

Heritability and genetic advance studies on fruit yield and ~~its~~ its attributes traits in brinjal (*Solanum melongena* L.)

Abstract

The present investigation was conducted at the Main Vegetable Research Station, Anand Agricultural University, Anand during the period 2023-2024. The experimental material comprised twelve generations viz., P₁, P₂, F₁, F₂, B₁, B₂, B₁₁, B₁₂, B₂₁, B₂₂, B_{1S} and B_{2S} of four families involving eight diverse cultivars of brinjal (*Solanum melongena* L.) used to study the heritability and genetic advance of brinjal for yield and shoot and fruit borer incidence. The experiment was laid out in a compact family block design with three replications. High broad and narrow sense heritability was recorded days to first flowering in the family AB 20-13 × CO 2; branches per plant in the family AB 20-19 × GAOB 2; plant height in the family AB 20-19 × GAOB 2 and GPBRJ 204 × Arka Harshitha; leaf blade length in the family GPBRJ 204 × Arka Harshitha; leaf blade width in the family AB 20-13 × CO 2; fruit length in all families viz., AB 20-19 × GAOB 2, AB 20-13 × CO 2, Anand Harit × GJB 3 and GPBRJ 204 × Arka Harshitha; fruit girth in the family AB 20-19 × GAOB 2 and Anand Harit × GJB 3; fruit weight in the family AB 20-19 × GAOB 2, AB 20-13 × CO 2 and GPBRJ 204 × Arka Harshitha; fruit yield per plant in the family AB 20-19 × GAOB 2, Anand Harit × GJB 3 and GPBRJ 204 × Arka Harshitha. The higher value of broad and narrow sense heritability shows higher selection efficiency, permitting plant breeders to efficiently select individuals or groups of individuals. In crops like brinjal, high narrow sense heritability estimates are particularly beneficial for developing enhanced varieties through the fixation of additive gene effects.

Keywords :- Brinjal, Broad sense heritability, Narrow sense heritability and Genetic advance

1. INTRODUCTION

Brinjal (*Solanum melongena* L.) is an important vegetable crop in the Solanaceae family and is a species of nightshade [1]. It is also referred to as eggplant, guinea squash, or aubergine which is widely grown in the temperate, subtropics and tropics regions [2]. *Solanum* is a very great genus and amongst the 22 Indian species of brinjal, all are diploid and have the somatic chromosome number $2n = 2x = 24$. It is cultivated worldwide and originated from the Indo-Burma region. It is extremely productive and generally called the poor man's crop. Brinjal is a self-pollinated crop but the extent of cross-pollination is reported as high as 29 per cent because of the heterostyly condition hence it has been divided

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as often cross-pollinated crop or a facultative cross-pollinated crop [3]. It comprises a high quantity of carbohydrates (6.4%), fat (0.3%), protein (1.3%), phosphorus (0.02%), iron (0.0013%), calcium (0.02%) and other mineral matters [4].

The ultimate goal of any plant breeding programme is to create improved genotypes that are better than their current ones in one or more traits that produce higher economic yield. To create an effective breeding strategy, one must have a sufficient understanding of the inheritance of quantitative traits as well as information about fruit yield heritability, its components and quality traits [5]. Heritability is defined as the amount of the total variation in a given phenotype within the population that is attributed to genetic variance. The genetic improvement of a plant and the surrounding environment control the phenotypic expression of the plant trait. Thus, the magnitude of variability existing in some key gainful traits and their heritability along with genetic advances will be fruitful to the breeders for selecting effectively and creating sound breeding programs. Information about heritability assists plant breeders in predicting the nature of the progeny, forming a proper selection and evaluating the increase of genetic advancement through selection [2]. An enhancement in yield and quality of brinjal is normally accomplished by selecting the genotypes with the required trait combination prevailing in nature or by hybridization [6]. Hence, the present study was carried out to evaluate the broad and narrow sense heritability and genetic advance for thirteen traits in brinjal.

2. Material and Methods

2.1 Field evaluation

The material comprised eight genetically diverse genotypes of brinjal (AB 20-13, GAOB 2, AB 20-13, CO 2, Anand Harit, GJB 3, GPBRJ 204 and Arka Harshitha) which were selected based on morphological characters. There were four hybrids (AB 20-13 × GAOB 2, AB 20-13 × CO 2, Anand Harit × GJB 3 and GPBRJ 204 × Arka Harshitha) obtained from Main Vegetable Research Station, Anand Agricultural University, Anand. Backcrossing was done in *Kharif-rabi* 2021-22 with its respective parents. Selfing of F_{1S} was done in the same season to get F_{2S} and also made fresh F_1 . Again, double backcross was done in *Kharif-rabi* 2022-23 with its respective parents. Selfing of B_1 and B_2 was done in the same season to get B_{1S} and B_{2S} . The evaluation trial was conducted in *Kharif-rabi* 2023-24 at the Main Vegetable Research Station, Anand Agricultural University, Anand. The experimental material consists of twelve generations (P_1 , P_2 , F_1 , F_2 , B_1 , B_2 , B_{11} , B_{12} , B_{21} , B_{22} , B_{1S} and B_{2S}) of each of the four families in Compact Family Block Design with three replications. Each

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replication was classified into four compact blocks. Each family of twelve generations was randomly allotted to each plot within a block. Inter and intra-row spacing was 90 cm and 60 cm, respectively. Standard agronomical practices were followed to raise for better yield and healthy crops. The observations were recorded on thirteen characters viz., days first flowering, branches per plant, plant height (cm), leaf blade length (cm), leaf blade width (cm), fruit length (cm), fruit girth (cm), fruit length/girth ratio, fruits per plant, fruit yield per plant (kg), total soluble solids ($^{\circ}$ Brix) and shoot and fruit borer (%) incidences. These thirteen traits were recorded for each family i.e. from five plants in P₁, P₂ and F₁, ten plants in B₁ and B₂ and twenty plants in F₂, B₁₁, B₁₂, B₂₁, B₂₂, B_{1S} and B_{2S} generations.

