

CORRELATION AND PATH COEFFICIENT ANALYSIS OF YIELD RELATED TRAITS IN F₃ POPULATIONS OF BRINJAL FROM INTRA-SPECIFIC HYBRIDIZATION

Abstract. In the present experiment the selected progenies of F₂ population [MLC-1 x Longai (oblong)] i.e. plant number 2, 12, 10, 3, 11, 19 and progenies of F₂ population [MLC-3 x Longai (oblong)] i.e. plant number 22, 26, 28, 105, 107, 109 along with their respective bulk populations evaluated based on eight quantitative traits. There was a significant difference among the genotypes for all the characters studied at 1 % level of significance. The phenotypic variance, phenotypic coefficients of variation were higher than the genotypic variance, genotypic coefficient of variation respectively in all the traits studied. Among all the genotypes high heritability coupled with high genetic advance as percent of mean except fruit length which indicating that all the traits were governed by additive gene action except fruit length. Characters *viz.*, number of fruits per plant, plant height, fruit weight, number of branches per plant recorded positive and significant association with yield per plant in the genotypes. Path coefficient analysis revealed that number of fruits per plant is important yield attributing trait because of their high direct effect and indirectly influencing number of branches per plant is another most important yield attributing trait.

Keywords: *Brinjal, Phenotypic coefficients of variation (PCV), Genotypic coefficient of variation (GCV), Heritability, Genetic advance as percent of mean.*

INTRODUCTION

Brinjal (*Solanum melongena* L, 2n = 24) belonging to family Solanaceae is grown round the year all over the country. It is called Brinjal in India, and Aubergine in Europe. The name 'eggplant' derived from the shape of the fruit of some varieties, which are white and very similar to chicken eggs. There are three main botanical varieties under the species *melongena* (Choudhury, 1976). The round or egg-shaped cultivars are grouped under var. *esculentum*, the long slender types are included under var. *serpentinum* and the dwarf brinjal plants are put under var. *depressum*. It is an important protective food with high nutritional value. One hundred gram of brinjal fruit contains 92.7% moisture, 0.3 gm fat, 4 gm carbohydrate and 1.4 gm protein. It is rich in fiber (1.3 gm), potassium (2 mg), vitamin B-6 and other phytonutrients like flavonoids. In Indian commercial cultivars the glycoalkaloid content varies from 0.37 mg to 4.83 mg/100 g fresh weight. It contains many essential minerals as 100 g of fruit contain calcium (18 mg), phosphorus (47 mg), iron (0.38 mg), sodium (3 mg), chromium (0.07 mg) and sulphur (44 mg). Its vitamin content per 100 g edible portion of fruit are Carotene (74 mg), Riboflavin (0.11 mg), Thiamin (0.03 mg), Niacin (0.9 mg), Folic acid (5 mg), vitamin C (1.2 mg) and Chlorine (52 mg) (Chen and Li, 1996).

Brinjal being rich in a number of nutrients like fiber, potassium, vitamin B-6 and flavonoids, lowers the risk of heart disease. White brinjal is used in many ayurvedic medicines. As brinjal is low in carbohydrates and high in fiber content, they are known to be good for people suffering from diabetes. Brinjal contains potassium, an important mineral, which plays a key role in maintaining electrolyte balance in the body. It also helps

Comment [AMA1]: You should write paragraph about selection in segregating generation in Brinjal and also about genetic advance

in neutralizing the effect of sodium on the body thereby aiding blood pressure control. Brinjal is rich in chlorogenic acid that acts as a powerful antioxidant agent, lowering cholesterol levels in the body.

Brinjal occupies the fourth position among vegetable crops in India covering 6.5 percent of the total vegetable area. Major brinjal producing states are Orissa, Bihar, Karnataka, West Bengal, Andhra Pradesh, Madhya Pradesh, Maharashtra and Uttar Pradesh. Brinjal is grown in India, over an area of 669 thousand hectares with an annual production of 12400 thousand metric tonnes with a productivity of 18.54 metric tonnes per ha (Anonymous, 2016-17) which is quite low. The reasons for low yield are the use of low yielding cultivars and the problems of diseases like damping off, phomopsis blight, little leaf, alternaria leaf spot, cercospora leaf spot, bacterial wilt and insect pests like fruit and shoot borer and jassids. Therefore, the development of high yielding brinjal varieties with good plant type, resistant to pests and diseases is needed which can help in increasing the productivity. Some Asian countries had conducted research on genetically modified insect resistant Bt brinjal containing Cry1Ac gene from the soil bacterium *Bacillus thuringiensis* for incorporating resistance to fruit and shoot borer there by stabilizing the yield of the crop. A variety developed using such technologies is still not accepted by consumers, as lot of questions still remains unanswered. Moreover, consumer preference varies from region to region in the Indian subcontinent, regarding shape and colour of the fruits. In addition to this, the adaptability of the crop also varies according to the ecological niche. These factors should be considered while developing an improved variety in this vegetable crop.

