



Analyzing Genetic Variation and Graphical Representation (Wr-Vr) in Brinjal (*Solanum melongena* L.) using the Hayman Approach in the Northwestern Region of India

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ABSTRACT

Background: Brinjal, also known as eggplant, is a resilient and widely cultivated vegetable crop in the Solanaceae family. It plays a crucial role in diets due to its rich supply of vitamins, minerals and dietary fiber, helping address the deficit in vegetable consumption recommended by the World Health Organization (WHO), which advises a daily intake of at least 400 grams of fruits and vegetables. Estimating genetic parameters is essential for understanding the genetic architecture of yield and its determining factors. Hayman's diallel cross analysis method is extensively utilized in plant breeding due to its capacity to provide comprehensive insights into diverse genetic parameters, including gene action, degree of dominance and heritability.

Methods: Nine parents with thirty six F_1 hybrids of brinjal derived using a half diallel mating design with nine brinjal genotypes, namely JBL-1, JBR-1, JBR-2, JBR-3, JBL-2, JBL-3, JBR-4, JBR-5 and JBR-6 were evaluated for yield and other yield attributing traits during *kharif* season 2023) using randomized block design (RBD) with three replications.

Result: The dominance effect (H_1) was significant and displayed a greater magnitude, indicating dominance gene action for yield per plant. The regression coefficient slope showed a significant deviation from zero, but not from unity, indicating the absence of non-allelic interaction. Furthermore, the regression line intersected the W_r axis below the origin, suggesting the presence of over-dominance for days to 50% flowering, fruit length (cm), number of primary branches per plant, plant height (cm), total fruit yield per plant (kg) and fruit borer infestation (%). The mean degree of dominance exceeding one indicated the prevalence of over-dominance for all traits except days to first picking, average fruit weight (gm), fruit girth (cm) and number of fruits per plant. These findings emphasize the importance of dominance variation in eggplant improvement, enabling successful heterosis breeding for advancing these populations and development of hybrids.

Key words: Brinjal, Degree of dominance, Genetic component, Hayman approach, Narrow sense heritability, W_r - V_r graph.

INTRODUCTION

Vegetables are essential for a healthy diet, providing vital vitamins, minerals, fiber and complex carbohydrates while being low in fat. In India, the average daily intake of fruits and vegetables is about 200 grams per person, significantly below the WHO's recommended 400 grams (Udikeri *et al.*, 2024). Brinjal (*Solanum melongena* L.), a resilient crop in the Solanaceae family, thrives under diverse conditions, resisting pests, diseases and environmental stresses (Malarkodi *et al.*, 2023; Palia *et al.*, 2021). In India, it is cultivated on 550,000 hectares, producing around 12 million tonnes annually (Rani *et al.*, 2018). Indian breeding programs focus on improving yield, quality and resistance, addressing local challenges like pests and diseases (Biradar *et al.*, 2023). Global breeding efforts also prioritize these traits, with collaborative genetic exchanges enhancing brinjal varieties.

Estimating genetic parameters is crucial for understanding the genetic architecture of yield and its determining factors (Datta *et al.*, 2021). Gene action analysis shows a prevalence of both non-additive and additive gene actions across diverse traits. In homozygous genotypes, genetic variation is solely additive and additive-epistatic, while segregating populations exhibit a

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combination of both additive and non-additive genes. Understanding the correlation between these traits and yield assists breeders in making precise selections (Shyadambi *et al.*, 2019). A deep understanding of gene actions and their influence on trait expression is essential for developing an effective selection program, particularly through the strategic use of suitable mating designs (Ginoya *et al.*, 2024).

