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### Estimation of heritability and genetic advance for fruit yield and its component traits in brinjal (*Solanum melongena* L.)

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#### ABSTRACT

The present investigation was conducted during Kharif seasons 2022-23 (Y1) and 2023-24 (Y2) to estimate heritability in the narrow sense and genetic advance in percent of mean using diallel mating design with ten diverse parents of brinjal. They were crossed in a diallel fashion (excluding reciprocals) for generating experimental material. All the ten parents and their 45 hybrids were grown in randomized block design with three replications. Observations were recorded for the twenty characters and the high heritability ( $h^2_{ns}$ ) coupled with high genetic advance as percent of mean were observed for fruit polar length, fruit equatorial circumference, length of calyx, average fruit weight, number of fruit per plant, fruit yield per plant, total phenol content in both the season (Y1, Y2) and over season pooled indicating thereby that these traits were less influenced by environment and were mainly under control of additive genes. This suggested that these characters could be improved through appropriate selection procedures.

**Keywords:** Brinjal, heritability, genetic advance, fruit yield.

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## INTRODUCTION

Brinjal, often referred to as aubergine or eggplant, is thought to have originated in India, where the cultivation of huge fruit types originally took place. Historical sources and botanical studies indicate that brinjal has been indigenous to Asia from ancient times. Renowned botanists such as De Candolle (1886) and Vavilov (1928) have determined that its origin can be traced back to the Indo-Burma region. Zeven and Zhukovsky (1975) observed the expansion of its presence in China during the 5th century B.C., followed by its subsequent distribution to Africa and Spain through Arabic traders.

Belonging to the Solanaceae family, brinjal comprises numerous species with a chromosome number of  $2n = 24$ . It exhibits significant morphological diversity in fruit shape and color, ranging from round to long, and white to deep purple. India, a leading producer of vegetables, cultivates brinjal over 0.758 million hectares, yielding 13.154 million tons annually with a productivity rate of 17.5 tonnes per hectare (Anonymous, 2021). Uttar Pradesh is a key region for brinjal cultivation, producing 2.75 million tons annually with high productivity. Nutritionally, brinjal is rich in proteins, vitamins, and minerals, and is widely used in dishes such as bhaji, stuffed brinjal, bharta, and pickles. Its medicinal properties are notable in treating diabetes, bronchitis, asthma, high blood pressure, osteoporosis, arthritis, Alzheimer's, and certain cancers (Sekar, *et al*, 2007 & Small, 2009). It also aids in curing stomach pains, abscesses, cracked nipples, fistula, piles, syphilitic eruptions, and various skin diseases (Matsubara *et al*, 2005).

Recent breeding efforts focus on improving traits like earliness, yield, and disease resistance. Hybridization has played a crucial role in enhancing these traits. Effective breeding programs require understanding the genetic components and selecting suitable parents for hybridization. The genetic factors, namely heritability and genetic progress, serve as valuable tools for breeders in selecting genotypes with favorable qualities for fruit output. The anticipated enhancement in the yield components is essentially contingent upon the characteristics and extent of the heritable fraction of the overall variance. The use of heredity alone may be deceptive, but when combined with genetic progress, the value of the heritability estimate improves.

## MATERIALS AND METHODS

The investigation conducted during *Khraif* seasons 2022-23 (Y1) and 2023-24 (Y2) to study the heritability in narrow sense and genetic advance in percent of mean by using diallel (except reciprocal) mating design at the Main Experiment Station (MES) of Department of Vegetable Science, Acharya Narendra Deva University of Agriculture and Technology, Narendra Nagar, Kumarganj, Ayodhya (U.P.) India. The experimental site is geographically, falls under a humid, sub-tropical climate and is located between 24.470 and 26.560 N latitude and 82.120 and 83.980 E longitude at an altitude of 113 m above the mean sea stratum in the Gangetic alluvial plains of Eastern Uttar Pradesh. The soil of the experimental site was sandy loam with average fertility level with pH in the range of 7.5-8.5. The selected parental lines i.e.; Pant Samrat (P1), Pant Rituraj (P2), Pusa Ankur (P3), NDB-Sel-19-1 (P4), NDB Sel-16-1 (P5), NDB - 3 (P6), Narendra Suyog (P7), KS-251 (P8), NDB - 2 (P9) and Co-2 (P10) were crossed in all possible cross combinations (excluding reciprocals) during year, 2021-22 to get 45 F<sub>1</sub>'s for the study of heritability in narrow sense and genetic advance in percent of mean. The mean of five plants was calculated and used for statistical analysis. A spacing of 1.2 m × 3 m was adopted and recommended agronomic practices were followed to raise a successful experimental crop. Observations were recorded for twenty characters as follows days to 50% Flowering, days to first fruit picking, fruit polar length (cm), fruit equatorial circumference (cm), plant height (cm), number of fruit per cluster, primary branches per plant, length of calyx (cm), length of pedicel (cm), leaf area (cm<sup>2</sup>), average fruit weight (g), number of fruits per plant, fruit yield per plant (kg), total phenol content (%), total soluble solid (T.S.S.) (brix), non-reducing sugar (%), total sugar(%), ascorbic acid (mg/100g), dry matter content (%). All the calculations were performed using the following formulae-

