

# Variability and selection indices in two F<sub>2</sub> populations of brinjal from intra-specific hybridization

## Abstract

Two F<sub>2</sub> populations of brinjal (*Solanum melongena* L.) from intra-specific hybridizations MLC-1 x Longai (oblong) and MLC-3 x Longai (oblong) attempted in 2015-16 were evaluated for eight quantitative traits using genetic variability parameters, heritability, genetic advance, genetic advance as per cent of mean, correlation and selection indices in the year 2017-18. The characters viz., number of fruits per plant (0.794) and number of branches per plant (0.633) recorded positive and highly significant correlations with yield per plant in F<sub>2</sub> plants of MLC-1 x Longai (oblong), whereas the characters viz., number of fruits per plant (0.819), average fruit weight (0.700) and fruit volume (0.593) recorded positive and highly significant correlations with yield per plant in F<sub>2</sub> plants of MLC-3 x Longai (oblong). Selection indices for yield selection were constructed in both the F<sub>2</sub> populations using the characters with highly significant yield correlations. Based on the efficient selection index, the genotypes were given scores or ranks and the best 5% plants were selected in both F<sub>2</sub> populations i.e., plant number 2, 12, 10, 3, 11 and 19 in F<sub>2</sub> plants of MLC-1 x Longai (oblong) and plant number 105, 28, 107, 26, 22 and 109 in F<sub>2</sub> plants of MLC-3 x Longai (oblong) for constituting the third generation, evaluated in the year 2018-19. A comparative evaluation of the performance of the two populations arising from one common parent i.e. Longai showed that population generated from cross MLC-1 x Longai (oblong) was more promising than MLC-3 x Longai (oblong).

**Keywords:** Brinjal, Phenotypic Coefficients of Variation (PCV), Genotypic Coefficient of Variation (GCV), heritability in broad sense, genetic advance, correlation, selection indices.

## 1. INTRODUCTION

Brinjal (*Solanum melongena* L.) is a common and popular vegetable crop with immense health benefits, belonging to the family *Solanaceae* with chromosome number  $2n=2x=24$  (Verma et al. 2021). Brinjal is a native of India, where large-fruited types were first domesticated. In his 1886 book "Origin of Cultivated Plants", De Candolle declared that the species *S. melongena* had been known in India from ancient times and was considered an Asian native (Chaudhary et al. 2017). Vavilov (1928) had the belief that the Indo-Burma region is the centre of origin of brinjal. Bangladesh and Myanmar are the centre of diversity (Isshiki et al. 1994) based on the isoenzyme and morphological variation noticed in an extensive germplasm collection from India. According to Zeven and Zhukovsky (1975), *S. melongena* originated in India but extended eastward and reached China in the 5<sup>th</sup> century B.C., becoming a secondary centre of variation. Brinjal is a self-pollinated annual to perennial vegetable extensively cultivated both in temperate and tropical zones of the world (Rahman et al. 2014) with cross pollination up to 29% (Ram, 1999).

Brinjal stands second in the area and production after China and occupies 730.4 thousand hectares with an annual production of 12800.8 thousand metric tonnes with productivity of 17.5 metric tonnes per ha (Anonymous, 2018). The demand for brinjal as a vegetable is increasing gradually worldwide because of its high nutritive value (Khandaker et al. 2020). In India great genetic diversity is present in brinjal (Chaurasia et al. 2018). Genetic improvement using these genetic resources has great potential to develop improved varieties. The information about variability is a prerequisite for implementing a successful breeding programme. Large genetic variability with regard to colour, size, maturity, fruit shape, culinary characters and spyness of plants exists in the indigenous genetic resources. Existence of more variability leads to more chances of improvement either from existing variability or variability created through hybridization. The segregating generations of hybridization programmes are expected to produce desirable segregants or transgressive segregants. The genetic improvement in any segregating population is based on the knowledge of the association between yield and yield-related traits that triggers the selection efficiency (Binodh et al. 2008). Character association between plant traits related to fruit yield is very important because these parameters will determine the future success of the breeding programme (Nalini et al. 2009).

Yield is a complex quantitative character influenced by environment and direct selection for yield is not reliable. High yield can often be achieved by implementing indirect selection for the yield attributing traits. Selection efficiency could be enhanced when we determine the relationship between various plant characters and yield through correlation analysis (Rekha and Celine, 2013). Selection index is commonly used in conventional breeding as an important selection criterion in order to reduce improvement complexity of trait relationship and to gain economic yield (Fotokian and Agahi, 2014). Thus, construction of selection indices will be highly helpful to discriminate desirable genotypes in crop improvement program. Selection indices will guide in deciding which genotypes will perform well from a segregating population. Appropriate selection

strategies help in retaining good gene combinations in a segregating population. These combinations manifest the contribution of yield attributes to the total yield of the genotypes. Given the above facts, the present study in brinjal investigated the following objectives: estimating the genetic variability parameters and constructing an optimum selection index for yield selection.

## 2. MATERIALS AND METHODS

The experiment was carried out during the *Rabi* season of 2017-18 at the Horticultural Experimental Farm, Assam Agricultural University, Jorhat, situated at the flood-free plains of upper Brahmaputra valley zone of Assam lying at 26°45' N latitude and 94°12' E longitude at an elevation of 86.6m above the mean sea level, in north-eastern of India. The details of the materials used and the methodologies adopted in the investigation are described below:

### 2.1 Plant materials

The experimental material used in the present study consisted of three parents and their two cross combinations in  $F_2$  generation along with two check varieties. All crosses were made during 2015-16 and  $F_1$  generation was raised in the year 2016-17. List of genotypes included in the present study and some of the morphological characters of the parents and checks are listed below based on the minimal descriptors of Agri-Horticultural crops, Part-II: Vegetable Crops published by National Bureau of Plant Genetics Resources, New Delhi (Srivastava et al. 2001). (Table1)

Longai (oblong) has good cooking quality, tender pulp, less seeds, big fruit size and good taste whereas MLC- 1 and MLC-3 has good adaptability. The  $F_1$ s of MLC-1 x Longai (oblong) and MLC-3 x Longai (oblong) were evaluated in the year 2016-17 and produced the seeds from these two  $F_1$ 's by selfing. In the present experiment these two  $F_2$  generations were evaluated during *Rabi* season 2017-18 in augmented randomized block design with three parents and two checks. Based on efficient selection indices, a number of single plants were selected in the  $F_2$  generation from the two populations separately. The single plant progenies were grown along with the bulk as the  $F_3$  generations and evaluated for further selection of individual superior plants for the next advanced generation.

