Study of genetic diversity and Genetic Advance in Brinjal for Morpho-Economic traits (*Solanum melongena* L.)

Abstract

In two distinct environments (E1 and E2), the current experiment was set up using a randomized block design with the goal of determining the extent of genetic diversity, heritability, and genetic advancement among 15 yield-related variables in brinjal. The analysis of variance results revealed that there were significant genetic variances across brinjal genotypes, indicating a significant degree of variability and boosting the opportunity for selection to improve the essential traits.There was a noticeable variance in mean values between the genotypes for several traits, from modest to wide. For most of the features under investigation, with the exception of days to 50% flowering, moderate to high genotypic coefficient of variation, moderate to high heritability, and genetic advancement as a percentage of mean were reported.

Keywords: - Variability, Heritability, Genetic Advance, crop improvement.

Introduction

Brinjal (*Solanum melongena* L.) also known as eggplant or aubergine is an important crop of sub-tropics and tropics. Brinjal is a self-pollinated crop, but cross-pollination has been reported as high as 48%. This is because it has pronounced heterostyly, which favours cross pollination. Fruit setting in long styled flowers varies from 70% to 86.70% in different varieties. In medium styled flowers, fruit set ranges from 12.5% to 55.60%. Earlier, brinjal cultivation was not practiced in the temperate hills but due to rise in temperature during last couple of decades this region has become ideal place for cultivation of brinjal. The period of April to September is suitable for longevity of thiscrop with remunerative yield of good quality fruits devoid of infestation of insect like borers.According to (Sato et al., 2011), eggplant was known in India in ancient times and probably a native of India was of the opinion that its center of origin was in the Indo Burma region (Vavilov 1928). It is believed that eggplant may have originated in China may be the secondary centre of origin which belongs to economically important family

Solanaceaewithbasic chromosome number (2n=2x=24). The first record of eggplant in Europe was in the fifteenth century, the name was probably derived from the white egg like, fruits. Brinjal is of much importance in the warm areas of far-east being grown extensively in India and other Asian countries like, Bangladesh, Pakistan and Philippines.According to Panse and Sukhatme (1967), it has many medicinal properties in ayurveda; it is used as asthma, appetiser, aphrodisiac, cardio tonic. In Unani system of medicine, roots of brinjal are used to alleviate pain, and fruit is used as cardiotonic, laxative, muturant and reliever of inflammation Ravali et al., (2017). Its leaves are used as narcotics and seeds as stimulant but they are apt to lead to dyspepsia and constipation. White brinjal is also said to be good for diabetic patients Pujer et al., (2017).A great genetic variation is available in brinjal throughout the country with regard to fruit size, shape, colour, growth habit, canopy bearing habit, yield, diseases & insect-pests resistance, as well as quality and adaptability for different localities and for different growing seasons. In addition, variation is also noticed for traits like vegetative growth, maturity and presence or absence of spines on leaves, stem and fruit calyx, among the indigenous material. It has been reported that on an average, the oblong-fruited eggplant cultivars are rich in total soluble sugars, whereas the long-fruited cultivars contain a higher content of free reducing sugars, anthocyanin, phenols, glycoalkaloids (such as solasodine), dry matter, and amide proteins Tirkey et al., (2018).Genetic variability plays an important role in a crop/vegetable in selecting the best genotypes for making rapid improvement in yield and other desirable characters as well as to select the potential parent for hybridization programmes. Genetic improvement of any crop mainly depends on the amount of genetic variability present in the population and the germplasm serves as a valuable source of base population and provide scope for wide variability Madavi et al., (2015). Further, the crop exhibits rich genetic diversity and scope for improvement forvarious horticultural traits.

Heritable variation can be effectively used with greater degree of accuracy when heritability is studied in conjunction with genetic advance Nayak and Nagre (2013). Heritability is the heritable portion of phenotypic variance. The estimates of heritability help the plant breeder in selection of elite genotypes from diverse genetic populations.Genetic advance estimated by the method of Madavi etal., (2015). Genetic advance denotes the improvement in the mean genotypic values of selected families over base population and thus helps the breeder to select the progenies in the earlier generation itself. An improvement in yield and quality of brinjal is normally achieved by selecting the genotypes with desirable character combination existing in nature or by hybridization. Categorization of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and genetic advance (GA) were done as per (Chaudhary*et al* 2014).