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2.2 Statistical Analysis

2.2.1 Broad sense heritability

The broad sense heritability h^2_b (a) in per cent was calculated by using the formula reported by [7] as follows.

$$h^2_b(a)(\%) = \frac{VF_2 - \sqrt{VP_1 \times VP_2}}{VF_2} \times 100$$

The broad sense heritability h^2_b (b) in per cent was calculated by using the formula reported by [8] as follows.

$$h^2_b(b)(\%) = \frac{VF_2 - \frac{(VP_1 \times VP_2) + VF_1}{3}}{VF_2} \times 100$$

The broad sense heritability (c) in per cent was calculated by using the formula reported by [8] as follows.

$$h^2_b(c)(\%) = \frac{VF_2 - \frac{(VP_1 + VP_2)}{2}}{VF_2} \times 100$$

The broad sense heritability (d) in per cent was calculated by using the formula reported by [9] as follows.

$$h^2_b(d)(\%) = \frac{VF_2 - \frac{(VP_1 + VP_2 + 2VF_1)}{4}}{VF_2} \times 100$$

Where,

h^2_b = Heritability in broad sense

VF_2 = Variance of F₂ generation

VF_1 = Variance of F₁ generation

VP_2 = Variance of P₂ generation

VP_1 = Variance of P₁ generation

2.2.2 Narrow sense heritability

The narrow sense heritability in per cent was calculated by using the formula reported by [10] as follows...

$$h^2_n (\%) = \frac{2VF_2 - (VB_1 + VB_2)}{VF_2} \times 100$$

Where,

h^2_n = Heritability in the narrow sense

VF_2 = Variance of F_2 generation

VB_1 = Variance of B_1 generation

VB_2 = Variance of B_2 generation

The above heritability estimate is based on the assumption that epistasis is absent.

2.2.3 Expected genetic advance

The expected genetic advance at 5 % selection intensity was estimated by using the formula suggested by [8] as follows...

$$G.A. = h^2_{(ns)} \times k \times \sigma_p$$

Where,

$h^2_{(ns)}$ = heritability in narrow sense

k = selection differential ($k = 2.06$ at 5 % selection intensity)

σ_p = phenotypic standard deviation

3. Results and Discussion

Together broad and narrow sense heritability estimations are vital. Yet, in segregating generations, calculating narrow sense heritability offers further accurate results. Hence, narrow sense heritability is further beneficial for choosing segregating populations in this study. The genetic advance is calculated based on the narrow sense of heritability toward confirming reliable results and enhancements in the mean genotypic value of certain families over the base population. These results for different traits studied in four families of brinjal (AB 20-19 \times GAOB 2, AB 20-13 \times CO 2, Anand Harit \times GJB 3, and GPBRJ 204 \times Arka Harshitha) are presented in Tables 1

3.1 Days First to Flowering

The broad sense heritability recorded for days first to flowering fluctuated from 18.69 to 65.23 %. AB 20-13 \times CO 2 depicted high broad sense heritability (65.23 %), while Anand Harit \times GJB 3 (37.19 %) and GPBRJ 204 \times Arka Harshitha (52.30 %) had moderate heritability. AB 20-19 \times GAOB 2 showed low broad sense heritability (18.69 %). Narrow sense heritability estimates for this trait fluctuated from 4.11 % to 121.85 %, with the higher values found in AB 20-19 \times GAOB 2 (70.93 %) and AB 20-13 \times CO 2 (121.85 %), whereas

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GPBRJ 204 × Arka Harshitha observed low narrow sense heritability. The genetic advance estimates ranged from 0.93 % to 42.68 %. Higher genetic advance was found in AB 20-19 × GAOB 2 (24.33 %) and AB 20-13 × CO 2 (42.68 %), while, GPBRJ 204 × Arka Harshitha (0.93 %) observed lower genetic advance. Anand Harit × GJB 3 showed that negative values of narrow sense heritability and genetic advance for this trait (Table 1).

Higher heritability (both broad and narrow sense) coupled with higher genetic advance in AB 20-13 × CO 2 depicted a significant additive gene effect, indicating that direct selection could effectively improve this character in subsequent generations. Similarly, higher narrow sense heritability along with higher genetic advance in AB 20-19 × GAOB 2 signifies that additive gene action predominates, making direct selection in segregating generations more effective. These findings are supported by Sujin *et al.* [11], Rameshkumar *et al.* [12], Verma *et al.* [13], Gazala *et al.* [14], Devaraju *et al.* [6] and Lodhi *et al.* [15] who found high narrow sense heritability coupled with high genetic advance. The negative values for narrow sense heritability and genetic advance in Anand Harit × GJB 3 are similar to those reported by Rathava *et al.* (2021).

3.2 Branches per Plant

For branches per plant, broad sense heritability estimates fluctuated from 33.99 to 47.00 %. All the families observed moderate broad sense heritability such as AB 20-19 × GAOB 2 (47.00 %), AB 20-13 × CO 2 (45.66 %), Anand Harit × GJB 3 (33.99 %) and GPBRJ 204 × Arka Harshitha (36.67 %). Narrow sense heritability for this trait ranged from 11.55 to 108.66 %, with the higher value in AB 20-19 × GAOB 2 (108.66 %). Anand Harit × GJB 3 (37.41 %) depicted moderate narrow sense heritability, while AB 20-13 × CO 2 (11.55 %) was lower narrow sense heritability. Genetic advance estimates ranged from 5.72 to 59.83 %. AB 20-19 × GAOB 2 (59.83 %) found higher estimate of genetic advance, whereas Anand Harit × GJB 3 (19.52 %) recorded moderate genetic advance and AB 20-13 × CO 2 (5.72 %) depicted lower genetic advance for branches per plant. Anand GPBRJ 204 × Arka Harshitha found that negative values of narrow sense heritability and genetic advance for this trait Table 1.

The higher to moderate broad sense heritability and higher narrow sense heritability couple with higher genetic advance recorded in AB 20-19 × GAOB 2, suggesting the predominant role of additive gene action in this trait's expression. Hence, selecting an increased number of branches per plant in succeeding generations has promising. The results similar with the findings of Sujin *et al.* [11], Gupta *et al.* [16], Tiwari *et al.* [17], Verma *et al.* [13], Balas *et al.* [1], Gazala *et al.* [14], Jirankaliet *et al.* [18], Devaraju *et al.* [6],

Anbarasi & Haripriya [19], Chithra *et al.* [20] and Rameshkumar *et al.* [12] who found high broad sense heritability along with high genetic advance. The findings are also consistent with Savaliya *et al.* [21] who noted moderate narrow sense heritability with higher genetic advance. The values of negative for narrow sense heritability and genetic advance in GPBRJ 204 × Arka Harshitha similar with earlier found by Mistry *et al.* [22].