Inheritance of quantitative character like yield is often influenced by variation in other component characters which may be due to pleiotrophy or genetic linkage (Hallard, 1939). Hence, knowledge of the association between yield and its component traits obtained through the estimation of correlations will guide a breeder for selecting appropriate genotypes. Though correlations give information about the components of a complex character like yield, but it could not provide an exact picture of relative importance of the direct and indirect contributions of the component characters to yield. Path coefficient analysis is an important method in which partitioning the correlation coefficients into direct and indirect effects of an independent variable on dependence variable.

MATERIALS AND METHODS

The present investigation was conducted during the *Rabi* seasons of 2018-19 under the Tropical Monsoon Rainforest Climate of Assam at the Horticultural Experimental Farm, Assam Agricultural University, Jorhat. The particulars of the materials used and the methodologies adopted in the examination are described below.

The experimental materials consist of the **six selected progenies of F₂ population [MLC-1 x Longai (oblong)]** i.e. T₃L₆- 2, T₃L₆- 12, T₃L₆- 10, T₃L₆- 3, T₃L₆- 11, T₃L₆- 19 and **six selected progenies of F₂ population [MLC-3 x Longai (oblong)]** i.e. T₃L₅- 22, T₃L₅- 26, T₃L₅- 28, T₃L₅- 105, T₃L₅- 107, T₃L₅- 109 along with their respective bulk populations i.e. T₃L₆ Bulk and T₃L₅ Bulk. The data recorded on different characters were subjected to different statistical analysis.

Comment [AMA2]: What is the difference between lines and bulk?
How you design your experiment to grown lines as individual plants and compare them with bulk?

Comment [AMA3]: You must write more details about the statistical analysis?

RESULTS AND DISCUSSION

Analysis of variance of the traits was done as per standard statistical procedure for Randomized complete block design as given by Panse and Sukhatme (1978). The analysis of variance of the selected F_2 plants (F_3) along with the bulks is presented in *Table 1*. The mean sum of squares due to genotypes or treatments was significant at both 5 percent and 1 percent level of significance for all quantitative characters. This is an indication of presence of good amount of genetic variability among the genotypes which is useful for brinjal improvement. The treatments and error mean sum of squares were further used for analysis of genotypic and phenotypic variances. Similar observations were recorded by Kumar and Arumugam (2013), Tripathy *et al.*, (2018), Hegade (2017), Chauhan *et al.*, (2018).

Comment [AMA4]: You should mention to the statistical procedure in Materials and Methods.

Mean performance of F_3 generation of two crosses along with the F_2 bulks

The mean performance of eight quantitative traits of the six selected progenies of F_2 population MLC-1 x Longai (oblong) i.e. $T_3L_6 - 2$, $T_3L_6 - 3$, $T_3L_6 - 10$, $T_3L_6 - 11$, $T_3L_6 - 12$, $T_3L_6 - 19$ and its bulk population as well as six selected progenies of F_2 population MLC-3 x Longai (oblong) i.e. $T_3L_5 - 22$, $T_3L_5 - 26$, $T_3L_5 - 28$, $T_3L_5 - 105$, $T_3L_5 - 107$, $T_3L_5 - 109$ and its bulk population, was presented in *Table.2*. Mean performance of individual parameter is described as below.

Among progenies of F_2 population MLC-1 x Longai (oblong) maximum plant height (73.18), number of fruits per plant (20.13) was observed in $T_3L_6 - 3$ and maximum number of branches per plant (13.60), fruit weight (224.09), fruit breadth (17.05), fruit volume (276.65), yield per plant (3571.87) was observed in $T_3L_6 - 12$. Highest fruit length (15.91) was observed in $T_3L_6 - 19$.