Materials and Methods

The present experiment was carried out at Horticultural Research Centre, H.N.B. Garhwal University, Srinagar, (Garhwal) Uttarakhand during kharif seasonsof the year 2016.The material for the present study comprised fifteen genotypes collected from different geographical regions of the country. The experiment was laid out in randomized block design having 15 genotypes replicated thrice to test the variation in genotypes (Gavade and Ghadage, 2015). The net plot size was 1.2 m × 3 m. The seedlings were planted in a fashion accommodating 10 plants in each treatment at spacing of 60cm line to line and 60cm plant to plant. 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, phomopsis blight diseases, white fly and leaf hopper. Five randomly marked plants were observed for recording various plant characters.

Experimental data

Five plants of each accession in each replication were randomly selected for recording the observations on 20 yield and its component characters viz. plant height (cm) at 15 days interval DAT, days to 50 per cent flowering, fruit setting percentage, number of flowers per cluster, number of fruits per cluster, number of clusters per plant,days to first fruit harvesting (Days),fruit length (cm),fruit breadth (cm),average fruit weight (g),number of fruits per plant,number of fruit per kg,number of seeds per fruit,weight of 1000 seeds in gram (Test weight),fruit yield per plant (kg),fruit yield per plot (kg),fruit yield per hectare (q/ha),ascorbic acid (mg/100g),total soluble solids (^{o}Brix)andincidence of shoot and fruit borer. The mean replicated data on various biometric traits were subjected to analysis of variance as per the standard statistical procedurePanse and Sukhatme (1967). Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated as per the formula suggested by)Burton and De-Vane (1953).Heritability (broad sense) was worked out using the formula given by Burton and De-Vane (1953). Genetic advance and genetic gain were calculated as per the formula suggested by Mohammad et al., (2015), Vidya and Kumar (2015), Reshmika et al., (2015), Pujer et al., (2017), Ravali et al., (2017), Tripathy et al., (2017), Rahangdale et al., (2022) and Tirkey et al., (2018).

Table 1: List of genotypes along with their sources

Sr. No.	Genotypes	Sources
1.	A-2	Solan, HP
2.	Aassly-14	Solan, HP
3.	Arka Keshav	IIHR, Bangaluru
4.	Arka Kusumakar	IIHR, Bangaluru
5.	Arka Neelkanth	IIHR, Bangaluru
6.	BH- 12	Solan, HP
7.	BRWER-5	Solan, HP
8.	CH-215	Solan, HP
9.	DWR-31	Solan, HP
10.	H-8	Solan, HP
11.	J C-1	Solan, HP
12.	Local-10	Solan, HP