4.3 Plant Height

The broad sense heritability estimates for plant height ranged from 27.32 to 82.05 %. Higher broad sense heritability noted in AB 20-19 × GAOB 2 (75.29 %), Anand Harit × GJB 3 (82.05 %) and GPBRJ 204 × Arka Harshitha (74.55 %), whereas AB 20-13 × CO 2 depicted lower broad sense heritability (27.32%). Narrow sense heritability estimates fluctuated from 53.53 to 144.09 %, with the higher values in AB 20-19 × GAOB 2 (144.09 %), GPBRJ 204 × Arka Harshitha (141.70 %) and AB 20-13 × CO 2 (71.24 %). Anand Harit × GJB 3 observed moderate narrow sense heritability (53.53 %). Genetic advance estimates varied from 5.72 to 59.83 %, with higher values in AB 20-19 × GAOB 2 (50.22 %), AB 20-13 × CO 2 (20.17 %) and GPBRJ 204 × Arka Harshitha (47.17 %). Anand Harit × GJB 3 had moderate genetic advance (16.61 %) in Table 1.

The higher heritability (both broad and narrow sense) along with higher genetic advance observed in AB 20-19 × GAOB 2 and GPBRJ 204 × Arka Harshitha, suggesting the predominant additive gene effect, indicates that direct selection could be effective for improving plant height in subsequent generations. The higher narrow sense heritability coupled with the moderate genetic advance in AB 20-13 × CO 2 also indicates the presence of additive gene effects, suggesting potential for improvement through selection in segregating generations. These above results are similar to the findings of Chaudhary & Kumar [23], Kumari *et al.* [24], Savaliya *et al.* [21], Sujin *et al.* [11], Gupta *et al.* [16], Verma *et al.* [13], Jirankaliet *et al.* [18], Jayalakshmi *et al.* [25], Patil *et al.* [26], Chithra *et al.* [20], Sailesh *et al.* [27] and Mohanty [28] who depicted higher broad sense heritability with higher genetic advance.

3.4 Leaf Blade Length

The broad sense heritability estimates for this trait ranged from 22.17 to 83.73 %. AB 20-13 × CO 2 (83.73 %) and GPBRJ 204 × Arka Harshitha (62.21 %) recorded higher broad sense heritability. While Anand Harit × GJB 3 (41.00 %) showed moderate broad sense heritability and AB 20-19 × GAOB 2 (22.17 %) found low broad sense heritability. The narrow sense heritability estimates for leaf blade length fluctuated from 12.94 to 74.31 %. Narrow sense heritability was higher in GPBRJ 204 × Arka Harshitha (74.31 %). AB 20-13 ×

CO 2 (58.10 %) observed a moderate estimate of narrow sense heritability, whereas AB 20-19 × GAOB 2 (15.83 %) and Anand Harit × GJB 3 (12.94 %) found lower narrow sense heritability. Genetic advance estimates ranged from 3.26 to 24.54 %. A higher estimate of genetic advance was noted in GPBRJ 204 × Arka Harshitha (24.54 %), whereas AB 20-13 × CO 2 (17.40 %) was the moderate estimate of genetic advance. The lower genetic advance was recorded in AB 20-19 × GAOB 2 (3.26 %) and Anand Harit × GJB 3 (3.41 %) in Table 1.

The higher heritability (both broad and narrow sense) along with higher genetic advance in GPBRJ 204 × Arka Harshitha, suggest an important additive gene effect which indicates that direct selection could be useful for improving this trait in subsequent generations. A similar finding was reported by Kumar *et al.* [29].

3.5 Leaf Blade Width

The broad sense heritability estimates for this leaf blade width ranged from 2.52 to 83.73 %. AB 20-13 × CO 2 (72.72 %) observed higher broad sense heritability, whereas Anand Harit × GJB 3 (41.23 %) showed moderate broad sense heritability. Low broad sense heritability was observed in AB 20-19 × GAOB 2 (2.52 %) and GPBRJ 204 × Arka Harshitha (21.20 %). The narrow sense heritability estimates ranged from 13.73 to 69.51 %. Higher narrow sense heritability was found in AB 20-13 × CO 2 (69.51 %). AB 20-19 × GAOB 2 (38.70 %). GPBRJ 204 × Arka Harshitha (54.38 %) depicted moderate narrow sense heritability, whereas Anand Harit × GJB 3 (13.73 %) had lower narrow sense heritability for leaf blade width. The genetic advance estimates fluctuated from 2.74 to 22.09 %. AB 20-13 × CO 2 (22.09 %) depicted higher genetic advance. The moderate genetic advance was noted in GPBRJ 204 × Arka Harshitha (13.50 %), whereas AB 20-19 × GAOB 2 (8.73 %) and Anand Harit × GJB 3 (2.74 %) were found to lower estimates of genetic advance for this trait in Table 1.

The higher broad and narrow sense heritability along with the higher genetic advance in AB 20-13 × CO 2 suggests the predominant role of additive gene action which indicates that this trait could be fixed and improved through direct selection. These findings agree with those of Kumar *et al.* [29].

4.6 Fruit Length

The broad sense heritability estimates for this trait ranged from 68.11 to 88.31 %. The results showed that all families had higher estimates of broad sense heritability. The narrow sense heritability estimates for fruit length ranged from 60.25 to 89.44 %. The AB 20-13 × CO 2 (89.44 %) found the higher value of narrow sense heritability followed by AB 20-19 × GAOB 2 (82.50 %), GPBRJ 204 × Arka Harshitha (82.44 %) and Anand Harit × GJB 3

(60.25 %). The estimates of genetic advance fluctuated from 26.69 to 34.43 %. Higher estimates of genetic advance observed in all families *i.e.*, AB 20-19 × GAOB 2 (34.43 %) followed by GPBRJ 204 × Arka Harshitha (33.21 %), AB 20-13 × CO 2 (28.59 %) and Anand Harit × GJB 3 (26.69 %)(Table 1).

