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# Assessment of genetic variability, heritability and genetic advance in Brinjal (*Solanum melongena* L.) Genotypes

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#### Abstract

Twenty diverse genotype of brinjal were assessed for nineteen qualitative and quantitative characters in Randomized Block Design with three replication at Vegetable Research Farm, College of Horticulture and Forestry, Central Agricultural University, Pasighat, Arunachal Pradesh during May to October, 2017-18. Genetic variability was studied for characters viz., plant height (cm), number of primary branches per plant, days to 50% flowering, days to 50% fruit set, days to 1<sup>st</sup> harvesting, number of fruits per plant, fruit weight (g), fruit length (cm), fruit girth (cm), number of flower per cluster, number of fruit per cluster, fruit yield per plant (kg). Highly significant differences were observed among the accession. High phenotypic and genotypic coefficient of variation was observed for number of fruit per cluster, fruit girth, fruit length, fruit yield per plant, fruit weight and number of fruit per plant indicating the existence of wider genetic variability for these traits in the germplasm. High heritability accompanied with high genetic advance was notice for number of fruit per cluster, fruit weight, plant height, fruit length, fruit yield per plant, number of primary branches per plant and fruit girth suggesting that they can be improved through direct selection due to predominant additive variation.

**Keywords:** Genetic variability, heritability, genetic advance, gene effects and fruit yield

#### Introduction

Brinjal (*Solanum melongena* L.) or eggplant is an important and popular vegetable crop of family Solanaceae, grown throughout the year all over the country. It is in cultivation since ancient times, playing important role to contribute in overall production of vegetable in India. This crop is also known as poor man's crop due to its affordable price and year round availability in all parts of the country. It has also occupied a prominence place in routine diet of all classes of society because of several luscious dishes prepared from its fruits. It is the most popular and widely cultivated vegetable crop in the central, southern and southeast Asia and some African countries. The crop is of great importance in the warmer areas of the Far East and is grown more extensively in China, Japan, Turkey, Egypt, Italy, Indonesia, Spain, Philippines, apart from India (Singh and Kalda, 2001) [26]. In India total production of brinjal is 12.80 million tonnes per annum covering 0.730 million hectare area with an average productivity of 17.45 metric tonnes per hectare (Horticultural Statistics at a Glance 2017). Brinjal is a stable vegetable in our diet since ancient times. The nutritional and medicinal properties make it imperative to grow it the year round. It is used in a variety of culinary preparations. The export of this crop is negligible and mostly it is consumed locally. Brinjal is a rich source of protective nutrients comparable to tomato, being the good source of calcium, phosphorous, iron and vitamin B. Fruits are excellent remedy for those suffering from liver troubles and high blood cholesterol. The de-cholesterolizing action is attributed to the presence of poly-unsaturated fatty acids (linoleic and lenolenic) in fruits. Piercing brinjal fruits with a needle and fried in sesame oil is a remedy for toothache. Aqueous extracts of fruit juice inhibits choline esterase activity of human plasma and dry fruit is reported to contain goitrogenic principles (Singh and Kalda, 2001) [26]. White brinjals are said to be a remedy for diabetic patients (Choudhury, 1976).

Despite the importance of brinjal in our daily life, less attention has been given to this crop in general and particularly in Northeastern Region for crop improvement in the past. Also, there is a need to fulfill the demand of ever increasing population. Therefore, it is essential to improve the yield potential through suitable breeding programme and collection of superior germplasm and its genetic analysis to get higher yield and desirable character.

The success of any crop improvement programme highly depends upon the nature and magnitude of the genetic variability present in the breeding material with which the breeders is working Prabhu *et al.* (2009) [20]. The total variability present in germplasm can be revealed through phenotypic coefficient of variation and genotypic coefficient of variation. The effectiveness of selection directly depends on the amount of heritability and genetic advance as a percent of mean for that character. Assessment of genetic variation is a prerequisite for initiating effective breeding programme, as it provides a basis for tailoring desirable genotypes. According to Chowdhary *et al.* (2013) [6] better knowledge on genetic variability could help to sustain long-term selection gain and conservation of plant genetic resources.

