Research Article

GENETIC VARIABILITY, HERITABILITY, GENETIC ADVANCE AND GENETIC DIVERSITY ANALYSIS FOR YIELD, YIELD RELATED COMPONENTS OF BRINJAL [*Solanum melongena L*] GENOTYPES

PUJER PARVATI[1], JAGADEESHA R.C.[1], SATISH D.[1], VENKATESHALU[2] AND MESTA R.K.[3]

[1]Department of Biotechnology and Crop Improvement, University of Horticultural Sciences, Bagalkot, Karnataka 587104, India
[2]Department of Entomology, University of Horticultural Sciences, Bagalkot, Karnataka 587104, India
[3]Department Of Plant Pathology, University of Horticultural Sciences, Bagalkot, Karnataka 587104, India
*Corresponding Author: Email- paru.hortico@gmail.com

Abstract- Eggplant or brinjal [*Solanum melongena* L.] is the most popular and widely cultivated vegetable crop in the central, Southern and Southeast Asia and in some African countries. In the present investigation 55 genotypes were collected and evaluated at the Research Farm of Department of Biotechnology and Crop Improvement during Khari season of 2015 to assess genetic variability, heritability, genetic advance and genetic diversity. Estimates of phenotypic coefficients of variability (PCV) and genotypic coefficients of variability (GCV) ranged for average fruit weight (18.00- 176.70) followed by plant spread (51.70-87.60) respectively. PCV were slightly higher than the corresponding GCV and the difference was very low for majority of the characters, suggesting that prevalence of more of genetic effects than environment in their expression. Heritability in broad sense (h^2), genetic advance (GA) and genetic advance as percentage of mean (GAM) ranged between 19-79-100%, 0.55-70.63, 23.17- 104.14 % respectively. High GCV, PCV, heritability coupled with high genetic advance indicating more of genetic inheritance and selection is effective. The genotypes CBB-23 (cluster XIV), A2 (cluster XIII), CBB-2 (cluster XII), CBB-50, CBB-49, A11, CBB-43, CBB-52 and CBB-64 (cluster XI) showed high genetic diversity giving room to improvement through hybridization between these genotypes. Therefore, direct selection helps in selecting good genotypes with high growth, yield and quality for brinjal hybrids.

Key words - *Solanum melongena, mean performance, genetic variability, heritability, genetic advance, genetic diversity*

Citation: Pujer Parvati, *et al*., (2018) Genetic variability, Heritability, Genetic Advance and Genetic Diversity Analysis for Yield, Yield Related Components of Brinjal [*Solanum melongena L]* Genotypes. International Journal of Genetics, ISSN: 0975- 2862 & E-ISSN: 0975-9158, Volume 10, Issue 6, pp.-460-463.

Introduction

Eggplant or brinjal [*Solanum melongena L.*] is the most popular and widely cultivated vegetable crop in the central, Southern and Southeast Asia and in some African countries. In the present investigation 55 genotypes were collected and evaluated at the Research Farm of Department of Biotechnology and Crop Improvement during *Khari* season of 2015 to assess genetic variability, heritability, genetic advance and genetic diversity. Estimates of Eggplant or brinjal [*Solanum melongena L.*] is the most popular and widely cultivated vegetable crop in the central, southern and Southeast Asia and in some African countries. The crop is extremely variable in India and for this reason, [1] regarded the crop as being of Indian origin. Genetic Variability The phenotypic expression of the plant character is mainly controlled by the genetic makeup of the plant and the environment, in which it is grown and the interaction between the genotypes and environment. Effectiveness of selection directly depends on the amount of heritability and genetic advance as per cent of mean for that character. Genetic diversity, the information on genetic divergence among the available germplasm is also vital to a plant breeder as it was also observed that the more diverse the parents, greater are the chances of obtaining high heterotic F_1s and broad spectrum of variability in the segregating generation. Of the several methods available, Mahalanobis generalized distance estimated by D^2 statistic serves to be a good index for estimating genetic diversity. So, this study aimed at justifying the real worth of the selection parameters that will be framed through comparative study of genetic variability and diversity parameters. The present studies were, therefore, initiated with an objective to determine genetic variability and diversity for fruit yield and related attributes along with quality components in relationships in a collection of 55 genotypes of brinjal.

