Short Communication

Morphological characterization and components of genetic variation in brinjal (*Solanum melongena* L.)

Sukhninder Kaur*, Mohinder Kaur Sidhu and Ajmer Singh Dhatt

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Solanum melongena L. (2n = 2x = 24) belongs to family Solanaceae (Nightshades), comprises around 98 genera and 2,700 species with huge diversity in terms of habitats, morphology and ecology. It is extensively cultivated vegetable crop in various countries parts of the world (Singh and Kalda 2001). However, India is the centre of diversity for this crop. Its primitive types are tall plants with broad and thorny leaves, clustered and andromonoecies flowers, small green fruits having bitter taste, hard pulp and thick peel. The domestication of primitive types, natural-outcrossing, mutation, hybridization and selection from different backgrounds created broad genetic diversity in cultivated brinjal throughout the world. Now a day, cultivars are diverse in shape, size and colour of fruits, earliness, yield and quality of the fruits. These morphological differences for plant growth pattern, leaf, flower, fruit and seed characteristics can be easily noticed among the genotypes. Therefore, wide range of diversity for various morphological, physiological and biochemical properties have been studied. The genetic divergence within crop species is pre-requisite for planning an efficacious breeding programme. Assessment of genetic diversity assists in selecting the suitable parents for hybridization programme and getting the desirable recombinants. The possibilities of acquiring the greater heterotic F₁s and wide spectrum variability in segregating generations are greater, when the selected parents are more diverse. To assess the genetic variation through morphological measures, ICAR-NBPGR has provided the standard

*Corresponding author, E-mail: sukhninderdhaliwal99@gmail.com

descriptors on the basis of highly heritable traits for the characterization of brinjal that can easily and rapidly discriminate various germplasm entries.

The present investigation was conducted with 110 brinjal germplasm lines developed and maintained at Punjab Agricultural University, Ludhiana during 2016-2017. The experiment was carried out in randomized block design with three replications on rainy season crop (June to December). Five healthy plants were selected for taking observations on various vegetative, flowering, fruiting and yield related traits. Observations for each trait in brinjal were taken as per standard descriptors of ICAR-NBPGR, New Delhi. The replicated data of each quantitative trait was statistically analyzed using CPCS1 software and the germplasm lines were compared with critical differences. However, the qualitative traits were examined as percent of total genotypes. Phenotypic and genotypic coefficients of variation were calculated as suggested by Burton and Devane (1953). Heritability in broad sense was calculated as suggested by Allard (1960) and the expected genetic advance was determined according to Al-Jibouri et al. (1958).

The characterization of brinjal with qualitative descriptors represented high morphological divergence among eggplant genotypes. Phenotypic observations related to leaf blade length and width, corolla colour, calyx spininess, fruit pedicel prickles, fruit shape, fruit bearing, fruit colour, seediness, seed colour and size are presented in Table 1. In general, intermediate growth habit occurred frequently among the genotypes belonging to different groups (big round, long and oblong) except for small round group, where the prostrate growth habit was dominating. The petiole colour was observed to be green in all the genotypes except for big round group, in which 45.45% genotypes had violet petiole colour. The dominating leaf blade colour was noted as green, but

