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Identification of Marker Linked with Little Leaf Resistance in Brinjal [*Solanum melongena* L.]

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ABSTRACT

The study was conducted during *kharif* (September, 2023 to February, 2024) at Main Vegetable Research Station, Anand Agricultural University, Anand, Gujarat, India to find out the linked marker to Little leaf disease resistant gene in brinjal. The experimental materials were comprised of $F_{2:3}$ segregating population of cross resistant parent AB 15–06 and susceptible parent GRB 5 against little leaf disease. Total 168 mapping population were developed from F_1 seeds derived from crosses of above refereed parents. F_1 hybrid seeds were collected in the year 2020–21. Total 168 F_2 mapping population were sown in the year 2021–22. In the year 2022–23, 168 F_2 mapping population collected seeds were sown as $F_{2:3}$ mapping population for morphophysiological characterizations. Phenotyping evaluation study in $F_{2:3}$ 168 mapping population was subjected for morphophysiological characters viz., days to initiation of flowering (24.6–55.4), plant height (62.3–111 cm), primary branches plant^{-1} (6.8–18.4), leaf length (12.7–24.1 cm), leaf width (7.1–18.3 cm), fruit volume (10–346.8 cc), no. of fruits plant^{-1} (10.3–55), fruit weight (34.4–95.5 g), fruit yield plant^{-1} (0.5–3.2 kg) and disease incidence (0–38.3%). Days to initiation of flowering (47), plant height (111 cm), no. of fruits plant^{-1}, fruit weight (35.9 g), fruit yield plant^{-1} (80.5 kg) were recorded higher in resistant parent. Correlation analysis indicated that morphophysiological traits like days to initiation of flowering and primary branches plant^{-1} positively correlated with the disease incidence.

KEYWORDS: Brinjal, little leaf disease, markers, regression analysis

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Data Availability Statement: Legal restrictions are imposed on the public sharing of raw data. However, authors have full right to transfer or share the data in raw form upon request subject to either meeting the conditions of the original consents and the original research study. Further, access of data needs to meet whether the user complies with the ethical and legal obligations as data controllers to allow for secondary use of the data outside of the original study.

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1. INTRODUCTION

Solanum melongena L., or brinjal, is a widely produced vegetable crop in tropical and subtropical regions that is valued for its tasty fruit, which is categorized as a berry by nature. It is commonly referred to as "aubergine" in Europe, "eggplant" in the Americas and Australia, and "brinjal" in South Asia, South-east Asia, and South Africa. In certain other regions of the world, it is also referred to as guinea squash, garden egg, or melongene. It is a member of the genus *Solanum* and family *Solanaceae*, having the diploid chromosome number 2n=2x=24. The main origin is thought to be Indo-Burma, and the secondary origin is thought to be China (Vavilov, 1928).

Brinjal production was primarily restricted by its high vulnerability to both abiotic and biotic stresses, in addition to its limited genetic base. It was afflicted with a number of illnesses, the most significant of which being little leaf disease brought on by phytoplasma, which results in significant financial losses (Rathnamma and Patil, 2017, Karkute et al., 2023, Chauhan et al., 2024). The afflicted plants exhibit small leaves, an abundance of new shoots, phyllody, and stunting. Following the disease's initial report in India by Thomas and Krishnaswami in 1939, various biological features of the illness have been identified. Thus far, phytoplasmas from six groups including 16SrI from Bangladesh, India, and Japan have been identified, 16SrII-D from Egypt, 16SrIII-J and 16SrIII-U from Brazil, 16SrVI-A and -D from Turkey and India, 16SrIX-C from Iran and 16SrXII-A from Russia (Tohidi et al., 2015; Kumar et al., 2017, Maheshwari et al., 2017; Darabakula et al., 2024) were reported to infect brinjal worldwide.

Brinjal is afflicted at various stages by a variety of diseases, which results in significant output losses. The insect vector of little leaf disease is *Hishimonus phycitis*, a member of the leafhopper family. In India, *Datura stramonium* was identified as a naturally occurring weed host for BLL phytoplasma. *Hishimonas phycitis*, a leafhopper, was found to be a possible vector (Karthikeyan et al., 2024).

Simple Sequence Repeats (SSR), also known as microsatellites, are the most extensively utilized and maybe the most informative molecular marker among all those that are accessible. They also require a little amount of DNA and are stable, locus specific, co-dominant, and highly polymorphic even within closely related lines. Because SSR markers are multi-allelic, they are a valuable marker system for marker-assisted selection and can detect higher levels of diversity (Khapte et al., 2018; Bhatt et al., 2022; Bhattacharjee et al., 2022).

In the early stages of QTL mapping research, Single Marker Analysis (SMA), a linkage map independent technique used for initial investigations on QTL mapping. SMA uses only one marker at a time to determine the QTL–marker connection. SMA can be carried out using ANOVAs, linear regressions, likelihood ratio tests, maximum likelihood estimation, and simple t tests (Sakure et al., 2024).

Generally, 6–7 backcrosses are required to transfer a gene into a new genotype, which is a labor intensive and time consuming process. Therefore, to facilitate the development of Brinjal little leaf resistant cultivars, there is need to find out the linked markers to the resistant gene, so that the requisite period for gene transfer can be reduced the identified linked marker will not only facilitate the transfer of disease-resistant gene in elite brinjal genotypes, but these will also help in identification of new genotypes resistant to little leaf disease. Therefore, the present investigation main aim was to find out the linked marker to Little leaf disease-resistant gene in brinjal.

2. MATERIALS AND METHODS

The study was conducted during *kharif* (September, 2023 to February, 2024) at Main Vegetable Research Station, Anand Agricultural University, Anand, Gujarat, India. The experimental material for present investigation comprised of $F_{2:3}$ segregating generation originating from a cross between a little leaf resistance parent of brinjal AB-15-06 (*S. melongena*) and a susceptible parent GRB-5 (*S. melongena*).

2.1. Phenotyping of mapping population for little leaf infection

Observations on days to initiation of flowering, plant height (cm), primary branches plant^{-1} (No.), leaf length (cm), leaf width (cm), fruit volume (cc), no. of fruits plant^{-1} (No.), fruit weight (gm), fruit yield plant^{-1} (kg) and disease incidence (%) were recorded from randomly selected five plant of the $F_{2:3}$ segregating population and their parents.

2.2. Days to initiation of flowering

The number of days were recorded from the date of transplanting to the appearance of first flower in plants.

2.3. Plant height

The height of selected plants was measured in centimeter from the base of the plant to the tip of the main stem at the time of maturity of randomly selected five plants.

2.4. Primary branches plant^{-1}

The total number of primary branches plant^{-1} were counted on the main stem at the time of maturity.

2.5. Leaf length

The leaf length measured in randomly selected five plants and average value was calculated.

2.6. Leaf width

The leaf width measured in randomly selected five plants

and average value was calculated.

2.7. Fruit volume

Fruit volume was measured by water displacement method as described by Konyak et al. (2020). Brinjal fruits after 6th picking were harvested and tested for fruit volume in a beaker filled with 1 l water. Water displaced by immersing of the fruit was measured and the volume was recorded which was considered as a fruit volume.

2.8. No. of fruit plant^{-1}

It was counted from the randomly selected five plant of the $F_{2:3}$ population and parents.

2.9. Fruit weight

Five randomly selected matured fruits line^{-1} of mapping population were tested and average/mean value of weight was calculated in gram.

2.10. Fruit yield plant^{-1}

The total fruits yield obtained from the randomly selected five plants from each picking were weighed in gram and their sum was calculated to obtain the fruit yield plant^{-1} in kilogram.

2.11. Disease incidence

Random observations of little leaf disease incidence in brinjal was carried out at weekly interval after 30 days of transplanting from September, 2023 to February, 2024. Based on per cent disease incidence, the brinjal mapping population was classified into five categories (Venkataravanappa et al., 2022).

(1) Immune (0%),

(2) Resistant (0.1–10%),

(3) Moderately resistant (10.1–20%),

(4) Susceptible (20.1–50%), and

(5) Highly susceptible (>50%)

2.12. Statistical analysis

2.12.1. Estimation of genetic variability parameters

2.12.1.1. Variance

Genotypic variance and phenotypic variance were calculated for various trait calculated as per Burton and Devane, (1953).

2.12.1.2. Genotypic variance (σ^2g)

It was the existence of variance among individuals brought about by variations in their genetic make-up or variance inherited from genetic sources.

$$\text{Genotypic variance } (\sigma^2g) = \frac{MSg - MSe}{r}$$

Where,

σ^2g=Genotypic variance

MSg=Mean sum of squares due to genotypes

MSe=Mean sum of squares due to error

r=Number of replications

2.12.1.3. Phenotypic variance (σ^2p)

It was the total variation caused by both environmental and genetic variables. It was calculated using the formula.

Phenotypic Variance (σ^2g)=$\sigma^2p+\sigma^2g$

Where,

σ^2p=Phenotypic variance

σ^2g=Genotypic variance

σ^2e=Error variance

2.12.1.4. Phenotypic (PCV) and genotypic (GCV) coefficients of variations

Phenotypic and genotypic co-efficient of variation was calculated by method described by Burton and Devane (1953).

2.12.1.5. Genotypic coefficient of variation (GCV%)

Genotypic coefficient of variation was calculated using the following formula given below.

$$GCV\% = \frac{\sqrt{\sigma^2g}}{\overline{X}} \times 100$$

Where,

$\overline{X}$=General mean of the character under study

σ^2g=Genotypic variance

2.12.1.6. Phenotypic coefficient of variation (PCV%)

Phenotypic coefficient of variation was calculated using the following formula described in below.

$$PCV\% = \frac{\sqrt{\sigma^2p}}{\overline{X}} \times 100$$

Where,

σ^2p=Phenotypic variance

$\overline{X}$=General mean of the character under study

Classification of PCV and GCV were done following the method as suggested by Robinson et al. (1949).

<10% Low

10–20% Moderate

>20% High

2.12.1.7. Heritability

The broad sense heritability (h^2b) was calculated for each traits by dividing genotypic variance and the phenotypic variance. The method followed was suggested by Johnson et al. (1955).

$$h^2b\ (\%) = \frac{\sigma^2g}{\sigma^2p} \times 100$$

h^2b=Heritability (broad sense)

σ^2g=Genotypic variance

σ^2p=Phenotypic variance

Classification of heritability was done by following a method as suggested by Robinson et al. (1949).

<30% Low

30-60% Moderate

>60% High

2.12.1.8. Genetic advance (GA)

It was measured the improvement rate in the mean of each line of mapping population value of selected plants over the parental population. It could be calculated by using the methodology suggested by Johnson et al. (1955) at 5% selection intensity using the constant 'k' as 2.06.