Materials and Methods

The present investigation was carried out at the research plot of Biotechnology and Crop Improvement during the *kharif* season of the year 2014-15. Experimental material consisted of 55 genotypes and it was laid out in Randomized Block Design (RBD) with 2 replications. All the scientific agronomic package of practices was followed to raise a healthy crop except spraying of insecticides to control the shoot and fruit borer, leaf hopper and white fly and phomopsis blight diseases.

Experimental data

Five plants of each accession in each replication were randomly selected for recording the observations on 14 yield and its component characters *viz.* plant height (cm) 90 DAT, stem girth (cm) 90 DAT, number of branches per plant 90 DAT, plant spread (cm) 90 DAT, days to first flowering, days to 50 per cent flowering, fruit diameter (cm), total phenol (%), reducing sugar (%), ascorbic acid (mg/100g), number of flowers per branches, number of fruits per plant, average fruit weight (g) and fruit yield per plant (kg). The mean replicated data on various biometric traits were subjected to analysis of variance as per the standard statistical procedure [2]. Phenotypic and genotypic components of variance, phenotypic and genotypic coefficients of variation, heritability, the expected genetic gain or advance under selection [9] were calculated.

Table-1 Analysis of variance for 14 characters of brinjal genotypes

SN	Characters	Df	Replication	Treatments	Error
			1	54	54
1	Plant height 90 DAS (cm)		1.570	139.12**	1.100
2	Stem girth 90 DAS (cm)		0.001	0.22**	0.002
3	Number of branches 90 DAS		0.082	5.49**	0.045
4	Plant spread 90 DAS (cm)		0.582	119.96**	0.311
5	Day to first flowering		0.525	97.95**	0.754
6	Days to 50 per cent flowering		0.265	88.68**	0.244
7	Fruit diameter (mm)		0.657	1.97**	0.010
8	Toatl phenol (%)		0.219	0.36**	0.002
9	Reducing sugar (%)		0.331	0.15**	0.003
10	Ascorbic acid (mg/100g)		3.247	21.48**	2.516
11	Number of flowers/branches		0.093	15.87**	0.059
12	Number of fruits per /plant		43.911	266.51**	10.763
13	Average fruit wieght (g)		3.746	2352.92**	0.625
FY/P	Fruit yield per plant (kg)		0.000	0.48**	0.010

Table-2 Estimation of mean, range, Phenotypic variance (PV), genotypic variance (GV), phenotypic coefficient of variance (PCV) genotypic coefficient of variance (GCV), heritability (h2), genetic advance (GA) and genetic advance as per cent of mean (GAM) for 14 characters of brinjal genotypes

SN	Mean	Range	GV	GCV (%)	PV	PCV (%)	h² (Broad Sense)	Genetic advance over mean
1	66.92	40.4-82	65.00	12.04	70.11	12.51	0.92	23.89
2	1.79	1.09-2.59	0.10	17.66	0.12	19.07	0.83	32.29
3	68.60	53.7-87.6	55.83	10.89	60.14	11.31	0.91	21.61
4	6.25	3.2-11.2	2.00	22.62	2.77	26.61	0.72	39.52
5	49.88	31.7-61.2	45.60	13.53	49.36	14.09	0.91	26.80
6	57.46	38.7-68.5	40.22	11.03	44.47	11.61	0.90	21.61
7	4.85	2.2-7.1	0.82	18.67	0.99	20.55	0.82	34.84
8	1.44	0.54-2.35	0.17	28.63	0.18	29.81	0.94	56.94
9	0.84	0.30-1.37	0.08	33.67	0.08	33.00	0.96	69.04
10	10.80	4.00-18.50	9.48	28.51	12.00	32.07	0.79	52.22
11	6.44	2.5-11.80	7.51	42.55	7.97	43.86	0.94	89.59
12	31.36	8.75-53.00	115.88	34.31	138.64	37.55	0.83	64.46
13	67.82	18.00-176.7	1001.15	46.65	1176.78	50.58	0.85	88.63
14	1.54	0.65-2.90	0.24	31.81	0.25	32.35	0.96	63.63