In progenies of F_2 population MLC-1 x Longai (oblong) maximum plant height (77.80), number of branches per plant (10.53), number of fruits per plant (14.53), fruit weight (286.81), fruit volume (448.05), yield per plant (4162.36), was found in $T_3L_5 - 105$ and fruit length (17.53), fruit breadth (19.86) was observed in $T_3L_5 - 26$.

The variation in the progenies is due to different combination of genes and furthermore the materials are of segregating generation of two different crosses where one parent is common. The wide amount of variability in brinjal for yield and yield contributing traits by many workers like Kumar and Arumugam (2013), Suhana *et al.* (2016), Chaudhary and Kumar (2017), Hegade (2017), Ravali *et al.* (2017), Chauhan *et al.* (2018), Tripathy *et al.* (2018).

GENETIC PARAMETERS

Components of variation

Phenotypic and genotypic variances were calculated according to the formula given by Johnson *et al.* (1955). The total variation among the genotypes was partitioned into three components viz. variance due to phenotype, genotype and environment. The estimates of variances due to these three components for eight characters are presented in *Table.3*. The magnitude of phenotypic variances was greater than genotypic variances. Maximum phenotypic and genotypic variance were observed for yield per plant followed by fruit volume, fruit weight, plant height, number of fruits per plant, fruit breadth, number of

branches per plant and fruit length. This indicated optimum amount of genetic variability in the evaluated progenies for the major yield contributing characters.

Phenotypic and genotypic coefficient of variation

Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were calculated by the formula suggested by Burton (1952) and classified as described by Sivasubramanian and Menon (1973) and presented in Table.3 and Fig.1. The high, moderate and low values considered were in accordance with Sivasubramanian and Menon (1973).

The PCV and GCV was found to be high in fruit volume followed by number of fruits per plant and fruit weight, moderate in yield per plant, number of branches per plant, fruit breadth, fruit length and low in plant height for all genotypes. PCV was higher than GCV; this might be due to the interaction of the genotypes with the environment to some degree. These results corroborate with the findings of Nayak and Nagre (2013), Gavade and Ghadage (2015), Hegade (2017), Ravali et al., (2017), Tirkey et al., (2018).

Heritability and genetic advance

Heritability, genetic advance in broad sense was estimated using formula suggested by Hanson *et al.* (1956), Allard (1960) respectively and presented in Table.3 and Fig.1. The high, moderate and low values of heritability and genetic advance as percent of mean considered were according to Johnson *et al.* (1955). High heritability was exhibited for the character fruit weight, fruit volume, number of fruits per plant, number of branches per plant, fruit breadth, plant height and yield per plant while moderate heritability noticed only in fruit length.

The genetic advance ranged from 1.34 (fruit length) to 695.39 (yield per plant). The genetic advance as per cent of mean varied from 8.57 to 51.80. Highest genetic advance as per cent of mean values were reported for fruit volume (51.80), number of fruits per plant (41.55), fruit weight (39.33), number of branches per plant (27.11), fruit breadth (20.153), and moderate values were reported for plant height (11.08). Whereas, the lowest value was reported for fruit length (8.57).

High heritability coupled with high genetic advance as percentage of mean was observed for all traits i.e. plant height, number of branches per plant, number of fruits per plant, fruit weight, fruit breadth, fruit volume and yield per plant except fruit length which indicated the predominance of additive gene action in the expression of most of the characters. These results are similar with the findings of Suhana *et al.*, (2016), Hegade (2017), Chauhan *et al.*, (2018), Tirkey *et al.*, (2018).

Correlation studies

Character association analysis is an important approach in a breeding programme. It gives an idea about relationship among the various characters and determines the component characters, on which selection can be used for genetic improvement in the fruit yield. The phenotypic correlation coefficient for fruit yield and its component character in brinjal are presented in Table.4 and Fig.2.

Comment [AMA5]: Heritability was 0.41 this is moderate or low. It is below than 50%. On which category you classified these values you should mention to it?

Comment [AMA6]: On which level of selection intensity to select your progeny?

Comment [AMA7]: There is some traits had low heritability (0.41) coupled with low GAM (8.57)

Significant positive relationship was observed between yield per plant and number of fruits per plant, plant height, fruit weight and number of branches per plant at phenotypic level. Whereas yield per plant showed negative non-significant correlation with fruit breadth, fruit volume and fruit length. Similar findings were found by Muniappan et al., (2010), Kumar and Arumugam (2013), Arunkumar et al., (2014), Bashar et al., (2015), Chauhan (2016), Shivkumar et al., (2016), Yadav Neha et al., (2017).