$GA=K\times h^2b\times\sigma p$

Where,

h^2 (bs) =Heritability in broad sense

σp=Phenotypic standard deviation of the trait

K=Standard selection differential which is 2.06 at 5% selection intensity

2.12.1.9. Genetic advance as per cent mean (GAM)

The genetic advance express as per cent of mean was calculated as per the formula suggested by Johnson et al. (1955).

$$GA\ (\%\ of\ mean) = \frac{GA}{\overline{X}} \times 100$$

0-10% : Low

1-20% : Moderate

20% and above : High

2.13. Test of normality

Skewness and kurtosis were calculated by the SPSS V20

2.14. Correlation analysis

Correlation analysis was performed by using R software V4.3.1

3. RESULTS AND DISCUSSION

The present study carried out morphophysiological characterization and singal marker analysis for little leaf resistance in brinjal. For that two two parents used in the study were AB 15–06 resistance and GRB 5 susceptible against little leaf disease maintained at Main Vegetable Research Station, Anand Agricultural University, Anand (Figure 1). These parental genotypes were further used to development of F_2 and $F_{2:3}$ segregating population F_1 hybrid was developed through crossing between both of the parents. Seeds of F_1 were used to development of 168 F_2 mapping population for genotypic analysis. Total 168 $F_{2:3}$ mapping population sown during the year *kharif*, 2023–24 along with their parents for morphophysiological characterization.

3.1. Phenotyping of mapping population to little leaf infection in brinjal

Parent GRB 5 was reported to be highly vulnerable to little leaf disease, whereas another parent AB 15–06 which did not exhibit any indications of the little leaf infection, was found highly resistant. F_1 plants did not exhibit any signs of infection. In F_2 mapping population 56 plants could not survived because of higher little leaf severity. Total 168 F_2 mapping population was used for morphophysiological characterization in $F_{2:3}$ segregating mapping population. In the field, Total 168 $F_{2:3}$ brinjal seedlings 30 days after germination were transplanted along with their parents viz; AB 15–06 and GRB 5. After 30 days of transplantation,

Phyllody of flowers: A. Healthy plant flower; B. Little leaf disease infected plant flower

A. Healthy plant leaves

B. Little leaf disease infected plant leaves

Figure 1: Continue...

A. Healthy plant B. Disease infected plant fruit

A. Healthy plant B. Little leaf disease infected plant

Figure 1: Differentiation of healthy and little leaf infected brinjal plant

little leaf disease infection screening was initiated. Data on the severity of little leaf disease incidence were recorded. Due to environmental effects on mapping population different disease severity was observed (Figure 2). The $F_{2:3}$ population disease progressions were tracked at 30-day intervals from the onset of the first symptom. Disease incidence was scored at 1–5 scaling level after 30 days of transplanting according to Venkataravanappa et al. (2022).

1. Immune (0%)
2. Resistant (0.1–10%)
3. Moderately resistant (10.1–20%)
4. Susceptible (20.1–50%), and
5. Highly susceptible >50%)

Throughout all the screened 168 mapping population of $F_{2:3}$ population, 72 genotypes were immune (disease scale-1), 26 resistant (disease scale-2), 30 moderately resistant (disease scale-3), 40 susceptible (disease scale-4) and no one genotype observed as highly susceptible (disease scale-5) (Figure 3).

3.2. Morphophysiological characterization of parents and $F_{2:3}$ mapping population

Total 168 $F_{2:3}$ populations were characterized for morphphysiological traits along with their parents. Data on days to initiation of flowering, plant height (cm), primary branches plant^{-1} (No.), leaf length (cm), leaf width (cm), fruit volume (cc), no. of fruits plant^{-1} (No.), fruit weight (gm), fruit yield plant^{-1} (kg) and disease incidence (%) were recorded from five plants of each mapping population and mean values have been presented in Table 1. followed by interpretation.

3.3. Days to initiation of flowering

Days of initiation of flowering was recorded from the date

Figure 2: Continue...

Figure 2: Disease severity in brinjal $F_{2:3}$ mapping population; Note: 1: Immune (0% disease incidence; 2: Resistance (0.1–10% disease incidence); 3: Moderately resistance (10.1–20% disease incidence); 4: Moderately susceptible (20.1–50% disease incidence); 5: Susceptible (>50% disease incidence)

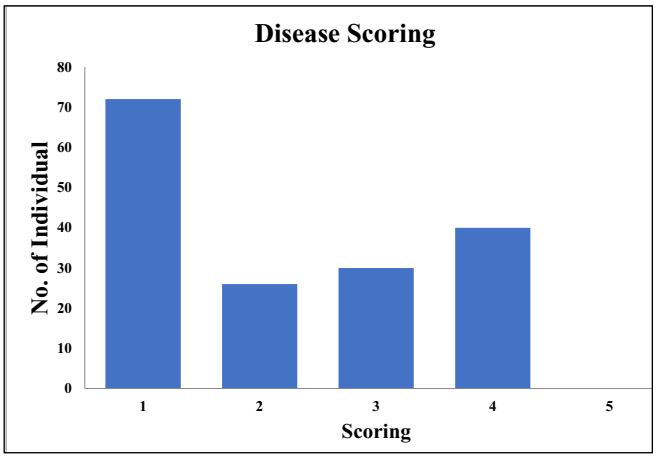


Figure 3: Distribution of $F_{2:3}$ mapping population according to disease scoring; Note: 1: Immune (0% disease incidence); 2: Resistance (0.1-10% disease incidence); 3: Moderately resistance (10.1-20% disease incidence); 4: Moderately susceptible (20.1-50% disease incidence); 5: Susceptible (>50% disease incidence)

of transplanting till the appearance of flowers in first plant of each line of mapping population. The highest mean value 55.4 was observed in line of mapping population 17 where as lowest mean value 24.6 was observed in line of mapping population 161. Resistant parent AB 15–06 had mean value 47 where as susceptible parent GRB 5 had mean value 44. Lines of mapping population 1 (44), 3 (45.4), 4 (42.8), 6 (44.6), 9 (45.4), 12 (46), 14 (46.2), 22 (38.8), 23 (36.8), 28 (43.6), 29 (45.4), 36 (46), 38 (37.8), 40 (36.6), 42 (41.4), 47 (36.2), 48 (45.6), 50 (37.6), 51 (44.2), 52 (46.2), 53 (38.6), 55 (44),57 (46.2), 59 (44) , 60 (48), 61 (45.8), 62 (43.6), 63 (49.2), 64 (44.2),65 (41.2), 67 (40.8), 68 (42.8), 70 (44.6), 70 (44.6), 73 (45.6), 74 (43.8), 75 (39.8), 78 (42.4), 81 (44), 82 (45.8), 86 (36.4), 91 (44), 93 (43.4), 94 (46), 95 (43), 97 (45.4), 98 (44.6), 99 (43), 100 (46.4), 102 (42.4), 103 (45), 107 (43), 108 (44), 111 (43),112 (39.2), 113 (43.2), 115 (45.6), 116 (40), 117 (36.4), 120 (45), 121 (46.4), 123 (44), 124 (43), 125 (46), 128 (40.6), 129 (45), 130 (42.8), 132 (43.4), 133 (40.6), 134 (44), 135 (45), 136 (40.4), 137 (46.4), 138 (38.4), 140 (42.6), 142 (41), 143 (44.6), 144 (46), 145 (41.4) 146 (43), 147 (37.8), 151 (46.6), 154 (46.2), 155 (38), 157 (43), 158 (44.6), 159 (46), 163 (45), 164 (45), 165 (44), 166 (43.2) and 167 (41.2) were recorded statistically higher over resistant plant AB 15-06.

The present study observed lower days to initiation compare to Konyak et al. (2020) recorded days to initiation flowering was ranged around 55.6–77.0 days. Saikia et al. (2021) observed days to initiation flowering was ranged between 62.89–117.5.

3.4. Plant height

As plant height data concerned in all 168 $F_{2:3}$ mapping

Table 1: Morphophysiological character in parents and $F_{2:3}$ mapping population of brinjal

Mapping population	FLO (days)	PH (cm)	BP (No.)	LL (cm)	LW (cm)	FV (cc)	NFP (No.)	FW (g)	FYP (kg)	DI (%)
1.	44.0	79.2	8.6	17.3	12.5	29.2	30.4	59.4	2.1	2.2
2.	51.6	68.8	8.0	16.1	11.2	74.2	27.9	56.4	1.6	0.0
3.	45.4	89.0	9.4	16.5	11.7	18.4	34.5	67.7	2.4	16.4
4.	42.8	106.0	10.2	17.9	14.8	96.4	23.9	87.1	3.0	0.0
5.	31.4	111.5	9.4	16.8	11.1	42.4	55.0	64.5	2.5	0.0
6.	44.6	97.5	9.4	19.8	14.0	92.8	43.5	73.8	2.5	0.0
7.	36.0	95.0	10.0	17.4	13.2	90.4	21.0	58.9	1.5	7.1
8.	25.8	58.9	8.2	16.2	10.4	21.4	11.1	38.2	0.7	38.3
9.	45.4	96.5	8.4	18.1	13.8	37.6	27.6	57.6	1.3	3.0
10.	48.2	49.8	7.6	19.7	13.7	14.0	11.8	36.0	0.6	36.9
11.	27.4	65.9	8.8	14.2	11.2	30.0	22.3	71.0	1.4	0.0
12.	46.0	84.1	13.0	19.3	13.8	105.0	32.1	59.3	3.1	2.5
13.	27.0	116.4	10.2	18.4	13.7	82.2	38.8	58.8	2.4	0.0
14.	46.2	79.2	11.6	18.6	12.4	22.2	36.4	53.6	2.8	0.0
15.	52.4	44.9	12.2	23.3	18.3	23.6	14.8	41.7	0.7	31.9
16.	26.6	89.7	9.2	19.4	15.5	33.4	36.0	63.9	2.4	4.8
17.	55.4	109.9	8.4	20.8	14.2	43.2	36.4	72.8	3.2	0.0
18.	54.2	101.0	9.8	16.1	11.4	35.2	23.2	50.7	1.5	0.0
19.	48.0	52.5	11.6	16.3	12.4	14.8	20.3	38.9	0.9	31.7
20.	25.6	93.1	10.4	18.9	12.7	105.2	26.8	81.6	2.4	9.0
21.	27.6	85.4	12.0	17.7	11.4	10.0	15.1	73.4	1.8	0.0
22.	38.8	94.2	10.2	16.6	10.3	15.8	24.0	45.1	1.3	0.0
23.	36.8	76.5	9.2	18.0	12.4	18.8	24.0	45.4	0.8	6.1
24.	26.2	73.5	10.4	16.3	10.4	45.8	13.6	51.6	1.6	12.3
25.	29.8	75.1	9.4	21.2	14.8	105.8	12.7	63.8	1.6	11.8
26.	48.0	82.4	8.4	18.4	12.8	54.8	15.0	48.2	0.9	0.0
27.	52.6	110.3	10.2	21.3	14.9	25.4	39.8	74.8	1.5	0.0
28.	43.6	84.3	8.2	19.3	14.0	65.4	19.1	66.6	2.1	10.2
29.	45.4	57.4	12.2	18.6	13.9	183.6	13.3	37.3	0.5	32.1
30.	50.2	78.0	9.0	19.2	11.8	109.0	27.0	62.4	1.5	12.9
31.	24.8	67.3	11.0	19.2	13.5	33.4	12.5	65.2	1.3	0.0
32.	31.8	70.1	11.8	20.8	14.2	54.0	16.7	56.1	1.0	11.7
33.	32.8	75.1	10.6	23.7	16.5	171.6	15.3	84.3	1.1	6.2
34.	28.8	69.2	11.8	22.1	16.2	12.8	34.7	67.8	2.4	0.0
35.	54.4	94.4	10.8	18.4	12.8	12.0	18.3	85.5	0.7	0.0
36.	46.0	79.6	9.4	18.3	13.6	21.6	13.1	64.4	0.8	0.6
37.	26.2	88.7	6.8	21.4	15.7	75.2	11.9	73.0	1.1	10.8
38.	37.8	77.1	10.4	18.7	13.2	25.6	17.4	36.6	1.2	0.3
39.	47.4	75.9	9.0	19.3	14.3	41.8	29.5	50.5	1.7	24.8
40.	36.6	89.9	11.0	20.4	15.6	48.0	27.4	64.3	1.3	0.0

