International Journal of Chemical Studies

P-ISSN: 2349–8528 E-ISSN: 2321–4902 www.chemijournal.com IJCS 2020; 8(4): 3286-3289 © 2020 IJCS Received: 10-05-2020 Accepted: 12-06-2020

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Genetic variability, heritability and genetic advance studies for yield and yield attributing traits in brinjal [Solanum melongena (L.)] genotypes

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DOI: https://doi.org/10.22271/chemi.2020.v8.i4ao.10158

Abstract

A field investigation was carried out to assess genetic variability, heritability and genetic advance of 17 brinjal genotypes at Department of Horticulture, College of Agriculture, Vijayapura during *kharif* season of 2018. The Higher GCV and PCV (>20%) were recorded for the traits like plant height, plant spread (at 90 DAT), fruit diameter, fruit length-diameter ratio, average fruit weight, number of fruits per cluster, number of fruits per plant, total yield per plant, yield per hectare and phenol content indicating the existence of broad genetic base, which would be amenable for further selection. High heritability (>60%) coupled with high genetic advance as per cent mean (>20%) which indicated the prevalence of additive gene action in expression of these traits and there by further improvement of these traits could be made by selection.

Keywords: Brinjal, traits, heritability genetic advance and variability

Introduction

Brinjal (*Solanum melongena* L.) belongs to the family Solanaceae, is an important and popular vegetable crop of India and it is native to Indo-Burma region and China (Vavilov, 1926)^[22]. In India it is cultivated in an area of 730 thousand hectare and producing 12801 tonns with the productivity of 17.5 per hectare (Anon., 2018)^[2]. It is considered as brain food and poor man's caviar. It is warm season vegetable grown under wide range of soil and climatic and tolerant to heat and drought conditions. As a self-pollinated crop sometimes certain percentage of cross pollination also noticed, herbaceous plant having erect or semi spreading growth habit. The immature fruit is primarily used for cooking and used in preparation of various dishes in different parts of the world.

It is an important source of carbohydrate (4.0 g), protein (1.40 g), fibre (1.30 g), vitamin A (124 IU), phosphorus (47 mg), potassium (2.0 mg) and iron (0.3 mg) and recommended for diabetes, asthma, cholera, bronchitis and it protects the brain cell membranes from damage. It has more regional preferences for specificity of fruits trait ranging from round to long fruit with green, purple, pink, white and stripped multicolours. Considering the potentiality of this crop, there is a prime need for improvement and to develop varieties suited to specific agro-ecological conditions and also for specific usage. The role of genetic variability in crops is of paramount importance in selecting the best genotypes for making rapid improvement in yield and related characters as well as to select the most potential parents for making the hybridization programme successful. The success of any crop improvement programme largely depends upon the nature and magnitude of the genetic variability existing in breeding material with which plant breeder is working (Prabhu *et al.*, 2009)^[18].

Material and Methods

The present experiment was carried out at Department of Horticulture, College of Agriculture, Vijayapura, University of Agricultural Sciences, Dharwad, Karnataka during 2018-19. The experiment was with laid out in Randomized block design with three replications, consisted seventeen genotypes of brinjal. Ridges and furrows prepared at a spacing of 75cm and then a five week old 15 seedlings of each genotype is transplanted in separate row by maintaining 60

cm plant to plant spacing (Anon., 2012)^[1]. Five randomly chosen plants in each replication of each genotype were labeled and used for recording the observations for the growth parameters viz., plant height (cm), plant spread (cm), number of primary branches per plant and stem girth (cm) at 90 days after transplanting. Earliness parameters viz., days to first flowering, days to 50 per cent flowering and days to first fruit maturity and yield parameters viz., fruit length (cm), fruit diameter (cm), fruit length-diameter ratio, average fruit weight (g), number of fruits per cluster, number of fruits per plant, total yield per plant (kg), yield per hectare (tonns) and also quality parameters recorded. Total phenol content of brinjal fruits were estimated by Folin Ciocalteu Reagent (FCR) method (Sadasivam and Manickam, 2005) [19]. Analysis of variance was carried out as per the procedure given by Panse and Sukhatme (1967)^[17]. The variability for different characters was estimated. Genotypic and phenotypic coefficients of variance (Burton and Devane, 1953)^[4], broad sense heritability (Falconer, 1981)^[5] and genetic advance as per cent over mean (Johnson et al., 1955) [6] worked out. Statistical analysis was carried out using WINDOSTAT 9.3 vr. software.