Path coefficient analysis

Path coefficient analysis carried out using the simple correlation coefficient suggested by Dewey and Lu (1959). Correlation studies in conjunction with path coefficient analysis revealed a better picture of the cause and effect relationship of different attributes. The direct and indirect effects as well as the correlation of different characters with yield were represented in the path analysis *Table.5*. In this analysis the phenotypic correlation among eight characters were taken into consideration. Among all the traits number of fruits per plant (1.082) exhibited maximum direct effect towards yield, followed by fruit weight (0.951). The character fruit breadth showed a very high direct negative effect (-0.206) which was counter balanced by the higher positive indirect effects through number of fruits per plant, number of branches per plant which resulted in higher correlation with fruit yield per plant.

Maximum yield attributing traits such as number of fruits per plant, fruit weight, fruit volume and number of branches per plant were having high positive direct effect towards yield per plant, and also exhibited higher positive correlation with yield except fruit volume. So, these traits were the most important selection criteria for improvement of fruit yield. Similar kind of results found by Muniappan et al., (2010), Kumar and Arumugam (2013), Arunkumar et al., (2014), Shivkumar et al., (2016).

Hence the knowledge of association of various yield components associated with traits of economic importance would help suitable selection criterion which could be used in future breeding programme. The residual effect of 0.04094 indicated that other possible characters which are not studied in the present experiment need to be included.

Table.1 Analysis of variance (ANOVA) of F₃ generation (F₂ Selected lines) of two crosses along with the F₂ bulks

	Df	PH	BP	FP	FW	FL	FB	FV	FY
Replication	2	4.17	0.26	1.10	314.58	0.55	0.82	239.91	95481.21
Treatment	13	61.13**	7.85**	30.64**	6769.64**	4.56**	11.32**	20052.31**	603432.81**
T ₃ L ₆ lines	5	6.66	0.27	1.52	460.70*	0.54	0.25	1329.99	254647.43*
T ₃ L ₅ lines	5	11.46*	0.76	4.12*	681.81*	0.35	0.82	960.29	191532.12*
T ₃ L ₆ lines Vs T ₃ L ₆ Bulk	1	3.57	0.21	0.36	265.97	0.79	0.14	385.75	112733.77
T ₃ L ₅ lines Vs T ₃ L ₅ Bulk	1	58.35*	0.01	10.49*	753.29	0.13	1.78	2417.61	751119.60*
F ₂ lines Vs F ₂ Bulk	1	9.92	0.04	1.52	258.48	0.30	0.04	576.68	174779.00
Error	26	5.24	0.43	1.20	452.21	1.47	0.71	747.29	87543.26
Total	41	70.54	8.54	32.94	7536.43	6.58	12.85	21039.50	786457.28

Comment [AMA8]: These lines still in F₃ generation and should have some variability. Why their no differences between them?

Comment [AMA9]: Not significant for T₃L₆ lines and T₃L₅ lines separately. This means there is no variability between them. How the treatment give significant?? Between lines their no significant Table 2. You should explain this results.

**P < 0.01, *P < 0.05, df : Degree of freedom, PH: Plant height (cm), BP: Number of branches per plant, FP: Number of fruits per plant, FW: fruit weight (gm), FL: Fruit length (cm), FB: Fruit breadth (cm), FV: Fruit volume (cc), FY: Yield per plant (gm), T₃L₆ - F₂ [MLC-1 x Longai (oblong)], T₃L₅ - F₂ [MLC-3 x Longai (oblong)].