### (a) Heritability

Following Mather and Jinks (1971), narrow sense heritability was obtained as:

$$h^2(n) = \left[ \frac{\frac{1}{2D} + \frac{1}{2}H_1 - \frac{1}{2}H_2 - 1/2F}{\frac{1}{2D} + \frac{1}{2}H_1 - \frac{1}{4}H_2 - \frac{1}{2}F + E} \times 100 \right]$$

Where,

$\hat{D}$  = components of variation due to additive effects of gene

$\hat{H}_1$  = components of variation due to dominance effects of gene

$\hat{H}_2$  = Dominance, indicating asymmetry of positive and negative effects of genes

$\hat{E}$  = The expected environmental component of variation

**(b) Genetic advance (GA)**

Expected genetic advance (Ga) was estimated by the formula suggested by Johnson *et al* (1995).

$$\begin{aligned} \text{G.A.} &= \frac{\sigma^2g \times k\sigma p}{\sigma^2P} \\ &= K\sigma p h^2 \end{aligned}$$

Where,

$\sigma^2g$  = Genotypic variance

$\sigma^2p$  = Phenotypic variance

$\sigma p$  = Phenotypic standard deviation

K = Selection different at 5% selection intensity (2.06),

$$\text{GA}(\%) = \frac{\text{Genetic advance}}{\bar{X}} \times 100$$

Where,

$\bar{X}$  = grand mean of the character

**RESULT AND DISCUSSION**

The estimates of heritability in narrow-sense and genetic advance in percent of mean were presented under Table- 1. The estimates of heritability in narrow-sense ( $h^2_{ns}$ ) have been classified by Kempthorne and Curnow (1961) into three categories viz., high (> 30%), medium (10- 30%) and low (<10%). In the first year (Y1), the high estimate of heritability in narrow sense was recorded for days to first fruit picking (33.50%), fruit polar length (cm) (77.40%), fruit equatorial circumference (cm) (79.70%), length of calyx (cm) (38.40%), length of pedicle (cm) (76.00%), average fruit weight (g) (79.40%), number of fruit per plant (62.10%), fruit yield per plant (kg) (35.30%) and total phenol content (%) (77.40%). A moderate estimate of heritability in narrow sense was observed for days to 50% flowering (28.20%), plant height (cm) (17.60%), primary branches per plant (10.10%), leaf area ( $\text{cm}^2$ ) (13.40%), reducing sugar (%) (11.20%), non-reducing sugar (%) (12.80%), total sugar (%) (11.60%), TSS (%) (12.40%) and ascorbic acid (mg/100g) (19.60%). A low estimate of heritability in narrow-sense was observed for the number of fruit per cluster (9.20%) and dry matter content (%) (8.90%).

In the second year (Y2), the high estimate of heritability in the narrow sense was recorded for days to first fruit picking (31.70%), fruit polar length (cm) (85.90%), fruit equatorial

circumference (cm) (80.90%), length of calyx (cm) (32.00%), length of pedicle (cm) (74.80%), number of fruit per cluster (59.70%), average fruit weight (g) (79.40%), number of fruit per plant (64.20%), fruit yield per plant (kg) (41.90%) and total phenol content (%) (58.20%). Moderate estimate of heritability in narrow sense was observed for days to 50% flowering (15.90%), plant height (cm) (18.50%), primary branches per plant (12.60%), leaf area (cm<sup>2</sup>) (15.20%), dry matter content (%) (11.10%), reducing sugar (%) (11.60%), non-reducing sugar (%) (26.20%), total sugar (%) (11.50%) and ascorbic acid (mg/100g) (20.40%). Low estimate of heritability in narrow-sense was observed for TSS (%) (9.80%).