1	Plant height 90 DAS (cm)	6	Days to 50 per cent flowering	11	Number of flowers/branches
2	Stem girth 90 DAS (cm)	7	Fruit diameter (cm)	12	Number of fruits per /plant
3	Number of branches 90 DAS	8	Total phenol (%)	13	Average fruit weight (g)
4	Plant spread 90 DAS (cm)	9	Reducing sugar (%)	FY/P	Fruit yield per plant (kg)
5	Day to first flowering	10	Ascorbic acid (mg/100g)		
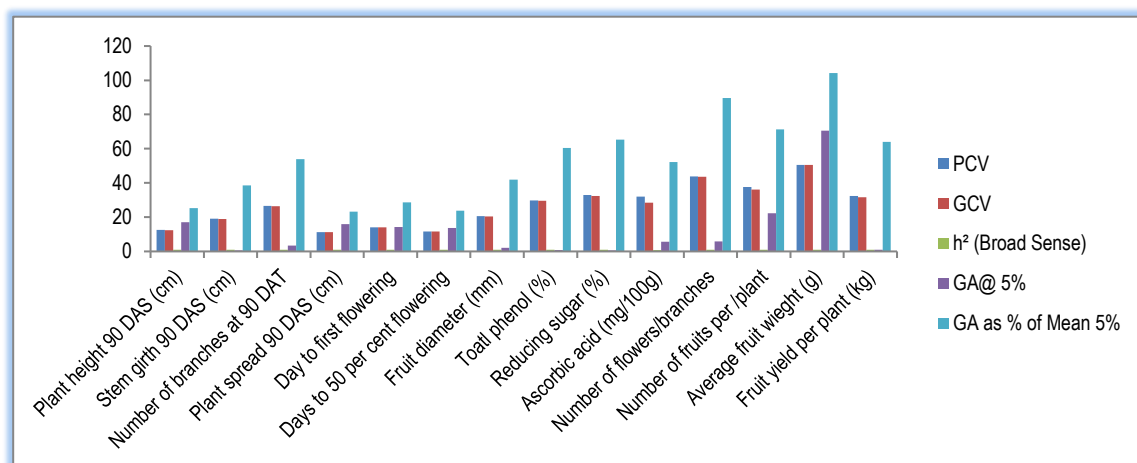
Fig-1 Estimation of phenotypic coefficient of variance (PCV) genotypic coefficient of variance (GCV), heritability (h2), genetic advance (GA) and genetic advance as per cent of mean (GAM) for 14 characters of brinjal genotypes

Results and Discussion
Analysis of variance and genetic variability
The genotypes in the experiment showed highly significant difference for the traits indicating the presence of sufficient variability in the experimental materials. The mean, range, genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) estimates for 14 quantitative traits in brinjal genotypes are presented in table 2. Mean and ranges are the simple measures of variability. The range of mean values also revealed sufficient variation for the characters under study. Maximum range of variability was observed for average fruit weight (18.00-176.70) followed by plant spread (51.70-87.60). These findings are in consonance with the findings of earlier workers [3-5]. The characters showing high range of variation have more scope for improvement. The lowest range of mean was recorded for ascorbic acid (0.30-1.37) indicating availability of low variation for its improvement in the experimental material used.

Table-3 Clustering pattern of fifty five genotypes of brinjal on the basis of genetic divergence

Cluster	Number of genotypes	Genotypes
I	2	CBB-32, CBB-57
II	2	CBB-24, CBB-38
III	2	CBB-41, CBB-37
IV	4	CBB-33, CBB27, A14, CBB-12
V	7	CBB-3, A1, CBB-29, CBB-31, CBB-2, CBB-44 , CBB-35
VI	16	CBB-13, CBB-19, CBB-58, CBB-51, CBB-36, CBB-56, CBB-54, A8, A13, CBB-7, CBB-14, CBB-36, A9, A10, CBB-20, CBB-4
VII	3	CBB-11, CBB-21, CBB-17
VIII	1	A12
IX	1	CBB-52
X	9	CBB-5, CBB-16, CBB30, CBB-34, CBB-40, CBB-59, CBB-6, CBB-18, CBB-1
XI	5	CBB-50, CBB-49, A11, CBB-43, CBB-64
XII	1	CBB-25
XIII	1	A2
XIV	1	CBB-23

