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Genetic variability, heritability and genetic advance studies in brinjal (*Solanum melongena* L.)

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Abstract

Thirteen parents along with thirty hybrids were evaluated during two successive years 2013-14 and 2014-2015 and pooled analysis was also carried out at VRC, GBPUAT Pantnagar, for twelve yield attributing characters. High phenotypic coefficient of variation (PCV) was recorded than their correspondent genotypic coefficient of variation (GCV). This was because of the reason that variability at phenotypic level includes both genotypic and environment variability. In pooled data high PCV was observed for the character number of unmarketable fruits per plant (44.07%), whereas high GCV was recorded for number of marketable fruits per plant (40.37%). High heritability coupled with high genetic advance as percent of mean was recorded for total number of fruits per plant (67.99%) indicating importance of additive gene action controlling this character.

Keywords: brinjal, variability, GCV, PCV, heritability, genetic advance

Introduction

Brinjal (*Solanum melongena* L.), is one of the most important vegetable crop. It is popular among people of all social strata and hence, it is rightly called as vegetable of masses (Patel and Sarnaik, 2003) [3]. The fruits of eggplant are widely consumed in various culinary preparations and are rich source of protective nutrients (Hedges and Lister, 2007) [7]. Eggplant is well known for its medicinal properties and has also been recommended as an excellent remedy for liver complaints and diabetic patients (Tiwari *et al.*, 2009) [25]. The eggplant phytochemical that have received most research attention is the phenolics, a powerful antioxidants (Vinson *et al.*, 1998) [26]. Polyphenols have shown to be beneficial for human health due to its many biological activities like free-radical scavenging, regulation of enzymatic activity and anti-cancer activities and regulator of cell signalling pathways (Sato *et al.*, 2011) [21]. Consequently, due to the multiple health benefits of eggplant, which include anti-oxidant, anti-diabetic, hypotensive, cardio protective and hepatoprotective effects, the demand for eggplant has been on a rapid and steady rise in the recent years (Ojiewo *et al.*, 2007) [17]. Brinjal is a self-pollinated crop but cross pollination also occurs to a considerable extent. This is because, it has pronounced heterostyly which favours cross pollination. Sixty to seventy percent fruit setting happens through pollination by insect, while 30-40% by selfing. Bumble bees (*Bombus* sp.) and honey bees (*Apis* sp.) are the vector which do most of the pollination. Brinjal is a day- neutral plant. Fruit setting is affected neither by natural light nor by relative humidity but mainly by the average maximum temperature (21-27 °C) and precipitation during first five days after flower opening. The selection of potential parents should be based on genetic distance which needs estimation of the magnitude of variability. Selection based on phenotypic performance is not single and only method for assessing genetic

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variability. Heritability is also an index for assessing the influence of environment on the expression of genotype. Effectiveness of selection directly depends on the amount of heritability and genetic advance as percent of mean for that character (Prabakaran, 2010) [19]. Hence, an insight into the magnitude of variability present in available accessions and hybrids of brinjal is of utmost importance to a plant breeder for starting a judicious breeding programme.

Materials and methods

Present investigation was conducted during autumn-winter season, 2013-14 and 2014-15 at the Vegetable Research Centre of Govind Ballabh Pant University of Agriculture and Technology, Pantnagar, Udham Singh Nagar (Uttarakhand), India. Thirteen genotypes of Brinjal including ten lines and three testers from germplasm maintained at Vegetable Research Centre of this University. The selected parental lines were agronomic ally and morphologically diverse for different traits. The genotypes were Swarn Syamli, PB71, BARI, SMB115, BB85, BRLVAR6, IBWL2001-1, PB66, LC7, PB70, Pant Samrat, Pant Rituraj and DBL02. Out of thirteen genotypes, ten were used as female (lines), viz. Swarn Syamli, PB71, BARI, SMB115, BB85, BRLVAR6, IBWL2001-1, PB66, LC7, PB70 and three as male (testers), viz. Pant Samrat, Pant Rituraj, DBL02. The seed of thirteen parents and thirty hybrids were sown in nursery on 14.6.2013 and transplanted on 20.7.2013 for 1st year evaluation and 2nd year in 2014-2015, nursery was sown on 16.6.2014 and transplanted on 16.7. 2014. Pooled analysis was also done. Experiment was laid out in Randomized Block Design (RBD) with three replications, each replication consists of forty three entries. Each row consists of ten plants, planted at a distance of 75 × 60 cm. All recommended cultural and agronomic practices and plant protection measures were followed as per recommendation to raise the normal crop. The observations were recorded for 12 characters viz. days to 50 % flowering, number of primary branches plant⁻¹, plant height (cm), fruit length (cm), fruit diameter (mm), number of marketable fruit plant⁻¹, weight of marketable fruits plant⁻¹ (Kg), number of unmarketable fruits plant⁻¹, weight of unmarketable fruits plant⁻¹ (Kg), total number of fruits plant⁻¹, total yield plant⁻¹ (Kg) and total yield hectare⁻¹ (q). The data were subjected to appropriate statistical analysis.