Table 1: Continue...

Mapping population	FLO (days)	PH (cm)	BP (No.)	LL (cm)	LW (cm)	FV (cc)	NFP (No.)	FW (g)	FYP (kg)	DI (%)
41.	49.6	75.9	10.4	18.9	12.5	77.0	19.4	54.1	1.4	10.0
42.	41.4	88.9	12.8	17.4	12.9	61.4	39.0	65.0	1.4	0.0
43.	51.0	60.4	9.2	20.1	13.7	55.8	36.6	44.9	1.4	5.3
44.	52.0	84.6	10.8	18.3	14.4	56.6	27.3	53.2	1.4	0.0
45.	51.4	99.2	9.6	20.2	14.3	16.2	35.9	75.7	1.4	0.0
46.	47.6	69.9	10.2	20.8	14.4	111.0	21.7	82.0	1.6	0.0
47.	36.2	100.4	15.0	18.1	13.3	252.0	37.0	74.5	1.5	0.0
48.	45.6	75.9	12.0	19.5	14.3	60.8	34.7	53.3	1.5	0.0
49.	32.4	73.1	12.0	18.2	14.5	23.8	24.8	82.5	1.4	7.1
50.	37.6	81.2	9.0	18.2	14.5	46.4	36.8	65.4	1.1	7.6
51.	44.2	70.1	10.0	18.6	13.5	40.6	25.0	74.2	1.8	0.0
52.	46.2	71.5	9.8	17.5	13.8	21.4	27.3	47.0	1.4	13.2
53.	38.6	80.3	9.2	19.5	14.6	23.6	21.0	60.7	1.7	13.7
54.	47.2	80.3	12.0	24.1	16.9	48.4	36.0	61.7	1.7	6.0
55.	44.0	57.4	11.2	19.3	13.5	37.2	14.8	46.0	0.8	31.8
56.	47.0	105.3	9.8	18.6	13.3	72.0	22.7	59.5	1.0	0.0
57.	46.2	109.1	11.0	19.4	13.9	218.4	32.2	56.1	2.3	0.0
58.	47.0	52.0	11.6	20.9	16.4	15.0	10.7	42.2	0.6	31.9
59.	44.0	49.2	12.6	23.3	18.1	22.2	12.2	41.2	0.9	32.1
60.	48.0	96.8	12.4	20.6	15.7	61.6	28.7	70.1	2.5	9.6
61.	45.8	95.1	11.0	18.8	14.0	130.0	29.3	60.8	1.4	0.0
62.	43.6	78.5	12.8	22.7	17.7	27.6	29.6	45.7	1.5	11.9
63.	49.2	98.3	10.2	22.1	15.6	62.0	23.2	57.3	1.5	10.1
64.	44.2	66.9	13.7	20.9	17.2	13.8	27.0	65.4	1.8	13.2
65.	41.2	72.0	10.4	21.7	16.3	12.4	34.3	52.9	1.1	0.0
66.	50.0	63.3	11.2	20.1	16.0	16.2	34.6	39.9	1.7	11.1
67.	40.8	80.5	12.6	21.0	12.6	47.6	21.1	63.8	1.4	0.0
68.	42.8	88.4	11.0	16.9	9.8	40.8	22.7	63.8	1.4	0.0
69.	51.0	77.3	10.0	17.6	11.5	20.8	26.3	74.3	1.6	8.4
70.	44.6	68.1	14.8	18.0	11.3	65.8	19.2	76.3	1.7	10.1
71.	44.8	75.2	13.0	16.0	10.4	24.4	29.8	55.2	1.4	5.8
72.	51.0	75.0	12.0	15.9	11.7	13.6	28.0	68.9	1.4	14.3
73.	45.6	75.5	12.4	18.6	11.2	13.2	32.1	77.1	2.1	12.6
74.	43.8	82.1	14.2	15.4	9.7	96.8	31.2	73.5	1.6	0.0
75.	39.8	68.6	14.6	15.5	10.7	95.2	35.0	65.6	1.6	6.5
76.	48.0	83.6	14.0	17.0	11.1	25.8	45.7	46.0	2.4	0.0
77.	49.0	53.0	16.2	15.5	10.5	19.6	16.2	43.4	0.7	36.1
78.	42.4	110.5	14.2	16.9	9.9	55.2	31.6	64.4	1.4	16.2
79.	49.0	93.2	15.2	17.4	9.7	84.8	21.0	79.7	1.3	24.6
80.	47.4	106.1	11.6	15.3	8.3	22.2	46.2	52.6	1.9	25.6
81.	44.0	101.1	11.4	19.6	12.4	173.4	12.6	92.3	0.9	0.0

Table 1: Continue...

Mapping population	FLO (days)	PH (cm)	BP (No.)	LL (cm)	LW (cm)	FV (cc)	NFP (No.)	FW (g)	FYP (kg)	DI (%)
82.	45.8	92.1	12.6	18.3	12.7	10.2	36.3	82.6	1.5	0.0
83.	50.2	71.3	13.0	15.7	10.1	24.0	32.9	47.5	1.0	14.4
84.	50.6	100.7	13.6	17.9	12.9	35.6	21.8	54.5	1.1	0.0
85.	49.4	66.2	13.8	17.9	12.4	95.4	30.7	70.8	1.8	8.4
86.	36.4	73.9	12.6	16.4	10.8	103.6	25.9	48.7	1.5	11.1
87.	50.0	101.0	13.4	16.2	11.4	105.8	26.9	85.5	1.6	15.1
88.	47.0	54.6	13.0	17.0	10.7	17.0	15.6	34.4	0.9	33.8
89.	50.0	90.6	10.4	17.4	13.0	15.4	16.1	73.8	1.4	5.4
90.	49.0	99.0	15.0	14.0	11.0	75.4	14.3	74.3	1.0	0.0
91.	44.0	103.2	12.6	14.3	7.1	45.8	15.6	64.3	1.1	0.0
92.	49.0	98.1	11.0	16.0	7.7	30.2	25.4	75.6	1.8	5.5
93.	43.4	91.8	13.4	15.8	10.9	46.6	36.1	54.8	1.1	0.0
94.	46.0	69.4	16.6	17.5	13.5	14.8	29.5	62.3	1.3	14.9
95.	43.0	83.3	13.6	14.2	9.0	193.8	13.9	70.2	1.3	0.0
96.	48.8	102.9	15.0	16.4	11.4	96.6	12.7	65.2	1.0	12.8
97.	45.4	95.5	15.2	15.4	9.9	285.2	24.0	77.6	1.4	0.0
98.	44.6	110.4	14.8	16.8	12.0	85.8	21.9	75.7	1.3	0.0
99.	43.0	111.8	16.0	13.8	9.6	27.8	46.1	62.3	1.7	7.0
100.	46.4	83.6	13.8	22.9	15.8	153.4	31.8	84.6	1.5	11.9
101.	48.0	103.3	16.0	18.2	13.1	18.8	14.0	57.4	1.4	0.0
102.	42.4	109.1	14.4	17.8	12.1	66.4	26.2	84.1	1.3	0.0
103.	45.0	98.6	14.8	18.6	13.2	94.8	46.9	56.1	1.4	0.0
104.	47.2	96.7	12.6	18.0	11.8	124.0	42.3	45.4	1.4	12.8
105.	55.2	104.6	13.8	15.4	11.8	124.2	31.2	64.4	1.3	0.0
106.	49.0	58.9	13.0	21.1	15.1	85.0	11.3	64.7	1.0	17.1
107.	43.0	95.7	11.6	17.6	11.1	105.6	45.8	49.6	1.5	0.0
108.	44.0	60.5	11.8	17.2	12.6	17.6	27.1	47.6	0.8	17.9
109.	49.2	107.3	13.4	16.5	11.4	26.2	37.6	45.2	1.5	0.0
110.	49.0	97.9	12.4	17.5	12.8	25.2	24.2	59.1	1.4	0.0
111.	43.0	112.4	13.0	19.4	11.5	23.8	34.7	65.6	1.4	0.0
112.	39.2	73.8	14.2	18.6	12.7	26.2	37.6	49.5	2.0	0.0
113.	43.2	66.4	9.6	19.6	12.1	127.4	38.2	47.6	1.4	11.8
114.	47.8	64.4	17.0	18.1	12.3	117.2	26.2	89.5	0.9	14.4
115.	45.6	72.8	12.2	21.9	13.5	93.6	19.5	62.3	1.5	31.8
116.	40.0	61.7	16.2	18.0	13.1	24.2	36.9	40.0	1.5	0.0
117.	36.4	60.8	17.2	15.1	11.9	26.6	13.4	33.4	0.7	23.8
118.	47.0	64.2	11.6	18.4	13.3	134.6	46.2	66.2	1.3	14.6
119.	51.0	72.4	11.0	16.1	12.0	16.0	54.8	45.7	1.5	13.6
120.	45.0	87.5	11.2	16.1	10.3	15.6	48.9	44.8	1.7	0.0
121.	46.4	53.0	12.6	15.6	9.4	53.0	16.3	34.8	0.8	31.9
122.	53.2	74.6	18.4	16.9	10.3	45.2	30.1	60.6	1.5	17.1

Table 1: Continue...

