Genetic variability studies in Brinjal (*Solanum melongena* L.) for quantitative and qualitative characters.

ABSTRACT

A study was carried out on brinjal to estimate variability, heritability, and genetic advance in the Department of Vegetable Science, College of Horticulture and Forestry, Pasighat.The high GCV and PCV (>20%) values for fruit diameter, fruit length, fruit weight, number of branches per plant, leaf area, number of fruits per plant, number of seeds per fruit, total phenol, anthocyanin, and solasodine content indicated high genetic variability among genotypes, making selection more effective for brinjal improvement. High heritability and high genetic advances were seen in the number of seeds per fruit, fruit yield per ha, leaf area, fruit weight, anthocyanin, and total phenol, which may be owing to additive gene action and selection from these traits being more successful.

Keywords: Genetic variability, PCV, GCV,Heritability,Genetic advance,

INTRODUCTION

Brinjal (*Solanum melongena* L.) is most important vegetable crop of night shade familywith chromosome number 2n=24. it is eulogized as Eggplant or Poor man's cup or Aubergine. It is annual, herbaceous, sometime perennial and basically self-pollinated in nature. Genus Solanum comprises around 2000 species categorized into 75 genera, in that important edible species are *Solanum melongena, Solanum torvum, Solanum nigrum, Solanum macrocarpon, Solanum ferox and Solanum aethiopicum*.Since people have been growing brinjal for the past 4,000 years in the subcontinent, it is believed to have its roots in India (Dunlop, 2006). India is the country where many large fruited cultivars were domesticated. The species *S. melongena* was well-known in India since antiquity (De Candolle 1886), and was thought to be a native of Asia and the Indo-Burma region is the center of origin according to Vavilov 1928. There are three main species in the genus "*Solanum,*" namely *escullantum* (large round), *serpentium* (long slender), and *depressum* (dwarf brinjal) (Choudhary, 1976).

Any crop improvement effort requires a good understanding of the level of genetic variability present in the genotypes for different traits. The important element of every population is variability. The heritable element of overall variability is represented by the genotypic coefficient of variation (GCV), which measures the genetic proportion of this variability. The chance of using a certain character in a selection programme increases with increasing GCV. Heritable variability cannot be calculated only based on genetic variability as measured by GCV. In addition, estimation of heritability and genetic advance as percent of the mean is also needed to assess the extent of genetic gain expected from effective selection. The variability available in the genotypes can be partitioned into heritable and nonheritable components, *viz.*, the coefficients of phenotypic and genotypic variation (PCV and GCV), heritability in a broad sense (H), genetic advance (GA), and genetic advance as a percent of the mean. Under varied climatic conditions, phenotypic variability changes, whereas genetic variability remains constant and is more valuable to a plant breeder for selection or hybridization. Since yield is a complex trait impacted by numerous yield-contributing components and significantly influenced by environmental factors, were estimations of heritability and genetic progress are relevant to selection.

MATERIALS AND METHODS

The experiment was conducted at Vegetable Experimental Farm, College of Horticulture and Forestry, Central Agricultural University, Pasighat, East Siang, Arunachal Pradesh, India, which is geographically situated between 28°04`N latitude and $95^{0}$22`E longitude at an elevation of 153 meters above the MSL which has a humid subtropical climatic condition, where the soil has the sandy loamy texture with p^{h} of 6-7.Genotype (Table 1) were evaluated for its growth, yield and quality attributing traits and seeds were sown in raised nursery bed and covered by the thin layer of sand and watered every day. Care was taken against damping off by drenching 0.1% of carbendazim. This study was carried out during March, 2022 to August, 2022. Parents were raised in a randomized complete block design with three replications. Thirty-five days-old seedlings raised in the nursery beds were transplanted on the mulched beds adopting a spacing of 60 × 60 cm. Ten plants were maintained for each parentin each replication. Recommended cultural practices were followed uniformly to all genotypesand grown well. Observations were recorded in five randomly selected plants in each replication. The data were analysed by the methods outlined by Panse and Sukhatme (1967) using the mean values at random plots in each replication from all genotypes to find out significanceof genotypic effect.