Diallel analysis is a widely used method for evaluating multiple parent screening genotypes in breeding and hybrid

development. It is preferred for its extensive application over other mating designs (Gangadhara *et al.*, 2021). Half-diallel crossbreeding provides breeders with greater control compared to full-diallel crossbreeding, simplifying the design and management by including one-directional crosses and reducing the complexity of reciprocal crosses. In homozygous genotypes, genetic dissimilarity arises from both additive and non-additive factors, including epistasis. (Ghannadha *et al.*, 1995). Hayman's diallel cross analysis method is widely used in plant breeding for its ability to offer insights into various genetic parameters, such as additive and dominance effects, gene distribution and heritability. Given eggplant's vulnerability to the fruit and shoot borer (FSB), particularly *Leucinodes orbonalis*, identifying resistant hybrids through gene action is a primary objective (Gami *et al.*, 2023).

MATERIALS AND METHODS

Plant material

These genotypes showed a variety of fruit features, including size, shape and color. JBR-1 produced small, spherical, purple fruits, whilst JBL-1 produced medium-sized, medium-long, violet fruits. Medium-sized, spherical fruits with hues of light purple-greenish and purple, respectively, were produced by JBR-2 and JBR-3. JBL-3 has medium-sized, long, pink fruits and JBL-2 had enormous, long, white fruits. JBR-5 had huge, round, green fruits with white stripes and JBR-4 featured medium-sized, round, white fruits with purple stripes. Lastly, JBR-6 produced spherical, medium-sized, violet-colored fruits with a nice shine. A semi-spreading plant type was displayed by all nine genotypes. The inheritance of several phenotypes in these genotypes were studied using them as parental lines.

Experimental layout

The study involved nine brinjal genotypes from the breeding program at Junagadh Agricultural University, Gujarat, which are currently being developed for hybrid and variety development. The genotypes were grown in a randomized

block design (RBD) with three replications at the experimental farm of LPU. Standard agronomic practices were followed, including irrigation, fertilization and pest management. Data were recorded on various quantitative and qualitative traits of agronomic importance, including days to first flowering, days to first picking, fruit length, average fruit weight, fruit girth, number of fruits per plant, number of primary branches per plant, plant height, total fruit yield per plant and fruit borer infestation. Infestation of BSFB to the shoots and fruits was monitored weekly after establishment of the plant in the field and continued to the last harvest of the brinjal fruits. Shoot damage was recorded by counting the infested shoots from 10 randomly selected plants. The percentage of shoot damage was calculated from damaged and healthy shoots. The number of infested and healthy brinjal fruits per plot were recorded at each harvest. The percentage of infestation by number was calculated using the number of infested and total brinjal fruits. At each count the affected shoots and fruits were removed and harvested.

Statistical analysis

Hayman's graphical approach

This approach, pioneered by Jinks and Hayman focuses on estimating components of variation. Hayman's method, characterized by its graphical Vr-Wr graph, provides insight into six components of variance: D (additive genetic variance), H_1 (dominance variance), H_2 (Overall dominance effects of heterozygous loci), E (expected environmental variance), F (mean of Fr over array) and h_2 (dominance effects) Hayman (1957) and jinks (1954).

RESULTS AND DISCUSSION

A genetic component analysis was performed on half diallel crossings and their corresponding parents, with a specific focus on yield and attributes related to yield. The results, presented in (Table 1), illustrate the application of this approach to discern the allelic content of parents involved in the diallel concerning both quantitative and polygenic traits. Furthermore, this analysis provided insights into the

Table 1: Estimation of genetic component proportions in the F_1 generation of brinjal.