The genotypic variation varied from 0.08 for reducing sugar (%) to 1001.15 for average fruit weight and genotypic coefficient of variation ranged from 10.89 % for plant spread at 90 DAT to 46.65 % average fruit weight. The highest genotypic coefficient variance was recorded for average fruit weight (46.65%) followed by number of flowers per branches (42.55%), number of fruits per plant (34.31%), reducing sugar (33.67 %), total phenol (28.63%), ascorbic acid (28.51%) and number of branches at 90 DAT (22.62). The highest phenotypic coefficient variance was recorded for average fruit weight (50.58%) followed by number of flowers per branches (43.86%), number of fruits per plant (37.55%), reducing sugar (33.00%), ascorbic acid (32.07 %), total phenol (29.81%), number of branches at 90 DAT (26.61) and fruit diameter (20.55%).In general for all the characters under study, PCV were slightly higher than the corresponding GCV indicating prevalence of environmental influence on expression of these traits. However, the difference between PCV and GCV being very low for majority of the characters suggesting more prevalence of genetic governance of these characters and thus selection on phenotypic basis would holds good. Slightly higher PCV to GCV were also obtained [6-10]. The PCV and GCV values were classified as low (<10.00 %), moderate (10.00- 20.00%) and high (>20.00%) as suggested [11]. High (>20.00%) GCV and PCV estimates are also evident from the studies [6-10]. In the present investigation it was also evident that difference between PCV and GCV were low for all the character studied. It indicates more of genetic control than environment in governing these traits and scope and importance of germplasm used in future selection for crop breeding.

Heritability and genetic advance
The result indicated that the heritability estimates were observed high for all the parameters studied in the experiment. The character fruit yield per plant (96.00%), reducing sugar (96.00%), total phenol (94.00%), number of flowers per branches (94.00%), plant height at 90 DAT (92.00 %), plant spread at 90 DAT (91.00 %), day to first flowering (91.00%), days to fifty per cent (90.00%), average fruit weight (85.00 %), stem girth at 90 DAT (83.00%), number of fruits per plant (83.00%), fruit diameter (82.00 %),1000 seed weight (81.00%), ascorbic acid (79.00%) and number of branches at 90 DAT (72.00 %) estimated very high heritability. Similar results reported by the scientist [3], [4] and [5]. Genetic advance and genetic advance as percentage of mean was calculated to predict the genetic gain and the result are presented in [table 2]. The highest estimate of genetic advance as percentage of mean was recorded for number of flowers per branches (89.59) followed by average fruit weight (88.63 %), reducing sugar (69.04%), number of fruits per plant (64.46%), fruit yield per plant (63.63 %), total phenol (56.94%), ascorbic acid (52.22 %), number of branches at 90 DAT (39.52%), fruit diameter (34.84 %), stem girth at 90 DAT (32.29 %), days to first flowering (26.80 %), plant height at 90 (21.43 %), day to 50 per cent flowering (21.61 %) and plant spread at 90 DAT (21.61 %). During the selection for the improvement of any character knowledge of both broad sense heritability and GAM are necessary because

broad sense heritability is based on total genetic variance and which includes both fixable (additive) and non-fixable (dominance and epistatic) variances. According to Percy and Turcotte, when heritability is mainly due to non- additive genetic effects (dominance and epistasis), genetic advance will be low, while in cases where heritability is chiefly due to additive gene effects, a high genetic advance may be expected. In the present investigation, except for first flowering node, high GAM coupled with high heritability has been observed for all the characters is the indication of prevalence of additive genetic effects (fixable) involved in their expression and predicted to show good response to phenotyped based selection in crop improvement programme. Hence, it is advisable for straight phenotype based selection to improve these characters. High heritability along with high GAM estimates are also obtained [6-10].