Mapping population	FLO (days)	PH (cm)	BP (No.)	LL (cm)	LW (cm)	FV (cc)	NFP (No.)	FW (g)	FYP (kg)	DI (%)
123.	44.0	95.8	13.4	16.6	10.7	24.4	25.5	62.9	1.4	0.0
124.	43.0	71.1	15.8	17.1	12.1	23.6	31.4	63.0	1.6	23.8
125.	46.0	89.1	14.4	20.6	13.4	24.8	43.5	75.9	1.5	12.0
126.	48.4	73.5	13.8	18.4	12.1	15.0	19.5	65.5	0.9	12.5
127.	48.2	104.5	15.2	20.9	13.1	34.4	37.7	64.0	1.3	0.0
128.	40.6	102.4	17.4	19.2	11.3	53.4	38.0	66.7	1.6	0.0
129.	45.0	106.5	12.8	20.4	12.4	14.8	24.0	56.2	1.0	0.0
130.	42.8	97.9	17.8	18.1	11.0	21.0	36.8	74.1	2.2	0.0
131.	49.0	73.8	15.6	19.3	13.1	163.8	33.0	85.0	2.6	0.0
132.	43.4	70.7	16.6	19.0	12.8	76.8	28.1	53.8	1.4	17.1
133.	40.6	58.7	13.6	16.4	9.9	66.0	48.2	52.4	2.1	0.0
134.	44.0	77.3	13.6	16.1	11.3	346.8	17.2	60.7	1.4	24.2
135.	45.0	60.7	14.6	16.9	10.7	38.0	31.4	64.6	2.4	0.0
136.	40.4	64.4	14.2	14.5	10.2	10.0	33.0	44.6	1.7	13.4
137.	46.4	90.1	12.2	15.5	11.0	44.0	32.9	46.1	2.3	0.0
138.	38.4	105.3	13.0	17.3	10.9	53.0	29.7	61.0	2.7	0.0
139.	50.0	97.2	14.8	16.3	10.4	34.0	37.0	46.5	1.3	0.0
140.	42.6	109.0	14.4	17.3	11.6	35.2	37.2	73.2	1.6	0.0
141.	50.0	106.0	13.8	15.4	10.7	25.0	36.0	57.9	2.9	0.0
142.	41.0	73.4	12.4	16.0	11.6	30.6	26.6	95.5	1.7	9.9
143.	44.6	83.8	14.2	17.1	11.1	33.0	31.8	84.8	1.8	13.1
144.	46.0	73.7	15.6	16.4	10.1	54.2	35.3	61.8	1.4	23.8
145.	41.4	63.6	15.0	14.8	9.8	64.4	21.2	61.5	1.4	12.7
146.	43.0	108.4	10.6	12.7	8.5	91.4	39.9	59.9	1.4	0.0
147.	37.8	106.4	15.4	14.9	10.0	42.0	36.6	74.6	1.1	0.0
148.	51.4	77.6	15.6	13.7	8.7	11.0	21.3	66.7	2.4	2.5
149.	47.2	109.9	11.6	15.3	9.6	77.4	25.3	47.6	2.0	0.0
150.	48.4	109.5	16.0	16.8	9.4	34.0	31.7	54.8	2.6	0.0
151.	46.6	95.6	17.0	14.6	9.6	334.0	16.6	63.7	1.4	0.0
152.	49.2	92.0	16.8	13.9	9.3	34.4	34.2	52.1	1.6	0.0
153.	51.0	89.0	14.4	16.9	11.4	35.2	30.5	49.5	1.2	13.2
154.	46.2	64.8	14.6	14.8	9.5	16.0	34.6	66.5	1.7	17.1
155.	38.0	91.7	16.0	19.0	11.5	25.6	21.2	46.2	1.2	0.0
156.	28.4	83.6	14.8	19.1	11.1	84.8	21.2	47.9	1.0	25.2
157.	43.0	87.2	13.2	19.6	12.4	12.0	18.8	46.3	1.0	5.3
158.	44.6	73.0	13.2	17.1	13.8	281.2	21.8	45.6	1.8	17.1
159.	46.0	92.4	16.2	20.1	13.4	25.8	26.5	54.8	1.4	31.9
160.	48.2	53.1	11.4	19.0	11.4	26.0	14.2	39.2	0.6	38.2
161.	24.6	66.9	15.8	21.0	12.3	54.8	13.8	78.1	1.3	23.8
162.	31.4	63.0	9.0	17.4	10.9	12.0	31.7	49.2	1.7	31.9
163.	45.0	57.2	10.2	21.3	11.8	16.0	10.3	36.0	0.6	36.4

Table 1: Continue...

Mapping population	FLO (days)	PH (cm)	BP (No.)	LL (cm)	LW (cm)	FV (cc)	NFP (No.)	FW (g)	FYP (kg)	DI (%)
164	45.0	61.3	9.0	19.6	10.8	25.0	11.9	41.3	0.8	37.4
165.	44.0	98.7	11.2	17.4	11.2	42.4	21.5	41.5	1.5	31.9
166.	43.2	60.5	15.6	18.6	11.6	55.4	21.4	64.3	1.3	30.5
167.	41.2	89.7	13.6	16.8	10.4	14.2	28.0	53.9	2.4	19.8
168.	47.0	70.3	10.4	15.4	11.1	147.4	24.5	72.7	2.3	31.9
Minimum	24.6	44.9	6.8	12.7	7.1	10	10.3	33.4	0.5	0.0
Maximum	55.4	116.4	18.4	24.1	18.3	346.8	55	95.5	3.2	38.3
AB 15-06	47.0	111.0	13.6	17.8	12.2	61.6	35.9	80.5	2.4	0.0
GRB 5	44.0	62.3	16.8	21.9	14.8	10.0	12.3	41.6	0.7	36.4
SEm±	4.37	9.07	0.83	0.91	0.82	3.09	2.41	3.83	0.11	1.07
CD (p=0.05)	12.11	25.19	2.30	2.52	2.28	8.57	6.68	10.62	0.31	2.97
CV %	22.37	24.44	14.89	11.26	14.94	11.48	19.74	14.18	16.63	24.82

Note: FLO: Days to initiation of flowering; PH: Plant height; BP: Primary branches plant^{-1}; LL: Leaf length; LW: Leaf width; FV: Fruit volume; NFP: No. of fruits plant^{-1}, FW: Fruit weight; FYP: Fruit yield plant^{-1} and DI: Disease incidence

population and both parents at the time of maturity stage. Minimum plant height 44.9 cm was found in line of mapping population 15 where as maximum plant height 116.4 cm was found in line of mapping population 13. Resistant parents AB 15–06 had mean value 111 cm where as susceptible parent GRB 5 had mean value 62.3 cm. Lines of mapping population 3, 4, 6, 7, 9, 16, 17, 18, 20, 22, 27, 35, 37, 40, 42, 45, 47, 56, 57, 60, 61, 63, 68, 78, 79, 80, 81, 82, 84, 87, 89, 90, 91, 92, 93, 96, 97, 98, 101, 102, 103, 104, 105, 107, 109, 110, 120, 123, 125, 127, 128, 129, 130, 137, 138, 139, 140, 141, 146, 147, 149, 150, 151, 152, 153, 155, 157, 159, 165 and 167 were observed statistically higher over resistant plant AB 15–06. Lines of mapping population 8, 10, 15, 19, 29, 43, 55, 58, 59, 77, 88, 106, 108, 116, 117 and 121 were statistically higher over susceptible parent GRB 5.

Finding of results are in accordance with Konyak et al. (2020) observed Plant height was ranged around 52.5–108.7 cm. Saikia et al. (2021) recorded plant height in the range of 50.45-115 cm.

3.5. Primary branches plant^{-1}

The data on numbers of primary branches were recorded at the time of maturity. Minimum primary branches plant^{-1} 6.8 was found in line of mapping population 37 where as Maximum primary branches plant^{-1} 18.4 were recorded in line of mapping population 122. Numbers of primary branches per plant were 13.6 and 16.8 in resistant parent AB 15-06 and susceptible parent GRB 5 respectively. Lines of mapping population 14, 15, 19, 29, 32, 34, 42, 48, 49, 54, 58, 59, 60, 62, 67, 72, 73, 80, 81, 82, 83, 86, 91, 93, 104, 107, 108, 109, 110, 111, 115, 118, 121, 123, 129, 137, 138, 142, 149, 157, 158 and 160 were statistically higher over resistant parent AB 15-06. Line of mapping population 70, 77, 79, 90, 94, 96, 97, 99, 101, 116, 124, 127, 131, 132, 135, 139, 144, 145, 147, 148, 150, 154, 155, 156, 159, 161 and 166 were statistically higher over susceptible parent GRB 5.

The result was concordant with the finding of Konyak et al. (2020) characterized no. of branches plant^{-1} of different genotypes was ranged from 11.5 to 22.5. Saikia et al. (2021) observed no. of primary branches plant^{-1} 5.26.

3.6. Leaf length

Fully expanded middle leaf was selected to measure the leaf length. Minimum leaf length 12.7 cm was observed in line of mapping population 146 where as maximum leaf length 24.1 cm was observed in line of mapping population 54. Leaf length recorded 17.8 cm in resistant parent AB 15–06 where as in susceptible parent GRB 5 had 21.9 cm. Lines of mapping population 1, 2, 3, 5, 7, 8, 18, 19, 22, 24, 42,52, 68, 69, 71, 72, 74, 75, 76, 77, 78, 79, 80, 83, 86, 87, 88, 89, 93, 94, 96, 97, 98, 105, 107, 108, 109, 110, 117, 119, 120, 121, 122, 123, 124, 133, 134, 135, 137, 138, 139, 140, 141, 142, 143, 144, 149, 153, 158, 162, 165, 167 and 168 were statistically higher over resistant parent AB 15–06. Lines of mapping population 6, 10, 16, 17, 25, 27, 32, 37, 40, 43, 45, 46, 48, 53, 57, 58, 60, 64, 65, 66, 81, 106, 111, 113, 125, 127, 157, 159, 161, 163 and 164 were statistically higher than the susceptible parent GRB 5.