Results and Discussion

Significant variance was observed for all the characters studied among all the genotypes are presented in Table 1. The estimates of genotypic and phenotypic coefficients of variation, heritability and genetic advance as per cent of mean are presented in Table 2. The phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the traits studied. High GCV and PCV (>20%) were observed for plant height and plant spread (at 90 DAT). The results were similar to the findings of Kumar et al. (2012)^[8], Shekar et al. (2012) ^[20] and Nayak and Nagre (2013) ^[15], presence of high variability in the germplasm for selection and even the differences between PCV and GCV values were minimum, indicating that traits under study were less influenced by environment. Hence, these characters can be relied upon and simple selection can be practiced for further improvement. For all the traits were PCV values found higher than the values of GCV indicating that apparent of variation is not only due to genotypes and also highly influenced by environmental effects and selection would be ineffective, which can be exploited through hybridization or heterosis.

Moderate estimates of GCV and PCV (11-20%) were observed for number of primary branches and stem girth (at 90 DAT). Several workers *viz.*, Das *et al.* (2010), Muniappan *et al.* (2010) ^[14], Kumar *et al.* (2011) ^[7], Arunkumar *et al.* (2013) ^[3], Kumar *et al.* (2013b) ^[9], Lokesh *et al.* (2013) ^[11] and Nayak and Nagre (2013) ^[15] reported similar findings. These results noticed. Lesser influence of environment in expression of these characters. Therefore, phenotypic variability may be a good measure of genotypic variability. High heritability (>60%) coupled with high genetic advance as per cent over mean (>20%) was recorded for the growth parameters *viz.*,

plant height, plant spread, number of primary branches and stem girth (at 90 DAT). These results suggested that the inheritance of such characters is governed mainly by additive gene effects and therefore, selection based on phenotypic performance may prove useful. Similar results were also reported by Sherly and Shanthi (2008)^[21], Muniappan *et al.* (2010)^[14], Kumar *et al.* (2012)^[8], Arunkumar *et al.* (2013)^[3] and Lokesh *et al.* (2013)^[11].

Low GCV and PCV were recorded for days to first flowering, days to 50 per cent flowering and days to first fruit maturity. These findings are in close agreement with the results obtained by Muniappan et al. (2010)^[14], Kumar et al. (2011) ^[7], Arunkumar et al. (2013) ^[3], Sao and Mehta (2009) and Shekar et al. (2012) [20]. Low GCV and PCV for both characters indicated the narrow genetic base. High heritability with moderate GAM observed for the traits like days to first flowering, days to 50 per cent flowering and days to first fruit maturity indicated that expression of this character as governed by non-additive gene action and could be exploited through heterosis breeding. These findings are similar to the reports of Muniappan et al. (2010)^[14] and Arunkumar et al. (2013)^[3] and days to first fruit maturity (Pramanick et al., 1994), Kushwah and Bandhyopadhya (2005) ^[10], Sao and Mehta (2009) and Shekar et al. (2012)^[20].

High (>20%) GCV and PCV were observed for most of yield and quality traits *viz.*, fruit diameter, fruit length-diameter ratio, average fruit weight, number of fruits per cluster, number of fruits per plant, total yield per plant, yield per hectare and phenol content. These results indicated the existence of sufficient variability in genetic stock studied and the environmental role is negligible. Hence, there is ample scope for improving these characters with direct selection. Several workers like Sherly and Shanthi (2008) ^[21], Sao and Mehta (2009), Das *et al.* (2010), Muniappan *et al.* (2010) ^[14], Kumar *et al.* (2012) ^[8], Arunkumar *et al.* (2013) ^[3], Lokesh *et al.* (2013) ^[11] and Nayak and Nagre (2013) ^[15] reported similar findings.

Moderate (11-20%) GCV and PCV were observed for fruit length indicating presence of moderate amount of variability for this trait. Moderate GCV and high PCV were observed for fruit length indicates that the apparent variation is not only due to genotypes but also due to the influence of environment on the expression of character. Selection for such traits may not give desired results. High heritability (>60%) estimates along with high GAM (>20%) was recorded for fruit length, fruit diameter, fruit length-diameter ratio, average fruit weight, number of fruits per cluster, number of fruits per plant, total yield per plant, yield per hectare and phenol content indicating predominance of additive gene component. Thus, there is ample scope for improving these characters with direct selection. Similar findings were also reported by several investigators like Sherly and Shanthi (2008)^[21], Sao and Mehta (2009), Das et al. (2010), Muniappan et al. (2010) ^[14], Kumar et al. (2012) ^[8], Arunkumar et al. (2013) ^[3], Lokesh et al. (2013)^[11] and Nayak and Nagre (2013)^[15].

