficient of variation was higher than the corresponding genotypic coefficient of variation for all the traits which might be due to interaction of the genotypes with the environment to some degree or other explaining environmental factors influencing the expression of these characters. High phenotypic and genotypic coefficient of variation was observed for number of fruits plant⁻¹, average fruit weight, fruit yield plot⁻¹, fruit yield hectare⁻¹, fruit yield plant⁻¹, fruit length and

fruit width which suggests greater phenotypic and genotypic variability among the genotypes and responsiveness of the attributes for making further improvement by selection. However, fruiting span showed low estimates of genotypic and phenotypic coefficient of variation indicating their limited scope for improvement.

Very high estimates of heritability were obtained for the traits viz., average fruit weight followed by days to 50% flowering, plant height at 90 DAT, fruit yield plant⁻¹, fruit yield plot⁻¹, fruit yield hectare⁻¹, plant height at 60 DAT and plant height at final harvest. However, it was recorded high for fruit length, number of fruit plant⁻¹, number of flower cluster⁻¹, days to 1st flowering, plant height at 30 DAT, fruit width, number of fruit cluster⁻¹ and days to 1st picking. High values of broad sense heritability for the above characters expressed that they were least influenced by environmental modification.

The highest estimate of genetic advance as percentage of mean was recorded for number of fruits plant⁻¹, average fruit weight, fruit yield plot⁻¹, fruit yield hectare⁻¹, fruit yield plant⁻¹ and fruit length.

High heritability coupled with high genetic advance as percentage of mean for traits like number of fruits plant⁻¹, average fruit weight, fruit yield plot⁻¹, fruit yield hectare⁻¹, fruit yield plant⁻¹ and fruit length suggested the preponderance of additive genes. It also indicated higher response for selection of high yielding genotypes as these characters are governed by additive gene actions.

High heritability supplemented with moderate genetic advance as percentage of mean were manifested by fruit width, number of fruits cluster⁻¹, number of flower cluster⁻¹ and days to 1st flowering which might be attributed to additive gene action conditioning their expression and phenotypic selection for their amenability can be brought about.

High heritability coupled with low genetic advance as percentage of mean was observed for plant height at 30 DAT, 60 DAT, 90 DAT and at final harvest, days to 50% flowering and days to 1st picking. This revealed the predominance of non-additive gene action in the expression of these characters.

The highest positive and significant correlation coefficient of fruit yield plant⁻¹ was noted with average fruit weight, plant height at final harvest, number of fruits plant⁻¹, fruit length and fruiting span, which indicated that effective improvement in brinjal yield through these components could be achieved. The yield attributing characters exhibited varying trend amongst them. Plant height at final harvest showed significant and positive correlation with fruit length followed by fruiting span, fruit yield plant⁻¹, number of fruits plant⁻¹ and number of branches plant⁻¹. Number of branches plant⁻¹ showed highly significant and positive correlation with fruit length, fruiting span and number of fruits plant⁻¹. Association of days to 1st flowering was recorded significant and positive with days to 50 per cent flowering, days to 1st picking and average fruit weight. Days to 50 per cent flowering was recorded highly significant and positive association with days to 1st picking and average fruit weight. Association of number of flowers⁻¹ cluster was recorded significant and positive with days to 1st picking. Days to 1st picking expressed significant and positive correlation with fruit width. Association of fruiting span was recorded significant and positive with fruit length, number of fruits plant⁻¹ and fruit yield plant⁻¹. Number of fruits plant⁻¹ expressed a highly significant and positive correlation coefficient with number of fruits cluster⁻¹, fruit length and fruit yield plant⁻¹. Fruit length expressed with highly significant and positively association with fruit yield plant⁻¹. Fruit width expressed with highly significant and positively association with average fruit weight.