**Table1** List of genotypes included in the present study

Plant material	Genotypes	Code	Location of collection	Morphological characters			
				Fruit colour	Fruit shape	Spines on plants	
						Leaf	Calyx
Parents	Longai (oblong)	T <sub>3</sub>	Farmer's Field, Karimganj, Assam	Light purple	Oblong	Absent	Present
	Manipur local -3 (MLC-3)	L <sub>5</sub>	Farmer's Field, Imphal, Manipur	Purplish green	Long	Absent	Present
	Manipur local -1 (MLC-1)	L <sub>6</sub>	Farmer's Field, Imphal, Manipur	Purplish green	Long	Absent	Present
$F_2$ Populations	MLC-1 x Longai(oblong)	T <sub>3</sub> L <sub>6</sub>					
	MLC-3 x Longai(oblong)	T <sub>3</sub> L <sub>5</sub>					
Check varieties	JC-1	T <sub>1</sub>	AAU, Jorhat, Assam	Purple	Long	Absent	Absent
	SM-6-7	T <sub>2</sub>	IIVR, Varanasi, Uttar Pradesh	Dark purple	Oval	Present	Present

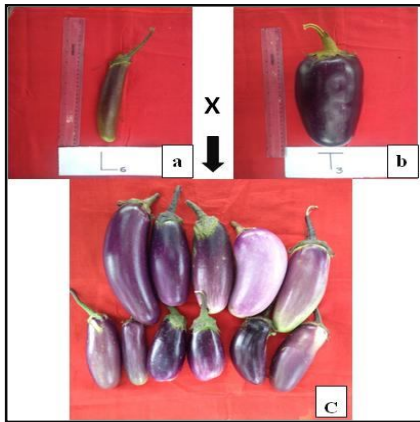
AAU-Assam Agricultural University; IIVR-Indian Institute of Vegetable Research

### 2.2 Data analysis methods

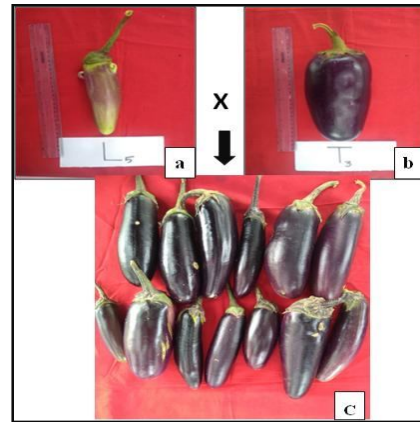
Analysis of variance of the characters was done as per standard statistical procedure for augmented randomized complete block design as given by Panse and Sukhatme (1978). Genotypic and phenotypic variances were estimated according to the formula given by Johnson et al. (1955). Genotypic and phenotypic co-efficient of variation were calculated by the formula suggested by Burton (1952). The phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) values were classified as described by Sivasubramanian and Menon (1973). Heritability in broad sense was computed as the ratio of genetic variance to the total phenotypic variance as suggested by Hanson et al.(1956) and expressed as percentage. Heritability in broad sense was categorized as per the classification given by Johnson et al.(1955). The genetic advance for different characters under selection was estimated using the formula suggested by Allard (1960). The range of genetic advance as per cent of mean was classified as suggested by Johnson et al. (1955). Selection indices were constructed using the component traits showing positive yield correlations only using the method given in Falconer (1989).

## 3. RESULTS AND DISCUSSION

The variability present in the fruits morphology and plants of two  $F_2$  populations is presented in the Fig. 1, Fig. 2 and Fig. 3. The analysis of variance for fruit yield and its contributing characters is presented in Table 2. The mean sum of squares for genotypes (parent, checks and crosses) were found to be significant for all the traits i.e. plant height (cm), number of branches per plant, number of fruits per plant, fruit weight (g), fruit length (cm), fruit breadth (cm), fruit volume (cc) and yield per plant (g) at 5 percent level of significance. The significant mean sum of squares of these characters indicated the presence of genetic variability present in the genotypes, providing the opportunity for improvement of the traits. Similar observations were recorded for plant height, primary branches, fruit length, and number of fruits for plant by Tirkey et al. (2018). Bashar et al. (2015), Chithra et al. (2021), Upadhyay et al. (2021), and Verma et al. (2021) recorded significant genetic variation for all traits except for fruit volume. Konyak et al. (2020) recorded genetic variation among the genotypes for all the traits which is related to present genotypes.



**Fig.1** (a) Manipur Local-1 (MLC-1), (b) Longai (Oblong) and (c) Variability in fruit morphology of  $F_2$  population of Manipur Local-1 x Longai (Oblong) hybrid



**Fig.2** (a) Manipur Local-3 (MLC-3), (b) Longai (Oblong) and (c) Variability in fruit morphology of  $F_2$  population of Manipur Local-3 x Longai (Oblong) hybrid.



