International Journal of Ecology and Environmental Sciences
www.ecologyjournal.in
Online ISSN: 2664-7133; Print ISSN: 2664-7125; Impact Factor: RJIF 5.28
Received: 20-09-2020; Accepted: 05-10-2020; Published: 26-10-2020
Volume 2; Issue 4; 2020; Page No. 251-253

Genetic variability studies for yield and its components in Brinjal (*Solanum melongena* L.) Germplasm

Praveen P Yankanchi[1*], Lakshmana D[2], Dhanalashmi TN[3], Onkarappa S[4], Prakash K[5]
[1-2] Department of Genetics and Plant breeding, College of Horticulture, Mudigere, UAHS, Shivamogga, Karnataka, India
[3] Department of Genetics and Plant breeding, College of Horticulture, Hiriyur, UAHS, Shivamogga, Karnataka, India
[4-5] Indian Council of Agricultural Research – Krishi Vigyan Kendra, Babbur Farm, Hiriyur, Karnataka, India

Abstract

The present investigation in brinjal (*Solanum melongena* L.) was carried out during *kharif* season of 2019-20 for yield and its components. Analysis of variance indicated highly significant differences among the genotypes for all the traits under study. The estimate of phenotypic coefficient of variation (PCV) was high (>20%) for number of flowers per cluster, fruit length, fruit girth and fruit weight whereas, genotypic coefficient of variation was high (>20%) for fruit length, fruit girth and fruit weight indicates the presence of high variability for these traits and offered better scope for improvement through selection. Low PCV and GCV (<10%) were recorded for days to 50% flowering and days to first pick indicating the narrow genetic base therefore selection for such traits may not give desirable results. High heritability (>60%) coupled with high genetic advance as percent over mean (>20%) was observed for number of secondary branches per plant, number of flowers per cluster, number of clusters per plant, number of fruits per plant, fruit length, fruit girth, fruit weight and fruit yield indicating that these traits were governed by additive genes and there is scope for improving these characters with direct selection.

Keywords: genetic variability, PCV, GCV, heritability, GAM

Introduction

Brinjal (*Solanum melongena* L.) a member of solanaceae family, is one of the most popular and widely cultivated vegetable crop in India and it is a self-pollinated annual herbaceous plant (Timmapur, 2007) [11] of tropics and subtropics particularly India, Japan, Indonesia. It is grown in an area of 7.3 lakh hectare with the production of 128.01 lakh tonnes and the productivity is 17.54 tonnes per hectare (NHB, 2018). The wide range of variability was observed in respect of all quantitative traits.

Large variability ensures the better chance of producing new forms. Estimation of coefficient of variation helps to assess variability in the population. Assessment of genetic variation in a species is a prerequisite for an efficient breeding program as it provides a basis for desirable genotypes. Association of variability parameters between various characters is significance in formulating an appropriate breeding strategy. Developing superior genotypes would be effective when greater variability exist in the chosen material.

Material and Methods

The present investigation on "Genetic variability studies for yield and its components in brinjal (*Solanum melongena* L.) Germplasm" was carried out in randomized complete block design (RCBD) with two replications during *kharif* season of 2019-20 among 33 brinjal genotypes at CoH, Hiriyur, Babbur Farm (Chitradurga). Tray sowing was carried out in 4th week of August-2019. The seedlings were transplanted to main field after 35 days at a spacing of 60 cm between rows and 45 cm between plants. All recommended cultural practices and plant protection measures were followed and observations were recorded for the traits like, plant height, number of primary and secondary branches per plant, days to 50% flowering, number of flowers per cluster, number of clusters per plant, days to first pick, number of fruits per plant, fruit length, fruit girth, fruit weight, fruit yield per plant and per hectare

Phenotypic and genotypic coefficient of variance was calculated using the formulae suggested by Burton De Vane (1952). Broad sense of heritability was calculated, genetic advance and genetic advance as percent over mean were estimated by the method suggested by Johnsons *et al.* (1955).