Department of Vegetable Science, Punjab Agricultural University, Ludhiana

Table 1: Morphological variation in qualitative traits in brinjal

Characters	Categories	Big-	Small-	Long	Oblong	
		round	round	(%)	(%)	
		(%)	(%)			
Plant	Upright	45.50	38.50	50.00	64.70	
growth	Intermediate	36.66	23.10	41.40	35.30	
habit	Prostrate	41.66	8.33	-		
Plant spread	Narrow	-	-	- 6.90		
1	Broad	45.45	61.54	48.28	47.06	
	Very broad	54.55	30.77	44.83	52.94	
Petiole	Green	31.82	61 54	70 69	6471	
colour	Greenish violet	9.09	-	517	-	
corour	Violet	45.45	38 46	22 41	35 29	
	Dark violet	13.45	-	1 72	-	
Loofblada	Voruwook	15.04		1.72	5 99	
Leaf Diade	Wash	4.55	-	1.72	22.00	
loong	Weak	4.55	20 10	24.14	25.55	
	Intermediate	50.00	38.46	55.45	41.18	
	Strong	36.36	46.15	18.97	29.41	
	Very strong	4.55	15.38	1.72	-	
Leaf blade	Very acute	-	-	3.45	-	
tip angle	Acute	59.09	53.85	58.62	88.24	
	Intermediate	9.09	46.15	-	-	
	Obtuse	31.82	-	37.93	11.76	
Leaf blade	Green	63.64	53.85	82.76	82.35	
colour	Dark green	27.73	23.08	6.90	11.76	
	Green violet	13.64	7.69	10.34	5.88	
	Violet	-	15 38	_	-	
Leaf	None	95.45	100	100	100	
prickles	For	1 55	100	100	100	
Corolla	White	9.00	-	20.60	5 88	
corona	Dele vielet	9.09	15 20	12.07	J.00	
coloui		9.09	13.30	12.07	20.41	
	Light violet	13.04	38.40	29.31	29.41	
	Violet	59.09	46.15	37.93	52.94	
~ .	Dark violet	9.09	-	-	-	
Calyx	Green	50.00	61.54	72.41	70.59	
colour	Light purple	4.55	7.69	8.62	11.76	
	Dark	45.45	30.77	18.97	17.65	
Calyx	Smooth	77.27	69.23	91.38	82.35	
spininess	Medium thorny	22.73	30.77	8.62	17.65	
Fruit	None	90.90	66.66	96.66	100	
pedicel	Few	9.09	33.33	3.33	-	
prickles						
Fruit	None	100	100	36.21	100	
curvature	Slightly curved	-	-	37.93	-	
	Curved	-	-	24.14	-	
	Sickle shaped	-	-	1.72	-	
Fruit	Solitary	68 18	15 38	34 48	47.06	
hearing	Cluster	31.82	84 62	65 52	52.94	
Eruit colour	Milky white	13.6	7 70	8.60	5 90	
i fuit coloui	Green	22 70	7.70	15 50	5.70	
	Dumla	21.00	22 10	12.00	5 00	
	Purple block	12.60	23.10 46.70	21.0	5000	
		13.00	40.70	10.20	17.00	
	Black	10.00	15.40	10.30	17.00	
	Light purple	18.20	-	12.10	5.90	
	Purple pink	-	-	3.40	-	
	Red	-	-	5.20	5.90	
Fruit colour	Uniform	86.36	100	81.03	76.47	
distribution	Mottled	4.55	-	3.45	5.88	
	Irregular stripped	9.09	-	15.52	17.65	
Fruit flesh	Very loose	-	-	1.72	-	
density	Loose	22.73	15.38	46.55	17.65	
	Compact	63.64	69.23	48.28	82.35	
	Very compact	13.64	15.38	3.45	-	
Seediness	Low	9.09	23.08	34.48	11.76	
	Medium	31.82	23.08	29.31	23.53	
	High	59.09	53.85	36.21	64.71	
Seed colour	Pale brown	72 72	25	73 33	25	
2000 001000	Brown	27.27	75	26.66	75	
Seed size	Small	9.00	23 08	13 70	,5	
Secu SIZE	Medium	7.09 77 77	61 54	75.96	88.24	
	Large	13.64	15 38	10 34	1176	
	Lu150	10.04	10.00	10.54	11./0	

pigmented leaves were also noticed in some genotypes of all the groups. The leaf prickles were observed only in big round group (4.55%). The corolla colour was generally violet and calvx colour green in all the groups except few genotypes. The calyx spininess was observed in some genotypes of all the groups. Fruit pedicel prickles were observed in some genotypes of round and long group. The maximum fruit length breadth ratio was observed in long group genotypes. The cluster bearing habit was mostly observed in small round and long genotypes. Fruit colour varied from white to almost black in different groups, however, dominating colour was purple and with uniform distribution in most of the genotypes. The degree of fruit curvature was observed only in long group as slightly, curved and sickle shaped. The pale brown, medium sized seed was observed in most of the genotypes. These results are in agreement with the findings of Hassan et al. (2015).

Analysis of variance showed that mean squares for all the traits were significant indicating the availability of sufficient variability in the experimental material. The morphological variation exhibited by germplasm lines of brinjal due to quantitative traits is shown in Table 2. The big round group exhibited maximum plant height, fruit breadth and average fruit weight. The genotypes of small round group appeared to be early in flowering. However, number of primary branches, petiole length, fruit pedicel length, fruit length, number of fruits per plant and fruit yield per plant was experienced on higher edge in long fruit group. Oblong fruited genotypes showed maximum vegetative growth and were entered late into flowering phase. Among all, the maximum fruit yield per plant was obtained in PBGL-401 (3.47 kg), followed by PMR-322 (3.06 kg), PBOB-508 (2.78 kg), PBGL-405 (2.83 kg) and PSL-423 (2.80). The highest number of fruits per plant were set on PBL-232 (48.87) followed by PSR-308 (43.17). However, the highest fruit weight was displayed in PMR-322 (358.02 g), followed by PBR-140 (316.67 g), PBRG-123 (312.50 g), PMRG-322 (300.00 g) and PBR-141 (300.00 g). These results are in agreement with the findings of Yadav et al. (2016)

In present investigation involving 110 genotypes, the genotypic coefficient of variance (GCV) remained lower than phenotypic coefficient of variance (PCV) for all the traits under observation (Table 2) The GCV ranged from 5.65% (Days to 50% flowering) to 50.68% (number of fruits per plant), while PCV from 7.40 (Days to 50% flowering) to 51.66 (number of fruits per plant). The maximum genotypic coefficient of variation was observed for the number of fruits per plant (50.68%) followed by average fruit weight (48.89%) and fruit