Table 1: Analysis of variance (mean sum of squares) for growth, earliness, yield and quality parameters in brinjal genotypes

S. No.	Source of variation/character	Replication	Genotypes (Treatment)	Error	CD (1%)	CD (5%)							
	Degrees of freedom	2	16	32									
	Parameters												
1.	Plant height at 90 DAT (cm)	102.29	469.43**	1.97	3.13	2.13							
2.	Plant spread at 90 DAT (cm)	24.71	331.77**	0.17	0.94	0.70							
3.	Number of primary branches at 90 DAT	0.85	0.70**	0.0078	0.06	0.04							
4.	Stem girth at 90 DAT (cm)	0.07	0.09**	0.01	0.27	0.20							
5.	Days to first flowering	13.31	45.71**	0.52	1.61	1.20							
6.	Days to 50 per cent flowering	7.84	52.70**	0.09	0.68	0.50							
7.	Days to first fruit maturity	7.84	42.02**	0.05	0.50	0.37							
8.	Fruit length (cm)	0.06	3.36**	0.06	0.55	0.41							
9.	Fruit diameter (cm)	0.04	4.20**	0.06	0.55	0.41							
10.	Fruit length-diameter ratio	2.50	0.30**	0.07	0.62	0.46							
11.	Average fruit weight (g)	172.13	2550.31**	7.70	6.20	4.61							
12.	Number of fruits per cluster	0.01	1.66**	0.08	0.64	0.47							
13.	Number of fruits per plant	46.46	68.98**	0.07	0.62	0.46							
14.	Phenol content (mg/100 g)	5.66	6526.70**	184.45	30.36	22.58							
15.	Total yield per plant (kg)	0.0015	0.60**	0.0003	0.04	0.03							
16.	Total yield per hectare (t)	26.07	232.97**	17.67	9.39	6.99							

**Significant at p=0.01 NS - Non- significant DAT- Days after transplanting

 Table 2: Estimates of range, mean, components of variance, heritability and genetic advance for growth, earliness, yield and quality parameters in brinjal genotypes

Sl. No.	Character	Range	Mean ±S.Em	GV	PV	GCV (%)	PCV (%)	h ² (%)	GA	GAM (%)		
	Parameters											
1.	Plant height at 90 DAT (cm)	41.63-79.36	59.89±0.786	155.82	157.79	20.84	20.97	98.80	25.55	42.66		
2.	Plant spread at 90 DAT (cm)	21.80-64.13	50.78±0.237	110.53	110.71	20.70	20.71	99.80	21.64	42.61		
3.	Number of primary branches at 90 DAT	1.73-3.53	2.49 ± 0.015	0.23	0.23	19.47	19.50	99.70	0.99	40.04		
4.	Stem girth at 90 DAT (cm)	0.87-1.54	1.16 ± 0.067	0.02	0.02	14.14	17.57	64.80	0.27	23.45		
5.	Days to first flowering	35.66-50.00	41.49±0.404	15.06	15.58	9.35	9.51	96.70	7.86	18.94		
6.	Days to 50 per cent flowering	38.33-57.00	47.09±0.170	17.54	17.64	8.89	8.91	99.50	8.60	18.27		
7.	Days to first fruit maturity	58.66-73.33	67.25±0.127	13.99	14.04	5.56	5.57	99.60	7.69	14.43		
8.	Fruit length (cm)	3.75-9.17	6.04 ± 0.061	1.10	1.16	17.37	17.84	94.70	2.10	34.82		
9.	Fruit diameter (cm)	2.27-7.20	4.58±0.138	1.04	1.46	25.84	26.39	95.80	2.39	52.10		
10.	Fruit length-diameter ratio	1.23-2.35	1.62 ± 0.157	0.07	0.15	16.80	24.14	48.80	0.39	24.12		
11.	Average fruit weight (g)	24.63-128.04	75.39±1.555	847.53	855.24	38.61	38.78	99.10	59.70	79.18		
12.	Number of fruits per cluster	1.00-3.00	1.33 ± 0.160	0.52	0.61	54.50	58.59	86.50	1.39	104.45		
13.	Number of fruits per plant	13.00-31.00	18.43±0.157	22.96	23.04	25.99	26.04	99.70	9.85	53.46		
14.	Phenol content (mg/100 g)	86.66-246.66	145.66 ± 7.607	2114.08	2298.54	31.56	32.19	92.00	90.83	62.39		
15	Total yield per plant (kg)	0.75-2.40	1.30 ± 0.012	0.20	0.20	34.34	34.37	99.80	0.92	70.69		
16	Total yield per hectare (t)	17.55-48.21	29.29±2.354	71.76	89.49	28.92	32.28	80.02	15.63	53.36		

GV = Genotypic variance PV =Phenotypic variance GCV =Genotypic coefficient of variance GA=Genetic advance h² =Heritability (broad sense) PCV =Phenotypic coefficient of variance GAM = Genetic advance (per cent mean) DAT= Days after transplanting

Conclusion

The results of genetic variability, heritability and genetic advance revealed that number of fruits per cluster, fruit length-diameter ratio, number of fruits per plant, average fruit weight and total yield per plant can be improved through direct selection from the existing germplasm stock, as the GCV and PCV were high for these traits indicated by the predominance of additive gene action in genetic variance.

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