Table.2 Mean table of F_3 generation (F_2 Selected lines) of two crosses along with the F_2 bulks

	PH	BP	FP	FW	FL	FB	FV	FY
T ₃ L ₆ - 2	67.28	12.33	17.80	190.05	14.58	14.90	264.16	3486.07
T ₃ L ₆ - 3	73.18	13.27	20.13	153.66	14.42	15.84	222.29	3250.00
T ₃ L ₆ - 10	69.32	12.73	19.80	163.75	14.26	15.15	220.99	3499.32
T ₃ L ₆ - 11	65.85	12.20	15.60	156.97	14.26	16.04	200.11	2589.10
T ₃ L ₆ - 12	67.18	13.60	16.13	224.09	14.80	17.05	276.65	3571.87
T ₃ L ₆ - 19	67.66	12.53	16.80	184.65	15.91	16.82	227.21	3077.09
T ₃ L ₆ bulk	62.17	12.40	15.07	156.45	14.41	14.88	195.09	2537.94
T ₃ L ₅ - 22	72.07	9.40	11.73	241.92	15.85	19.26	360.48	2852.95
T ₃ L ₅ - 26	77.03	10.00	12.47	228.41	17.53	19.86	336.35	2860.78
T ₃ L ₅ - 28	75.81	9.13	11.33	267.06	17.40	18.92	382.62	3028.17
T ₃ L ₅ - 105	77.80	10.53	14.53	286.81	16.88	18.45	448.05	4162.36
T ₃ L ₅ - 107	73.11	9.60	11.00	260.63	16.90	19.61	366.84	2866.01
T ₃ L ₅ - 109	72.05	9.67	11.60	271.80	16.78	19.30	376.14	3149.98
T ₃ L ₅ bulk	71.97	9.07	11.27	236.37	15.63	18.59	350.64	2678.54
Overall Mean	70.89	11.18	14.66	215.90	15.69	17.56	301.97	3115.01
S.E.	1.87	0.53	0.90	17.36	0.99	0.69	22.32	241.58
C.D. 5%	4.03	1.15	1.93	37.50	2.14	1.48	48.21	521.83

PH: Plant height (cm), BP: Number of branches per plant, FP: Number of fruits per plant, FW: fruit weight (gm), FL: Fruit length (cm), FB: Fruit breadth (cm), FV: Fruit volume (cc), FY: Yield per plant (gm), T₃L₆ - F₂ [MLC-1 x Longai (oblong)], T₃L₅ - F₂ [MLC-3 x Longai (oblong)].

Table.3 Genetic parameters in F_3 generation (F_2 Selected lines) of two crosses along with the F_2 bulks

	PH	BP	FP	FW	FL	FB	FV	FY
V _p	23.87	2.90	11.01	2558.02	2.50	4.24	7182.29	259506.44
V _g	18.63	2.48	9.81	2105.81	1.03	3.54	6435.01	171963.18
PCV	6.89	15.43	22.63	23.43	10.08	11.73	28.06	16.35
GCV	6.09	14.25	21.37	21.25	6.48	10.71	26.56	13.31
h ² (b.s)	0.78	0.85	0.89	0.82	0.41	0.83	0.90	0.66
G.A (5%)	7.86	2.99	6.09	85.77	1.34	3.54	156.42	695.39
G.A as % of Mean (5%)	11.08	27.11	41.55	39.73	8.57	20.15	51.80	22.32

PH: Plant height (cm), BP: Number of branches per plant, FP: Number of fruits per plant, FW: fruit weight (gm), FL: Fruit length (cm), FB: Fruit breadth (cm), FV: Fruit volume (cc), FY: Yield per plant (gm), PCV=Phenotypic coefficient of variability, GCV= Genotypic coefficient of variability, h² (b.s) = Heritability (broad sense), GA =Genetic Advance.

Comment [AMA10]: Why bulk had the lower mean for all traits???

Comment [AMA11]: Please check these values for all traits

Comment [AMA12]: This is the calculation of environmental variance
 $V_e = MSe / r$

Comment [AMA13]: Genotypic variance
 $V_g = (MSg - Mse) / 3.14$
 Phenotypic variance = $V_g + V_e$

Table.4 Phenotypic correlations among yield and yield contributing characters of of F3 generation (F2 Selected lines) of two crosses along with the F2 bulks

	PH	BP	FP	FW	FL	FB	FV	FY
PH	1							
BP	-0.445**	1						
FP	-0.306*	0.881**	1					
FW	0.673**	-0.611**	-0.648**	1				
FL	0.575**	-0.565**	-0.544**	0.608**	1			
FB	0.636**	-0.766**	-0.774**	0.802**	0.640**	1		
FV	0.715**	-0.698**	-0.669**	0.910**	0.572**	0.784**	1	
FY	0.369*	0.358*	0.443**	0.364*	0.040 ^{NS}	-0.063 ^{NS}	0.282 ^{NS}	1

Comment [AMA14]: Correlation r at 6 degrees of freedom
0.05 = 0.707
0.01 = 0.834
Check the significance.