Components/Ratios	DFF	DFP	FL (cm)	AFW (gm)	FG (cm)	NFP	NPBP	PH (cm)	TFYP (kg)	FBI (%)
D	13.21	39.41*	7.28*	1002.68*	13.60*	20.73*	0.11	24.86*	0.06*	24.85*
H_1	148.20*	36.77*	7.80*	714.47*	7.22*	11.19*	2.36*	51.39*	0.18*	42.64*
H_2	133.31*	33.99*	4.98*	625.06*	5.99*	10.20*	2.22*	46.46*	0.15*	33.07*
h_2	25.65	0.19	0.12	1.56	-0.03	7.00	3.37*	11.64	0.01	1.88
F	7.80	6.55	-0.49	-511.83	5.14*	3.47*	0.01	-6.98	-0.07	10.51
E	0.64	0.27	0.03	26.39	0.08	0.06	0.02	0.79	0.004	0.05
$(H_1/D)1/2$	3.39	0.96	1.03	0.84	0.73	0.73	4.58	1.44	1.73	1.31
$H_2/4H_1$	0.22	0.23	0.16	0.22	0.21	0.23	0.24	0.23	0.21	0.19
$[\sqrt{4DH_1}+F/\sqrt{4DH_1}] - F$	1.19	1.18	0.94	0.54	1.70	1.26	1.02	0.82	0.49	1.38
h_2/H_2	0.19	0.01	0.03	0.002	-0.005	0.69	1.52	0.25	0.04	0.06
Heritability (ns) %	23	67	80.5	81.4	75.5	77.8	16.8	59.7	65.8	59
t^2	21.42	0.60	2.51	4.79	0.03	0.94	37.13	6.93	8.14	0.16

presence or absence of epistasis. Heritability in the broad sense (h_2) quantifies the genetic contribution to the total phenotypic variance observed, providing insights into the potential for genetic improvement through selective breeding. For instance, traits such as days to first flowering (DFF) exhibit a moderate genetic influence with an h_2 value of 25.65. In contrast, high heritability percentages for traits like flower length (FL) at 80.5% and average fruit weight (AFW) at 81.4% indicate strong genetic control, making these traits excellent candidates for selective breeding programs. These findings highlight the importance of both dominance and additive genetic effects across a range of traits, including days to first picking (DFP), fruit girth (FG), number of fruits per plant (NFP), number of primary branch per plant (NPBP), plant height (PH), total fruit yield per plant (TFYP) and fruit borer infestation (FBI). The substantial genetic control over these traits underscores their potential for significant improvement through targeted breeding efforts, ensuring the development of superior plant varieties with desirable agronomic characteristics.

Genetic component analysis unveiled that while the additive effect lacked significance, the dominance effect (H_1) emerged as notably significant and pronounced, which was in accordance with previous investigations by (Joshi *et al.*, 2023). This implies a predominant influence of dominance gene action across various traits including DFF, DFP, FL (cm), AFW (gm), FG (cm), NFP, NPBP, PH (cm), TFYP (kg) and FBI (%). The significant (H_2) genetic variance indicates a symmetric allele distribution for the mentioned traits. However, in some instances, both additive and dominance effects (D , H_1 and H_2) were significant (Harshita *et al.*, 2023), indicating the involvement of both gene actions in the expression of traits such as days to first picking, FL (cm), AFW (gm), FG (cm), NPBP, PH (cm), NFP, TFYP (kg) and FBI (%). Notably, a significant additive effect without a significant dominance effect was observed for DFP, FL (cm), AFW (gm), FG (cm), NFP, PH (cm), TFYP (kg) and FBI (%). Additionally, a positive value of F_r indicated an excess proportion of dominance alleles relative to recessive alleles for all traits except FL (cm), AFW (gm), PH (cm) and TFYP (kg), which were in accordance with (Kumar *et al.*, 2020). Environmental component (E) exhibited a positive but non-significant influence on all studied traits, indicating its role in shaping the modification of traits (Barik *et al.*, 2022).

The mean degree of dominance exceeded one, suggesting the prevalence of overdominance for all traits except for DFP, AFW (gm), FG (cm) and NFP. Moreover, the ratio of H_2 to $4H_1$ was below 0.25, indicating an asymmetric distribution of dominant and recessive alleles among the parents for all traits (Kasara *et al.*, 2023). The calculated value of $[\sqrt{4DH_1} + F/\sqrt{4DH_1}] - F$ exceeded one, suggesting an abundance of dominant genes relative to recessive genes among the parents for all traits except for FL (cm), AFW (gm), PH (cm) and TFYP (kg). Furthermore, the lower narrow-sense heritability across all traits indicated that dominance variance outweighed additive variance (Sujin