**Fig. 3** Variability present in plants of two  $F_2$  populations and their parents. (a) Manipur Local-1 (MLC-1), (b) Longai (Oblong), (c) Manipur Local-3 (MLC-3), (d) Manipur Local-1 X Longai (Oblong), (e) Manipur Local-3 X Longai (Oblong).

**Table 2** Analysis of variance (ANOVA) for augmented randomized block design based on different quantitative characters of parents,  $F_2$  populations and check varieties

Source of variation	DF	PH	BP	FP	FW	FL	FB	FV	FY
Replication	2	6.32	0.17	0.33	246.44	0.41	1.18	264.02	189925.35
Entries (Parents + Checks + $F_2$ Plants)	244	118.82*	6.39*	21.48*	3938.55*	17.49*	12.68*	18705.31*	616587.82*
Error	8	2.85	0.20	0.42	445.58	0.81	0.33	170.87	217052.00

\*P<0.05 DF - Degrees of freedom, PH: Plant height (cm), BP: Number of branches per plant, FP: Number of fruits per plant, FW: Fruit weight (g), FL: Fruit length (cm), FB: Fruit breadth (cm), FV: Fruit volume (cc), FY: Yield per plant (g).

### 3.1 Mean performance of different quantitative characters

Mean performance of two F<sub>2</sub> populations of brinjal MLC-1 x Longai (oblong), MLC-3 x Longai (oblong), their parents and check varieties for yield and yield contributing characters are presented in Table3. Among parent's maximum fruit weight, fruit breadth, fruit volume and yield per plant was observed in Longai (oblong). The highest number of branches per plant and number of fruits per plant for parents was observed in MLC-3. Maximum plant height and fruit length was observed in MLC-1.

Out of two F<sub>2</sub> populations maximum value for plant height, fruit weight, fruit length, fruit breadth, fruit volume and yield per plant was observed in MLC-3 x Longai (oblong). Maximum number of branches per plant and number of fruits per plant was recorded in MLC-1 x Longai (oblong). The reason for significant variation for these traits in the present study could be due to hybridization between parents of diverse origin that evolved at different regions or agro-climatic zones of the country. Moreover, the materials used in the study were the first segregating generation of two successful crosses. Thus, variation is due to different combinations of genes in the progenies. In brinjal, high extent of variability has been reported for yield and yield attributing characters by many workers (Bashar et al. 2015; Suhana et al. 2016; Sujin et al. 2017, Konyak et al. 2020; Chithra et al. 2021 and Verma et al. 2021).

**Table3** Mean performance of different quantitative characters of parents, F<sub>2</sub> populations and check varieties

	Quantitative characters							
	PH	BP	FP	FW	FL	FB	FV	FY
Longai (oblong)	60.85	7.83	7.82	273.74	14.79	24.47	379.81	2684.45
MLC-3	74.72	12.07	9.78	134.18	15.69	14.52	196.57	2024.05
MLC-1	76.01	10.43	9.28	146.61	18.60	13.57	200.93	1404.86
JC-1	66.11	9.04	8.83	331.71	22.15	19.17	595.71	3199.95
SM-6-7	49.76	9.77	13.15	140.00	9.34	15.19	221.54	1839.66
Mean	65.49	9.83	9.77	205.25	16.11	17.39	318.91	2230.59
Coefficient of variation (%)	2.58	4.55	6.67	8.40	5.59	3.30	4.38	15.60
Standard Error (mean)	0.97	0.26	0.38	12.19	0.52	0.33	7.55	268.98
Critical Difference (5%)	3.18	0.84	1.23	39.74	1.70	1.08	24.61	877.19
Range Lowest	49.76	7.83	7.82	134.18	9.34	13.57	196.57	1404.86
Range Highest	76.01	12.07	13.15	369.66	22.15	24.47	595.71	3199.95
<b>Mean of F<sub>2</sub> populations</b>								
MLC-3 x Longai (oblong)	68.44	8.72	7.44	207.78	16.52	19.51	358.43	1585.64
MLC-1 x Longai (oblong)	64.68	10.81	12.19	123.64	15.93	15.33	172.06	1541.43

PH: Plant height (cm), BP: Number of branches per plant, FP: Number of fruits per plant, FW: fruit weight (g), FL: Fruit length (cm), FB: Fruit breadth (cm), FV: Fruit volume (cc), FY: Yield per plant (g).

### 3.2 Genetic parameters

#### 3.2.1 Phenotypic and genotypic coefficient of variation

The PCV and GCV measure the extent of variation present in a population for different characters. The high, moderate and low values for PCV and GCV are in accordance with the study by Sivasubramanian and Menon (1973).

Among parents and check varieties the extent of PCV and GCV of all eight traits are presented in Table 4.1, Fig.4 reflecting that high PCV and GCV was found in fruit volume (64.47, 64.32), yield per plant (55.71, 53.48), fruit weight (43.08, 42.26), fruit length (29.85, 29.32), fruit breadth (26.02, 25.81), number of fruits per plant (21.40, 20.33) and moderate in plant height (16.60, 16.4) and number of branches per plant (16.50, 15.86). These results corroborated the findings of Bashar et al. (2015), Chaudhary and Kumar (2017), Tirkey et al. (2018), and Konyak et al. (2020).

From the Table 4.2, Fig.5 in F<sub>2</sub>population MLC-1 x Longai(oblong) high PCV and GCV was observed for yield per plant (49.86, 39.66), number of fruits per plant (42.87, 42.53), fruit length (34.56, 34.09), fruit volume (28.02, 26.97), number of branches per plant (25.90, 25.57), fruit weight (24.48, 17.55) and moderate in plant height (19.35, 19.17) and fruit breadth (15.22, 14.75).Several workers (Suhana et al. 2016; Sujin et al. 2017; Chithra et al. 2021; Patil et al. 2021 and Verma et al. 2021) also reported similar genetic variation in terms of PCV and GCV parameters.