Clustering pattern of genotypes
The D^2 value between any two genotypes was calculated as the sum of squares of the differences between the mean values of all the yield and yield related characters and is used for the final grouping of the genotypes. Tocher statistical procedure was employed to group genotypes of brinjal into 14 clusters. Clustering pattern of brinjal genotypes was presented in [fig 2] and [table 3]. Cluster VI (CBB-13, CBB-19, CBB-58, CBB-51, CBB-36, CBB-56, CBB-54, A8, A13, CBB-7, CBB-14, CBB-36, A9, A10, CBB-20 and CBB-4) constituted maximum number of genotypes (16) followed by cluster x (CBB-5, CBB-16, CBB30, CBB-34, CBB-40, CBB-59, CBB-6, CBB-18 and CBB-1) containing 9 genotypes and cluster V (CBB-3, A1, CBB-29, CBB-31, CBB-2, CBB-44 and CBB-35) bearing 7 genotypes. Further, cluster XI (CBB-50, CBB-49, A11, CBB-43 and CBB-64), cluster IV (CBB-33, CBB27, A14, CBB-12) cluster VII (CBB-11,CBB-21, CBB-17) cluster I (CBB-32, CBB-57) cluster II (CBB-24,CBB-38) cluster III (CBB-41,CBB-37) accommodated 5, 4, 3, 2, 2 and 2 genotypes respectively. Cluster VIII (A12), cluster IX (CBB-52), cluster XII (CBB-25), cluster XIII (A-2) and cluster XIV (CBB-23) had a single genotype each. Larger the divergence between the genotypes, higher will be the heterosis [12]. Hence, crossing between the genotypes of more divergent clusters would be helpful in getting novel recombinants with high heterosis. Similar results were reported [13-17]. It will be fruitful to select genotypes of cluster combinations VI and XIV, XIII and XIV, XII and XIV, XI and XIV and IV and XIV as parents for hybridization as they were highly divergent.

Mean intra and inter cluster distances
Mean intra and inter cluster distances were presented in [table 4]. The intra cluster D^2 values ranged from 0.000-3946.06. Maximum intra cluster distance was recorded in cluster x followed by cluster IX, cluster V, cluster IV, cluster III, cluster II and cluster I while no intra cluster distance was noticed in clusters VI, VII, VIII, XI, XII, XIII and XIV as they were solitary clusters. The inter cluster D^2 values ranged from 1025.22-31727.60. Maximum inter cluster distance was observed between clusters VI and XIV, followed by clusters XIII and XIV, cluster XII and cluster XIV, cluster II and cluster XIV, cluster V and cluster XIV, cluster XI and cluster XIV and cluster IV and cluster XIV indicating the presence of distant genetic divergence among the genotypes of these clusters, while lowest inter cluster distance was reported between cluster I and cluster III followed by cluster I and cluster VIII cluster I and cluster VII and clusters IV and V denoting narrow genetic diversity. The scientists [18], [19] and [20] suggested same results for distant divergence and narrow divergence of different genotypes. Being primary centre of origin, India has accumulated a wide range of variability in brinjal. The existing variability can be used to further enhance the yield level of the brinjal cultivars by following appropriate breeding strategies. Diverse genotypes can be utilized for hybridization programme also. Major yield contributing characters is identified and selection for these traits will be helpful in getting increased yield of this crop. Based on the results obtained it was concluded that high genetic variability and heritability estimates obtained for most of the earliness, growth, yield and its components including quality indicated the prevalence of additive genetic effects (fixable) governing their expression. Therefore, direct selection based on these combinations of traits help in harnessing for selecting good genotypes with high yield per plant in improvement programmes. The genotypes CBB-23 (cluster XIV), A2 (cluster XIII), CBB-2 (cluster XII), CBB-50, CBB-49, A11,

Table-4 Intra (diagonal) and inter cluster distance D_2 values among fifty five brinjal genotypes

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
I	191.28	6207.76	1025.22	4560.61	5951.92	10780.07	1524.35	1503.57	2779.24	3613.18	3240.49	7939.03	7883.78	8673.89
II		192.25	5518.91	2400.96	1357.92	3677.81	11049.21	6421.87	4583.72	10852.44	2381.40	4571.83	6548.80	23683.08
III			893.85	3432.01	5021.09	8357.21	1707.84	1186.86	2812.03	2918.01	3541.14	6572.50	7288.75	9415.81
IV				1380.94	1974.15	2566.66	7069.92	3977.11	4934.59	6611.91	2655.26	2571.31	4094.10	20112.32
V					1463.61	2886.83	9469.95	5112.51	5162.87	8943.71	3192.66	3261.05	5156.26	22433.51
VI						0.000	13718.42	8883.46	10435.79	11850.15	5416.46	1538.73	3327.39	31727.60
VII							0.000	1436.45	5229.48	2250.71	7494.55	10812.41	10525.92	5682.64
VIII								0.000	3559.38	2628.20	5346.97	7118.42	7831.29	8314.90
IX									2373.84	6185.19	4194.56	9267.26	11217.20	10765.37
X										3946.06	8375.19	9730.75	10412.85	8774.96
XI											0.000	3549.29	4583.08	20424.58
XII												0.000	1157.85	28024.75
XIII													0.000	28877.63
XIV														0.000