In spite of obvious importance in our daily life, little attention has been given to this crop in the past for the yield improvement. Use of traditional varieties and less variability affected by diseases and pest is the important constraint for low yield potentiality. Collection of germplasm and its genetic analysis can help to get a suitable genotype for higher yield or any other desirable character. To meet the demand of ever-increasing population, there is need to enhance the productivity levels of brinjal crop. Simultaneously, demand is increasing for varieties for different culinary purposes. Moreover, in view of very high local preferences for colour, shape and taste, there are specific genotypes suitable for specific locality since it is not possible to have one common cultivar suitable for different localities and local preferences. Therefore, it is essential to improve the yield potential of available genotypes through suitable breeding programme. It is one of very few self-pollinated crops where exploitation of hybrid vigour has been commercially successful because of high number of seeds obtained from a cross. The success of any crop improvement programme largely depends upon the nature and magnitude of the genetic variability existing in breeding material with, which the plant breeder is working (Prabhu *et al.*, 2009; Meena and Bahadur., 2013) [20].

Variability is the basic requirement for any crop improvement programme. The total variability present in germplasm can be divided into heritable and non-heritable components through genetic parameters like phenotypic and genotypic coefficients of variation, heritability and genetic advance, however, heritability is the heritable portion. It is an important index of characters transmission from parents to offspring (Falconer, 1981). The effectiveness of selection directly depends on the amount of heritability and genetic advance as per cent of mean for that character. According to Sharma and Jana (2002) [13], assessment of genetic variation is a prerequisite for initiating efficient breeding programme, as it provides a basis for tailoring desirable genotypes. Knowledge on genetic information obtained through the analysis of genetic variability and relatedness between or within species is prerequisite towards effective utilization and conservation of plant genetic resources (Chaudhuri *et al.*, 1976). Better knowledge on genetic variability or genetic similarity could help to sustain long-term selection gain (Chowdhary *et al.*, 2013) [6] In spite of obvious importance in our daily life, little attention has been given to this crop in the past for the yield improvement. Use of traditional varieties and less variability affected by diseases and pest is the important constraint for low yield potentiality. Collection of germplasm and its genetic analysis can help to get a suitable genotype for higher yield or any other desirable character. To meet the demand of ever-

increasing population, there is need to enhance the productivity levels of brinjal crop. Simultaneously, demand is increasing for varieties for different culinary purposes. Moreover, in view of very high local preferences for colour, shape and taste, there are specific genotypes suitable for specific locality since it is not possible to have one common cultivar suitable for different localities and local preferences. Therefore, it is essential to improve the yield potential of available genotypes through suitable breeding programme. It is one of very few self-pollinated crops where exploitation of hybrid vigour has been commercially successful because of high number of seeds obtained from a cross. The success of any crop improvement programme largely depends upon the nature and magnitude of the genetic variability existing in breeding material with, which the plant breeder is working (Prabhu *et al.*, 2009; Meena and Bahadur., 2013) [320].

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### Materials and Methods

This experiment was conducted at Vegetable Research Farm, College of Horticulture and Forestry, Central Agricultural University, Pasighat, East Siang, Arunachal Pradesh, India during 2017-2018. The research farm is situated in the foot hills of Eastern Himalayan Range at an altitude of 153 m above mean sea level, 28°04'N latitude and 95°22'E longitude. The climate of this area is humid, sub-tropical and maximum rainfall occurs between May-September. The experimental material for the present study consisted of 20 diverse genotypes of Brinjal (Table 1). The experiment was laid out in Randomized block design (RBD) with three replications. The standard cultural practices were followed as

mentioned in Package of Practices for Vegetable Crops. The seeds were sown in black plastic pot trays and covered by thin layer of cockpit and water every day. Five week old seedling raise in nursery were transplanted on raised beds adopting a spacing of 60 x 60 cm under polyhouse condition. The recommended dose of fertilizer were applied as on recommended time to grow healthy crop. Other agronomic practices were done to maintain the crop. The observations were recorded in five randomly selected plants in each replication for parameters *viz.*, plant height (cm), number of primary branches per plant, days to 50% flowering, days to 50% fruit set, days to first harvesting, number of fruit per plant, fruit weight (g), fruit length (cm), fruit girth (cm), number of flower per cluster, number of fruit per cluster, fruit yield per plant (kg).