et al., 2019). Graphical representations of W_r - V_r , along with regression coefficients and their standard errors for each of the 10 traits, are depicted in (Fig 1 to 10). Parents closer to the origin have excessive dominant genes and parents above the regression line have duplicate gene activity, while parents below the regression line have complementary gene action. This information is shown by the location of parents along the regression line Bhimireddy *et al.* (2023). For all analyzed traits, the slope of the regression coefficient significantly deviated from zero but maintained proximity to unity, suggesting the lack of non-allelic interaction. Notably, the regression lines intersected the W_r axis below the origin, suggesting the existence of overdominance for FL and FG. Conversely, an interception above the origin indicated partial dominance for DFF, DFP, AFW, NFP, NPBP, PH and TFYP. Complete dominance for FBI was indicated by an interception at the origin. These observations are consistent with findings reported by Ramani *et al.* (2017).

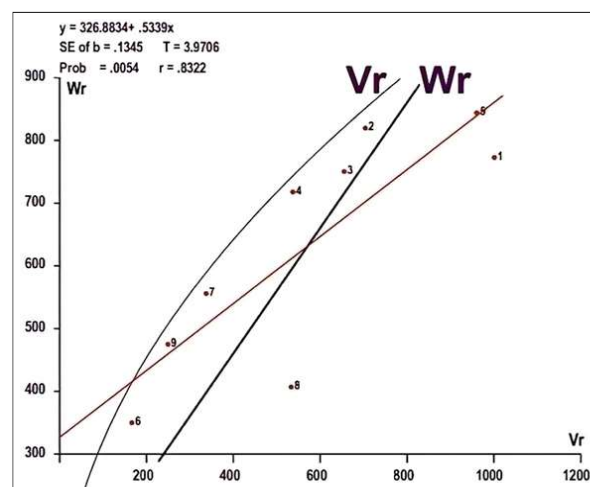


Fig 1: Days to 50% flowering.

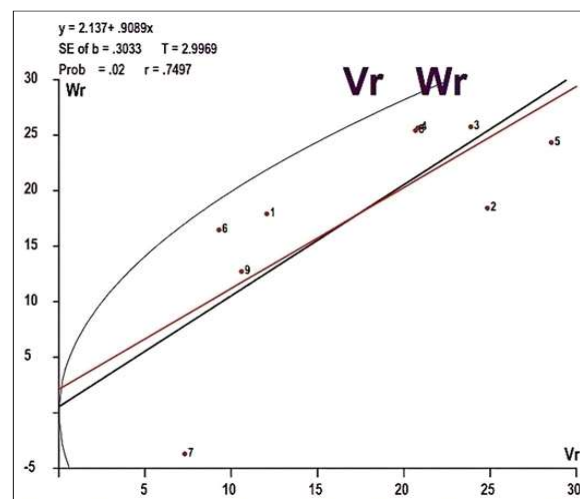


Fig 2: Days to first picking.

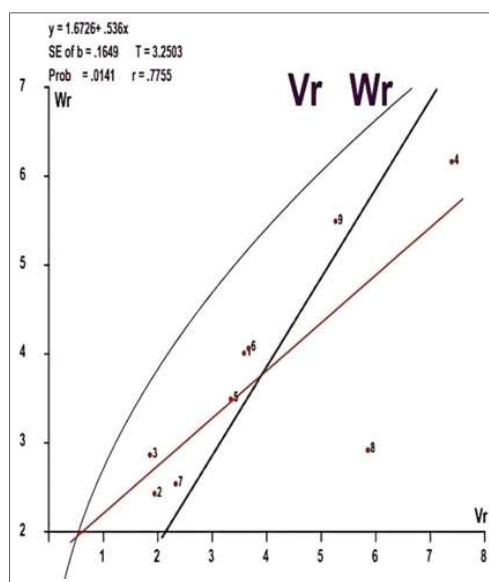


Fig 3: Fruit length (gm).