The results were in concurrence with the findings of Shilpa et al. (2018) observed leaf length (12.78–24.97 cm) in brinjal. Kaur et al. (2018) measured leaf length 12.78–33.97 cm where as Begum et al. (2022) observed leaf length 9.26–24.51 cm.

3.7. Leaf width

Fully expanded middle leaf was selected to measure the leaf

width. Minimum leaf width 7.1 cm was observed in line of mapping population 91 where as maximum leaf width 18.3 cm was observed in line of mapping population 15. Leaf width was recorded 12.2 cm and 14.8 cm in resistant parent AB 15–06 and susceptible parent GRB 5 respectively. Lines of mapping population 2, 3, 5, 8, 11, 18, 21, 22, 24, 30, 69, 70, 71, 72, 73, 75, 76, 77, 83, 86, 87, 88, 90, 93, 96, 98, 102, 104, 105, 107, 109, 111, 113, 117, 119, 120, 122, 123, 124, 126, 128, 130, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 147, 153, 155, 156, 160, 162, 163, 164, 165, 166, 167 and 168 were statistically higher over resistant parent AB 15-06. Lines of mapping population 6, 7, 9, 10, 12, 13, 17, 20, 26, 28, 29, 31, 32, 35, 36, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 55, 56, 57, 61, 67, 82, 84, 94, 101, 103, 108, 110, 112, 115, 116, 118, 125, 127, 131, 132, 158 and 159 were statistically higher over susceptible parent GRB 5.

The present findings were analogous with the results of Begum et al. (2022) and Kaur et al. (2018) measured leaf width 2.72–8.14 cm and 5.16–18.50 cm, respectively.

3.8. Fruit volume

Fruit volume data measured at 6th picking stage. Mean values of fruits volume was recorded 61.6 and 10.0 in resistant parent AB 15–06 and susceptible parent GRB 5 respectively. Minimum fruit volume recorded was 10 cc in line of mapping population 21 where as maximum fruit volume observed was 346.8 cc in line of mapping population 134. Lines of mapping population 42 (61.4 cc), 43 (55.8 cc), 44 (56.6 cc), 78 (55.2 cc), 128 (53.4 cc), 144 (54.2), 161 (54.8 cc) and 166 (55.4) were statistically higher over resistant parent AB 15–06.

The present results are in conformity with the reports of Konyak et al. (2020) recorded fruit volume 44.17–316.67 cc in brinjal.

3.9. No. of fruit plant^{-1}

The data pertaining to no. of fruit plant^{-1} was recorded at the different picking stages. Results reveled that minimum no. of fruit plant^{-1} 10.3 observed in line of mapping population 163 where as maximum no. of fruit plant^{-1} recorded was 55 in line of mapping population 5. Mean values for number of fruits plant^{-1} was recorded 35.9 and 12.3 in resistant parent AB 15–06 and susceptible parent GRB 5 respectively. Lines of mapping population were 12 (32.1), 39 (29.5), 43 (36.6), 48 (37.7), 57 (32.2), 61 (29.3), 62 (29.6), 65 (34.3), 66 (34.6), 71 (29.8), 73 (32.1), 74 (31.2), 78 (31.6), 83 (32.9), 93 (29.5), 104 (31.2), 111 (34.7), 122 (30.1), 131 (33), 135 (31.4), 136 (33), 137 (32.9), 138 (29.7), 143 (31.8), 144 (35.3), 150 (31.7), 152 (34.2), 153 (30.5), 154 (34.6) and 162 (31.7) statistically higher over resistant parent AB 15–06. Lines of mapping population 8 (11.1), 10 (11.8), 37 (11.9), 58 (10.7), 106 (11.3), 163 (10.3) and 164 (11.9) were recorded statistically higher over susceptible parent GRB 5.

The results are in harmony with the findings Balasubramaniyam et al. (2021) was recorded no. of fruit per plant 9.25–43.14 in brinjal.

3.10. Fruit weight

The data pertaining to fruit weight was recorded at the different picking stages. Results reveled that minimum fruit weight 33.4 observed in line of mapping population 117 where as maximum fruit weight 95.5 g was recorded in line of mapping population 142. Fruit weight was observed 80.5 g and 41.6 g of resistant parent AB 15–06 and susceptible parent GRB 5 respectively. Lines of mapping population 17 (72.8 g), 27 (74.8 g), 37 (73 g), 45 (75.7 g), 47 (74.5 g), 51 (74.2 g), 60 (70.1 g), 69 (74.3 g), 70 (76.3 g), 73 (77.1 g), 74 (73.5 g), 79 (79.7 g), 85 (70.8 g), 89 (73.8 g), 90 (74.3 g), 92 (75.6 g), 95 (70.2 g), 97 (77.6 g), 98 (75.7 g), 130 (74.1 g), 140 (73.2 g), 147 (74.6 g), 161 (78.1 g) and 168 (72.7) were statistically higher over resistant parent AB 15–06 statistically at par with resistant parent AB 15–06. Lines of mapping population 10 (36 g), 38 (36.6 g), 88 (34.4 g), 116 (40 g), 117 (33.4 g), 121 (34.8 g), 160 (39.2 g), 163 (36 g), 164 (41.3 g) and 165 (41.5 g) were statistically higher over than the susceptible parent GRB 5.

The present results observed lower fruit weight compared to Balasubramaniyam et al. (2021) recorded fruit weight 23.12–105.01 g in brinjal.

3.11. Fruit yield plant^{-1}

The data pertaining to fruit yield plant^{-1} was recorded at the different picking stages. Based on data minimum number of fruit yield plant^{-1} 0.5 kg was observed in the line of mapping population 29 and maximum number of fruit yield plant^{-1} 3.2 kg was observed in the line of mapping population 17. Fruit yield plant^{-1} was recorded 2.4 kg and 0.7 kg of resistant parent AB 15–06 and susceptible parent GRB 5. Lines of mapping population were 1 (2.1 kg), 28 (2.1 kg), 57 (2.3 kg), 73 (2.1 kg), 130 (2.2 kg), 133 (2.1 kg), 137 (2.3 kg) and 168 (2.3 kg) were noted statistically higher over resistant parent AB 15–06. Lines of mapping population 10 (0.6 kg), 29 (0.5 kg), 58 (0.6 kg), 160 (0.6 kg) and 163 (0.6 kg) were observed statistically higher over than the susceptible parent GRB 5.

The present findings were in concurrence with Balasubramaniyam et al. (2021) recorded fruit weight 0.48–2.42 kg and Nagar et al. (2024) observed fruit weight 0.447–1.990 kg.

3.12. Disease incidence

Disease incidence was recorded at weekly bases of transplanting to the maturity stage of both of the parents and 168 $F_{2:3}$ segregating population. On the based on data

minimum number of disease incidence 2.2% observed in line of mapping population 1 and maximum number of disease incidence 38.3% observed in the line of mapping population 8 where as other 0% indicated immune plants against little leaf disease. Resistant parent AB 15–06 observed 0% disease incidence where as susceptible parent GRB 5 recorded 36.4% disease incidence. Lines of mapping population 1 (2.2%), 12 (2.5%), 38 (0.3%) and 148 (2.5%) were statistically higher at par with resistant parent AB 15-06. Line of mapping population 79 (36.1%) and 88 (33.8%) were recorded statistically higher at par than the susceptible parent GRB 5.

3.13. Correlation study of disease incidence with morphophysiological traits

The pearson's correlation (Figure 4) revealed a significant negative association between primary branches per plant with leaf length (r 0.24**) and leaf width (r 0.31***) and positive correlate with disease incidence(r 0.01), fruit volume (r 0.10), plant height (r 0.06), fruit weight (r 0.09), no. of fruit per plant (r 0.10), and days to initiation of flowering (r 0.14). Days to initiation of flowering correlated non significant with each parameters. Fruit yield plant^{-1} significant negative association with disease incidence (r-0.40***) and positive correlate with plant height (r 0.35), no. of fruit plant^{-1} (r 0.50***) and fruit weight (r 0.30), no. of fruit plant^{-1} significant negative association with disease incidence (r-0.39***), leaf length (r-0.15*) were as plant height (r 0.34***) correlate positively. Fruit weight significant negative association with disease incidence (r-0.39***) were as plant height (r 0.36***) and fruit volume (r 0.24**) positively correlate respectively. Plant height significant negative association with disease incidence (r-060***), leaf length (r-0.18*), leaf width (r-0.20*), Fruit volume shown negative non significant over result over disease incidence (r-0.08), leaf length (r-0.05) and leaf width (r-0.01). Leaf width was positive correlated with leaf length (r 0.83***) and negative correlate with disease incidence (r-0.05). Leaf length was also negative correlate with disease incidence (r-0.14).

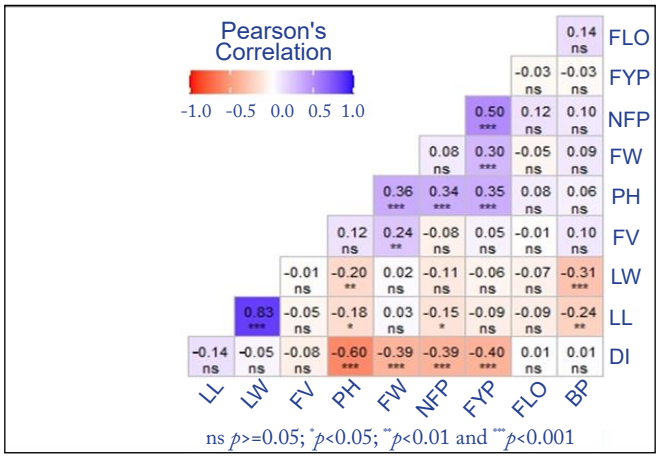


Figure 4: Correlation coefficient analysis of morphophysiological characters in $F_{2:3}$ mapping population in brinjal; Note: FLO: Days to initiation of flowering; FYP: Fruit yield plant^{-1}; NFP: No. of fruits plant^{-1}; FW: Fruit weight; PH: Plant height; FV: Fruit volume; LW: Leaf width; LL: Leaf length; DI: Disease incidence; BP: Primary branches plant^{-1}

Results found that characters like plant height, fruit volume, number of fruits plant^{-1}, fruit weight, leaf length, leaf width and fruit yield plant^{-1} were recorded significant negative correlated with disease incidence while remaining morphophysiological parameters days to initiation of flowering and primary branches plant^{-1} positively correlated in Figure 4.

The present investigation were accordance with Frary et al. (2014), Konyak et al. (2020) and Vethamonai et al. (2020) carried out correlation analysis from different morphological characters. viz., plant height, fruit volume, no. of fruits per plant^{-1}, fruit weigh and fruit yield ranges significantly negative correlated with each other that was similar to our finding results.