In case of pooled, the high estimate of heritability in narrow sense was recorded for days to first fruit picking (39.00%), fruit polar length (cm) (83.80%), fruit equatorial circumference (cm) (81.80%), length of calyx (cm) (37.30%), length of pedicle (cm) (78.00%), number of fruit per cluster (44.40%), average fruit weight (g) (79.60%), number of fruit per plant (65.70%), fruit yield per plant (kg) (39.90%) and total phenol content (%) (71.30%). Moderate estimate of heritability in narrow sense was observed for days to 50% flowering (24.80%), plant height (cm) (19.30%), primary branches per plant (12.30%), leaf area (cm<sup>2</sup>) (15.20%), dry matter content (%) (11.90%), reducing sugar (%) (11.00%), non-reducing sugar (%) (16.50%), total sugar (%) (11.20%), TSS (%) (13.10%) and ascorbic acid (mg/100g) (20.50%). Low estimate of heritability in narrow-sense ( $h^2_{ns}$ ) was not observed for any character in pooled.

Genetic advance was classified into three groups such as (i) high (> 20%) (ii) moderate (> 10% to 20%) and (iii) low (< 10%). In first season ( $Y_1$ ) high genetic advance in per cent of mean were estimated for leaf area (cm<sup>2</sup>) (20.67%), fruit polar length (cm) (38.14%), fruit equatorial circumference (cm) (40.56%), length of calyx (cm) (29.89%), length of pedicle (cm) (20.39%), average fruit weight (g) (53.96%), number of fruit per plant (40.44%), fruit yield per plant (kg) (36.05%), total phenol content (24.86%), reducing sugar (46.50%), non-reducing sugar (38.30%), total sugar (28.80%) and ascorbic acid (31.03%). The moderate genetic advance was estimated for plant height (11.42%), primary branches per plant (6.42%), number of fruit per cluster (7.51%), dry matter content (6.20%) and TSS (9.23%). The low genetic advance was recorded for days to 50% flowering (1.41%) and days to first fruit picking (1.21%).

**Table-1: Estimates of heritability in narrow sense and genetic advance in per cent of mean for twenty characters in brinjal over two years Y1 (2022-23), Y2 (2023-24) and over season pooled.**

S. No.	Characters	Heritability ( $h^2_{ns}\%$ )			Genetic advance in per cent of mean		
		Y1	Y2	Pooled	Y1	Y2	Pooled
1.	Days to 50% flowering	28.20	15.90	24.80	1.41	1.10	1.82
2.	Days to first fruit picking	33.50	31.70	39.00	1.21	1.18	1.72
3.	Plant Height (cm)	17.60	18.50	19.30	11.42	11.53	14.05
4.	Primary branches per plant	10.10	12.60	12.30	6.42	14.33	11.64
5.	Leaf area (cm <sup>2</sup> )	13.40	15.20	15.20	20.67	17.56	20.16
6.	Fruit Polar Length (cm)	77.40	85.90	83.80	38.14	37.94	38.61
7.	Fruit equatorial circumference (cm)	79.70	80.90	81.80	40.56	40.84	40.86
8.	Length of calyx (cm)	38.40	32.00	37.30	29.89	32.35	30.78
9.	Length of pedicle (cm)	76.00	74.80	78.00	20.39	18.20	20.75
10.	Number of fruit per cluster	9.20	59.70	44.40	7.51	3.21	4.85
11.	Average fruit weight (g)	79.40	79.40	79.60	53.96	53.56	55.42
12.	Number of fruit per plant	62.10	64.20	65.70	40.44	42.16	41.38
13.	Fruit yield per plant (Kg)	35.30	41.90	39.90	36.05	32.34	35.93
14.	Total phenol content (%)	77.40	58.20	71.30	24.86	22.19	23.44
15.	Dry matter content (%)	8.90	11.10	11.90	6.20	5.22	7.73
16.	Reducing sugar (%)	11.20	11.60	11.00	46.50	36.99	41.28
17.	Non reducing sugar (%)	12.80	26.20	16.50	38.30	37.27	34.25
18.	Total sugar (%)	11.60	11.50	11.20	28.80	24.45	26.18
19.	TSS (%)	12.40	9.80	13.10	9.23	7.06	9.85
20.	Ascorbic acid (mg/100g)	19.60	20.40	20.50	31.03	29.07	30.51

