

Correlation and Path Coefficient Analysis of Yield Related Traits in F₃ Populations of Brinjal from Intra-specific Hybridization

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Authors' contributions

This work was carried out in collaboration among all authors. Authors KS, PS and DS designed the study, performed the statistical analysis, wrote the protocol and wrote the first draft of the manuscript. Authors PKB and SG managed the analyses of the study. Authors KS and PS managed the literature searches. All authors read and approved the final manuscript.

Article Information

DOI: 10.9734/CJAST/2020/v39i1030628

Editor(s):

(1) Dr. Tushar Ranjan, Bihar Agricultural University, India.

(2) Dr. Ahmed Mohamed El-Waziry, Alexandria University, Egypt.

Reviewers:

(1) Ahmed Mohamed Abdelmoghny, Cotton Research Institute, Agricultural Research Center, Egypt.

(2) Janilson Pinheiro de Assis, Federal Rural University of the Semi-Arid (UFERSA), Brazil.

Complete Peer review History: <http://www.sdiarticle4.com/review-history/56896>

Received 05 March 2020

Accepted 12 May 2020

Published 19 May 2020

Original Research Article

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.

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Keywords: *Brinjal; phenotypic coefficients of variation (PCV); genotypic coefficient of variation (GCV); heritability; genetic advance as percent of mean.*

1. 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* [1]. 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) [2].

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 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 [3] 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.

Brinjal demand is progressively increasing because of high nutritive value and low price [4], so to meet the demand of brinjal potential hybrids or improved varieties need to be developed. Crop improvement can be possible with the help of hybridization programme. The desirable segregants or transgressive segregants are expected to produce in hybridization programme. For implementing successful breeding programme the information about variability is prerequisite. Genetic improvement of any character is difficult without having sufficient genetic variability. Variability is a measure estimated from mean, phenotypic and genotypic coefficient of variation, heritability, genetic advance and genetic advance as percent of mean. Characters with high estimates of heritability are of great importance to the plant breeder as it enables them selection for the character is easy because heritability is the transmissibility of characteristics from parents to offspring. Based on the estimate of heritability (broad sense) the estimates of genetic advance in broad sense can be measured. The genetic gain expressed for a particular character through selection is the product of its heritability, phenotypic standard deviation and selection

differential as proposed by Burton and Devane [5]. Genetic advance is the improvement in the mean genotypic value of selected plants in the population and it is the measure of genetic gain under selection. Due to masking influence of environment upon traits concerned, values of genetic advance exhibit 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.

Inheritance of quantitative character like yield is often influenced by variation in other component characters which may be due to pleiotropy or genetic linkage [6]. 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.

2. MATERIALS AND METHODS

The present investigation was conducted in a randomized complete block design with three replications at a spacing of 75 cm row to row and 60 cm plant to plant 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 F_2 population [MLC-1 x Longai (oblong)] i.e. T_3L_6 - 2, T_3L_6 - 12, T_3L_6 - 10, T_3L_6 - 3, T_3L_6 - 11, T_3L_6 - 19 and 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 along with their respective bulk populations i.e. T_3L_6 Bulk and T_3L_5 Bulk. The seeds from all the F_2 population plants were mixed to generate Bulk separately for both the F_2 populations. Based on the efficient selection indices constructed using the method given by Falconer [7] the 5% plants

selected separately as lines out of 120 F_2 plants in each F_2 population in the year 2017-18.

The data recorded on different characters were subjected to different statistical analysis. Analysis of variance of the traits was done as per standard statistical procedure Randomized complete design as given by Panse and Sukhatme [8]. Phenotypic and genotypic variances were calculated according to the formula given by Johnson et al. [9]. Phenotypic and Genotypic co-efficient of variation were calculated by the formula suggested by Burton [10] and classified in to Low (less than 10%), Moderate (10-20%) and High (More than 20%) as described by Sivasubramanian and Menon [11]. Heritability in broad sense was computed as the formula suggested by Hanson et al. [12] and expressed as percentage categorized in to Low (less than 30%), Moderate (30-60%) and High (More than 60%) as per the classification given by Johnson et al. [9]. Genetic advance was estimated using formula suggested by Allard [13] and the range of genetic advance as per cent of mean was classified in to Low (less than 10%), Moderate (10-20%) and High (More than 20%) as suggested by Johnson et al. [9]. Path coefficient analysis carried out using the simple correlation coefficient suggested by Dewey and Lu [14].

3. RESULTS AND DISCUSSION

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 [15], Tripathy et al. [16], Hegade [17], Chauhan et al. [18].