The phenotypic and genotypic coefficient of variability was calculated as per formula given by Burton and de Vane (1953)<sup>[4]</sup>. PCV and GCV were classified as low, moderate or high suggested by Shivasubramanian and Menon (1973). Heritability ( $h^2$ bs) was calculated as per formula given by Burton and de Vane (1953)<sup>[4]</sup>. The expected genetic advance resulted from selection of 5 percent superior individuals were worked out as suggested by Johnson *et al.* (1955)<sup>[10]</sup>. The genetic advance as percentage of mean was categorised into low, moderate and high as suggested by Johnson *et al.* (1955)<sup>[10]</sup>. < 20 = Low, 20 – 30 = Moderate, >30 = High.

## Results and Discussion

Analysis of variance indicated significant differences among genotypes for all the characters indicating that the present genotypes were appropriate and hence suitable for further genetic analysis. A wide range of variation was observed for all characters studied, particularly for plant height, number of primary branches, days to 50% flowering, days to 50% fruit set, days to first harvesting, fruit weight, fruit girth, fruit length, fruit yield per plant. The characters showing high degree of variations have more scope for their further improvement Mohanty (2002)<sup>[16]</sup>. A better understanding about variability can be gained by comparing the relative amount of coefficient of phenotypic and genotypic variance for the actual strength of variability. From the experiment conducted, it was observed that magnitude of phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV) for all the characters under study which is an indicator of additive gene effect influenced by environment on the expression of the traits. Similar finding were also reported by Shekar *et al.* (2012)<sup>[24, 25]</sup>. In other words, it is likely that genetic factors were predominantly responsible for expression of those attributes and selection could be made effectively on the basis of phenotypic performance.

The phenotypic coefficient of variation ranged from 2.29% for flavonoid content to 70.47% for reducing sugar content. The phenotypic coefficient of variation was highest for reducing sugar content (70.47%), followed by characters *viz.*, non-reducing sugars (59.78%) number of fruit per cluster (52.57%), fruit girth (52.55%), Solasodine content (52.25%), fruit length (50.74%), fruit yield per plant (43.66%), fruit weight (38.01%), total sugar content (34.48%), number of fruit per plant (32.49%), anthocyanin content (31.69%) and number of flower per cluster (30.46%) indicating that, these characters would respond very well to the selection. Similar findings were also reported by Doshi *et al.* (1999)<sup>[8]</sup>.

Genotypic coefficient of variation varied from 0.31% for flavonoid content to 62, 93% for reducing sugar content. High

genotypic coefficient of variation was noted for reducing sugar content (62.93%) followed by characters *viz.*, number of fruit per plant (52.03%), non-reducing sugar (49.69%), fruit length (46.52%), fruit yield per plant (38.19%), fruit girth (36.20%), fruit weight (35.95%), solasodine content (34.60%), total sugar content (25.84%), plant height (21.52%) and number of primary branches (21.25%). Similar results were reported by Mohanty (2002)<sup>[16]</sup> for number of fruits per plant and fruit weight, Prasad *et al.* (2004) for fruit length, fruit girth, average fruit weight, number of fruits per plant and fruit yield per plant, Kushwaha and Bandhyopadhy (2005) for fruit weight, number of fruits per plant and fruit girth, Babu and Patil (2005) for number of fruits per plant, fruit diameter and fruit yield per plant, Patel *et al.* (2004) for yield per plant and single fruit weight. The high values of GCV suggested greater genotypic variability among the genotypes and responsiveness of the attributes for making further improvement by selection. However, it has been suggested that GCV values alone are not sufficient to determine the amount of variation which is heritable.