The higher broad and narrow sense heritability combined with the higher genetic advance observed in all four families, indicates the predominant role of additive gene action in the expression of the fruit length. This suggests that direct selection may effectively fix and improve the trait. These above results conform with the reports of Chaudhary & Kumar [23], Kumari *et al.* [24], Ravali *et al.* [30], Sujin *et al.* [11], Gupta *et al.* [16], Tiwari *et al.* [17], Balas *et al.* [1], Devaraju *et al.* [6], Jayalakshmi *et al.* [25], Kumar *et al.* [29], Anbarasi & Haripriya [19], Bidaramali *et al.* [31], Prajapati *et al.* [32], Durga *et al.* [3], Soumya *et al.* [34], Lodhi *et al.* [15], Verma *et al.* [34] and Sailesh *et al.* [27] as they recorded high estimates of heritability along with high genetic advance.

3.7 Fruit Girth

Broad sense heritability estimates for this trait ranged from 60.91 to 80.41 %. The broad sense heritability depicted higher in GPBRJ 204 × Arka Harshitha (80.41 %), AB 20-13 × CO 2 (61.17 %), Anand Harit × GJB 3 (60.91 %) and AB 20-19 × GAOB 2 (69.40 %). The narrow sense heritability estimates for fruit girth ranged from 48.83 to 91.69 %. The higher value of narrow sense heritability had found in GPBRJ 204 × Arka Harshitha (91.69 %) and AB 20-19 × GAOB 2 (76.67 %), while it was moderate in AB 20-13 × CO 2 (51.98 %) and Anand Harit × GJB 3 (48.83 %). The estimates of genetic advance varied from 17.67 to 22.10 %. Higher estimates of genetic advance were depicted in Anand Harit × GJB 3 (21.96 %) and GPBRJ 204 × Arka Harshitha (20.37 %). AB 20-13 × CO 2 (18.39 %) and AB 20-19 × GAOB 2 (17.93 %) recorded moderate genetic advance (Table 1).

Higher heritability (both broad and narrow sense) and higher genetic advance were observed in GPBRJ 204 × Arka Harshitha, indicating the significant role of additive gene effects. These present results conform with the reports of Chaudhary & Kumar [23], Gavade & Ghadage [35], Kumari *et al.* [24], Ravali *et al.* [30], Sujin *et al.* (2017), Dineshkumar *et al.* [4], Balas *et al.* [1], Gazala *et al.* [14], Jayalakshmi *et al.* [25], Datta *et al.* [2], Prajapati *et al.* [32], Chithra *et al.* [20], Rameshkumar *et al.* [12], Lodhi *et al.* [15], Verma *et al.* [34] and Sailesh *et al.* [27] as they found higher values of broad heritability coupled with higher genetic advance and also Savaliya *et al.* [21] who reported higher narrow sense heritability along with higher genetic advance.

3.8 Fruit Length/Girth Ratio

Broad sense heritability for this trait ratio ranged from 51.12 to 80.78 %. Higher broad sense heritability was found in GPBRJ 204 × Arka Harshitha (80.78 %), whereas it had found moderate in AB 20-13 × CO 2 (56.31 %), Anand Harit × GJB 3 (55.12 %) and AB 20-19 × GAOB 2 (51.12 %). The estimate of narrow sense heritability for this trait varied from 32.33 to 46.60 %. Moderate narrow sense heritability was reported in GPBRJ 204 × Arka Harshitha (46.60 %), AB 20-13 × CO 2 (46.31 %) and AB 20-19 × GAOB 2 (32.33 %) with the rest of the family III showing negative values. The estimate of genetic advance ranged from 8.66 to 17.67 %. Moderate genetic advance was depicted in AB 20-13 × CO 2 (17.67 %) and GPBRJ 204 × Arka Harshitha (17.10 %), while AB 20-19 × GAOB 2 (8.66 %) reported a lower estimate of genetic advance and the rest of family III was negative values (Table 1).

Higher broadsense and narrow sense heritability along with moderate genetic advance observed in AB 20-13 × CO 2 and GPBRJ 204 × Arka Harshitha revealed the involvement of additive gene action, suggesting that direct selection for improving this trait in segregating generations of these families would be more effective. In AB 20-19 × GAOB 2, the moderate estimate of narrow sense heritability and low genetic advance indicated a preponderance of non-additive gene effects for the inheritance of the character, making it difficult to improve through direct selection. Therefore, heterosis breeding is recommended for the improvement of this character. These present findings were analogous to the results of Datta *et al.* [2] who found high heritability along with high genetic advance.

3.9 Fruit Weight

The broad sense heritability estimates for this trait ranged from 51.68 to 83.47 %. The Anand Harit × GJB 3 (83.47 %) and AB 20-19 × GAOB 2 (77.33 %) recorded higher broad sense heritability, while GPBRJ 204 × Arka Harshitha (59.04 %) and AB 20-13 × CO 2 (51.68 %) found moderate estimate of broad sense heritability. The estimates of narrow sense heritability for fruit weight fluctuated from 60.91 to 80.41 %. All the families *viz.*, AB 20-19 × GAOB 2 (89.41 %), Anand Harit × GJB 3 (87.17 %) and GPBRJ 204 × Arka Harshitha (72.80 %) exhibited higher narrow sense heritability, while in AB 20-13 × CO 2 (38.74 %) showed moderate estimate of narrow sense heritability. The genetic advance estimates fluctuated from 16.27 to 51.38 %. AB 20-13 × CO 2 (16.27 %) was a moderate genetic advance, while AB 20-19 × GAOB 2 (51.38 %), GPBRJ 204 × Arka Harshitha (50.18 %) and Anand Harit × GJB 3 (49.18 %) showed higher estimate of genetic advance for fruit weight in Table 1.

Higher broad and narrow sense heritability coupled with the higher genetic advance in Anand Harit \times GJB 3 and GPBRJ 204 \times Arka Harshitha revealed the predominant role of additive gene effect in the expression of the trait. This suggests that the trait could be effectively fixed and improved through direct selection. These present results conform with the finding of Chaudhary & Kumar [25] Ravali *et al.* [30], Savaliya *et al.* [21], Sujin *et al.* [11], Gupta *et al.* (2018), Dineshkumar *et al.* [4], Tiwari *et al.* [17], Gazala *et al.* [14], Jirankaliet *al.* [18], Kumar *et al.* [29], Anbarasi & Haripriya [19], Bidaramaliet *al.* [31], Rameshkumar *et al.* [12], Sailesh *et al.* [27], Sonagara *et al.* [36], Verma *et al.* [34], Mohanty [28] and Rathod *et al.* [37] as they noted higher estimates of heritability coupled with higher genetic advance.