3.14. Test of normality

Discrete variation in the population was expressed by quantitative characters. For a given characteristic, skewness and kurtosis were computed to determine the frequency distribution of a mapping population and their genetic relationships.

The frequency distribution curve for the morphophysiological features of the $F_{2:3}$ mapping population displayed in Figure 5. Skewness and kurtosis measured $F_{2:3}$ mapping population showed in Table 2.

Kurtosis describes how peaked a distribution was, while skewness indicated how far a distribution deviates from symmetry. Positive skewness suggested complementing

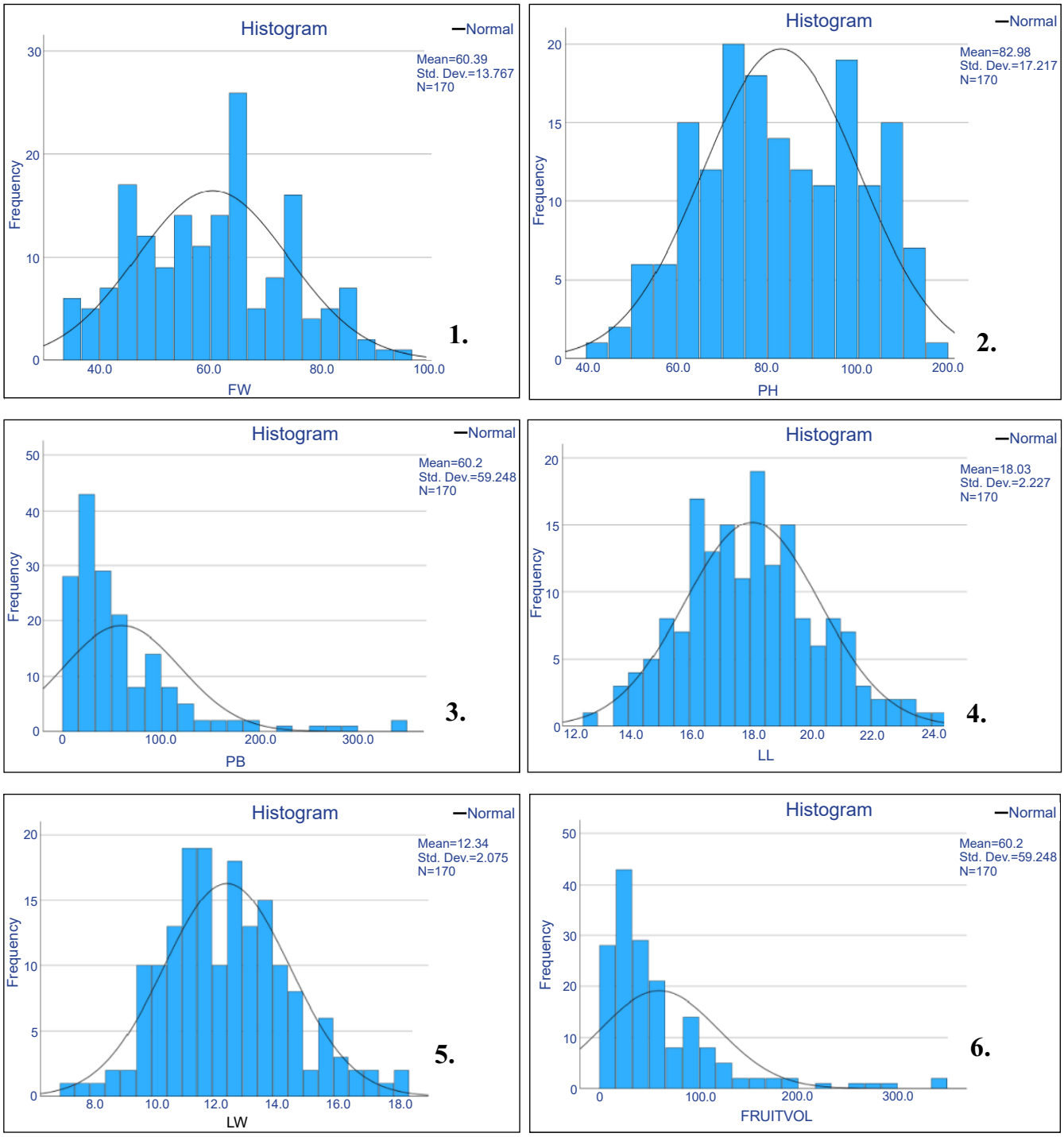
Table 2: Skewnness and kurtosis for morphophysiological traits of $F_{2:3}$ mapping population

Sl. No.	Traits	Skewness	Kurtosis
1.	Days to initiation of flowering	-1.221	1.249
2.	Plant height	-0.027	-1.007
3.	Primary branches plant^{-1}	2.442	7.295
4.	Leaf Length	0.302	-0.133
5.	Leaf Width	0.404	0.148
6.	Fruit volume	2.442	7.295
7.	No. of Fruit plant^{-1}	0.276	-0.419
8.	Fruit weight	0.172	-0.619
9.	Fruit yield plant^{-1}	0.753	0.505
10.	Disease incidence	0.988	-0.228

epistatic gene action for the trait under study, and it also showed that genetic gain occurred more quickly under intense selection than it does under mild selection. When skewness wasnegative, that indicated the presence of duplicate epistasis gene activity. Under mild selection, genetic gain occurred more quickly, but under strong selection, it occurred more quickly.

Mesokurtic referred to a regular normal distribution with a kurtosis of 0. The visual representation of an elevated kurtosis (>1) was a narrow "bell" with a high peak, while a lower kurtosis denoted a broadening of the apex and the tails' "thickening." Kurtosis <1 was considered platykurtic, whereas >1 was considered leptokurtic (Yankanchi et al., 2022).

Morphophysiological and biochemical characters like primary branches plant^{-1} (2.442), leaf length (0.302), leaf width (0.404), fruit volume (2.442), no. of fruit plant^{-1}



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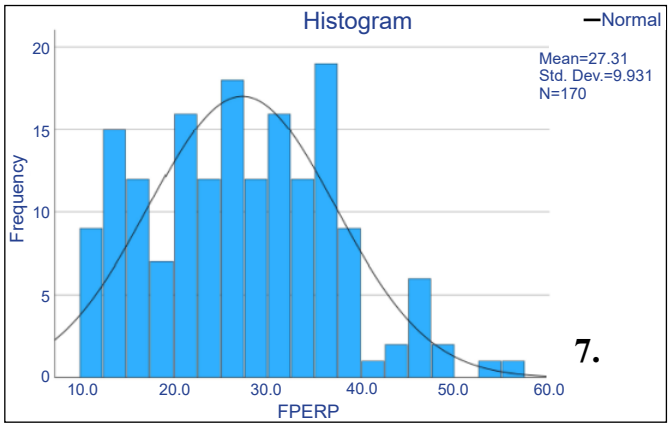