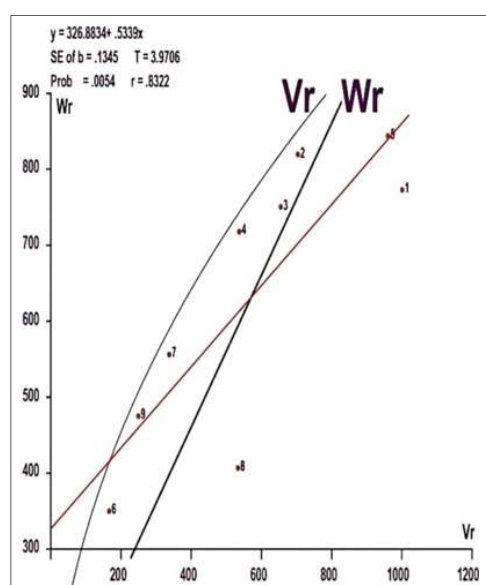


Fig 4: Average fruit weight (gm).

Frequency of dominant and recessive genes among parents for various traits categorizes parents in Table 2, based on whether they possess more dominant genes, more recessive genes, or an equal frequency of both for various traits. For the trait DFF, parent JBL-3 carries more dominant genes, JBL-2 shows more recessive genes and JBR-3 has an equal frequency of both gene types. Regarding the trait DFP, JBL-2 has a greater number of recessive genes, JBR-4 possesses a larger frequency of dominant genes and JBL-1 has an equal distribution of both. Parents JBR-1 and JBR-2 have more dominant genes for the trait FL (cm), while JBR-3 has more recessive genes and JBL-3 has an equal frequency of both. For AFW (gm), JBL-3 is dominant, JBL-2 is recessive and JBR-3 is balanced. JBR-6 has more dominant genes in terms of FG (cm), whereas JBL-2 and JBR-3 are recessive and JBL-2 and JBL-1 have equivalent frequencies. For NFP, JBL-3 and JBR-2 are balanced, JBR-4 exhibits dominance and JBL-2 exhibits recessiveness. In NPBP, JBR-3 is dominant, JBR-1 is recessive and JBL-3 and JBR-2 have equal frequencies. JBR-1 and JBL-3 are balanced for PH (cm), while JBR-4 has more dominant genes and JBR-2 has more recessive genes. For TFYP (kg), JBR-3 contains more recessive genes, JBL-2 has more dominant genes and JBR-1 has an equal distribution of genes. Lastly, for FBI (%), JBR-1 is dominant, JBR-2 and JBL-1 are recessive and JBR-4 has equal frequencies of both gene types. Future research can utilize this categorization to study genetic inheritance patterns and the impact of gene dominance on trait expression. This data provides a foundation for selecting parent strains in breeding programs aimed at enhancing desirable traits while maintaining genetic diversity.

The mean degree of dominance exceeded one, indicating the prevalence of overdominance for all traits except DFP, AFW, FG and NPBP. Understanding the breadth of gene groups demonstrating dominance and their influence on specific traits is crucial for genetic advancement through selection processes. In this study, it was observed that the h_2/H_2 value was generally low across most cases, except for the number of primary

Table 2: The distribution of dominant and recessive genes among parents across various traits.

Characters	Parents with more dominant genes	Parents with more recessive genes	Parents with equal frequency of both genes
DFF	JBL-3	JBL-2	JBR-3
DFP	JBR-4	JBL-2	JBL-1
FL (cm)	JBR-1, JBR-2	JBR-3	JBL-3
AFW (gm)	JBL-3	JBL-2	JBR-3
FG (cm)	JBR-6	JBR-3, JBL-2	JBR-2, JBL-1
NFP	JBR-4	JBL-2	JBL-3, JBR-2
NPBP	JBR-3	JBR-1	JBL-3, JBR-2
PH (cm)	JBR-4	JBR-2	JBR-1, JBL-3
TFYP (kg)	JBL-3, JBL-2	JBR-3	JBR-1
FBI (%)	JBR-1	JBR-2, JBL-1	JBR-4