The GCV, PCV interpreted as low (0–10%), moderate (11–20%), high (>20%), heritability (h2) and GAM sorted as low (0–30%), moderate (31–60%), high (>60%). Genetic advance as mean was low (0–10%), moderate (11–20%), high (>20%) worked out (Burton and De-Vane 1953 and Hanson et al. 1956, Johnson et al. 1955, respectively). The data obtained in respect of all the characters has been subjected to the statistical tool WINDOSTAT software tool.

$$\text{Genotypic coefficient of variation (GCV\%)} = \frac{\text{Genotypic standard deviation}}{\text{Grand mean}} \text{X100}$$

Phenotypic coefficient of variation (PCV %) $=\frac{\text{Genotypic standard deviation}}{\text{Grand mean}}$ X100

Heritability in broad sense is the ratio of genotypic variance to the total phenotypic variance is symbolized as h2 (BS) and estimates of heritability expressed in percentage. Estimation of heritability was done as per the formula given by Hanson et al. (1956).

$H(\%)=\frac{\text{Genotypic variance}}{\text{Phenotypic variance}}$

Genetic advance (GA) is improvement in the mean genotypic value of selected plant over the parental population. It was calculated by the formula as suggested by Johnson et al. (1955) and Lush (1949).

$GA=\frac{\text{Genotypic variance}}{\text{Phenotypic variance}}$Xk X$\sigma$p

Where, σp = Phenotypic standard deviation

k = Selection differential, a constant value is 2.06 at 5% selection intensity

Sl. No.	Genotype	Collected from	Symbol
1.	Pusa Purple Cluster	IARI New Delhi	P1
2.	Rajendra Baingan-2	BAU Sabour	P2
3.	Swarna Mani	BAU Sabour	P3
4.	Tripura Local	West Tripura	P4
5.	Muktakeshi	BAU Sabour	P5
6.	Haritha	KAU Kerala	P6
7.	CO-2	TNAU	P7
8.	Arunachal Local	Arunachal Pradesh	P8

Table 1. Details of the parents used in the present study.

Source of variations	Df	DFF	DFIF	DFH	FD (cm)	FL (cm)	FW(g)	NBP	LA (cm^2)
Replication	2	6.24	0.03	1.38	0.09	0.22	2.52	0.10	7.67
Genotypes	7	67.59*	29.30*	38.94*	10.53*	56.16*	5168.81*	21.55*	6094.96*
Error	14	1.73	1.98	1.86	0.20	0.32	4.33	0.31	5.95
S. Em (±)		0.76	0.81	0.79	0.26	0.33	1.20	0.32	1.41
C.D at 5%		2.31	2.46	2.39	0.78	0.99	3.64	0.98	4.27
CV		3.15	3.00	2.60	4.00	2.91	4.67	2.83	6.16

Source of variations	Df	NFP	NSP	FYP (kg)	FYPH(q)	PH (cm)	TPC mg/100g	ANT mg/100g	SOL mg/100g
Replication	2	1.86	21.40	0.83	38.40	7.30	4.66	0.62	0.10
Genotypes	7	218.86*	88833.00*	1.01*	18511.30*	313.25*	440.29*	1543.28*	11.74*
Error	14	1.26	51.45	0.10	21.12	3.25	1.71	1.20	0.19
S. Em (±)		0.65	4.14	0.18	2.65	1.04	0.75	0.63	0.25
C.D at 5%		1.97	12.56	0.55	8.05	3.16	2.29	1.92	0.76
CV		7.31	12.26	5.43	6.37	5.02	3.24	3.76	3.64

Table 2: Analysis of variance (ANOVA) for yield and quality attributing traits in brinjal genotypes

* Significance at 5%

DFF-Days to First Flowering, DFIF-Days to 50% flowering, DFH- Days to first fruit Harvest, FD (CM)- Fruit Diameter, FL-Fruit length (cm), FW-Fruit weight (gm), NBP-No. of branches per plant, LA (cm2)- Leaf area, NFP- No. of fruits per plant, NSF-No. of seeds per fruit, FYP- Fruit Yield per plant (kg), FYPH- Fruit yield per Ha, PH-Plant height (cm), TP – Total Phenol (mg/100g), ANT- Anthocyanin (mg/100g), SOL- Solasodine (mg/100g).