From the Table 4.3, Fig.6 in F<sub>2</sub>population MLC-3 x Longai (oblong) high PCV and GCV was observed for yield per plant (44.64, 33.60), fruit volume (36.62, 36.44), number of fruits per plant (30.71,

29.44), fruit weight (25.95, 23.87) and moderate in number of branches per plant (19.80, 19.12), fruit breadth (17.07, 16.81), fruit length (13.00, 11.80) and plant height (12.73, 12.49). Suhana et al. (2016), Kasera et al. (2018), Tirkey et al. (2018) reported similar findings with respect to PCV and GCV parameters.

Broad difference between PCV and GCV indicated their sensitiveness to environmental fluctuation. The high values of GCV suggested greater genotypic variability among the genotypes and response of these attributes for making further improvement by selection.

### **3.2.2 Heritability and Genetic advance as per cent of mean**

Heritability provides information regarding transmissible genetic variation and determines genetic improvement and response to selection. Broad sense heritability includes both additive and non-additive gene effects. The consideration for high, moderate and low heritability was in agreement with the study of Johnson et al. (1955).

Among parents and check varieties the amount of heritability (broad sense) of all eight traits (Table 4.1, Fig.7) revealed high heritability in fruit volume (0.99) and fruit breadth (0.98) followed by plant height (0.98), fruit length (0.95), fruit weight (0.96), number of branches per plant (0.92), yield per plant (0.92) and number of fruits per plant (0.90). In the F<sub>2</sub> population MLC-1 x Longai (oblong) the heritability (broad sense) estimates were high for number of fruits per plant (0.98) and plant height (0.98) followed by number of branches per plant (0.97), fruit length (0.97), fruit breadth (0.94), fruit volume (0.93), yield per plant (0.63) and moderate in fruit weight (0.51) (Table 4.2, Fig.8). In the F<sub>2</sub> population MLC-3 x Longai (oblong) the heritability (broad sense) estimates were very high for fruit volume (0.99) and fruit breadth (0.97) followed by plant height (0.96), number of branches per plant (0.93), number of fruits per plant (0.92), fruit weight (0.85), fruit length (0.82) and moderate in yield per plant (0.57) (Table 4.3, Fig.9). These results corroborated with the findings of Chaudhary and Kumar (2017), Sujin et al. (2017), Kasera et al. (2018), Tirkey et al. (2018). Heritability itself does not provide any indication towards the amount of genetic progress (Kumar and Sasivannan, 2006). Heritability estimates along with genetic advance are normally more helpful in predicting genetic gain under selection (Johnson et al. 1955). Genetic advance and heritability are the major factors in the improvement of mean genotypic value of selected plants over the parental population.

Among eight characters yield per plant showed highest genetic advance in all the genotypes viz., parents and check varieties, F<sub>2</sub> population MLC-1 x Longai (oblong), F<sub>2</sub> population MLC-3 x Longai (oblong). Lowest genetic advance was recorded for number of branches per plant in parents and check varieties, F<sub>2</sub> population MLC-3 x Longai (oblong), and in F<sub>2</sub> population MLC-1 x Longai (oblong) lowest genetic advance was recorded for fruit breadth.

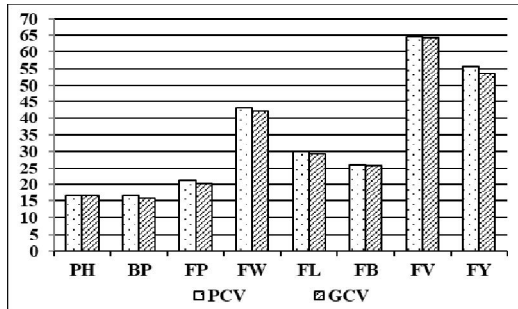
Due to masking influence of environment upon traits concerned, values of genetic advance exhibit high fluctuations. Therefore, to attain relative comparison of the characters in relation to environment, genetic advance as percentage of mean was calculated to predict the genetic gain (Tables 4.1, 4.2 and 4.3). The high, moderate and low values were considered as in accordance with Johnson et al. (1955).

Among parents and check varieties the high genetic advance as percent of mean was observed for fruit volume (132.19%) followed by yield per plant (105.77%), fruit weight (85.38%), fruit length (59.33%), fruit breadth (52.73%), number of fruits per plant (39.80%), plant height (33.37%) and number of branches per plant (31.41%) (Table 4.1, Fig.7).

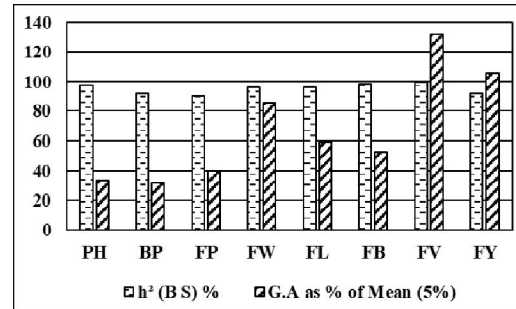
The F<sub>2</sub> population MLC-1 x Longai (oblong) exhibited high genetic advance as percent of mean for number of fruits per plant (86.94%) followed by fruit length (69.29%), yield per plant (64.98%), fruit volume (53.48%), number of branches per plant (52.00%), plant height (39.14%), fruit breadth (29.45%) and fruit weight (25.91%) (Table 4.2, Fig.8).

The F<sub>2</sub> population MLC-3 x Longai (oblong) exhibited the high genetic advance as percent of mean for fruit volume (74.70%) followed by number of fruits per plant (58.13%), yield per plant (52.11%), fruit weight (45.25%), number of branches per plant (38.05%), fruit breadth (34.11%), plant height (25.23%) and fruit length (22.06%) (Table 4.3, Fig.9).