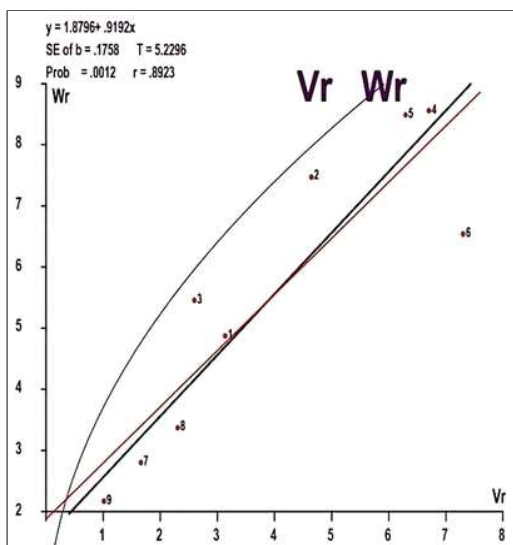


Fig 5: Fruit girth (cm).

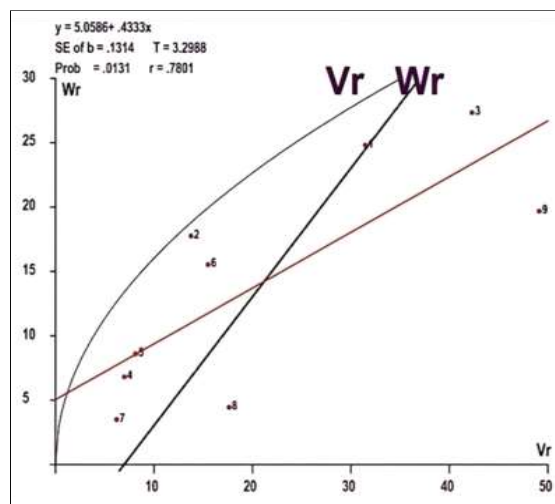


Fig 8: Plant height (cm).

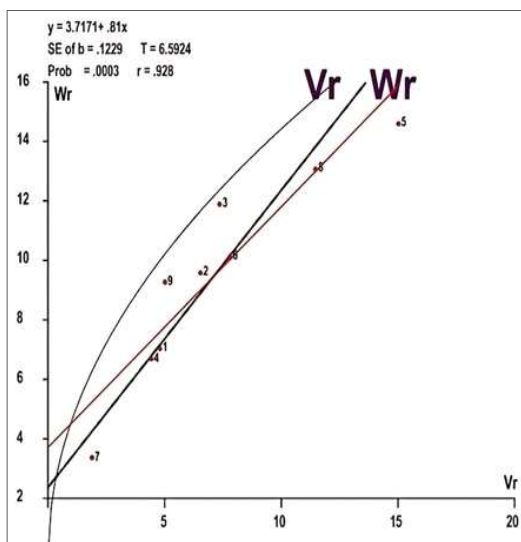


Fig 6: Number of fruits/plant.

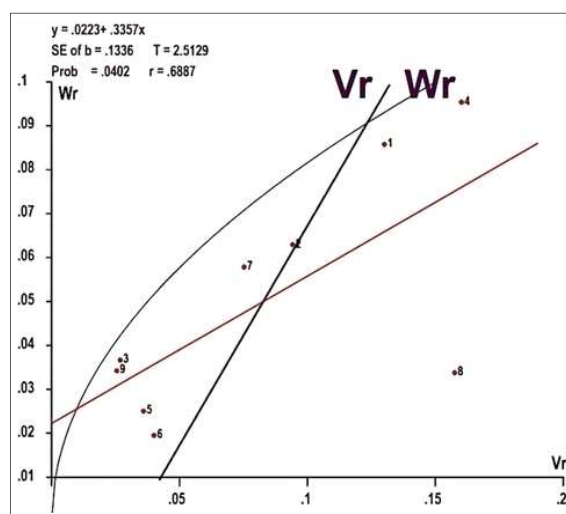


Fig 9: Total fruit yield per plant (kg).