However, fruit yield plant⁻¹ exhibited significant and negative association with fruit width and days to 1st picking. Highly significant and negative association of plant height at final harvest was observed with number of branches plant⁻¹ at final harvest, fruiting span and fruit length. Number of branches plant⁻¹ was found significant and negative association with fruit width, average fruit weight and days to 1st picking. Days to first flowering were found significant and negative with number of fruits plant⁻¹, fruit length and fruiting span. Days to 50 per cent flowering exhibited significant and negative association with number of fruits plant⁻¹, fruiting span and fruit length. Significant and negative association of number of flowers cluster⁻¹ was observed with fruiting span. Correlation coefficient of days to 1st picking was

showed significant and negative association with fruiting span, fruit length and number of fruits plant⁻¹. The correlation coefficient of number of fruits plant⁻¹ was recorded to negative and significant association with fruit width and average fruit weight. Correlation coefficient of fruit length was showed significant and negative association with fruit width. The correlation coefficient of fruit width was recorded to negative and significant association with fruit yield plant⁻¹.

Path coefficient analysis revealed that average fruit weight, number of fruits plant⁻¹, fruiting span, fruit length and number of branches plant⁻¹, number of fruits cluster and fruit width are the most important characters contributing towards fruit yield and hence purposeful and balanced selection based on these characters would be rewarding for improvement in brinjal.

The D² analysis provides valuable information on the extent of variation present in the crop under improvement. Selection of parent or lines based on individual attributes may not be as advantageous as the one based on a number of improvement traits collectively. In any breeding programme inclusion of such genetically diverse parent is essential to generate variability and desirable recombinants.

On the basis of D² analysis the 41 genotypes were grouped into seven clusters, irrespective of the geographic divergence, indicating no parallelism between geographic and genetic diversity.

Days to 50% flowering showed maximum contribution towards total divergence followed by fruit yield plant⁻¹, average fruit weight, fruit length, plant height at final harvest, number of fruit plant⁻¹ and fruit width. Thus, these traits should be given almost consideration for the purpose of further selection and choice of parents for improvement programme.

The intra cluster distance was highest in cluster III, IV and II and the minimum inter cluster distance was observed between cluster V, VI and VII while the maximum inter cluster distance was exhibited by cluster VI and cluster VII followed by cluster IV and V. It would therefore logical to make crosses between genotypes belonging to these different cluster separated by

high estimated statistical distances to create wider spectrum of variability and to exploit hybridization.

The inter cluster means was wide for cluster V [viz. plant height at final harvest, days to 1st flowering, days to 50% flowering and fruit yield plant⁻¹] followed by cluster VI [viz. number of branches plant⁻¹, fruit length and average fruit weight], cluster IV for fruiting span and number of fruits plant⁻¹, cluster VII for days to 1st picking and cluster I for fruit width. It suggested that characters which showed the variations are responsible for the variability in open pollinated and hybrid cultivars.

Crossing among the genotypes in cluster V (2017/BRL VAR-2), cluster VI (2016/BRL VAR-6) and cluster VII (2017/BRR VAR-11) were identified as genetically diverse parents, which can be utilized for future crop improvement programme may lead to maximum diversity in the segregating population and develop high yielding varieties in brinjal.

Expression of 6 distinguishing morphological traits was observed visually at plant and fruit levels to categorize the genotypes as per National test Guidelines DUS test developed by ICAR.

At plant and fruit level, the expression of 6 morphological characters at different stages of plant and fruit was observed to categorize the genotypes. leaf colour, fruit shape, fruit colour, colour of calyx and colour of flower are the most stable and uniform distinguishing characters for verification of brinjal genotypes at field level.

Significantly minimum 9.00% incidence of shoot borer was recorded in genotypes 2017/BRLVAR-2 followed by 2016/BRRVAR-5, 2016/BRRVAR-7, and 2017/BRLVAR-3. However, genotype 2017/BRRVAR-12 was observed highly susceptible to incidence of shoot and fruit borer under field condition.

An overall observation of quantitative and qualitative characters genotype 2016/BRRVAR-2 was recorded highest fruit yield followed by 2016/BRRVAR-7 and 2016/BRLVAR-3 and these were suitable for cultivation in Kymore Plateau and Satpura hills agro-climatic region of M.P.