3.1 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

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
Treatments	13	61.13**	7.85**	30.64**	6769.64**	4.56**	11.32**	20052.31**	603432.81**
T ₃ L ₆ F ₂ Selected lines	5	6.66	0.27	1.52	460.70*	0.54	0.25	1329.99	254647.43*
T ₃ L ₅ F ₂ Selected lines	5	11.46*	0.76	4.12*	681.81*	0.35	0.82	960.29	191532.12*
T ₃ L ₆ F ₂ Selected 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 F ₂ Selected 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 Selected 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

**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 F₃ generation (F₂ selected lines) of two crosses along with the F₂ 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)]

of F₂ population MLC-3 x Longai (oblong) i.e. T₃L₅ – 22, T₃L₅ – 26, T₃L₅ – 28, T₃L₅ – 105, T₃L₅ – 107, T₃L₅ -109 and its bulk population, was presented in Table 2. Mean performance of individual parameter is described as above.

Among progenies of F₂ population MLC-1 x Longai (oblong) maximum plant height (73.18), number of fruits per plant (20.13) was observed in T₃L₆ – 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 T₃L₆ – 12. Highest fruit length (15.91) was observed in T₃L₆ – 19.

In progenies of F₂ 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 T₃L₅ – 105 and fruit length (17.53), fruit breadth (19.86) was observed in T₃L₅ – 26.

The variation with in the progenies i.e. T₃L₆ F₂ selected lines and T₃L₅ F₂ selected lines is less because these are already selected lines out of 120 F₂ plants (i.e. 5 % of plants) cultivated in the previous year i.e. 2017-18. Whereas the variation between the both the F₂ selected lines or progenies is more because the parents of the

both the cross combination is different. 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 reported in brinjal for yield and yield contributing traits by many workers like Kumar and Arumugam [15], Suhana et al. [19], Chaudhary and Kumar [20], Hegade [17], Ravali et al. [21], Chauhan et al. [18], Tripathy et al. [16].

3.2 GENETIC PARAMETERS

3.2.1 Components of variation

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.

3.2.2 Phenotypic and Genotypic Coefficient of Variation

Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were presented in Table 3 and Fig. 1. 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 [22], Gavade and Ghadage [23], Hegade [17], Ravali et al. [21], Tirkey et al. [24].

3.2.3 Heritability and Genetic Advance

Heritability, genetic advance and genetic advance as per cent of mean was presented in Table 3 and Fig. 1. 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 percent of mean values were reported for fruit volume (51.80), number of fruits per plant (41.55), fruit weight (39.73), number of branches per plant (27.11), fruit breadth (20.15), 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 most of the 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, [19], Hegade [17], Chauhan et al. [18], Tirkey et al. [24].

3.3 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.

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. [25], Kumar and Arumugam [15], Arunkumar et al., [26], Bashar et al. [27], Chauhan [28], Shivakumar et al. [29], Yadav Neha et al. [30], Tiwari et al. [31], Onyia et al. [32].

Table 3. Genetic parameters in F₃ generation (F₂ selected lines) of two crosses along with the F₂ 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 in %)	78.06	85.29	89.10	82.32	41.28	83.39	89.60	66.27
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

Table 4. Phenotypic correlations among yield and yield contributing characters 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

**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 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)

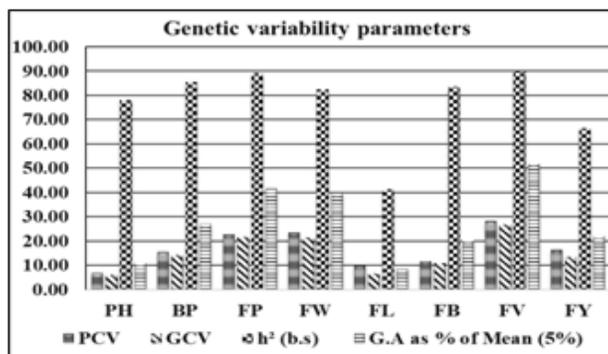


Fig. 1. PCV, GCV, heritability and genetic advance as percent of mean of quantitative traits

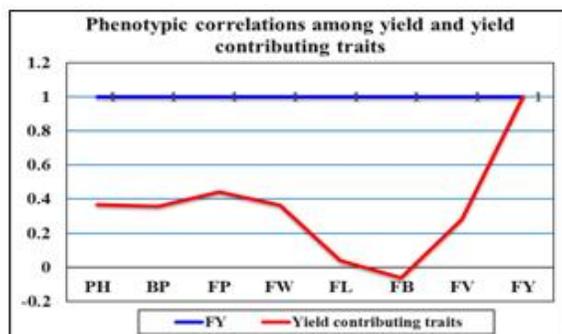


Fig. 2. Phenotypic correlations among yield and yield contributing traits

3.4 Path Coefficient Analysis

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 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. [25], Kumar and Arumugam [15], Arunkumar et al. [26], Shivakumar et al. [29], Bende et al. [33].

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.

4. 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 moderate heritability, low genetic advance as percent of mean was reported, indicating that most of the

traits were governed by additive gene effects except fruit length. 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.

5. 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 and 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.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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