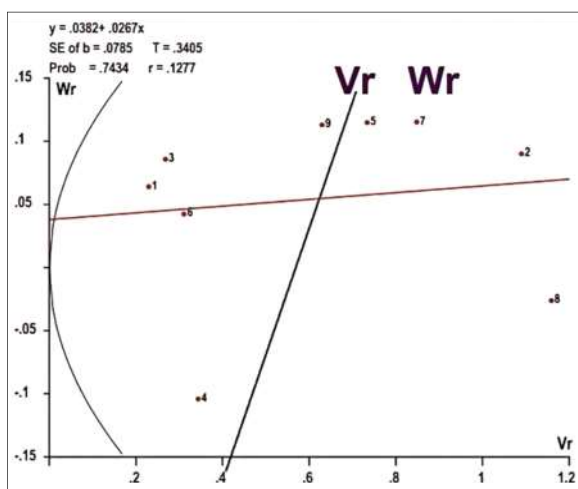


Fig 7: Number primary branches/plant.

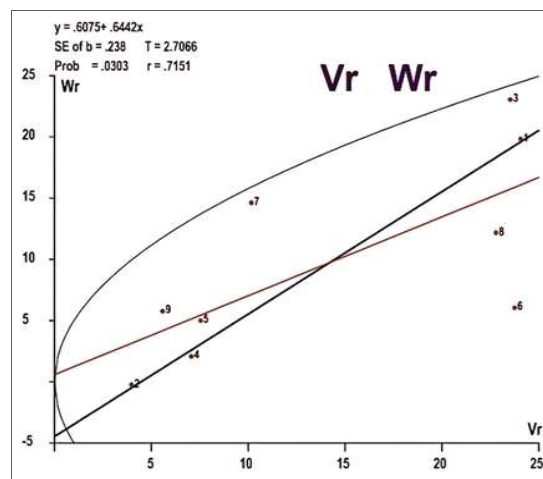


Fig 10: Fruit borer infestation (%).

branches, suggesting challenges in accurately estimating the number of gene groups involved (Mishra *et al.*, 2023) and (Tiwari *et al.*, 2023). A population exhibiting a dominance of additive genetic variance would facilitate character enhancement through selection in the segregating generation. Conversely, when non-additive effects play a significant role, hybridization becomes more advantageous, implying breeding techniques such as biparental mating, heterosis breeding and selection breeding (Kasera *et al.*, 2020).

CONCLUSION

This study highlights the genetic complexity and potential for breeding improvements in brinjal. Genetic analysis revealed significant dominance effects across various traits, indicating a strong influence of non-additive gene actions. Traits such as days to first flowering, fruit length and average fruit weight exhibited high heritability, making them prime candidates for selective breeding. The findings underscore the importance of understanding both additive and dominance genetic effects to enhance traits effectively. The prevalence of overdominance for most traits suggests the utility of hybrid breeding approaches. The identification of gene actions and their impact on traits provides valuable insights for developing resistant hybrids, especially against pests like the fruit and shoot borer and enhancing overall yield and quality. Future breeding programs should focus on exploiting these genetic variations through strategic hybridization and selection methods in both segregating generations and hybrid development to achieve significant improvements in brinjal cultivation.

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Authors contributions

Experiments were conducted by S. Anvesh, I.R. Delvadiya, Harshita Thota and M. Yasaswini, I.R. Delvadiya designed the study, while S. Anvesh, I.R. Delvadiya and Harshita Thota contributed to drafting the manuscript. All authors have reviewed and endorsed the final version of the manuscript.

Compliance with ethical standards

Ethical issues: None.

Conflict of interest

The authors declare no conflicts of interest.

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