13.	Local-17	Solan, HP
14.	Pusa Purple Cluster	IARI, New Dehli
15.	Rajendra-9	Solan, HP

RESULTS AND DISCUSSION

Analysis of variance and genetic variability

The ANOVA (Table 1) showed highly significant differences among the genotypes for all the traits indicating thereby the presence of sufficient variability inthe experimental materials. The mean performances of the different genotypes for different trait are presented.The quality contributing traits the mean performance recorded as, the genotype H-8 (12.47 mg) for ascorbic acidshowed recorded maximumand minimum by the genotype DWR-31 (4.47 mg), for total soluble solids by the genotype Arka Neelkanth (5.31) showed recorded maximum andminimum by the genotype BH-12 (2.50), for fruit and shoot borer incidence observed by genotype H-8 (13.33%) showed recordedminimum and maximum by the genotype BH-12 (56.67%), for fruit lengthobserved by the genotype JC-1 (15.14 cm) heightand by the genotype A-2 (6.73 cm) recorded small fruit, for maximum fruit breadth recorded by the genotype A-2 (6.20 cm) and lowest by Pusa Purple Cluster (3.26 cm).The yield contributing traits are very important for selecting best high yielding hybrids therefore, the genotypeBRWRES-5 (103.32 g) foraverage fruit weight observed recorded maximum and minimum showed by the genotypeArka Keshav (57.90 g),fornumber of fruit per kg the genotype Arka Keshav(17.30 kg) recorded maximum and minimum showed by the genotypeDRWRES-5 (9.68), fornumber of fruits per plant the observed by genotypeArka Keshav (25.07) showed recorded maximum andminimum showed by the genotypeJC-1 (6.47),fornumber of seed per fruit the genotypeLocal-17 (671) showed recorded maximumandminimum showed by the genotype BH-12 (248), for weight of 1000 seeds observed by the genotypeRajendra-9 (4.70 g) showed recorded maximum and minimum showed by the genotypeJC-1 (2.49 g), and for fruit yield per plant observed by the genotype Arka Keshav (1.990 kg) showed recorded maximum and minimum showed by the genotypeJC-1 (0.447 kg), for fruit yield per plot bythe genotype Arka Keshav (19.90 kg) recorded maximum and minimum showed by the genotype JC-1 (4.47 kg), for fruit yield per hectareshowed maximum mean performance by the genotype Arka Keshav (552.78 q)and minimum by the genotype JC-1(124.08 q), Arka Keshav recorded highest mean performance for plant height (102.93 cm) and lowest by BH-12 (79.43 cm), for early 50 per cent flowering the genotype Arka Keshav (39.33 days) showed and late 50 per cent flowering genotyperecorded by DWR-31 (58.67 days), for fruit set percentagethe genotype Arka Keshav (78.34 %), recorded maximum and the genotype JC-1 (56.90 %) minimum, for number of flowers per cluster Arka Keshav(5.64) genotype showed highest and the lowest genotype JC-1 (2.04), for number of fruits per clusterthe genotype showed maximumArka Keshav (4.41) and by the genotype JC-1(1.17) minimum, for number of clusters per plant the genotype showed Arka Keshav (18.50)maximum and by the genotypeJC-1(10.20) minimum,for minimum days to first fruit harvestingthe genotype showed Arka Keshav (57.33 days) and maximum days to first fruit harvesting showed by BRWRES-5 (68.00 days), The high mean performance helps in identifying the best genotypes for developing the hybrids with good growth, earliness, and quality and yield parameters.

The estimates of mean, range, genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for 20 quantitative traits in brinjal genotypes are presented in Table 3.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 by number of seeds per fruit(248 - 671)followed by fruit yield per hectare (124.08-552.78).These findings are in consonance with the findings of earlier workers [9], [13], [18].The characters showing high range of variation have more scope for improvement. The lowest range of mean was recorded for fruit yield per plant (0.447 - 1.990) indicating availability of low variation for its improvement in the experimental material used.The estimate of phenotypic coefficient of variance (PCV) and genotypic coefficient of variance ranged from (6.34- 63.71) and (5.71- 61.58) respectively (Table 3).The PCV was highest for number of fruits per plant (63.71%),fruit and shoot borer incidence % (51.58%), number of fruits per cluster (42.79), fruit yield per hectare (38.10%), fruit yield per plot (38.10%), fruit yield per plant (38.10%), number of seeds per fruit (36.59%), ascorbic acid (36.15%). Similarly, GCV was also highest for number of fruits per plant (61.58%), fruit and shoot borer incidence % (38.93 %), number of seeds per fruit (35.19%), fruit yield per plant (34.85%), fruit yield per plot (34.85%), fruit yield per hectare (34.85%), number of fruits per cluster (34.29),number of flowers per cluster (31.01%), Ascorbic acid (30.81%), and fruit length (30.63).The PCV and GCV were lowest forPlant height at 60 and fruit set percentage DAT (6.34 &5.71).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.The PCV and GCV values were classified as low <15.00 %), moderate (15-30%) and high (>30%).In the present investigation PCV and GCV were high for number of fruits per plant (63.71 & 61.58),fruit and shoot borer incidence % (51.58 &38.93), number of fruits per cluster (42.79 & 34.29), fruit yield per hectare (38.10& 34.85), fruit yield per plot (38.10& 34.85), fruit yield per plant (38.10& 34.85), number of seeds per fruit (36.59&35.19), ascorbic acid (36.15& 30.81).The characters like, average fruit weight (20.95), stem girth (19.07% & 18.90 %), plant spread (11.31% & 11.28%), days to first flowering (14.09% & 13.98%), days to 50 per cent flowering (11.61% 7 11.56%) has moderate PCV.average fruit weight (20.95&19.75), number of fruits per kg (20.36& 18.89),test weight of seeds (22.86&19.99),number of clusters per plant (19.52& 16.49), fruit breadth (18.46& 16.27). 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