3.10 Fruits per Plant

Broad sense heritability estimates for fruits per plant ranged from 31.65 to 56.96 %. All families exhibited moderate broad sense heritability. Narrow sense heritability for this trait ranged from 20.55 to 114.09 %. Anand Harit \times GJB 3 (114.09 %) and AB 20-13 \times CO 2 (61.29 %) found the higher narrow sense heritability, while moderate values recorded in AB 20-19 \times GAOB 2 (27.96 %) and GPBRJ 204 \times Arka Harshitha (20.55 %). In these four families, narrow sense heritability estimates were higher than broad sense heritability because of gene \times environment interactions. Estimates of genetic advance fluctuated from 7.05 to 31.23 %. The higher genetic advance was showed in AB 20-13 \times CO 2 (31.23 %) and Anand Harit \times GJB 3 (27.50 %), while moderate in AB 20-19 \times GAOB 2 (11.38 %) and lower in GPBRJ 204 \times Arka Harshitha (7.05 %) in Table 1.

Anand Harit \times GJB 3 and AB 20-13 \times CO 2 depicted higher broad and narrow sense heritability along with higher genetic advance which indicates the predominant role of additive gene effect in the inheritance of fruits per plant. This suggests the potential for fixing and improving this trait through direct selection in subsequent generations. These results agree with the reports of Chaudhary & Kumar [25], Mistry *et al.* [22], Kumari *et al.* [24], Ravali *et al.* [30], Sujin *et al.* [11], Dineshkumar *et al.* [4], Verma *et al.* [13], Balas *et al.* [1], Gazala *et al.* [14], Jirankaliet *al.* [18], Pandey *et al.* [38], Pramila *et al.* [39], Devaraju *et al.* [6], Kumar *et al.* [29], Bidaramaliet *al.* [31], Prajapati *et al.* [32], Patil *et al.* [26], Rameshkumar *et al.* [12], Lodhi *et al.* [15], Sonagara *et al.* [36], Mohanty [28] and Rathod *et al.* [37] as they exhibited higher estimates of heritability coupled with higher genetic advances.

3.11 Fruit Yield per Plant

The broad sense heritability estimates for fruit yield per plant varied from 27.08 to 88.84 %. AB 20-19 × GAOB 2 (131.51 %), Anand Harit × GJB 3 (143.99 %) and AB 20-13 × CO 2 (31.23 %) recorded moderate estimates of broad sense heritability and GPBRJ 204 × Arka Harshitha (102.04 %) depicted lower values of broad sense heritability. The estimates of narrow sense heritability for fruit weight fluctuated from 51.52 to 143.99 %. The estimates of narrow sense heritability were extremely higher in Anand Harit × GJB 3 (143.99%), AB 20-19 × GAOB 2 (131.51 %) and GPBRJ 204 × Arka Harshitha (102.04 %). Moderate narrow sense heritability was found in AB 20-13 × CO 2 (51.52 %). The estimates of genetic advance ranged from 27.45 to 119.83 %. All the families exhibited high genetic advances in fruit yield per plant in Table 1.

AB 20-19 × GAOB 2, AB 20-13 × CO 2 and Anand Harit × GJB 3 recorded moderate to higher estimates of broad and narrow sense heritability coupled with higher genetic advance. This indicates the importance of additive gene action, suggesting that direct selection for improving this trait in the segregating generation of these families would be rewarding. These results were in concurrence with the findings of Chaudhary & Kumar [25], Kumari *et al.* [24], Ravali *et al.* [30], Sujin *et al.* [11], Dineshkumaret *al.* [4], Tiwari *et al.* [17], Verma *et al.* [13], Gazala *et al.* [14] Pandey *et al.* [38], Pramila *et al.* [39], Anbarasi & Haripriya [19], Chithra *et al.* [20], Datta *et al.* [2], Prajapati *et al.* [32], Patil *et al.* [26], Durga *et al.* [3], Sailesh *et al.* [27], Soumya *et al.* [33], Verma *et al.* [34], Mohanty [28] and Rathod *et al.* [37] who recorded higher heritability along with higher genetic advance as observed in present study.

3.12 Total Soluble Solids

The broad sense heritability estimates for total soluble solids ranged from 25.39 to 42.94 %. Anand Harit × GJB 3 (42.94 %), followed by AB 20-13 × CO 2 (34.55 %), AB 20-19 × GAOB 2 (34.39 %) and GPBRJ 204 × Arka Harshitha (25.39 %) recorded moderate estimates of broad sense heritability. Narrow sense heritability for this trait fluctuated from 30.84 to 57.89 %. Anand Harit × GJB 3 recorded the higher narrow sense heritability (57.89 %), followed by GPBRJ 204 × Arka Harshitha (36.56 %) and AB 20-13 × CO 2 (34.55 %), while the remaining families had negative values. Genetic advance estimates fluctuated from 11.24 to 18.43%, with Anand Harit × GJB 3 (18.43 %), GPBRJ 204 × Arka Harshitha (13.71 %), and AB 20-13 × CO 2 (11.24 %) exhibited higher genetic advance in Table 1.

The moderate estimates of broad and narrow sense heritability along with higher genetic advance in AB 20-13 × CO 2, Anand Harit × GJB 3 and GPBRJ 204 × Arka Harshitha indicate that direct selection for improvement of this trait in the segregating

generation may be useful. These above findings confirm the reports of Sailesh et al. (2023), who recorded moderate broadsense heritability. The above results are similar to the findings of Chaudhary & Kumar [25], Gazala *et al.* [14], Bidaramali *et al.* [31], Chithra *et al.* [20], Sonagara *et al.* [36] and Rathod *et al.* [37] who reported higher genetic advance for this trait.