Genotypic and phenotypic coefficients of variation (GCV and PCV) were obtained by the method suggested by Burton and De Vane (1952) [3]. Heritability in "Broad sense" was calculated as the ratio between genotypic variance and expressed as percentage Burton and De Vane (1952) [3] and Allard (1960) [1]. The expected genetic advance (GA.) was estimated as per Lush (1940) [11] and further used by Burton and De Vane (1952) [3] and Johnson *et al.* (1955) [8].

Results and Discussion

Analysis of variance for above mentioned twelve characters of pooled analysis is depicted in table 1. The mean square due to genotypes for all the characters was highly significant. These results clearly indicate that there was substantial genotypic variation between the genotypes for the character studied. Estimation of range, general mean, PCV, GCV, ECV, heritability, genetic advance, genetic advance as percent of mean for twelve characters are presented in Table 2. The present findings revealed that the estimates of PCV were generally higher than their corresponding GCV for all the characters studied. This was because of the reason that variability at phenotypic level includes both genotypic and

environment variability. Pooled over the years data indicated that high PCV value was recorded in number of unmarketable fruits plant⁻¹ (44.07%) followed by weight of unmarketable fruits plant⁻¹ (42.27%), number of marketable fruits plant⁻¹ (40.37%), total number of fruits plant⁻¹ (37.70%) and fruit diameter (30.97%), while high GCV value was recorded in number of marketable fruit plant⁻¹ (36.82%) followed by number of unmarketable fruits plant⁻¹ (36.62%), total number of fruits plant⁻¹ (35.27%) and weight of unmarketable fruits plant⁻¹ (35.23%). For most of characters, the differences in estimates of PCV and GCV were less, indicating that these characters were less affected by environment and therefore more stable. Similar results were reported by Mohanty (1999) [13], Kumar *et al.* (2000) [9], Naliyadhara *et al.* (2007) [16] and Singh *et al.* (2013) [23]. The concept of heritability is important to determine whether the phenotypic differences observed among various individuals, are due to differences in their genetic makeup or simply as a result of environmental factors. The knowledge of heritability of a character is also important to breeder as it indicates the possibility and extent to which genetic gain is possible through selection Robinson *et al.* (1949) [20]. The knowledge of the heritability along with genetic advance drawing valuable conclusion for effective selection based on phenotypic performances Johnson *et al.* (1955) [8]. Pooled data over the years indicated that the high value of genetic advance as percent of mean for number of marketable fruits plant⁻¹ (69.19%), total number of fruits plant⁻¹ (67.99%), number of unmarketable fruits plant⁻¹ (62.68%) and weight of unmarketable fruits plant⁻¹ (60.50%). The character showing lowest value for genetic advance as percent of mean were number of primary branches plant⁻¹ (35.49%), days to 50% flowering (14.05) and plant height (10.17%). High heritability coupled with high genetic advance was observed for number of marketable fruits plant⁻¹ and total number of fruits plant⁻¹ indicating the importance of additive gene action controlling these characters. Simple selection therefore, could be effective for improvement of number of marketable fruits plant⁻¹ and total number of fruits plant⁻¹. In brinjal, high heritability coupled with high genetic advance for number of fruits plant⁻¹ was reported by Singh and Gopala Krishnan (1999) [24], Mohanty (2001) [14], Baswana *et al.* (2002) [2], Singh and Kumar (2005) [22], Naik *et al.* (2010) [15], Daka and Soni (2012), Kumar *et al.* (2012) [10], Singh *et al.* (2013) [23] and Mili *et al.* (2015) [12]. High to moderate heritability for characters number of primary branches plant⁻¹ and days to 50% flowering coupled with low genetic advance as per cent was observed indicating that these traits improved by development of hybrid varieties or utilization of transgressive segregants in heterosis breeding programme was reported by Chaudhary and Pathania (1998) [5], Chaudhary (1999) [6], Singh and Gopala Krishnan (1999) [22, 23], Mohanty (2001) [14] and Singh *et al.* (2013) [22, 23].