Estimates of heritability in broad sense (h2), genetic advance (GA) and genetic advance as percentage of mean (GAM) are presented in Table 3.Heritability, GA and GAM values ranged between16.18- 92.48%,4.73 - 69.71%, 0.71 - 249.08% respectively.The heritability values were classified as low (<50.00%), moderate (50.00- 80.00%) and high (>80.00%) while, GA and GAM as low (< 25.00%), moderate (25-50%) and high (>50.00%) as suggested byJohanson *et al.* [16]. Estimates of heritability were high (>80.00%) for all the traits viz, for number of seeds per fruit (92.48%), fruit length (90.78%), average fruit weight (88.80%), Plant height at 15 DAT (88.03%),30 DAT (87.89%), 45 DAT (87.05%), number of fruits per plant (86.15%),number of fruits per kg (86.04%,) 60 DAT (83.73%), fruit yield per plant (83.66%), fruit yield per plot (83.66%) and fruit yield per hectare (83.66%). Similar results reported by the scientistGavade and Ghadage (2015), Madhavi et al., (2015), Patel et al., (2015), Shende et al., (2014), Vidya and Kumar (2015), Ravali et al., (2017), Sujin et al., (2017)**.**The estimates of GAM were also high (>50)for number of seed per fruit (69.71%), number of fruits per plant (67.82),fruit yield per plant (65.67%), fruit yield per plot (65.67%), fruit yield per hectare (65.67%), Fruit and shoot borer incidence (60.53%), number of fruits per kg (59.31%), fruit length (57.27%). number of fruits per cluster (56.61%) and ascorbic acid (52.83%). The moderate GAM (25-50%) was recorded for number of flowers per cluster (46.49%),Average fruit weight (38.33%), TSS (38.27%), test weight of seeds (36.02%), Plant height at 15 DAT (30.78%), fruit breadth (29.33%) and number of clusters per plant (28.70). 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. 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 phenotypic 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 Singh et al., (2013a), Kumar et al., (2013b), Chaudhary and Kumar (2014) and Mili et al., (2014) and Barela et al., (2022).

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.Major yield contributing characters is identified and selection for these traits will be helpful in getting increased yield of this crop.Diverse genotypes can be utilized for hybridization programme also.

Conclusion

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.

Table 2: Analysis of variance (ANOVA) for 20 quantitative characters in brinjal (*Solanum melongena* L.).

S.NO	**Source of variance**	**Mean sum of square**		
		Replication	**Treatment**	**Error**
	D.F.	**2**	**14**	**28**
1.	**Plant height at 15 DAT**	4.505	0.216**	0.195
	Plant height at 30 DAT	8.309	0.665**	0.364
	Plant height at 45 DAT	5.139	1.743**	0.715
	Plant height at 60 DAT	40.444	7.248**	2.459
	Plant height at 75 DAT	177.817	0.820**	16.231

2.	**Days to 50% flowering**	0.622	70.707**	14.479
3.	**Fruit set percentage**	14.566	115.929**	24.633
4.	**No. of flower per cluster**	0.127	2.558**	0.283
5.	**No. of fruits per cluster**	0.014	2.054**	0.093
6.	**No. of clusters per plant**	1.408	15.286**	0.975
7.	**Days to first fruit harvesting**	11.82	150.16**	36.89
8.	**Fruit length (cm)**	1.036	24.080**	1.072
9.	**Fruit breadth (cm)**	0.039	2.143**	0.187
10.	**Average fruit weight (g)**	5.985	732.36**	29.544
11.	**No. of fruit per plant**	1.719	74.238**	3.776
12.	**No. of fruit per kg**	0.118	20.316**	1.042
13.	**No. of seed per fruit**	1236.26	48711.28**	1578.33
14.	**Seed test weight**	0.005	1.773**	0.164
15.	**Fruit yield per plant(kg)**	0.002	0.453**	0.027