3.13 Shoot and Fruit Borer Incidence

The broad sense heritability estimates for this trait fluctuated from 26.90 to 65.82 %. AB 20-13 × CO 2 (65.82 %) recorded a higher estimate of broad sense heritability. Anand Harit × GJB 3 (42.67 %) was found moderate and also GPBRJ 204 × Arka Harshitha (29.03 %) depicted lower values of broad sense heritability. The estimates of narrow sense heritability for fruit weight fluctuated from 22.92 to 68.53 %. The higher value of narrow sense heritability was observed in AB 20-13 × CO 2 (68.38 %). Anand Harit × GJB 3 (22.93 %), AB 20-19 × GAOB 2 (22.92 %) exhibited moderate narrow sense heritability. Genetic advance estimates fluctuated from 7.84 to 37.38 %, with AB 20-13 × CO 2 (37.38 %) exhibiting high genetic advance. AB 20-19 × GAOB 2 (11.81 %) depicted moderate genetic advance and also Anand Harit × GJB 3 (7.84 %) revealed lower genetic advance for this trait. While the remaining family IV had negative values (Table 1).

AB 20-13 × CO 2 exhibited higher estimates of broad and narrow sense heritability along with higher genetic advance. This suggests the importance of additive gene action which indicates that direct selection for improving this trait in the segregating generation of these crosses would be effective. These results are in agreement with the findings of Ravali *et al.* [30], Savaliya *et al.* [21] who found high narrow sense heritability with high genetic advance, Sujin *et al.* [11], Dineshkumar *et al.* (2018), Verma *et al.* [13], Balas *et al.* [1], Jirankali *et al.* [18], Durga *et al.* [3] and Rameshkumar *et al.* [12] who recorded high broad sense heritability coupled high genetic advance.

Table 1 Estimates of heritability and genetic advance for different traits in four families in Brinjal

Family	Broad sense heritability (%)					Narrow sense heritability (%)	Genetic advance (% of mean)
	h ² bs (a)	h ² bs (b)	h ² bs (c)	h ² bs (d)	h ² bs Mean		
1. Days to first flowering							
Family-I	24.71	@	11.63	20.22	18.85	70.93	24.33
Family-II	63.88	@	63.64	68.16	65.23	121.85	42.68
Family-III	30.64	@	30.33	50.59	37.19	@	@
Family-IV	53.40	@	51.20	@	52.30	4.11	0.93

Maximum	63.88	@	63.64	68.16	65.23	121.85	42.68
Minimum	24.71	@	11.63	20.22	18.69	4.11	0.93
2. Branches per plant							
Family-I	32.87	76.50	32.87	45.74	47.00	108.66	59.83
Family-II	48.95	61.93	47.55	24.22	45.66	11.55	5.72
Family-III	31.97	43.71	26.29	@	33.99	37.41	19.52
Family-IV	@	36.67	@	@	36.67	@	@
Maximum	48.95	76.50	47.55	45.74	47.00	108.66	59.83
Minimum	31.97	36.67	26.29	24.22	33.99	11.55	5.72
3. Plant height (cm)							
Family-I	75.74	@	74.75	75.37	75.29	144.09	50.22
Family-II	33.37	@	32.89	15.69	27.32	71.24	20.17
Family-III	88.21	@	88.03	69.89	82.05	53.53	16.61
Family-IV	77.25	@	76.57	69.81	74.55	141.70	47.27
Maximum	88.21	@	88.03	75.37	82.05	144.09	50.22
Minimum	33.37	@	32.89	15.69	27.32	53.53	16.61
4. Leaf blade length (cm)							
Family-I	23.01	9.97	@	33.51	22.17	15.83	3.26
Family-II	80.52	87.90	88.11	78.39	83.73	58.10	17.40
Family-III	49.88	41.15	44.54	28.44	41.00	12.94	3.41
Family-IV	70.39	50.93	68.28	59.25	62.21	74.31	24.54
Maximum	80.52	87.90	88.11	78.39	83.73	74.31	24.54
Minimum	23.01	9.97	44.54	33.51	22.17	12.94	3.26
5. Leaf blade width (cm)							
Family-I	@	@	@	2.52	2.52	38.70	8.73
Family-II	73.54	78.39	72.61	66.37	72.73	69.51	22.09
Family-III	38.34	59.91	33.62	33.06	41.23	13.73	2.74
Family-IV	25.81	6.22	25.72	27.04	21.20	54.38	13.50
Maximum	73.54	78.39	77.61	66.37	72.73	69.51	22.09
Minimum	25.81	6.22	25.72	2.52	2.52	13.73	2.74
6. Fruit length (cm)							
Family-I	86.49	58.34	80.59	47.03	68.11	82.50	34.43
Family-II	76.11	87.13	75.48	72.87	77.90	89.44	28.59
Family-III	76.55	73.79	74.22	77.69	75.56	60.25	26.29
Family-IV	88.64	93.40	88.70	82.49	88.31	82.67	33.21
Maximum	88.64	93.40	88.70	82.49	88.31	89.44	34.43
Minimum	76.11	58.34	74.22	47.03	68.11	60.25	26.69
7. Fruit girth (cm)							
Family-I	81.09	70.09	71.31	55.10	69.40	76.67	17.93
Family-II	69.71	63.28	59.70	52.00	61.17	51.98	18.39
Family-III	34.32	@	75.56	72.85	60.91	91.69	21.96
Family-IV	84.42	82.05	84.08	71.07	80.41	48.83	20.37
Maximum	84.42	82.05	84.08	72.85	80.41	91.69	21.96
Minimum	34.32	63.28	59.70	52.00	60.91	48.83	17.93
8. Fruit length/girth ratio							
Family-I	62.73	66.73	50.00	25.00	51.12	32.33	8.66
Family-II	62.75	75.00	50.00	37.50	56.31	46.31	17.67
Family-III	54.83	76.14	50.22	39.29	55.12	@	@