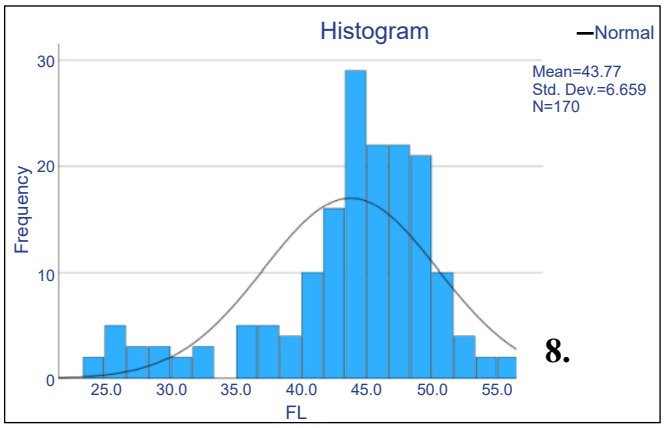

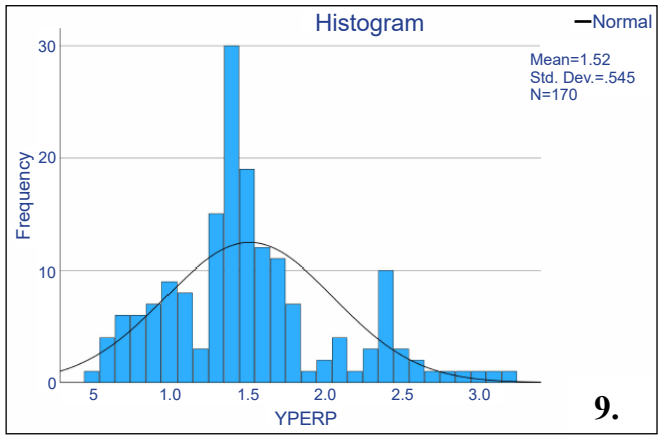

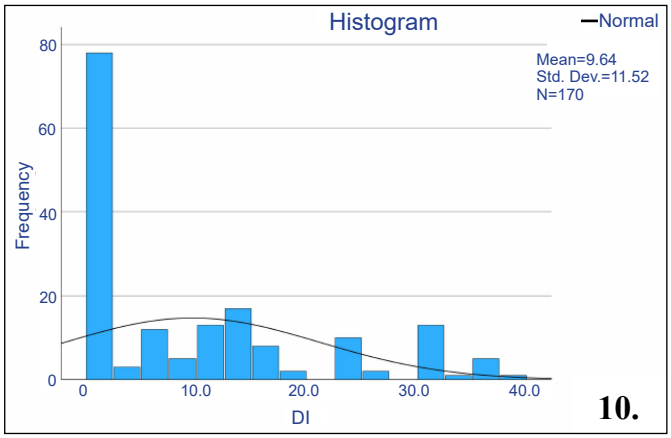

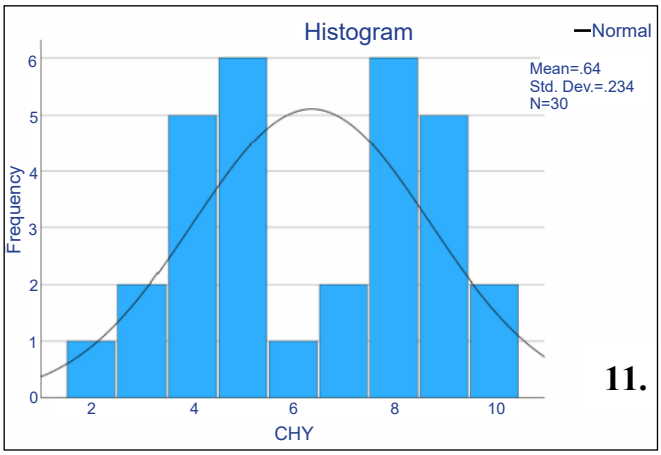

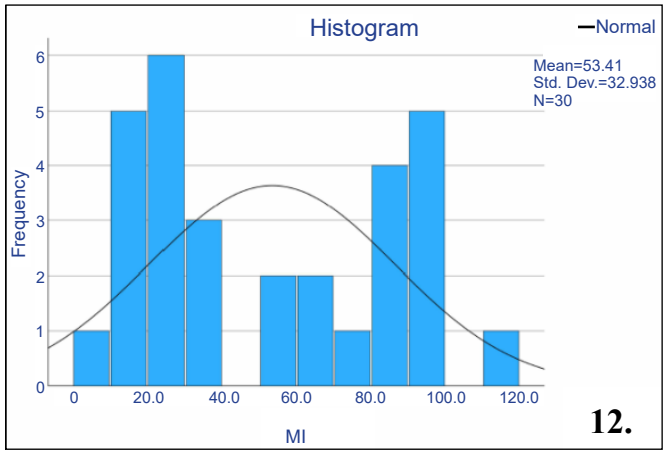

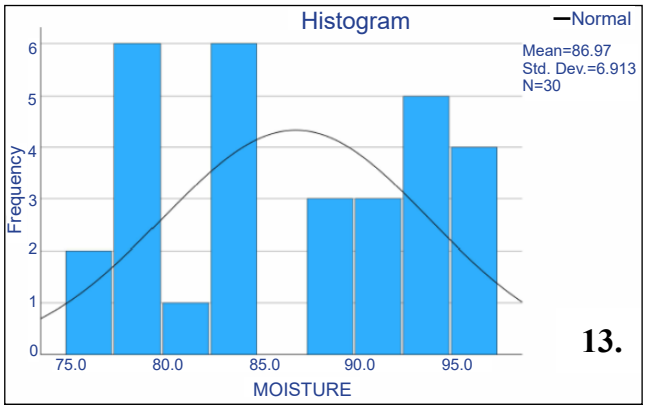

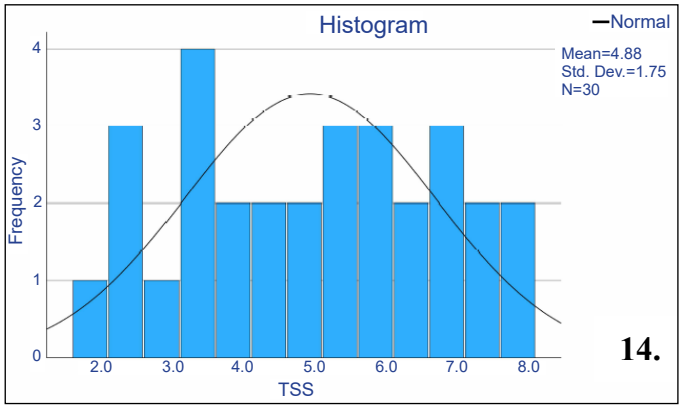

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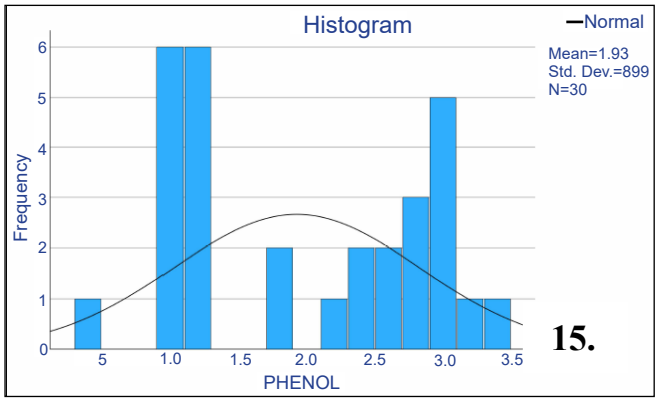

Figure 5: Frequency distribution of morphophysiological and biochemical characters in $F_{2:3}$ population of brinjal; Note: FLO: Days to initiation of flowering; FYP: Fruit yield plant^{-1}; NFP: No. of fruits plant^{-1}; FW: Fruit weight; PH: Plant height; FV: Fruit volume; LW: Leaf width; LL: Leaf length; DI: Disease incidence; BP: Primary branches plant^{-1}

(0.276), fruit weight (0.172), fruit yield per plant^{-1} (0.753), disease incidence (0.988) showed positive skewness. This indicated that a greater number of genotypes than would be predicted from a normal distribution were below the mean. Other characters like days to initiation of flowering (-1.221) and plant height (-0.027) detected negative skewness. This indicated that more genotypes that would be predicted from a normal distribution were above the mean.

For kurtosis, days to initiation of flowering (1.249), primary branches plant^{-1} (7.295), leaf width (0.148), fruit volume (7.295), fruit yield per plant^{-1} (0.0505) showed positive kurtosis which indicated a leptokurtic distribution, which represented the average level of complementary gene activity. Some of the morphophysiological characters like disease incidence (-0.228), plant height (-1.007), no. of fruit per plant^{-1} (-0.419), fruit weight (-0.619) detected negative kurtosis which meant average level of complementary gene activity though to be platykurtic that indicated the presence of numerous small gene progressively greater effects controlled activity of the genes.

Bhanushree et al. (2019) observed skewness and kurtosis of morphological character like plant height (0.28 and -0.07) and fruit weight ranges varied from 0.23 to -0.37 in brinjal, respectively. This was noted to agreement with our finding result.

Uddin et al. (2021) found skewenes and kurtosis of morphological characters like plant height (0.21 and 2.25), days to initiation of flowering (-2.25 and 3.27), fruit weight (0.14 and 2.69), no. of fruit per plant^{-1} (2.25 and 7.16) fruit yield plant^{-1} (0.54 and 5.41). Ranges were agreement with our finding results.

Tassone et al. (2022) found skewness and kurtosis of fungal wilts caused by Fusarium oxysporum f. sp. melongenae disease incidence in brinjal. Ranged from 0.455 and -1.502. The range was accordance with our finding result.

Yankanchi et al., (2022) observed skewness and kurtosis of morphological character like plant height (0.046039 and 2.1009), no. of primary branches plant^{-1} (-0.15774 and 2.78912), number of fruits plant^{-1} (-0.80198 and 3.13263), fruit weight (1.0577 and 3.34928), fruit yield plant^{-1} (0.45725 and 2.0653).

3.15. GCV, PCV, Heritability, GA of Morphophysiological traits of $F_{2:3}$ mapping population

Any breeding effort could benefit from using population variability estimates and heritable component analysis to improve a plant trait. The majority of the variation present must be heritable in order to advance a character through selection. Therefore, it was crucial for breeding to understand the genotypic and phenotypic coefficients of variation as well as the heritability of the trait. For this reason, the variability among various traits was assessed using the co-efficient of variation that was computed at the phenotypic and genotypic levels. Heritability provided an estimate of the relative amount of heritable portion of variation, while GCV and PCV indicated the existence of the moderate to high values were observed which potential for scope for improvement through selection.

Table 3: Variability analysis for morphophysiological and biochemical traits of $F_{2:3}$ population

Sl. No.	Traits	Range	Mean	GCV (%)	PCV (%)	h²B (%)	GAM (%)
1.	Days to initiation of flowering	24.6–55.4	43.76	11.56	25.15	21.1	10.94
2.	Plant height (cm)	44.9–116.4	83	17.63	30.14	34.23	21.25
3.	Primary branches per plant^{-1}	6.8–18.4	12.46	18.76	23.95	61.34	30.26
4.	Leaf length (cm)	12.7–24.1	18.03	11.31	15.96	50.23	16.52
5.	Leaf width (cm)	7.1–18.3	12.34	15.45	21.49	51.65	22.86
6.	Fruit volume (cc)	10–346.8	60.2	98.29	98.96	98.65	201.1
7.	No. of fruit per plant^{-1}	10.3–55.0	27.31	35.28	40.43	76.15	63.42
8.	Fruit weight (g)	33.4–95.5	60.39	21.9	26.09	70.45	37.86
9.	Fruit yield plant^{-1} (kg)	0.5–3.2	1.52	35.21	38.94	81.76	65.58

Heritability value in combination with high genetic advancement provided an accurate estimate of the amount of genetic advancement resulting from the selection of the finest individuals reported by Burton and Devane, (1953) and Johnson et al., 1955. Values between 10–20% were regarded as medium, values less than 10% were regarded as low, and values beyond 20% were considered high for both genotypic and phenotypic coefficients of variation. For heritability, value was below 30% and higher than 60% that considered being low heritability and high heritability respectively. Value between 30–60% was represented moderate heritability (Johnson et al.,1955).

Variability analysis for morphophysiological and biochemical traits of $F_{2:3}$ mapping population were mentioned in Table 3.

3.16. Days to initiation of flowering

The ranges for days to initiation of flowering (24.6–55.4) while moderate values of genotypic coefficient of variation and phenotypic coefficient of variation shown high value i.e., GCV (11.56) and PCV (25.15%), which was suggested phenotypic coefficient of variation greater than genotypic coefficient of variation that indicated role of environment for trait development. Moderate per cent mean of genetic advance (10.94%) and low estimates of heritability (21.1%) which influenced by environmental effects and genetic improvement through selection would be difficult due to masking effect of the environment on the genotypic effect and limited chance for crop improvement.

The results were in confirmation with finding of Mat sulaiman et al. (2020) who recorded high value of GCV and PCV with moderate per cent mean of genetic advance and low heritability.

3.17. Plant height

The wide range for plant height 44.9 to 116.4 cm while moderate values recorded for genotypic and phenotypic coefficient of variation i.e., GCV and PCV (17.63 and 30.14%) which suggested the presence of moderate amount of variability which could be utilized through selection of effective breeding programme. More importantly moderate estimates of heritability (34.30) and moderate per cent mean of genetic advance (21.25%) which suggested moderately scope for this trait improvement.

The result obtained here was concordant with the findings of Anbarasi et al. (2021) who reported moderate variability in reference population for the trait.

3.18. Primary branches plant^{-1}

Primary branches plant^{-1} wide ranged 6.8 to 18.4 while moderate values found for GCV and PCV (12.46% and 18.76%) which indicated the moderate variability which could be utilized through selection programme. The higher estimates of heritability (61.34%) coupled with high values per cent mean of genetic advance (30.26%) which indicated the presence of additive gene and a better chance for selection which would be rewarding.

The above results were in agreement with finding of Mahmoud et al. (2018) who reported moderate GCV and PCV with high heritability and per cent mean of genetic advance.