Table 3 : Mean, range, variability, heritability, and genetic advance as per cent of mean yield and quality attributing traits of brinjal.

Sl. No	**Traits**	**Mean**	**Range**		**Variability**		**Heritability**	**Genetic advance**	**Genetic advance as per cent of mean**
			Min	**Max**	**GCV (%)**	**PCV (%)**			
1	Days to first flowering	54.97	46.25	62.17	8.52	8.85	92.68	9.29	16.91
2	Days to 50 percent flowering	66.02	59.70	69.48	4.57	5.04	82.16	5.64	8.54
3	Days to first harvest	71.49	65.66	76.76	4.92	5.27	86.94	6.75	9.45
4	Fruit diameter (cm)	4.97	1.32	6.82	37.34	38.40	94.54	3.72	74.79
5	Fruit length (cm)	11.05	3.80	16.18	39.04	39.38	98.30	8.81	79.74
6	Fruit weight (g)	92.64	17.96	144.79	44.79	44.84	99.75	85.36	92.14
7	Number of branches per plant	10.96	6.94	14.80	24.28	24.81	95.80	5.36	48.96
8	Leaf area (cm^2)	96.58	60.03	187.29	46.65	46.72	99.71	92.67	95.95
9	Number of fruits per plant	17.31	10.61	36.66	49.21	49.63	98.29	17.39	100.49

10	Number of seeds per fruit	419.62	185.19	691.51	41.00	41.03	99.83	354.07	84.38
11	Fruit yield per plant (kg)	1.80	0.78	2.55	30.73	35.31	75.74	0.99	55.09
12	Fruit yield per hectare (q)	331.43	171.32	414.57	23.69	23.73	99.66	161.45	48.71
13	Plant height (cm)	64.61	50.65	81.95	15.73	15.98	96.95	20.62	31.92
14	Total phenol (mg/100g)	52.72	40.13	74.53	22.94	23.07	98.85	24.76	46.98
15	Anthocyanin (mg/100g)	31.83	11.79	75.63	71.22	71.30	99.77	46.65	146.55
16	Solasodine (mg/100g)	5.23	2.81	8.58	37.55	38.47	95.29	3.95	75.51

GCV- Genotypic coefficient of variance, PCV- Phenotypic coefficient variance

RESULTS AND DISCUSSION

The magnitude of variability existing in crop species is of almost importance, as it provides the basis for effective selection the total variance i.e., phenotypic variance present in the population arises due to combined action of genotypic and environmental effects. Phenotypic variability is the observable variation present in a character in the population, it includes both genotypic and environmental components of variations and as a result, its magnitude different under different environmental condition. Genotypic variation, on the other hand, is the components of variation, which is due to the genotypic difference among individual with in a population and is the main concern of plant breeders. The analysis of variance revealed that significant variations were observed in genotypes almost for all the characters. The significant variation among the parent were found for days to first flowering , days to fifty percent flowering, days to first harvest, fruit diameter, fruit length, fruit weight, number of branches per plant, leaf area, number of fruits per plant, number of seeds per plant, fruit yield per plant, fruit yield per ha, plant height, total phenol content, and anthocyanin content and solasodine content, it indicated sufficient scope for bringing genetic improvement in brinjal. In crop improvement, only the genetic components of variation are important since only this component is transmitted to the next generation, the extent of contribution of the phenotypic variation for the fruits yield in a population is ordinarily expressed as the ratio of genetic variation to the total variance, which is known as heritability.

The improvement in genotypic value of the new population compared to the original population is estimated as genetic advance. It is the degree of gain obtained in a particular character. High heritability coupled with high genetic advance offers the most suitable condition for selection. With these points in view, the variability results for 16 quantitative traits were evaluated in the present investigation and discussed here under.