Family-IV	76.17	92.97	76.09	77.90	80.78	46.60	17.10
Maximum	54.83	92.97	76.09	77.90	80.78	46.60	17.67
Minimum	76.17	66.73	50.00	25.00	51.15	32.33	8.66
9. Fruit weight (g)							
Family-I	81.25	@	81.23	69.50	77.33	89.41	51.38
Family-II	52.15	@	52.12	50.76	51.68	38.74	16.27
Family-III	87.80	@	80.52	82.08	83.47	87.17	49.18
Family-IV	62.93	@	56.96	54.25	59.04	72.80	50.18
Maximum	87.80	@	81.23	82.08	83.47	89.41	51.38
Minimum	52.15	@	52.12	50.76	51.68	38.74	16.27
10. Fruits per plant							
Family-I	64.16	29.39	64.09	70.19	56.96	27.96	11.38
Family-II	59.68	@	49.80	54.71	54.73	61.19	31.23
Family-III	51.97	42.41	51.69	35.99	45.52	114.09	27.50
Family-IV	9.62	@	54.47	30.85	31.65	20.55	7.05
Maximum	64.16	42.41	64.09	70.19	56.96	114.09	31.23
Minimum	9.62	29.39	49.80	30.85	31.65	20.55	7.05
11. Fruit yield per plant (kg)							
Family-I	89.02	92.04	88.78	85.51	88.84	131.51	119.83
Family-II	59.08	94.86	55.55	67.74	69.31	51.52	27.45
Family-III	86.75	85.95	80.75	70.81	81.07	143.99	100.16
Family-IV	33.74	46.58	5.64	22.39	27.08	102.04	96.90
Maximum	89.02	94.86	88.78	85.51	88.84	143.99	119.83
Minimum	33.74	46.58	5.64	22.39	27.08	51.52	27.45
12. Total soluble solid (°Brix)							
Family-I	@	34.39	@	@	34.39	@	@
Family-II	34.53	46.37	34.32	22.99	34.55	30.84	11.24
Family-III	61.71	46.35	58.16	5.54	42.94	57.89	18.43
Family-IV	23.77	38.64	23.53	15.60	25.39	36.56	13.71
Maximum	61.71	46.37	58.16	22.99	42.94	57.89	18.43
Minimum	23.77	34.39	23.53	5.57	25.39	30.84	11.24
13. Shoot and fruit borer incidence (%)							
Family-I	@	@	@	@	@	22.93	11.81
Family-II	65.11	64.09	64.40	69.69	65.82	68.53	37.38
Family-III	34.59	9.45	34.54	29.03	26.90	22.92	7.84
Family-IV	41.23	@	36.84	49.92	42.67	@	@
Maximum	65.11	64.09	64.40	69.69	65.82	68.53	37.38
Minimum	41.23	9.45	34.54	29.03	26.90	22.92	7.84

@ = Negative estimates

4. Conclusion

Higher estimates of heritability (broad and narrow sense) coupled with higher genetic advance depicted for fruit yield per plant in family I (AB 20-19 × GAOB 2) and family III (Anand Harit × GJB 3) which suggest the predominance of additive/fixable gene actions. This trait would be further improved by adopting selection in succeeding segregating generations. Conversely, lower narrow sense heritability along with lower genetic advance, it showed that

Comment [F22]:

Comment [F23]:

there for days to first flowering in IV, leaf blade length and width in family III and fruits per plant in family IV, suggest the preponderance of non-additive gene action and heterosis breeding or population improvement approaches may be useful for these traits.

5. References

1. Balas, A., Jivani, L. L., Valu, M. G., Sakriya, S. G., Gamit, U. C. & Rathod, R. K. (2019). Study of genetic variability and heritability in brinjal (*Solanum melongena* L.). *The Pharma Innovation Journal*, 8 (9), 44-46.
2. Datta, D. R., Rafii, M. Y., Misran, A., Jusoh, M., Yusuff, O., Sulaiman, N. M. & Momodu, J. (2021). Genetic diversity, heritability and genetic advance of *Solanum melongena* L. from three secondary centres of diversity. *Bangladesh Association of Plant Taxonomists*, 28 (1), 155-69.
3. Durga, H., Kumar, C. H., Uma J. K. Kumara, U., Kranthi, R. G. & Paratpara, R. M. (2022). Studies on variability, heritability and genetic advance in F^2 generation of Brinjal (*Solanum melongena* L.) for different yield attributing characters. *The Pharma Innovation Journal*, 11 (5), 2121-23.
4. Dineshkumar, S., Praneetha, S. & Manikandapoobathi, N. (2018). Variability, heritability and genetic advance for qualitative and quantitative characters in brinjal (*Solanum melongena* L.). *International Journal of Chemical Studies*, 6 (3), 280-82.
5. Rathava, K. V., Acharya, R. R. & Damor, A. S. (2021). Studies on heritability and genetic advance for fruit yield and its component traits in segregating generations of brinjal (*Solanum melongena* L.). *The Pharma Innovation*, 10(10), 1652-1655.
6. Devaraju, Indires, K. M., Srinivasa, V., Lakshmana, D., Singh, T. H., Devappa, V. & Venugopalan, R. (2020). Studies on variability components for yield and its attributes in Brinjal (*Solanum melongena* L.) under hill zone of Karnataka. *Journal of Pharmacognosy and Phytochemistry*, 9 (2), 2200-03.
7. Mahmud, I. & Kramer, H. H. (1951). Segregation for yield, height and maturity following soybeans cross 1. *Agronomy Journal*, 43 (12), 605-609.
8. Allard, R. W. (1960). *Principles of Plant Breeding*. John Wiley and Sons. Inc. New York.
9. Mather, J. & Jinks, J. L. (1971). *Biometrical Genetics*. 3rd edition, Chapman and Hall Ltd., London, pp. 126-33.
10. Warner, J. N. (1952). Method for estimating heritability. *Agronomy Journal*, 44, 427-30.

11. Sujin, G. S., Karuppaiah, P. & Saravanan, K. (2017). Genetic variability and correlation studies in brinjal (*Solanum melongena* L.). Indian Journal of Agricultural Research, 51 (2), 112-19.
12. Rameshkumar, D., Swarna, P. R., Savitha, B. K. & Ravikesavan, R. (2022). Genetic variability and correlation analysis in F₂ segregating population in brinjal (*Solanum melongena* L.). Journal of Applied and Natural Science, 14 (SI), 151-54.
13. Verma, P., Kushwaha, M. L., & Panchbhaiya, A. (2018). Studies on variability, heritability and genetic advance for yield attributing traits in brinjal (*Solanum melongena* L.) for two different seasons. International Journal of Current Microbiology and Applied Sciences, 7 (9), 1543-52.
14. Gazala, N., Jabeen, N., Mushtaq Chatto, M., Hussain, K., Afroza, B. & Berges, S. (2019). Variability, Heritability and Genetic Advance studies in Brinjal (*Solanum melongena* L.). International Journal of Botany Studies, 5 (1), 114-17.
15. Lodhi, S. K., Kumar, P., Jatav, V., & Bhati, D. (2023). Studies on genetic variability, heritability and genetic advance in brinjal (*Solanum melongena* L.). International Journal of Advanced Biochemistry Research, 7 (2), 399-402.
16. Gupta, R. A., Ram, C. N., Chakravati, S. K., Deo, C., Vishwakarma, M. K., Arya, R. & Pal, B. (2018). Studies on variability, heritability and genetic advance in brinjal (*Solanum melongena* L.). Journal of Pharmacognosy and Phytochemistry, 7(1), 3195-98.
17. Tiwari, D., Yadav, G. C., Kumar, A., Maurya, V. K. & Singh, D. (2018). Genetic variability, heritability and genetic advance in brinjal (*Solanum melongena* L.). International Journal of Chemical Studies, 6 (6), 2567-70.
18. Jirankali, J. P., Reddy, N., Gangaprasad, S. & Manohara, S. N. (2019). Genetic variability for quantitative and qualitative characters in brinjal (*Solanum melongena* L.). International Journal of Current Microbiology and Applied Sciences, 8(3), 476-84.
19. Anbarasi, D. & Haripriya, K. (2021). Genetic variability, heritability and genetic advances in brinjal (*Solanum melongena* L.). Annals of Plant and Soil Research, 23 (2), 196-99.
20. Chithra, K., Devaraju, M., Srinivasa, V., Varalakshmi, B. & Asha, A. B. (2022). Genetic investigation in segregating generation of brinjal (*Solanum melongena* L.). National Academy Science Letters, 45, 5-8.