The efficiency of selection for particular character is best reflected by the extent of its heritability. Heritability is a measure of genetic relationship between parent and progeny and has been widely used in determining the degree to which a character may be transmitted from parents to off springs. High heritability in broad Estimation of heritability in broad sense gives the extent of heritable component of variation. According to Robinson *et al.* (1949)<sup>[10]</sup> heritability values are categorized as low from 0-30%, moderate from 30-60% and above are high. In the present investigation the characters like number of fruit per cluster, fruit weight, plant height, fruit length, fruit yield per plant, number of primary branches had high heritability. High heritability for different traits indicated that large proportion of phenotypic variance has been attributed to genotypic variance and suggested that selection could be made for these traits on the basis of phenotypic expression. Burton (1952)<sup>[24, 25]</sup> also suggested that a genotypic coefficient of variation along with high heritability gives clear picture of gain to be expected from selection. The high heritability values for yield and component characters corroborates with the findings of Singh *et al.* (2013)<sup>[29]</sup>, Prabakaran *et al.* (2013)<sup>[19]</sup>, Kumar and Arumugam (2013)<sup>[24, 25]</sup> and Yadav *et al.* (2014)<sup>[17]</sup>. Moderate heritability value was recorded in days to 50% fruit set, days to first harvesting and fruit girth. The finding concluded that the lowest heritability value was found in number of fruit per plant and number of flower per cluster. The summarized result in corroborates with the findings of Singh *et al.* (2013)<sup>[29]</sup>, Prabakaran *et al.* (2013)<sup>[24, 25]</sup>, Kumar and Arumugam (2013)<sup>[13]</sup> and Yadav *et al.* (2014)<sup>[17]</sup>.

Genetic advance is the improvement in the mean genotype value of selected plants over the parental population. It is the measure of genetic gain under selection. In the present study, genetic advance as percentage of mean ranged between 7.35% for number of flower per cluster to 116.87% for fruit length. The highest estimate of genetic advance as percentage of mean was recorded for fruit length (116.87%), followed by number of fruit per cluster (106.07%), fruit weight (93.16%), fruit yield per plant (91.54%), fruit girth (68.32%), plant height (55.73%), number of primary branches (45.66%) and number of fruit per plant (16.05%). Moderate value of genetic advance as percentage of mean was observed in days to first harvesting (14.56%), days to 50% flowering (14.10%), days to 50% fruit set (13.09%) and number of flower per cluster which might be attributed to additive gene action conditioning

their expression and phenotypic selection for their amenability can be brought about. These results was as per the guidelines agreement with Choudhary *et al.* (2010) for the characters like plant height, number of primary branches per plant, fruit yield per plant, and number of fruit per plant. In order to have a clear predictability of the breeding value, heritability along with genetic advance was found to be more effective and reliable in predicting the result and effect of selection. Heritability and Genetic Advance when estimated together are more useful for predicting the genetic progress in selection as high heritability coupled with high genetic advance reflect preponderance of additive gene action Mili *et al.* (1994) <sup>[14]</sup> for adoption of appropriate breeding procedures. Further, Johnson *et al.* (1955) <sup>[10]</sup> reported that high heritability estimates along with high genetic gain were useful than heritability alone for effective selection. According to Johnson *et al.* (1955) <sup>[13]</sup> genetic advance as a percent of mean are classified as low (<10%, moderate (10-20%) and high (>20%). Therefore in the present study high heritability coupled with high genetic advance was recorded high in plant

height, number of primary branches per plant, fruit weight, fruit length, fruit girth, number of fruit per cluster and fruit yield per plant. Also, moderate heritability coupled with genetic advance value was observed in days to 50% flowering, days to 50% fruit set, days to first harvesting and number of fruit per plant. The lowest heritability coupled with genetic advance value was shown by number of flower per cluster. This result agrees with the finding of Shekar *et al.* (2012) <sup>[24, 25]</sup> and Arunkumar *et al.* (2013) <sup>[2]</sup>. Similarly, the characters like plant height, number of fruits per plant, fruit weight, fruit length, fruit girth and fruit yield per plant recorded high heritability with high genetic advance which indicated that most likely the heritability is due to additive gene effect Panse (1957) <sup>[17]</sup> and would respond well to selection. High value of genetic coefficients of variation and heritability estimates supplemented with greater genetic gains also indicated additive gene effect regulating the inheritance of such traits. These findings were in agreement with Karak *et al.* (2012) <sup>[11]</sup>, Prabakaran *et al.* (2013) <sup>[19]</sup>, and Yadav *et al.* (2014) <sup>[30]</sup>.