Table 1: Analysis of variance pooled

Source of Variation	df	Cropping Season	MS											
			Days to 50% flowering	Number of primary branches plant ⁻¹	Plant height (cm)	Fruit length (cm)	Fruit diameter (mm)	No. of marketable fruits plant ⁻¹	Wt. of marketable fruits plant ⁻¹ (Kg)	No. of unmarketable fruits plant ⁻¹	Wt. of unmarketable fruits plant ⁻¹ (Kg)	Total number of fruits plant ⁻¹	Total yield plant ⁻¹ (Kg)	Total yield hectare ⁻¹ (q)
Replication	2	pooled	14.248060	0.008837	85.373120	2.028377	22.935390	7.617148	0.034657	0.061171	0.000167	6.407955	0.030096	912.980900
Treatment	42	pooled	210.901071**	2.842001**	295.576760**	88.555817**	1362.332103**	248.616387**	0.910520**	19.519516**	0.181158**	368.072051**	1.746183**	86255.165979**
Error	210	pooled	3051.08527	0.108933	59.868680	2.100850	18.044435	8.262501	0.048660	1.364182	0.012353	8.525857	0.048872	2568.065303

* indicates level of significance at 5%, ** indicates level of significance at 1%

Table 2: Estimation of different genetic parameters of various characters

Characters	Cropping Season 2013-1 and 2014-15	Range	General mean \pm SE (m)	Coefficient of variation (%)			Heritability (%)	Genetic advance (GA)	Genetic advance As per cent of mean
				PCV	GCV	ECV			
Days to 50% flowering	pooled	60.66-84.00	69.94 \pm 1.52	9.81	8.18	5.41	69	9.83	14.05
No. of primary branches /plant	pooled	2.2-5.3	3.51 \pm 0.13	21.35	19.18	9.38	80	1.24	35.49
Plant height (cm)	pooled	61.43-92.54	80.99 \pm 3.07	12.20	7.76	9.41	40	8.24	10.17
Fruit length (cm)	pooled	7.00-24.49	15.73 \pm 0.58	25.82	24.12	9.21	87	7.30	46.42
Fruit diameter(mm)	pooled	29.83-83.81	50.23 \pm 1.71	30.97	29.79	8.45	92	29.66	59.04
No. of marketable fruits plant ⁻¹	pooled	8.03-37.40	17.19 \pm 1.14	40.37	36.82	16.55	83	11.89	69.19
Wt. of marketable fruits plant ⁻¹ (Kg)	pooled	0.79-2.48	1.45 \pm 0.08	29.96	25.97	14.94	75	0.67	46.39
No. of unmarketable fruits plant ⁻¹	pooled	2.32-11.08	4.75 \pm 0.47	44.07	36.62	24.52	69	2.97	62.68
Wt. of unmarketable fruits plant ⁻¹ (Kg)	pooled	0.12-0.87	0.47 \pm 0.04	42.27	35.23	23.34	69	0.28	60.50
Total number of fruits plant ⁻¹	pooled	10.68-48.49	21.29 \pm 1.17	37.70	35.27	13.30	87	14.92	67.99
Total yield ⁻¹ plant (Kg)	pooled	0.97-3.15	1.93 \pm 0.089	29.75	27.45	11.42	85	1.10	52.26
Total yield hectare ⁻¹ (q)	pooled	216.99-700.90	430.17 \pm 20.23	29.83	27.46	11.65	84	224.01	52.07

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