CBB-43, CBB-52 and CBB-64 (cluster XI) showed high genetic diversity giving room to improvement through hybridization between these genotypes. To develop high yielding and quality brinjal by selecting diverse genotypes.

Research Category: Yield and quality

Abbreviations
CBB- College of Bagalkot Brinjal

*Research Guide or Chairperson of research: Dr R C Jagadeesha
University: University of Horticultural Sciences, Bagalkot, Karnataka 587104, India
Research project name or number: PhD Thesis

Author Contributions: All author equally contributed

Author statement: All authors read, reviewed, agree and approved the final manuscript

Conflict of Interest: None declared

Ethical approval: This article does not contain any studies with human participants or animals performed by any of the authors.

Reference
[1] Vavilov N.I. (1928) *Proc. V. Int. Cong. Genet*.
[2] Panse V. G. and Sukhatme P. V. (1985) *Indian council of Agricultural Research, New Delhi, India*. p.63-69.
[3] Karak C., Ray S., Akhtar A., Naik. and Hazra P.(2012) *Journal of Crop and Weed* ,8,1: 86-89 .
[4] Arunkumar B., Kumar S. V. S. and Prakash C. G. (2013) *Bioinfolet*, 10, 739-744.
[5] Patel K., Sarnaik D., Asati B., Tirkey T. (2004) *Agric Sci Digest*, 24, 256-259.
[6] Kumar S. R., Arumugam T., Anandakumar C. R. and Premalakshmi, V. (2013) *African Journal of Agricultural Research*, 8, 4956-4959.
[7] Mohammad R. N. R., Mahdiyeh P., Abdolrahim G. and Javad A. (2015) *Journal of Agricultural and Biological Science New York*, pp. 342.
[8] Mili C., Bora G. C., Das B., Paul S. (2014) *Direct Res Agric Food*. 2,192-194.
[9] Babu S. and Patil R. (2005) *Madras J. Aric Res*. 95,1-6,18-23.
[10] Sing O. and Kumar J. (2005) *Indian J. Hort*., 62, 265-267.
[11] Sivasubramanian S and Menon M. (1973) *Madras Agricultural Journal* 60: 1139.
[12] Johnson H.W., Robinson H.F. and Comstock R.S. (1955) *Agronomy Journal* 47, 314-318.
[13] Ravali B., Ravinder B.R., Saidaiah P. and Shivraj N. (2017) *Int. J. Curr. Microbiol. App. Sci,* 6 ,6, 48-54.
[14] Islam M.A., Nasrin A.I., Mian M.A.K., Shahadat M.K. and Shahjahan M. (2011) *Libyan Agri. Res. Center J. Inter*., 2, 1, 15-19.
[15] Dutta R., Mandal A.K., Maity T. K. and Hazra P. (2009) *Journal of Crop and Weed*, 5, 1, 67-70.
[16] Bansal S. and Mehta A. K. (2007) *Haryana J. Hort. Sci*., 36, 319-320.
[17] Kumar S., Singh A. K., Sharma J. P. and Sharma N. (2007) *Haryana J. Hortl sci.*, 68, 3, 95-96.
[18] Ramesh S. K., Arumugam T. and Ulaganathan V.(2013a) *Sabrao J. Breeding Gene,* 48 ,2, 162-171.
[19] Dhaka S. K. and Soni A. K. (2012) *Asian J. Hort*., 7, 2, 537-540.
[20] Chowdhury M. S. I. (2005) *An M. Sc. thesis. Dept. of Horticulture, BSMRAU, Salna, Gazipur*.