21. Savaliya, P. G., Patel, N. B., Mungala, R. A. & Movaliya, H. M. (2017). Estimation of gene action, heterosis, genetic advance and other components in brinjal (*Solanum melongena* L.). *International Journal of Chemical Studies*, 5, 1858-65.
22. Mistry, C. Kathiria, K. B., Sabolu, S. & Kumar, S. (2016). Heritability and gene effects for yield related quantitative traits in eggplant. *Annals of Agricultural Science*, 61 (2), 237-46.
23. Chaudhary, P. & Kumar, S. (2014). Variability, heritability and genetic advance studies in eggplant (*Solanum melongena* L.). *Plant Archives*, 14 (1), 483-86.
24. Kumari, R., Akhtar, S., Solankey, S. S. & Rani, N. (2017). Genetic variability in Indian and exotic brinjal genotypes for morpho-biochemical characters. *New Agriculturist*, 28 (2), 345-51.
25. Jayalakshmi, K., Praneetha, S., & Poobalan, V. (2020). Genetic variability studies in Tamilnadu land races of brinjal (*Solanum melongena* L.). *Journal of Pharmacognosy and Phytochemistry*, 9(1), 2135-38.
26. Patil, V., Gangaprasad, S. & Kumar, D. (2021). Studies on variability, heritability, genetic advance and transgressive segregating in brinjal (*Solanum melongena* L.). *The Pharma Innovation Journal*, 10 (8), 1763-66.
27. Sailesh, M., Singh, A. K., Suman M., Mishra, D. & Rathour, A. (2023). Genetic variability, heritability and advancement in brinjal (*Solanum melongena* L.). *The Pharma Innovation Journal*, 12 (9), 1672-75.
28. Mohanty, B. K. (2024). Variability, heritability and genetic advance studies in brinjal (*solanum melongena* L.). *Indian Journal of Agricultural Research*, 36 (4), 290 - 92.
29. Kumar, M., Ram, C. M., Yadav, G. C., Kumar, S. & Kumar, R. (2020). Studies on genetic variability, heritability in narrow sense and genetic advance in percent of mean in brinjal (*Solanum melongena* L.). *The Pharma Innovation Journal*, 9 (9), 300-03.
30. Ravali, B., Reddy, K. R., Saidaiah, P. & Shivraj, N. (2017). Variability, heritability and genetic advance in brinjal (*Solanum melongena* L.). *International Journal of Current Microbiology and Applied Sciences*, 6 (6), 42-47.
31. Bidaramali, V., Akhtar, S., Kumari R., Das, A., Ahmad, M. F. & Roy C. (2021). Studies on Variability and Correlation for Nutrients, Biochemicals and Yield Contributing traits in Brinjal (*Solanum melongena* L.). *International Journal of Current Microbiology and Applied Sciences*, 10 (10), 90-101.

32. Prajapati, D. R. Patel, D. A. & Patel, D. K. (2021). Study of genetic variability in brinjal (*Solanum melongena* L.). International Journal of Chemical Studies, 9 (2), 945-947.
33. Soumya, B. K., Deo, C., Singh, S., Bhutia, N. D., Tayeng, T., Hazarika, B. N. & Dutta, R. (2023). Genetic Variability Studies in Brinjal (*Solanum melongena* L.) for Quantitative and Qualitative Characters. International Journal of Environment and Climate Change, 13 (10), 4463-73.
34. Verma, B., Sharma, D. & Trivedi, J. (2023). Genetic variability and heritability studies in brinjal (*Solanum melongena* L.). The Pharma Innovation Journal, 12 (7), 3097-98.
35. Gavade, R. T., & Ghadage, B. A. (2015). Genetic variability, heritability and genetic advance in segregating generation of brinjal (*Solanum melongena* L.). Bioinfolet-A quarterly journal of life sciences, 12(1), 325-28.
36. Sonagara, M. K., Patel, B. N., Acharya, R. R., Parihar, A., Patel, R. & Vaghela, U. (2022). Assessment of genetic variability, heritability and genetic advance in brinjal (*Solanum melongena* L.). The Pharma Innovation Journal, 11 (12), 1981-83.
37. Rathod, D., Tandel, T., Sarker. M., Ahlawat, T. R., Patel, A. I., Vashi, J. M. Bambharolia, R. P., Varshney, N., Emmi, S. & Chaudhari B. N. (2024). Genetic variability analysis in brinjal (*Solanum melongena* L.). International Journal of Advanced Biochemistry Research, 8 (1), 04-06.
38. Pandey, S., Mishra, S., Kumar, N., Yadav, G. C. & Pandey, V. P. (2019). Studies on heterosis, combining ability and gene advance for the quantitative characters in brinjal or eggplant (*Solanum melongena* L.). Journal of Pharmacognosy and Phytochemistry, 8 (1), 19-22.
39. Pramila, Kushwaha, M. L., Kumar, U. & Yadav L. M. (2019). Genetic variability, heritability and genetic advance studies in brinjal (*Solanum melongena* L.). International Journal of Chemical Studies, 6, 592-95.