Character	Mean	Range			GCV	PCV	Heritability	Genetic	
		Big round	Small round	Long	Oblong	(%)	(%)	% (bs)	advance (%)
Plant height (cm)	99.58	74.67-145.67	82.67-119.33	56.67-142.33	65.67-132.00	18.08	20.76	64.72	33.25
No. of Primary Branches	4.13	2.33-6.33	2.33-5.00	2-6.67	1.67-5.67	22.95	26.86	29.90	28.83
Petiole length (cm)	4.17	2.83-5.73	2.83-4.83	2.67-7.50	3.10-6.00	19.45	22.43	28.77	23.74
Leaf blade length (cm)	15.01	9.67-19.73	9.17-16.33	10.33-20.73	12.50-21.33	16.69	20.49	51.61	28.53
Leaf blade width (cm)	9.26	6.83-11.67	6.17-10.33	6.17-15.50	5.26-15.50	19.37	24.71	46.65	32.07
Days to 50% flowering	66.39	57-73.33	56.57-72.33	57.33-74	64.67-74	5.65	7.40	43.53	9.05
Fruit pedicel length (cm)	4.60	3.00-5.83	3.17-4.67	2.83-7.60	2.83-7.17	18.05	23.95	39.65	28.01
Fruit length (cm)	12.52	6.83-13.70	4.93-10.93	7.97-23.83	7.00-13.67	36.57	39.47	75.18	69.78
Fruit breadth (cm)	5.09	4.83-9.97	4.03-6.80	2.73-6.27	3.77-8.33	29.11	32.14	69.53	54.31
Average fruit weight (g)	127.40	50.00-358.62	27.78-110	35-233.33	55.56-225	48.89	49.00	99.98	85.06
Number of fruits per	19.79	3.5-23.67	9.72-43.17	8.92-48.87	1.42-29.97	50.68	51.66	67.76	95.40
plant									
Fruit yield (kg/plant)	1.63	0.43-3.06	0.75-1.89	0.87-3.47	0.47-2.78	39.70	40.92	75.42	32.79

Table 2: Morphological variability and heritability for quantitative traits in brinjal

yield per plant (39.70%). The highest phenotypic coefficient of variation was observed in number of fruits per plant (51.66%) followed by average fruit weight (49.00%) and fruit yield per plant (40.92%). A close correspondence between genotypic and phenotypic coefficient of variation for most the traits highlighted the negligible influence of the environment in the expression of these traits. The highest genotypic and phenotypic coefficient of variation was observed for the traits viz., number of fruits per plant, average fruit weight, fruit yield per plant, fruit length, fruit breadth, and number of primary branches. High value of GCV and PCV for the above mentioned traits indicated that these were responsible for considerable amount of genetic variability in 110 genotypes. It further suggested the potential use of these traits for selection of parents in hybridization programmes. These results for high GCV in average fruit weight, fruit yield per plant, fruit breadth and number of fruits per plant were substantiated with the reports of Ravali et al. (2017) and Yadav et al. (2016). Moderate PCV and GCV were observed for the leaf blade width, fruit pedicel length, plant height, petiole length and leaf blade length were corroborated with the findings of Yadav et al. (2016). All the characters can be improved by the vigorous selection. However, lower PCV (7.40%) and GCV (5.65%) was exhibited for the days to 50% flowering, which suggests the adoption of source having high variability for the further improvement of this trait. The results for days to 50% flowering were in line with the findings of Ansari et al. (2011).

The heritability of different quantitative traits and their expected genetic advance in further generations is presented in (Table 2). The highest level of heritability was experienced in average fruit weight (99.98%) followed by fruit yield per plant (75.42%), fruit length (75.18%), and fruit breadth (69.53%) that specified the least influence of the environment in their expression.

The highest genetic advance was acknowledged in number of fruits per plant (95.40%) followed by average fruit weight (85.06%), fruit length (69.78%), and fruit breadth (54.31%). High heritability and high genetic advance in average fruit weight, fruit yield per plant, number of fruits per plant, plant height, fruit length and fruit breadth revealed preponderance of additive gene action. These results were in agreement with the findings of Prasad et al. (2010) and Ravali et al. (2017). Moderate heritability and high genetic advance in leaf blade length, leaf blade width and fruit pedicel length unveiled the occurrence of additive gene action, where moderate heritability was due to environment effects. Yadav et al. (2016) also reported moderate heritability and high genetic advance for leaf blade length and width. High genetic advance in number of primary branches and petiole length revealed the preponderance of additive gene action and low heritability was as a result of significant influence of the environment and these results were supported with the findings of Ansari et al. (2011). High heritability in comparison to the GA for some traits indicated the negligible effect of environmental changes on their expression that made the phenotypes true representative of their genotypes. The selection based on phenotypic performance would be highly helpful in such traits. Moderate heritability and low genetic advance in days to 50% flowering, disclosed nonadditive gene action, where the selection may not be rewarding. The similar results were reported by Ansari et al. (2011) and Yadav et al. (2016) for days to 50% flowering. It was concluded that there was huge variability in the different vegetative, flower, fruit and seed traits of the genotypes under investigation. This variability along with heritability and genetic advance may provide an effective foundation for the selection of diverse parents in hybridization programme on the basis of most favourable traits and may help in the achievement of better transgressive segregants in future.

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