6.2 Conclusions

- 1) Analysis of variance revealed highly significant variance for all the traits depicting greater variability in the existing material.
- 2) Variation was high for fruit yield plant⁻¹ followed by fruit yield hectare⁻¹, fruiting span, average fruit weight, days to 1st picking, plant height at final harvest, plant height at 90 DAT, 60 DAT and 30 DAT, days to 50 per cent flowering and days to 1st flowering. The PCV was higher than the GCV for all the characters. The PCV and GCV were highest for characters, number of fruits plant⁻¹, average fruit weight, fruit yield plot⁻¹, fruit yield hectare⁻¹, fruit yield plant⁻¹, fruit length and fruit width indicating greater diversity for these traits and their further improvement through selection. High heritability coupled with high genetic advance as percentage of mean for traits like number of fruits plant⁻¹, average fruit weight, fruit yield plot⁻¹, fruit yield hectare⁻¹, fruit yield plant⁻¹ and fruit length Suggested that the preponderance of additive genes. It also indicated higher response for selection of high yielding genotypes as these characters are governed by additive gene actions.
- 3) Correlation coefficient of fruit yield plant⁻¹ was recorded highly significant and positive with average fruit weight, plant height at final harvest, number of fruits plant⁻¹, fruit length and fruiting span. Significant and negative association was exhibited with fruit width and days to 1st picking. The highest positive and significant correlation coefficient of fruit yield plant⁻¹ was noted with these characters indicating that these characters are the primary yield determinant in brinjal.
- 4) Path coefficient analysis revealed that average fruit weight, number of fruits plant⁻¹, fruiting span, fruit length and number of branches plant⁻¹, number of fruits cluster⁻¹ and fruit width are the most important characters contributing towards fruit yield and hence purposeful and balanced selection based on these characters would be rewarding for improvement in brinjal.

- 5) Study of genetic divergence revealed a high inter cluster distance between cluster VI and cluster VII and cluster IV and V may be considered in a crossing programme to get better segregants for improvement of brinjal. Also high contribution of traits like days to 50% flowering, fruit yield plant⁻¹, average fruit weight, fruit length, plant height at final harvest, number of fruit plant⁻¹ and fruit width towards total divergence suggested selection of parents based on these characters for exploitation of hybrid vigour. Crossing among the genotypes in cluster V (2017/BRL VAR-2), cluster VI (2016/BRL VAR-6) and cluster VII (2017/BRR VAR-11) were identified as genetically diverse parents, which can be utilized for future crop improvement programme may lead to maximum diversity in the segregating population and develop high yielding varieties in brinjal.
- 6) The finding will help to a great extent in maintenance breeding, quality seeds production, seed certification and seed testing programme. It also used for screening of genotypes for quality and high yield. Brinjal genotypes in active seed multiplication chain at national level may be verified with the help of observed distinguishing, stable and uniform morphological traits at plant and fruit level viz., leaf colour, fruit shape, fruit colour, colour of calyx and colour of flower.
- 7) An overall observation of quantitative and qualitative characters genotype 2016/BRRVAR-2 was recorded highest fruit yield followed by 2016/BRRVAR-7, 2016/BRLVAR-3 and lowest incidence of shoot borer in genotype 2017/BRLVAR-3 were identified as best genotypes for cultivation in Kymore Plateau and Satpura hills agro-climatic region of M.P.

6.3 Suggestions for further work

1. Stability of distinct traits of brinjal should be established over the years.
2. Traits identified for high heritability coupled with high or moderate genetic gain may be considered in selection for the improvement of crop.
3. Characters having desirable association and direct effects with fruit yield should be given due consideration for genetic improvement in brinjal.
4. Crossing among the genotypes in cluster V (2017/BRL VAR-2), cluster VI (2016/BRL VAR-6) and cluster VII (2017/BRR VAR-11) were identified as genetically diverse parents, which can be utilized for future crop improvement.