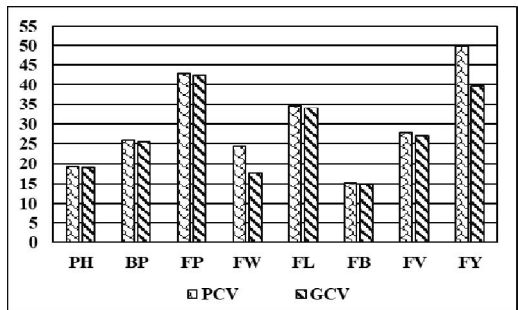
High to moderate heritability coupled with high genetic advance as percent of mean was recorded for all the quantitative characters which was an indication that additive gene action was present (Fig.7, Fig.8 and Fig.9). These findings were similar to the reports of Sujin et al. (2017), Kasera et al. (2018), Konyak et al. (2020), Balasubramaniyam et al. (2021) and Chithra et al. (2021). Thus, selection of progenies from the base population using these highly heritable characters could help in creating an improved new population in the next generation.



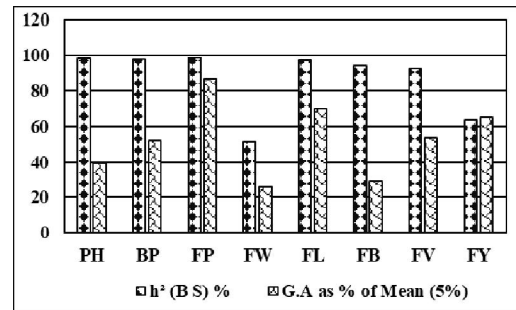
**Fig. 4** Phenotypic and genotypic coefficients of variation of the parents and the check varieties



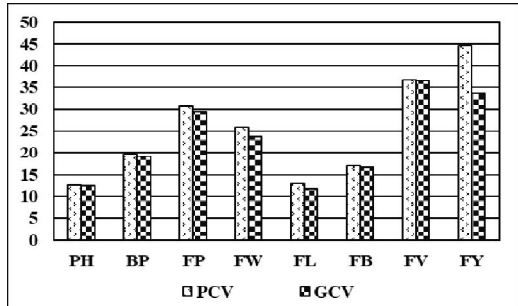
**Fig. 7** Heritability and Genetic advance as per cent of mean of the parents and the check varieties



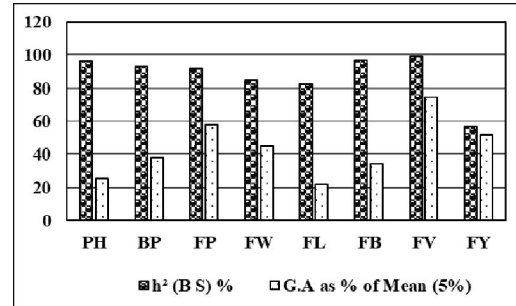
**Fig. 5** Phenotypic and genotypic coefficients of variation of F<sub>2</sub> population MLC-1 x Longai (oblong)



**Fig. 8** Heritability and Genetic advance as percent of mean of F<sub>2</sub> population MLC-1 x Longai (oblong)



**Fig. 6** Phenotypic and genotypic coefficients of variation of F<sub>2</sub> population MLC-3 x Longai (oblong)



**Fig. 9** Heritability and Genetic advance as percent of mean of F<sub>2</sub> population MLC-3 x Longai (oblong)

**Table 4.1** Estimates of genetic parameters of parents and check varieties for quantitative traits

	PH	BP	FP	FW	FL	FB	FV	FY
PCV (%)	16.6	16.5	21.4	43.08	29.85	26.02	64.47	55.71
GCV (%)	16.4	15.86	20.33	42.26	29.32	25.81	64.32	53.48
h <sup>2</sup> <sub>bs</sub>	0.98	0.92	0.9	0.96	0.97	0.98	0.99	0.92
h <sup>2</sup> <sub>bs</sub> (%)	97.60	92.40	90.30	96.20	96.50	98.40	99.50	92.20
GA (5%)	21.86	3.09	3.89	214.45	9.56	9.17	394.22	3158.72
GA, as % of Mean (5%)	33.37	31.41	39.8	85.38	59.33	52.73	132.19	105.77

**Table 4.2** Estimates of genetic parameters of F<sub>2</sub> population MLC-1 x Longai (oblong) for quantitative traits

	PH	BP	FP	FW	FL	FB	FV	FY
PCV (%)	19.35	25.9	42.87	24.48	34.56	15.22	28.02	49.86

<b>GCV (%)</b>	19.17	25.57	42.53	17.55	34.09	14.75	26.97	39.66
<b>h<sup>2</sup><sub>bs</sub></b>	0.98	0.97	0.98	0.51	0.97	0.94	0.93	0.63
<b>h<sup>2</sup><sub>bs</sub> (%)</b>	98.18	97.45	98.45	51.37	97.32	93.95	92.65	63.26
<b>GA (5%)</b>	25.31	5.62	10.6	32.03	11.04	4.51	92.02	1001.65
<b>GA, as % of Mean (5%)</b>	39.14	52	86.94	25.91	69.29	29.45	53.48	64.98

**Table 4.3** Estimates of genetic parameters of F<sub>2</sub> population MLC-3 x Longai (oblong) for quantitative traits