**Table 1:** List of brinjal genotypes and there sources

Sl. No.	Genotypes	Sources
1	CHFP-1	Nagaland
2	CHFP-2	Tripura
3	CHFP-3	West Bengal
4	CHFP-4	West Bengal
5	CHFP-5	West Bengal
6	CHFP-6	Riga (Arunachal Pradesh)
7	CHFP-7	Itanagar (Arunachal Pradesh)
8	CHFP-8	Pasighat (Arunachal Pradesh)
9	CHFP-9	Nari (Arunachal Pradesh)
10	CHFP-10	Mizoram (Arunachal Pradesh)
11	CHFP-11	Mirem (Arunachal Pradesh)
12	CHFP-12	Roing (Arunachal Pradesh)
13	CHFP-13	Yingkyong (Arunachal Pradesh)
14	CHFP-14	Boleng (Arunachal Pradesh)
15	CHFP-15	Sine (Arunachal Pradesh)
16	CHFP-16	Mebo (Arunachal Pradesh)
17	CHFP-17	AAU, Assam.
18	CHFB-18	AAU, Assam.
19	Kashi Taru	KVK, Pasighat (Arunachal Pradesh)
20	Pusa Purple Long	AAU, Assam.

**Table 2:** Anova Table

Sl. No.	Source of variation	Replication	Treatment	Error
1	Plant Height(cm)	31.18	1,797.48**	68.88
2	No. of primary branches/plant	1.59	10.24**	1.77
3	Days to 50% flowering	612.13**	186.33*	87.85
4	Days to 50% fruit set	465.24**	182.13*	77.28
5	Days to first harvest	439.88**	204.94**	69.56
6	Number of fruit per plant	68.28	58.01	34.95
7	fruit weight (mg)	11.86	2,849.71**	107.74
8	Fruit length (cm)	3.62	59.38**	3.53
9	Fruit girth (cm)	2.36	12.57**	3.39
10	Number of flower per cluster	1.34	0.75	0.58
11	Number of fruit per cluster	2.34	0.85	0.78
12	Fruit yield per plant (kg)	0.07	1.29**	0.12

**Table 3:** Genetic parameters for yield and yield attributing characters in Garden pea genotypes

S.N.	Characters	Range		Variance		Coefficient of variability (%)		Heritability %	Genetic advance	Genetic advance as % of mean (Genetic gain)
		Min	Max	Phenotypic	Genotypic	PCV	GCV			
1.	Plant height (cm)	60.6	151.1	645.08	576.20	22.77	21.52	89.32	62.16	55.73
2.	Nos. of primary branches/ plant	4.67	10.93	4.60	2.83	27.11	21.25	61.48	3.61	45.66
3.	Days to 50% flowering	44.66	72.66	120.67	32.82	18.92	9.87	27.20	8.19	14.10
4.	Days to 50% fruit set	56.77	83.00	112.23	34.95	15.34	8.56	31.14	9.04	13.09
5.	Days to 1 <sup>st</sup> harvesting	65.80	90.50	114.69	45.13	13.51	8.47	39.35	11.55	14.56
6.	Number of fruit per plant	36.67	12.17	42.64	7.69	32.49	13.80	18.03	3.23	16.05
7.	Fruit weight (g)	120.26	43.66	1021.73	913.99	38.01	35.95	89.46	78.35	93.16
8.	Fruit length (cm)	24.43	4.40	22.15	18.62	50.74	46.52	84.06	10.84	116.87
9.	Fruit girth (cm)	8.80	0.92	6.45	3.06	52.55	36.20	47.44	3.30	68.32
10.	Number of flower per cluster	3.47	1.10	0.64	0.06	30.46	9.04	8.81	0.19	7.35
11.	Number of fruit per cluster	1.00	3.40	0.437	0.428	52.57	52.03	97.01	1.33	106.07
12.	Fruit yield per plant (kg)	2.83	1.04	0.51	0.39	43.66	38.19	76.52	1.50	91.54

## Conclusion

As per the assessment of the genotypes, various important traits are fulfilling all the breeding objective and expressing potential for further crop improvement programme. High PCV and GCV was recorded in the parameters like number of fruit per plant, fruit weight, fruit girth and fruit yield per plant. Similarly, high heritability coupled with high genetic advance was observed for number of flower per cluster, fruit weight, plant height, fruit length and number of primary branches per plant. These characters are therefore, governed by additive gene effects. It may also be concluded that selection on the basis of these characters will be more useful for the improvement of this crop towards attaining higher fruit yield per plant. Thus, the investigation indicated that the present germplasm provided a wide base of variability and an appropriate genetic background for further selection to improve the yield and yield components of brinjal.

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