16.	**Fruit yield per plot(kg)**	0.220	45.320**	2.769
17.	**Fruit yield per hectare (q)**	192.82	34878.97**	20.72.95
18.	**Ascorbic acid**	3.480	19.042**	1.352
19.	**TSS**	0.236	2.510**	0.316
20.	**Fruit and shoot borer %**	15.555	673.650**	125.079

**Significant at 5% level.

Table 3 Estimates of genetic parameters of variations for various characters in brinjal

Sr. No.	**Characters**	**Range**	**Mean**	**Coefficients of variation (%)**		**Heritability (%)**	**Genetic gain (%)**	**Genetic advance**
				Phenotypic	**Genotypic**			
1.	Plant height (cm)15 DAT	5.30 – 9.83	7.53	16.97	15.93	88.03	2.32	30.78
	30 DAT	12.23 – 18.77	14.39	12.06	11.31	87.89	3.14	21.83
	45 DAT	30.77 – 38.80	34.20	6.87	6.41	87.05	4.21	12.32
	60 DAT	56.63 – 67.77	61.30	6.34	5.80	83.73	6.71	10.94
	75 DAT	79.43 - 102.93	90.31	9.27	8.13	76.84	13.25	14.68
2.	Days to 50% flowering (days)	39.33 – 58.67	48.62	11.21	9.31	69.09	7.75	15.94
3.	Number of clusters per plant	10.20 - 18.50	13.17	19.52	16.49	71.36	3.76	28.70
4.	Fruit set percentage (%)	56.90 - 78.34	65.92	14.20	5.71	16.18	3.12	4.73

5.	Number of fruits per cluster	1.17 - 4.41	2.22	42.79	34.29	64.22	1.25	56.61
6.	Number of flowers per cluster	2.04 - 5.64	3.27	26.45	31.01	72.79	1.53	46.49
7.	Days to first fruit harvesting (days)	57.33 - 82.66	68.84	12.85	9.24	51.73	9.43	13.69
8.	Fruit length (cm)	6.73 - 15.14	9.54	29.18	30.63	90.78	5.47	57.27
9.	Fruit breadth (cm)	3.26 - 6.20	4.96	18.46	16.27	77.73	1.47	29.33
10.	Average fruit weight (g)	57.91 - 103.32	77.52	20.95	19.75	88.80	29.71	38.33
11.	Number of fruits per plant	6.47 – 25.07	13.66	38.22	63.71	86.15	9.27	67.82
12.	Number of fruits per kg	9.68 - 17.30	13.42	20.36	18.89	86.04	4.84	36.09
13.	Number of seeds per fruit	248 - 671	357.33	36.59	35.19	92.48	249.08	69.71
14.	Weight of 1000 seeds	2.49 - 4.70	3.67	22.86	19.99	76.51	1.32	36.02
15.	Fruit yield per plant (kg)	0.447 - 1.990	1.08	38.10	34.85	83.66	0.71	65.67
16.	Fruit yield per plot (kg)	4.47 - 19.90	10.80	38.10	34.85	83.66	7.10	65.67
17.	Fruit yield per hectare (q)	124.08-552.78	300.19	38.10	34.85	83.66	197.66	65.67
18.	Fruit and shoot Borer Incidence (%)	13.33 - 56.67	33.75	51.58	38.93	56.97	20.43	60.53
19	TSS (^{0}Brix)	2.50-5.31	4.02	21.90	25.83	71.92	4.51	38.27
20.	Ascorbic acid (mg/100g),	4.47-12.47	8.53	36.15	30.81	63.90	4.46	52.83

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