	<b>PH</b>	<b>BP</b>	<b>FP</b>	<b>FW</b>	<b>FL</b>	<b>FB</b>	<b>FV</b>	<b>FY</b>
<b>PCV (%)</b>	12.73	19.80	30.71	25.95	13.00	17.07	36.62	44.64
<b>GCV (%)</b>	12.49	19.12	29.44	23.87	11.8	16.81	36.44	33.60
<b>h<sup>2</sup><sub>bs</sub></b>	0.96	0.93	0.92	0.85	0.82	0.97	0.99	0.57
<b>h<sup>2</sup><sub>bs</sub> (%)</b>	96.25	93.30	91.88	84.67	82.39	97.03	99.01	56.67
<b>GA (5%)</b>	17.27	3.32	4.33	94.02	3.64	6.65	267.74	826.33
<b>GA, as % of Mean (5%)</b>	25.23	38.05	58.13	45.25	22.06	34.11	74.70	52.11

PH: Plant height (cm), BP: Number of branches per plant, FP: Number of fruits per plant, FW: fruit weight (g), FL: Fruit length (cm), FB: Fruit breadth (cm), FV: Fruit volume (cc), FY: Yield per plant (g), PCV=Phenotypic coefficient of variability, GCV= Genotypic coefficient of variability, h<sup>2</sup><sub>bs</sub> = Heritability in broad sense, GA = Genetic Advance.

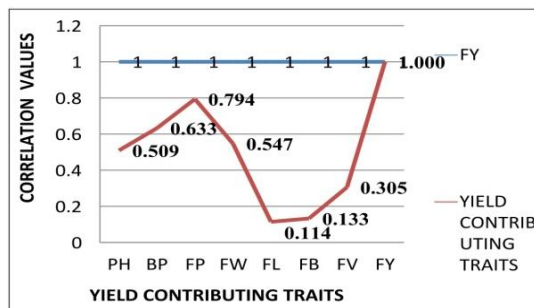
### 3.3 Correlation studies

The correlation between different characters helps to find out the degree of relationship between two characters. As plant yield is a complex character and is polygenically inherited, direct selection for yield may not be much effective. Selecting various component characters which are correlated to yield and have simple inheritance with less environmental influence would aid in effective selection.

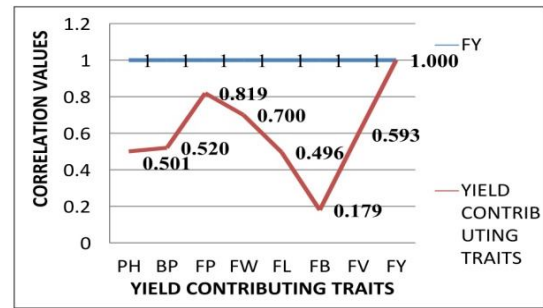
Phenotypic correlations among yield and yield contributing traits of F<sub>2</sub> population MLC-1 x Longai (oblong) presented in the Table 5.1, Fig.10. In the F<sub>2</sub> population of MLC-1 x Longai(oblong), a positive relationship was observed for yield per plant with number of fruits per plant(0.794), number of branches per plant (0.633), fruit weight (0.547), plant height (0.509) and fruit volume (0.305) at phenotypic level. The results were in agreement with the findings of Bashar et al. (2015), Patel et al. (2015), Yadav Neha et al. (2017) and Konyak et al. (2020).

Phenotypic correlations among yield and yield contributing traits of F<sub>2</sub> population MLC-3 x Longai (oblong) presented in the Table 5.2, Fig.11. Positive relationship was observed for yield per plant with number of fruits per plant (0.819), fruit weight (0.700), fruit volume (0.593), number of branches per plant (0.520), plant height (0.501) and fruit breadth (0.179) at phenotypic level. These results closely corroborated the findings of Mohammad et al. (2015), Chauhan et al. (2016), Sujin et al. (2017), and Upadhyay et al. (2021).

This implies that indirect selection through these traits would also be helpful for improvement of yield in segregating populations of brinjal crosses.



**Fig. 10** Phenotypic correlations among yield and yield contributing traits of F<sub>2</sub> population MLC-1 x Longai (oblong)



**Fig. 11** Phenotypic correlations among yield and yield contributing traits of F<sub>2</sub> population MLC-3 x Longai (oblong)

**Table 5.1** Phenotypic correlations among yield and yield contributing characters of F<sub>2</sub> population MLC-1 x Longai (oblong)

	<b>PH</b>	<b>BP</b>	<b>FP</b>	<b>FW</b>	<b>FL</b>	<b>FB</b>	<b>FV</b>	<b>FY</b>
<b>PH</b>	1							

<b>BP</b>	0.561**	1						
<b>FP</b>	0.530**	0.685**	1					
<b>FW</b>	0.310**	0.196*	0.085 <sup>NS</sup>	1				
<b>FL</b>	0.201*	0.083 <sup>NS</sup>	0.141 <sup>NS</sup>	0.108 <sup>NS</sup>	1			
<b>FB</b>	-0.075 <sup>NS</sup>	-0.046 <sup>NS</sup>	-0.013 <sup>NS</sup>	0.249**	0.062 <sup>NS</sup>	1		
<b>FV</b>	0.093 <sup>NS</sup>	0.117 <sup>NS</sup>	-0.058 <sup>NS</sup>	0.685**	0.088 <sup>NS</sup>	0.274**	1	
<b>FY</b>	0.509**	0.633**	0.794**	0.547**	0.114 <sup>NS</sup>	0.133 <sup>NS</sup>	0.305**	1

**Table 5.2** Phenotypic correlations among yield and yield contributing characters of F<sub>2</sub> population MLC-3 x Longai (oblong)

	<b>PH</b>	<b>BP</b>	<b>FP</b>	<b>FW</b>	<b>FL</b>	<b>FB</b>	<b>FV</b>	<b>FY</b>
<b>PH</b>	1							
<b>BP</b>	0.341**	1						
<b>FP</b>	0.566**	0.482**	1					
<b>FW</b>	0.304**	0.253**	0.250**	1				
<b>FL</b>	0.407**	0.334**	0.298**	0.486**	1			
<b>FB</b>	0.156 <sup>NS</sup>	0.064 <sup>NS</sup>	0.091 <sup>NS</sup>	0.169 <sup>NS</sup>	0.115 <sup>NS</sup>	1		
<b>FV</b>	0.306**	0.303**	0.246**	0.735**	0.385**	0.410**	1	
<b>FY</b>	0.501**	0.520**	0.819**	0.700**	0.496**	0.179*	0.593**	1

PH: Plant height (cm), BP: Number of branches per plant, FP: Number of fruits per plant, FW: fruit weight (g), FL: Fruit length (cm), FB: Fruit breadth (cm), FV: Fruit volume (cc), FY: Yield per plant (g).