Results and Discussion

The analysis of variance for all characters showed significant difference among treatments (table 1.). The genotypic and phenotypic coefficient of variation measures the extent of variability among different traits presented in table 2. The estimate of PCV was higher than GCV for all characters and is due to the interaction of genotypes with the environment. The estimate of phenotypic coefficient of variation (PCV) was high (>20%) for number of flowers per cluster (), fruit length (31.36%), fruit girth (27.87%) and fruit weight (21.68%) whereas, genotypic coefficient of variation (GCV) was high (>20%) for fruit length (30.31%), fruit girth (26.55%) and fruit weight (20.07%) indicating high variability in the genotypes used for direct selection. Moderate PCV (10% to 20%) was observed for number of fruits per plant (19.57%), number of clusters per plant (19.22%), fruit yield per plant (18.39%), number of secondary branches per plant (17.18%), number of primary branches per plant (15.45%) and plant height (11.30%) while, GCV was moderate for number of flowers per cluster (17.87%), umber of clusters per plant (17.82%), number of fruits per plant

(17.11%), fruit yield per plant (15.17%), number of secondary branches per plant (14.20%) and number of primary branches per plant (12.08%). Akpan *et al.* (2016) [1], Kaundinya *et al.* (2017), Pujer *et al.* (2018) [10], Bende *et al.* (2019) [3], Dasmohapatra *et al.* (2019) [5] and Jirankali *et al.* (2019) [6] found the similar results.

High heritability (>60%) was observed for fruit length (93.43%) followed by fruit girth (90.77%), number of clusters per plant (86.00%), fruit weight (85.68%), number of fruits per plant (76.42%), number of flowers per cluster (69.59%), number of secondary branches per plant (68.36%), fruit yield per plant (68.06%), plant height (65.75%), days to 50% flowering (61.41%), days to first pick (61.25%) and number of primary branches per plant (61.09%). The high value of genetic advance as percent over mean (>20%) were observed for fruit length (60.37%), fruit girth (52.12%), fruit weight (38.27%), number of clusters per plant (34.06%), number of fruits per plant (30.81%), number of flowers per cluster (30.71%), fruit yield per plant (25.79%) and number of secondary branches per plant (24.19%) the results were accordance with Verma *et al.* (2018) [12], Dasmohapatra *et al.* (2019) [5], Balas *et al.* (2019), Jirankali *et al.* (2019) [6] and Bende *et al.* (2019) [3]. This indicates the predominance of additive gene component. Thus, there is scope for improving these characters with direct selection.

Table 1: Analysis of variance (ANOVA) for fruit yield and its components in brinjal

Sl. No	Sources	Replications	Genotypes	Error
	Degree of freedom (df)	1	32	32
01	Plant height (cm)	1.368	55.548*	11.476
02	Primary branches/plant	1.084	0.852*	0.205
03	Secondary branches/plant	8.367	7.430*	1.396
04	Days to 50% flowering	141.885	47.941*	11.458
05	Number of flowers per cluster	1.773	0.654*	0.117
06	Number of clusters per plant	0.903	2.981*	0.224
07	Days to first picking	45.251	89.909*	21.604
08	Number of fruits per plant	0.386	8.614*	1.151
09	Fruit length (cm)	2.463	21.560*	0.731
10	Fruit girth (cm)	1.221	11.245*	0.543
11	Fruit weight (g)	33.605	268.788*	20.716
12	Fruit yield per plant (g)	2531.697	20008.206*	3801.814
13	Fruit yield (t/ha)	1.005	354.875*	5.292

* Significant at 5 % level

Table 3: Genetic parameter of variation for fruit yield and its components in brinjal.