3.19. Leaf length

Observations on leaf length revealed the values in between 12.7 to 24.1 cm while moderate values of GCV (11.31%) and PCV (15.96%) which suggested the presence of moderate amount of variability which could be utilized through selection for efficient breeding programme. The moderate estimates of heritability (50.23%) with moderate values per cent mean of genetic advance (16.52%) suggested limited chances for improvement through selection.

The results were in accordance with kaur et al. (2018) reported moderate values of GCV (16.09%) and PCV (20.49%) with moderate heritability (51.61%) and per cent mean of genetic advance (28.53%).

3.20. Leaf width

For leaf width, it was ranged in between 7.1 to 18.3 cm while moderate values of GCV (15.45%) and high value of PCV (21.49%) which suggested phenotypic coefficient of variation greater than genotypic coefficient of variation that indicated role of environment for trait development. The moderate estimates of heritability (51.65%) with high values per cent mean of genetic advance (22.86%) suggested that preponderance of additive gene effects. The moderate heritability beign exhibited due to moderate environmental effects. Selection might be fair chances for crop improvement.

The result was in coherence with kaur et al. (2018) reported moderate values of GCV (19.37%) and PCV (24.71%) with moderate heritability (46.65%) and per cent mean of genetic advance (32.07%).

3.21. Fruit volume

Observations on fruit volume revealed the values in between 10 to 346.8 cc was observed along with closely association of GCV (98.29%) with PCV (98.96%) which indicated the presence of good amount of variability and little influence of environment on the expression of trait. The high estimates of heritability (98.65%) with high values per cent mean of genetic advance (201.1%) which suggested the involvement of additive gene action in the inheritance of these trait and selection segregating generation of these populations would be effective for further improvement in this trait.

High values of GCV (51.74%) and PCV (52.04%) with high heritability (98.87) and per cent mean of genetic advance (105.98) was reported by kaur et al. (2018).

3.22. Number of fruits per plant^{-1}

Number of fruits plant^{-1} ranged in between 10.3 to 55.0 while moderate values found for GCV (35.28%) and PCV (40.43%) suggested the moderate variability which could be utilized through selection for breeding programme. The high estimates of heritability (76.15%) along with high values per cent mean of genetic advance (63.42%) indicated that the involvement of additive gene action in the inheritance of these trait and selection segregating generation of these populations would be effective for further improvement in this trait.

3.23. Fruits weight

Fruit weight ranged in between 33.4 to 95.5 g while moderate values found for GCV (21.90%) and PCV (26.09%) were measured which might be due to presence of good amount of variability of all the mapping populations for traits. Presence of high variability indicated less environmental influence hence selection might be rewarding. The high estimate of heritability (70.45%) with high values per cent mean of genetic advance (37.86%) were recorded for these trait which indicated the presence of additive gene and less environmental influence and selection would be effective. The above results were in agreement with Sangam et al. (2020) with high values of GCV and PCV with high heritability and high values per cent mean of genetic advance.

3.24. Fruit yield plant^{-1}

Fruit yield plant^{-1} ranged in between 0.5 to 3.2 kg while high values found for GCV (35.21%) and PCV (38.94%) which indicated high variation among the mapping population due to fruit yield plant^{-1}. The high estimates of heritability (81.76%) with high values per cent mean of genetic advance (65.58%) for this trait which indicated almost all populations revealed involvement of additive gene action and direct selection of improvement of this trait in segregating generation of this population would be lucrative.

These findings were accordance with Nagar et al. (2024) with high values of GCV and PCV with high heritability and per cent mean of genetic advance.

3.25. Identification of marker trait association for little leaf resistance

3.25.1. Single marker analysis (SMA)

Single marker analysis was for each marker locus,

Table 4: Detailed of linked marker associated with little leaf resistance in brinjal

Trait	Sr. No.	Marker	Primer sequence 5' to 3'		Product size (bp)	*p* value	R^2 (%)
FP	1	CSM44	F: CGTCGTTGTAACCCATCATC	P1	233	0.025**	2.95
			R: TTGCCAAATTCCTTGTGTTC	P2	244		
	2	smSSR03	F: ATTGAAAGTTGCTCTGCTTC	P1	195	0.026*	2.92
			R: GATCGAACCCACATCATC	P2	215		
DI	3	emh11G21	F: ATGTGTGAACTCAAATGGAAGGGA	P1	282	0.0097**	3.95
			R: GTTTCGAATTGCTTTTTGGTGCATGTAG	P2	306		
	4	emk03O04	F: ATGATTTGGGCAGCCACTTTTGTA	P1	284	0.0004**	12.17
			R: GTTTGGAACCAACTAAACTTAGGGCA	P2	314		
	5	CSM16	F: ACGTGCCATTTCAAACTTGG	P1	212	0.0002**	13.76
			R: TCCTTTTCTTGAGCTGAATTTG	P2	243		
	6	emd05B11	F: ATTGCTTCAATTAAGGCTGAGAGGG	P1	193	0.0001**	15.96
			R: GTTTGGATTAGCATGTGGAGGACTGAA	P2	214		
	7	emb01A21	F: TCATGGTAGGTGGAGACAGAACCA	P1	249	0.0027**	5.25
			R: GTTTGGATTAGCATGTGGAGGACTGAA	P2	223		
FYPP	8	emh05B02	F: ATACCAAAGACACGTTGGGATCAT	P1	185	0.029*	2.8
			R: GTTTCTAGGAGAGCATCTCCCTCCCT	P2	176		
	9	emf11D18	F: AGAGACAGGGAGAGTGCATTCTATG	P1	234	0.023*	3.06
			R: GTTTGCAGTTCATAAGGTTGCATCAATAC	P2	247		
	10	CSM78	F: AGGGAGGAGCTCTCGTGTG	P1	267	0.0084**	4.10
			R: CAATAACGTAGCTTAATTACTCCCAAG	P2	295		

Note: FP: Fruit plant^{-1}; DI: Disease incidence; FYPP: Fruit yield plant^{-1}

disregarding data from other loci into genotypic groups was based on the presence or absence of particular marker locus. It also indicated whether the genotype classes and the marker locus differ significantly from one another. It revealed the association between molecular marker and trait of interest.

3.25.2. Validation of marker trait association

One-way ANOVA was carried out for single marker analysis to detect SSR markers (as an independent variable) associated with quantitative traits (dependent variables). An association between the marker and the phenotypic trait was revealed by a significant F-value (p<0.01 and 0.05).

When combining marker data with phenotypic data, the analysis indicated that these variables together contribute significantly to the observed variation among the groups. The F-statistic significantly exceeds the critical F-value, indicated that the differences between groups were highly significant from a statistical standpoint. So, reject the null hypothesis, indicating that there was indeed a significant disparity in means among the groups under consideration. On the other hand, the variation within groups reflected the inherent variability of individual data points around their respective group means.

A simple linear regression was calculated for little leaf resistance in brinjal mapping population using the 48 SSR markers. The significance of the regression coefficient was considered for establishing the potential association between the marker and trait. The marker with the best relationship could be evaluated from its PVE (phenotypic variance as explained). The percent PVE demonstrated variability of the specified trait explained by the marker.

A total of ten SSR markers were found to be linked with fruit per plant, disease incidence and fruit yield per plant^{-1}. CSM44 and smSSR03 markers significantly linked with fruit yield per plant^{-1}. The R^2 value of CSM44 and smSSR03 was ranged 2.92% and 2.92%, respectively. Lower R^2 value indicated the model was explaining far more variance than actually existed in the data. Total five markers associated with disease incidence viz., emh11G21, emk03O04, CSM16, emd05B11 and emb01A21. Three markers name emk03O04, CSM16, emd05B11 had maximum R^2 value 12.17%, 13.76%, 15.96% that indicated that 12-16% phenotypic variation has been explained by these three marker. Phenotypic variation in the dependent variable (presumably influenced by these markers) could be explained by the independent variables represented by these markers. This suggested that these markers have some degree of association with the little leaf disease resistance. emb01A21 marker had lower R^2 value (5.25%) compare to other disease incidence marker, suggested that this marker's variability contributed minimally to study the variability in the dependent variable (disease incidence) within the model. It implied that the relationship between emb01A21 marker (in depended variable) and the disease incidence (dependent variable) was weak or not well-captured by the model. emh05B02, emf11D18 and CSM78 markers associated with fruit yield plant^{-1} with R^2 value 2.8%, 3.06% and 4.10%, respectively. The product amplified by different SSR markers associated for fruit plant^{-1}, disease incidence and fruit yield plant^{-1} indicted in Table 4.

Frary et al. (2003) identified markers linked with morphological characters in eggplant. For leaf length two marker association was identified on linkage groups 11 and 12 and leaf width four marker were identified with R^2 value 22%, Days to flowering was located on linkage group 2 with 28% of the variation in flowering time. No. of fruits plant^{-1} linked on linkage group 3, 4, 7 and 10 with R^2 value 26%, plant height was linked on linkage group 2, 5, 10 and 12 with R^2 value 28%.

Portis et al. (2014) identified markers association in egg plant of each morphological traits viz; No. of flower inflorescence^{-1}, fruit weight, fruit diameter, fruit length, leaf prickliness had seven marker association with 4 and 93% of the phenotypic variance (PV).

Wei et al. (2020) also carried out QTL analysis for different morphlogocal characters viz; main stem height (msh), fruit length (fl), fruit diameter (fd), fruit shape (fs), leaf lobing (llob), leaf prickle number (lpn), leaf prickle color (lpc), and vein color (vc) with 4.08-55.23% phenotypic variance.

Narayanswami et al. (2023) identified two resistant markers against phomosis blight in brinjal. emf11A03 marker with LOD, phenotypic explained (%) and additive effect was detected 4.203, 7.393%, 13.41, respectively while marker name emk03O04 had LOD score 3.079, phenotypic variation 5.501% with additive effect 14.58.

The present results were in conformity with Sakure et al. (2024) who identified SSR markers linked with root knot nematode resistance and leaf thickness in tobacco by validation of marker trait association through marker analysis with R^2 ranged from 2.2-20.45%.

4. CONCLUSION

Present investigation revealed total ten SSR markers were found to be linked with fruit plant^{-1}, disease incidence and fruit yield plant^{-1}. Two markers CSM44 and smSSR03 significantly linked with number of fruit plant^{-1}. Total five markers associated with disease incidence were emh11G21, emk03O04, CSM16, emd05B11 and emb01A21. From these, three markers namely emk03O04, CSM16, emd05B11 were strongly linked with little leaf resistance in brinjal. Three markers emh05B02, emf11D18 and CSM78 were found associated with fruit yield plant^{-1}.

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