**P < 0.01, *P < 0.05, PH: Plant height (cm), BP: Number of branches per plant, FP: Number of fruits per plant, FW: fruit weight (gm), FL: Fruit length (cm), FB: Fruit breadth (cm), FV: Fruit volume (cc), FY: Yield per plant (gm).

Table.5 Path coefficient analysis among yield and yield contributing characters of of F3 generation (F2 Selected lines) of two crosses along with the F2 bulks

	PH	BP	FP	FW	FL	FB	FV	FY
PH	-0.082	-0.046	-0.331	0.639	0.034	-0.131	0.285	0.369*
BP	0.036	0.102	0.954	-0.581	-0.033	0.158	-0.278	0.358*
FP	0.025	0.090	1.082	-0.616	-0.032	0.160	-0.266	0.443**
FW	-0.055	-0.063	-0.702	0.951	0.036	-0.165	0.362	0.364*
FL	-0.047	-0.058	-0.589	0.578	0.059	-0.132	0.228	0.040 ^{NS}
FB	-0.052	-0.078	-0.838	0.762	0.038	-0.206	0.312	-0.063 ^{NS}
FV	-0.059	-0.071	-0.723	0.865	0.034	-0.162	0.398	0.282 ^{NS}

Residual effect = 0.04094 **P < 0.01, *P < 0.05, PH: Plant height (cm), BP: Number of branches per plant, FP: Number of fruits per plant, FW: fruit weight (gm), FL: Fruit length (cm), FB: Fruit breadth (cm), FV: Fruit volume (cc), FY: Yield per plant (gm).

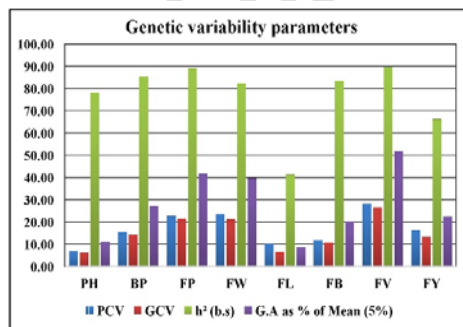


Fig.1 PCV, GCV, Heritability and Genetic advance as percent of mean of quantitative traits.

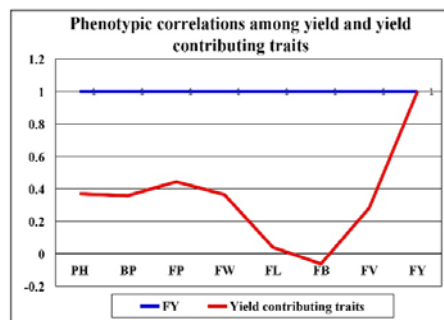


FIG.2 Phenotypic correlations among yield and yield contributing traits

Conclusion

Based on the results of investigation it can be concluded significant phenotypic and genetic variability were found for yield per plant and its components. High amount of phenotypic and genotypic coefficient variations was observed for all the quantitative traits. High estimates of heritability were observed for all the quantitative characters **except fruit length in which moderate heritability was present**. Heritability along with high genetic advance as percent of mean was registered for all the quantitative traits studied except for **fruit length** where the both the values were low indicating that all the traits were governed by additive gene effects. Phenotypic correlation studies revealed that significant positive relationship was observed between yield per plant and number of fruits per plant, plant height, fruit weight and number of branches per plant. Path coefficient analysis showed that numbers of fruits per plant is important yield attributing trait because of their high direct effect and indirectly influence other yield attributing trait like number of branches per plant which showed significant phenotypic correlation with the yield per plant.

Comment [AMA15]: Here low while in results is moderate?????
Indicating non additive gene controlled fruit length.

Suggestions for further works

Materials generated in this study can be used for further evaluation to select high yielding genotypes with better adaptability. Emphasis should be given to the yield components which showed high significant correlation as well as direct and indirect effects on yield per plant for further improvement. Quality analysis particularly for total phenol content, total soluble solids will be very useful for brinjal quality improvement work. The genotypes should be screened against biotic stresses (disease & insect pests) particularly phomopsis blight, bacterial wilt and fruit and shoot borer. Further hybridization and selection programme would be most effective for the lines which give better performance than the check varieties.

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