Genetic advance was classified into three groups such as (i) high (> 20%) (ii) moderate (> 10% to 20%) and (iii) low (< 10%). In first season ( $Y_1$ ) high genetic advance in per cent of mean were estimated for leaf area ( $\text{cm}^2$ ) (20.67%), fruit polar length (cm) (38.14%), fruit equatorial circumference (cm) (40.56%), length of calyx (cm) (29.89%), length of pedicle (cm) (20.39%), average fruit weight (g) (53.96%), number of fruit per plant (40.44%), fruit yield per plant (kg) (36.05%), total phenol content (24.86%), reducing sugar (46.50%), non-reducing sugar (38.30%), total sugar (28.80%) and ascorbic acid (31.03%). The moderate genetic advance was estimated for plant height (11.42%), primary branches per plant (6.42%), number of fruit per cluster (7.51%), dry matter content (6.20%) and TSS (9.23%). The low genetic advance was recorded for days to 50% flowering (1.41%) and days to first fruit picking (1.21%).

In second season ( $Y_2$ ) high genetic advance in per cent of mean were estimated for leaf area ( $\text{cm}^2$ ) (17.56%), fruit polar length (cm) (37.94%), fruit equatorial circumference (cm) (40.84%), length of calyx (cm) (32.35%), average fruit weight (g) (53.56%), number of fruit per plant (42.16%), fruit yield per plant (kg) (32.34%), total phenol content (22.19%), reducing sugar (36.99%), non-reducing sugar (37.27%), total sugar (24.45%) and ascorbic acid (29.07%). The moderate genetic advance was estimated for plant height (11.53%), primary branches per plant (14.33%), number of fruit per cluster (3.21%), dry matter content (5.22%) and TSS (7.06%). The low genetic advance was recorded for days to 50% flowering (1.10%) and days to first fruit picking (1.18%).

While in pooled season high genetic advance in per cent of mean were estimated for leaf area ( $\text{cm}^2$ ) (20.16%), fruit polar length (cm) (38.61%), fruit equatorial circumference (cm) (40.86%), length of calyx (cm) (30.78%), length of pedicle (cm) (20.75%), average fruit weight (g) (55.42%), number of fruit per plant (41.38), fruit yield per plant (kg) (35.93), total phenol content (23.44), reducing sugar (41.28%), non-reducing sugar (34.25%), total sugar (26.18%) and ascorbic acid (30.51%). The moderate genetic advance was estimated for plant height (14.05), primary branches per plant (11.64), number of fruit per cluster (4.85%), dry matter content (7.73%) and TSS (9.85%). The low genetic advance was recorded for days to 50% flowering (1.82%) and days to first fruit picking (1.72%).

High heritability coupled with high genetic advance were observed for fruit polar length, fruit equatorial circumference, length of calyx, length of pedicle, average fruit weight, number of fruit

per plant, fruit yield per plant, total phenol content in the year over season pooled. These results are in close conformity with the findings of Singh and Kumar (2005), Mili *et al.* (2014), Madhvi *et al.* (2015), Tabasum *et al.* (2024) and Sreevandana and Jana (2024).

Moderate heritability coupled with high genetic advance were observed for plant height, primary branches per plant, number of fruit per cluster, dry matter content and TSS. Whereas, the character days to 50% flowering, leaf area shows moderate heritability coupled with low genetic advance, while reducing sugar, non-reducing sugar, total sugar and ascorbic acid indicates moderate heritability coupled with high genetic advance.

Similar finding for moderate estimate of narrow sense heritability for different brinjal traits have been also reported by previous workers Chaudhary *et al.* 2023, Lodhi *et al.* 2023 and Nagar *et al.* 2024.

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