Fruit yield per ha showed high genotypic and phenotypic coefficient of variation (>20%), high heritability and high genetic advance. The genotypes displayed significant differences for all the traits through analysis of variance study. The characters considered for the present study had PCV a little higher in magnitude than the corresponding GCV. Thus, indicating the reliability of selection based on these traits as possibly the environmental factors have played a lesser role in the expression of these characters. Consequently, simple selection for traits can be practiced for further improvement. The results of Ravali*et al*. (2017) and Lokesh *et al*. (2013) were in agreement with the present findings. Yield per plant recorded maximum genotypic coefficient of variation and phenotypic variation (>30%). Similar results were also reported by Vaishya *et al.* (2017), Mangai *et al*. (2017) and Lokesh *et al*. (2013).Fruit diameter exhibited high genotypic and phenotypic coefficient of variation (>30%) with high heritability. The findings are in close harmony with those of Manpreet *et al*. (2013), Milli *et al*. (2014). Fruit length showed high genotypic and phenotypic coefficient of variation and high heritability. The findings are in close harmony with those of Singh and Kumar

(2005), Manpreet *et al*. (2013), Milli *et al*. (2014). Fruit weight showed high genotypic and phenotypic coefficient of variation (>40%), high heritability and high genetic advance. The results of Lokesh *et al*. (2013) were in agreement with the present findings.

Number of fruits per plant revealed high GCV and PCV with moderate heritability and high genetic advance. Similar results were also reported by Sonagara*et al*. (2022). Number of seeds per fruit exhibited high genotypic and phenotypic coefficient of variation with high heritability, high genetic advance and similar reports were found by Rad *et al*. (2015). High genotypic and phenotypic coefficients of variation were observed for leaf area. Heritability and genetic advance as per cent of mean were also found to be high. The results are in conformity with the observations of Bansal (2007).The estimates of heritability and genetic advance per cent of mean for number of branches per plant revealed high genotypic and phenotypic coefficient of variation with low genetic advance. These results were in accordance with the observations of Karak *et al*. (2012), Singh and Kumar (2005).

High heritability coupled with high GA was observed for total phenol and high genetic advance which was agreeable with earlier findings of Sonagara*et al*. (2022). Anthocyanin reported high genotypic and phenotypic coefficient of variation with high heritability and high genetic advance and results are in accordance with reports ofSonagara*et al*. (2022). Solasodine showed high genotypic and phenotypic coefficient of variation coupled with high heritability and low genetic advance and findings were in accordance with Sharmin *et al*. (2010) and Roychowdhury *et al.* (2011).Lower GCV and PCV (<20%) were observed in days to first flowering, days to fifty percent flowering, days to first harvest and plant height. Thus, these traits were less influenced by environment. Similar results were recorded by Madhavi *et al*. (2015) and Sujin *et al*. (2017).

High heritability in the broad sense helps identify appropriate characters for selection and enables the breeder to select superior genotypes based on phenotypic expression of quantitative characters. High yield can be achieved by the selection of characters that have high heritability coupled with genetic advances. Selection of one trait invariably affects several associated traits which evoke the necessity of determining interrelationships of various yield components among them and with yield. (Konyak *et al*. 2020). Heritability in broad sense was estimated highest in number of seeds per fruit, anthocyanin, fruit weight, fruit yield per ha and indicating that the traits is least influence by environment. Further, there is abundant range for improving these traits in desirable direction with direct selection. Similar findings were also reported by earlier investigation Kumar (2016) and Konyak *et al*. (2020).High genetic advance per cent of mean were recorded for anthocyanin followed by number of fruits per plant, leaf area, fruit weight, solasodine indicates significance of additive gene action governing this trait. So, further selection will improve this trait. Similar results were obtained for some of these characters by Sharma and Swaroop (2000), Sunitha and Bandhopadhya (2005).

CONCLUSION

For each trait investigated in this study, the phenotypic coefficients of variability were larger than the genotypic coefficients of variability. High GCV and PCV (>20%) values for fruit diameter, fruit length, fruit weight, number of branches per plant, leaf area, number of fruits per plant, number of seeds per fruit, fruit yield per plant, fruit yield per ha, total phenol, anthocyanin, and solasodine content indicated enormous genetic variability among genotypes, making selection more effective for brinjal improvement.

The number of seeds per fruit, fruit yield per ha, leaf area, fruit weight, anthocyanin, and total phenol showed high heritability along with significant genetic advance, which may be owing to additive gene action and selection from these traits being more successful. Fruit length, fruit diameter, number of branches per plant, days first harvest, days first flowering, solasodine, and yield per plant all showed low genetic advance, suggesting that these traits were influenced by non-additive gene action and that heterosis breeding from these traits may be more successful.

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