			
2015/BRLVAR-1	2015/BRLVAR-2	2015/BRLVAR-3	2015/BRLVAR-4
			
2015/BRLVAR-5	Kashi Taru	Punjab Sadabahar	2016/BRLVAR-1
			
2016/BRLVAR-2	2016/BRLVAR-3	2016/BRLVAR-4	2016/BRLVAR-5
			
2016/BRLVAR-6	2016/BRLVAR-7	2016/BRLVAR-8	2016/BRLVAR-9

Plate I: Genotype of Brinjal showing fruit shape, colour and size

			
2016/BRRVAR-1	2016/BRRVAR-2	2016/BRRVAR-4	2016/BRRVAR-5
			
2016/BRRVAR-7	2016/BRRVAR-8	2016/BRRVAR-9	2017/BRRVAR-1
			
2017/BRLVAR-2	2017/BRLVAR-3	2017/BRLVAR-4	2017/BRLVAR-5
			
2017/BRLVAR-6	2017/BRLVAR-7	2017/BRLVAR-8	2017/BRLVAR-9

Plate II: Genotype of Brinjal showing fruit shape, colour and size

		
2017/BRRVAR-1	2017/BRRVAR-2	2017/BRRVAR-3
		
2017/BRRVAR-4	2017/BRRVAR-5	2017/BRRVAR-8
		
2017/BRRVAR-10	2017/BRRVAR-11	2017/BRRVAR-12

Plate III: Genotype of Brinjal showing fruit shape, colour and size

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APPENDICES

Appendix–I Analysis of variance table showing the mean sum of squares

Source of variance	D.F.	Plant height (cm) at			
		30DAT	60DAT	90DAT	Final harvest
Replications	2	3.433	17.365	6.668	32.198
Genotypes	40	148.706**	247.961**	336.872**	462.422**
Error	80	9.130	7.757	9.367	16.245

Source of variance	D.F.	No. of branches plant ⁻¹ at final harvest	Days to 1 st flowering	Days to 50% flowering	No. of flower cluster ⁻¹
Replications	2	2.588	11.934	4.130	0.141
Genotypes	40	5.652**	102.190**	113.367**	2.531**
Error	80	1.924	5.376	3.113	0.117

Source of variance	D.F.	Days to 1 st picking	Fruiting span	No. of fruits plant ⁻¹	No. of fruits cluster ⁻¹
Replications	2	22.853	22.373	2.021	0.129
Genotypes	40	240.235**	197.816**	47.510**	0.869**
Error	80	24.428	26.015	1.850	0.061

Source of variance	D.F.	Fruit length (cm)	Fruit width (cm)	Av. fruit weight (g)	Fruit yield plant ⁻¹
Replications	2	3.416	0.419	21.029	0.014
Genotypes	40	39.901**	6.695**	2777.893**	0.403**
Error	80	1.444	0.427	72.983	0.011

Source of variance	D.F.	Fruit yield plot ⁻¹	Fruit yield hectare ⁻¹	Incidence of fruit and shoot borer (%)
Replications	2	5.875	1480.018	52.073
Genotypes	40	161.359**	40639.415**	194.200
Error	80	4.657	1172.953	169.858

CURRICULAM VITAE

Name of the author- Deepa Kulesh

Place- Village- Lalpur, Th- Dindori,

District- Dindori (M.P.) - 481880

Date of Birth- 1st January 1994



The author of this thesis **Miss Deepa Kulesh**, D/o Shri Karam Singh Kulesh and Smt. Panchwati Kulesh was born on, 1st January 1994 at Village Lalpur, Th -Dindori, Dist -Dindori (M.P.). She has joined the following institutions and successfully completed the degree of M.Sc. (Ag.) during the year 2017 -18 with 7.86 OGPA with 10 point scale.

She has got the following degrees,

S. No.	Decreases granted	Institution	University/ Board	Percentage	Year
1	M.Sc. (Ag.)	JNKVV, Jabalpur	JNKVV, Jabalpur	78.60	2018
2	B.Sc.(Ag.)	JNKVV, Jabalpur	JNKVV, Jabalpur	73.00	2016
3	12 th	Govt. Boys H S School, Harrai Chhindwara	M.P. Board Bhopal	78.20	2011
4	10 th	Govt. High School, Tendni Chhindwara	M.P. Board Bhopal	58.83	2009

She has following scientific interests-

For the partial fulfillment of the master's degree programme she was allotted a research problem on **“Genetic studies on advance lines of Brinjal”** which was successfully conducted by her and being submitted in the form of the thesis.