SL. No.	Characters	Mean	Range		PCV (%)	GCV (%)	h^2 (%)	GAM (%)
			Max.	Min.				
01	Plant height (cm)	51.20	61.53	41.42	11.30	9.16	65.75	15.31
02	No. primary branches/plant	4.708	6.10	3.13	15.45	12.08	61.09	19.45
03	No. secondary branches/plant	12.22	15.24	8.10	17.18	14.20	68.36	24.19
04	Days to 50% flowering	58.69	67.50	47.00	9.285	7.27	61.41	11.74
05	Number of flowers per cluster	2.899	4.22	1.71	21.42	17.87	69.59	30.71
06	Number of clusters per plant	6.586	9.51	4.45	19.22	17.82	86.00	34.06
07	Days to first picking	85.64	102.40	73.95	8.719	6.82	61.25	11.00
08	Number of fruits per plant	11.29	14.77	6.17	19.57	17.11	76.42	30.81
09	Fruit length (cm)	10.64	17.59	4.45	31.36	30.31	93.43	60.37
10	Fruit girth (cm)	8.711	13.53	4.76	27.87	26.55	90.77	52.12
11	Fruit weight (g)	55.48	84.67	39.81	21.68	20.07	85.68	38.27
12	Fruit yield per plant (g)	593.18	796.01	454.37	18.39	15.17	68.06	25.79
13	Fruit yield per hectare (t)	21.97	29.48	16.82	18.39	15.17	68.06	25.79

PCV: Phenotypic coefficient of variation
GA: Genetic advance
GCV: Genotypic coefficient of variation
GAM: Genetic advance as percent of mean
h^2: Broad sense heritability

Conclusion

High magnitude of PCV and GCV were recorded for number of flowers per cluster, fruit length, fruit girth and fruit weight and high heritability coupled with high genetic advance as percent over mean was estimated for number of secondary branches per plant followed by number of flowers per cluster, number of clusters per plant, number of fruits per plant, fruit length, fruit girth, fruit weight and fruit yield per plant indicating high variability in the genotypes used for direct selection indicating additive gene action in genetic variance.

References

1. Akpan NM, Ogbonna PE, Onyia VN, Okechukwu EC, Atugwu IA. Variability studies on ten genotypes of eggplant for growth and yield performance in south eastern Nigeria. The J Animal & Pl. Sci. 2016; 26(4):1034-1041.
2. Balas A, Jivani LL, Valu MG, Sakriya SG, Gamit UC, Rathod RK, *et al*. Study of genetic variability and heritability in brinjal (Solanum melongena L.). The Pharma Innovation Journal. 2019; 8(9):44-46.
3. Bende TS, Bagade AB, Deshmukh JD, Shinde AV. Variability studies for yield and yield components in brinjal (Solanum melongena L.). International Journal of Chemical Studies. 2019; 7(2):56-58.
4. Burton GW, Devane EW. Estimating heritability in tall fescue (Festuca arundinaceae) from replicated clonal material. Breed. J. 1953; 45:478481.
5. Dasmohapatra A, Sharma D. Mean performance & variability analysis in long fruited brinjal (Solanum melongena L.) for chattisgarh. Bull. Env. Pharmacol. Life Sci. 2019; 8(2):28-31.

6. Jirankali JP, Reddy N, Gangaprasad S, Manohara SN. Genetic variability for quantitative and qualitative charactersin brinjal (Solanum melongena L.). Int. J Curr. Microbiol. App. Sci. 2019; 8(3):476-484.
7. Johnson HW, Robinson HF, Comstock RE. Estimated of genetic environmental variability in soybean. Agron. J. 1955; 47:314-318.
8. Koudinya AVV, Das A, Layek S, Chowdhury R, Pandit MK. Genetic variability, character association and path analysis for yield and fruit quality componenets in brinjal. Journal of Applied and Natural Science. 2017 9:1343-49.
9. NHB. Indian Horticulture Database-2018, National Horticulture Board, Ministry of Agriculture, Government of India, 2018.
10. Pujer P, Jagadeesha RC, Cholin S. Genetic variability, heritability and genetic advance for yield, yield related components of brinjal (Solanum melongena L.) genotypes. International Journal of Pure and Applied Biosciences. 2015; 5:872-78.
11. Timmapur PH. Heterosis and combining ability studies in brinjal (Solanum melongena L.). M. Sc. Thesis, Department of Horticulture, University of Agricultural Sciences, Dharwad, India, 2007.
12. Verma P, Kushwaha ML, Panchbhaiya A. Studies on variability, heritability and genetic advance for yield attributing traits in brinjal (Solanum melongena L.) for two different seasons. Int. J Curr. Microbiol. App. Sci. 2018; 7(9):1543-1552.