### 3.4 Selection indices

The selection index is the best linear prediction of an individual's breeding value and it takes the form of a multiple regression of breeding value on all the source of information. Efficiency of selection is calculated by comparing the expected responses to index selection i.e. genetic advance of different combinations of yield contributing characters and to simple selection i.e. genetic advance of yield, assuming same intensity of selection. The product of higher index, regression values with phenotypic values of the characters gives the rankings of genotypes which may be helpful in selecting superior genotypes.

#### 3.4.1 F<sub>2</sub> (T<sub>3</sub>x L<sub>6</sub>) MLC-1 x Longai (oblong)

In MLC-1 x Longai (oblong) F<sub>2</sub> population, two characters viz., number of fruits per plant, number of branches per plant along with yield per plant were used to construct selection indices and their respective genetic advances were estimated (Table 6.1). Three selection indices based on these characters were constructed. The maximum genetic advance was observed for three-character combination yield per plant + number of branches per plant + number of fruits per plant (1161.08) followed by yield per plant + number of fruits per plant (1160.76) and for yield per plant (1001.65). The highest selection efficiency was obtained for three-character combination, fruit yield per plant + number of branches per plant + number of fruits per plant (115.92%). Utilizing the highest efficient indices (yield per plant + number of branches per plant + number of fruits per plant), the selection scores were calculated. On the basis of selection score, out of 120 plants in the F<sub>2</sub> population MLC-1 x Longai (oblong) the top 6 individual plants were selected (i.e. 5 percent plants selected) (Table 6.2.) It was found that the plant number 2, 12, 10, 3, 11 and 19 in F<sub>2</sub> population of cross combination MLC-1 x Longai (oblong) were genetically the best among all the plants as these plants had higher selection scores.

**Table 6.1** Selection indices of F<sub>2</sub> population MLC-1 x Longai (oblong)

Index	GA (5%)	GA, as % of mean (5%)	Selection efficiency in %
I <sub>1</sub>	1001.65	64.98	100.00
I <sub>12</sub>	1160.76	75.30	115.88
I <sub>123</sub>	1161.08	75.32	115.92

I<sub>1</sub> (Yield per plant), I<sub>12</sub> (Yield per plant, Number of fruits per plant), I<sub>123</sub> (Yield per plant, Number of branches per plant, Number of fruits per plant), GA =Genetic Advance.

**Table 6.2** Genotype rankings of F<sub>2</sub> population MLC-1 x Longai (oblong)

Plant Number	Selection score
2	218756.39
12	211301.51

10	189252.10
3	185251.99
11	182371.88
19	181741.19

### 3.4.2F<sub>2</sub> (T<sub>3</sub>XL<sub>5</sub>) MLC-3 x Longai(oblong)

In MLC-3 x Longai (oblong) F<sub>2</sub> population three characters viz., number of fruits per plant, average fruit weight, fruit volume along with yield per plant were used to construct selection indices and their respective genetic advances were estimated (Table 6.3). Four selection indices based on three characters were constructed along with yield per plant. The maximum genetic advance was observed for four-character combination yield per plant + fruit volume + fruit weight + number of fruits per plant (1473.78) followed by yield per plant + fruit weight + number of fruits per plant (1452.22), yield per plant + number of fruits per plant (1205.81) and for yield per plant (826.33). The highest selection efficiency was obtained for four-character combination yield per plant + fruit volume + fruit weight + number of fruits per plant (178.35) using which, the selection scores were calculated. On the basis of selection score, out of 120 plants of the F<sub>2</sub> population MLC-3 x Longai (oblong) the top 6 individual plants were selected (i.e. 5 percent plants selected) (Table 6.4) It was observed that the plant number 105, 28, 107, 26, 22 and 109 in F<sub>2</sub> population of cross combination MLC-3 x Longai (oblong) were genetically best among all the plants as these plants had higher selection scores.

**Table 6.3** Selection indices of F<sub>2</sub> population MLC-3 x Longai (oblong)

Index	GA (5%)	GA, as % of mean (5%)	Selection efficiency in %
I <sub>1</sub>	826.33	52.11	100.00
I <sub>12</sub>	1205.81	76.05	145.92
I <sub>123</sub>	1452.22	91.59	175.74
I <sub>124</sub>	1473.78	92.94	178.35

I<sub>1</sub> (Yield per plant); I<sub>12</sub> (Yield per plant, number of fruits per plant); I<sub>123</sub> (Yield per plant, fruit weight, number of fruits per plant); I<sub>1234</sub> (Yield per plant, fruit volume, fruit weight, number of fruits per plant), GA =Genetic Advance.

**Table 6.4** Genotype rankings of F<sub>2</sub> population MLC-3 x Longai (oblong)

Plant Number	Selection score
105	2409036.94
28	1506936.79
107	1482552.50
26	1480786.67
22	1471796.64
109	1451197.32

In the present study, addition of characters one by one in the construction of selection index resulted in the increased estimates of genetic advance. These findings are in tune with the results of Bashar et al. (2015), where he also found higher relative efficiencies over straight selection for yield/plant (g) in brinjal when selection index was constructed using characters like yield per plant (g), fresh weight per fruit (g), number of fruits in inflorescence per plant, number of fruits in solitary per plant, number of secondary branches per plant, harvesting period and fruit circumference (cm). Hence, these results indicate that selection index based on several characters with significant positive correlation and heritability exhibited high selection efficiency in improvement of yield per plant in brinjal.

To test the efficacy of selection during *Rabi*, season 2018-19 the selected progenies viz., T<sub>3</sub>L<sub>6</sub> - 2, T<sub>3</sub>L<sub>6</sub> - 3, T<sub>3</sub>L<sub>6</sub> - 10, T<sub>3</sub>L<sub>6</sub> - 11, T<sub>3</sub>L<sub>6</sub> - 12, T<sub>3</sub>L<sub>6</sub> - 19 along with T<sub>3</sub>L<sub>6</sub> bulk population and the selected progenies viz., T<sub>3</sub>L<sub>5</sub> - 22, T<sub>3</sub>L<sub>5</sub> - 26, T<sub>3</sub>L<sub>5</sub> - 28, T<sub>3</sub>L<sub>5</sub> - 105, T<sub>3</sub>L<sub>5</sub> - 107, T<sub>3</sub>L<sub>5</sub> - 109 along with T<sub>3</sub>L<sub>5</sub> bulk population were evaluated.

The percent of improvement of yield per plant of the six selected progenies of both the F<sub>2</sub> populations over both bulk populations (Table 6.5) showed that in the progenies of F<sub>2</sub> population MLC-1 x Longai (oblong) maximum percent of improvement of yield per plant was observed in T<sub>3</sub>L<sub>6</sub>-12 (10.40) and in progenies of F<sub>2</sub> population MLC-3 x Longai (oblong) maximum improvement was observed in T<sub>3</sub>L<sub>5</sub>- 105 (14.84).

In both the populations as Longai (oblong) was the common parent, a comparative analysis was done to record the performance of the two populations arising out of its combination with MLC-1 and MLC-3. The percent of yield improvement of cross T<sub>3</sub>L<sub>6</sub> [MLC-1 x Longai (oblong)] was observed to be more than the cross combination T<sub>3</sub>L<sub>5</sub> [MLC-3 x Longai (oblong)] (Table 6.5). So, this cross combination T<sub>3</sub>L<sub>6</sub> was observed to be more promising for future breeding work.

**Table 6.5** Improvement of yield per plant in F<sub>3</sub> generation (F<sub>2</sub> Selected lines) of two crosses over their F<sub>2</sub> bulks.

Lines	Mean values of yield per plant (g) of F <sub>3</sub> generation (F <sub>2</sub> Selected lines)	Percentage improvement of yield per plant in F <sub>3</sub> generation (F <sub>2</sub> Selected lines) over bulk (F <sub>3</sub> )	Yield per plant of F <sub>2</sub> generation (g)
T <sub>3</sub> L <sub>6</sub> – 2	3486.07	9.48	3011.00
T <sub>3</sub> L <sub>6</sub> – 3	3250.00	7.12	2988.00
T <sub>3</sub> L <sub>6</sub> – 10	3499.32	9.61	3124.00
T <sub>3</sub> L <sub>6</sub> -11	2589.10	0.51	2580.00
T <sub>3</sub> L <sub>6</sub> – 12	3571.87	10.40	3010.50
T <sub>3</sub> L <sub>6</sub> – 19	3077.09	5.39	2780.00
<b>Overall mean of F<sub>2</sub> selected lines of T<sub>3</sub>L<sub>6</sub></b>	<b>3245.58</b>	<b>7.08</b>	
<b>Mean of T<sub>3</sub>L<sub>6</sub> bulk (F<sub>3</sub>)</b>	<b>2537.94</b>		
T <sub>3</sub> L <sub>5</sub> – 22	2852.95	1.74	2693.00
T <sub>3</sub> L <sub>5</sub> – 26	2860.78	1.82	2930.00
T <sub>3</sub> L <sub>5</sub> – 28	3028.17	3.50	2882.00
T <sub>3</sub> L <sub>5</sub> – 105	4162.36	14.84	2880.00
T <sub>3</sub> L <sub>5</sub> – 107	2866.01	1.87	2860.00
T <sub>3</sub> L <sub>5</sub> – 109	3149.98	4.71	2816.00
<b>Overall mean of F<sub>2</sub> selected lines of T<sub>3</sub>L<sub>5</sub></b>	<b>3065.46</b>	<b>3.87</b>	
<b>Mean of T<sub>3</sub>L<sub>5</sub> bulk (F<sub>3</sub>)</b>	<b>2678.54</b>		

#### 4. CONCLUSION

Significant phenotypic and genetic variability were observed for yield per plant and its components. High estimates of phenotypic and genotypic coefficient variations and heritability were observed for all the quantitative characters under study. High heritability and high genetic advance as percent of mean were registered for all the quantitative traits, which was an indication of additive gene effects for these traits. At phenotypic level the yield per plant exhibited high positive correlation with number of fruits per plant, number of branches per plant in the F<sub>2</sub> plants of MLC-1 x Longai (oblong). In the F<sub>2</sub> plants of MLC-3 x Longai (oblong) yield per plant exhibited high positive correlation with number of fruits per plant, fruit weight, fruit volume, and number of branches per plant. Selection for the yield based on multiple yield component characters with high correlation were used for construction of index and the top 5 percent plants in F<sub>2</sub> populations MLC-1 x Longai (oblong) and MLC-3 x Longai (oblong) were identified for further breeding works. Comparative analysis showed that the population generated from cross T<sub>3</sub>L<sub>6</sub> [MLC-1 x Longai (oblong)] was more promising than the population T<sub>3</sub>L<sub>5</sub> [MLC-3 x Longai (oblong)] for future breeding works.

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