



International Journal of Research in Agronomy

E-ISSN: 2618-0618
P-ISSN: 2618-060X
© Agronomy
NAAS Rating (2026): 5.20
www.agronomyjournals.com
2026; 9(6): 211-215
Received: 02-04-2026
Accepted: 08-05-2026

Vishal D Gal
M.Sc. Scholar, Department of
Genetics and Plant Breeding,
College of Agriculture, Junagadh
Agricultural University, Junagadh,
Gujarat, India

RS Parmar
Associate Professor & Head,
Department of Genetics and Plant
Breeding, College of Agriculture,
Junagadh Agricultural University,
Mota Bhandariya-Amreli, Gujarat,
India

SB Chaudhari
Assistant Professor, Department of
Soil science and Chemistry, College
of Agriculture, Junagadh
Agricultural University, Mota
Bhandariya-Amreli, Gujarat, India

GK Sapra
Assistant Research Scientist, Main
Oilseeds Research Station,
Junagadh Agricultural University,
Junagadh, Gujarat, India

Corresponding Author:
Vishal D Gal
M.Sc. Scholar, Department of
Genetics and Plant Breeding,
College of Agriculture, Junagadh
Agricultural University, Junagadh,
Gujarat, India

Genetic components of variance for fruit yield and its contributing traits in Brinjal [*Solanum melongena* L.]

Vishal D Gal, RS Parmar, SB Chaudhari and GK Sapra

DOI: <https://www.doi.org/10.33545/2618060X.2026.v9.i6c.5689>

Abstract

A half diallel analysis was carried out using nine parental lines and their 36 F₁ hybrids of brinjal (*Solanum melongena* L.), along with a standard check (GJBH-4), to estimate heterosis and genetic components of variance governing fruit yield and its component traits. The experiment was conducted in a randomized block design with three replications during *rabi* 2025-26 at the Vegetable Research Station, College of Agriculture, Junagadh Agricultural University, Junagadh. Observations were recorded on five randomly selected competitive plants per replication for 16 characters viz., days to first flowering, days to first picking, number of fruits per plant, fruit length, average fruit weight, fruit girth, number of primary branches per plant, plant height, days to last picking, number of pickings, total fruit yield per plant, total soluble solids, fruit and shoot borer infestation, vitamin-C content and total anthocyanin pigment and the mean values were subjected to analysis of variance for genetic component analysis following Hayman's approach. The estimates of genetic components of variance revealed that dominance components (H₁ and H₂) were higher in magnitude than the additive component (D) for most of the traits, indicating the predominance of non-additive gene action in the inheritance of these characters. The average degree of dominance (H₁/D)^{1/2} was greater than unity for all traits, suggesting over-dominance. The estimates of H₂/4H₁ indicated unequal distribution of positive and negative alleles among the parental lines. The KD/KR ratio further revealed a preponderance of dominant alleles over recessive ones for most of the traits except plant height. The environmental component (E) was non-significant for most of the traits, indicating minimal environmental influence on their expression. Heritability estimates were generally moderate for most characters, while high heritability was observed for traits like days to first flowering, number of fruits per plant, number of primary branches per plant and shoot borer infestation and low heritability for Vitamin-C content.

Overall, the present investigation indicated the predominance of non-additive gene action for fruit yield and most of its component traits. Therefore, heterosis breeding would be an effective approach for improving fruit yield and associated traits in brinjal.

Keywords: Brinjal, Half-diallel analysis, genetic components of variation

Introduction

Brinjal (*Solanum melongena* L., 2n = 24) is an important vegetable crop belonging to the family *Solanaceae*, widely cultivated in tropical and subtropical regions of India. It is known by various vernacular names such as *Ringan*, *Baingan*, *Vangi* and *Katharikai* is believed to have originated in the Indo-Burma region. Due to its high yield potential, adaptability and affordability, it is often referred to as the "poor man's vegetable". Brinjal is nutritionally rich, containing vitamins such as ascorbic acid, niacin and vitamin B-complex, along with essential minerals and antioxidant compounds like anthocyanins.

India is the second largest producer of brinjal in the world, with wide cultivation across major states including Gujarat. The crop exhibits considerable genetic variability in plant growth and fruit characteristics, offering great scope for genetic improvement. However, fruit yield is a complex quantitative trait governed by multiple component characters and their interactions. Therefore, understanding the genetic architecture of yield and its contributing traits is essential for effective selection and crop improvement.

Diallel analysis based on Hayman's approach provides a detailed understanding of gene action by partitioning genetic variance into additive (D), dominance (H₁ and H₂) and environmental (E)

components. These parameters also help in estimating the degree of dominance and distribution of alleles among parental lines. Knowledge of these genetic components is useful in deciding appropriate breeding strategies, where additive effects favor selection methods, while dominance effects support heterosis breeding.

Thus, the study of genetic components of variance plays a crucial role in identifying suitable parents and developing high yielding hybrids or varieties for sustainable improvement in brinjal.

Materials and Methods

The experimental material comprised of parents and their F_1 's derived by crossing among nine parents viz., JBR-24-14, JBR-24-13, JBR-24-12, JBR-24-11, GJB-3, GJLB-4, GRB-7, Pant Rituraj and Pusa Kranti in a half-diallel fashion (Table 1). Row to row and plant to plant spacing was maintained at 60 cm $\times$ 30 cm. To produce a better crop, the recommended agronomic practices of the region were followed. The nine parental lines were selected based on morphological variability for growth, maturity, fruit size, fruit shape, fruit yield and yield contributing traits in brinjal. The experiment was laid out in a randomized block design with three replications during *rabi* 2025-26 at the Vegetable Research Station, Junagadh Agricultural University, Junagadh.

Observations were recorded on sixteen characters viz., days to first flowering, days to first picking, number of fruits per plant, fruit length (cm), average fruit weight (g), fruit girth (cm), number of branches per plant, plant height (cm), days to last picking, number of pickings, total fruit yield per plant (kg), total soluble solids, fruit borer infestation (%), shoot borer infestation (%), Vitamin-C content and total anthocyanin pigment and the mean data were used for statistical analysis.

The total variation among F_1 hybrids was analyzed following Hayman's diallel approach (³Hayman, 1954a, ⁴Hayman 1954b) to estimate genetic components of variance. The genetic parameters viz., additive variance (D), dominance variance (H_1 and H_2), covariance of additive and dominance effects (F) and environmental component (E) were estimated. Further, the degree of dominance (H_1/D)^{1/2}, proportion of positive and negative alleles ($H_2/4H_1$) and the ratio of dominant to recessive genes (KD/KR) were computed to understand the nature and distribution of gene effects.

Results and Discussion

The estimate of the components of variation revealed significant differences was examined for variance due to additive genetic effect (D) for all the traits (except days to first flowering, days to first picking, number of fruits per plant, fruit length, number of primary branches per plant, plant height, total fruits yield per plant and vitamin-c) implying importance of both additive and non-additive gene effect. Notwithstanding, additive component was lower in magnitude than both dominance components for all the traits, which showing the predominance of non-additive gene action in the expression of all the traits. (Table 1)

Genetic analysis exhibited that T_2 values were non-significant for all the characters (except fruit length, fruit girth, number of primary branches per plant, days to last picking, total soluble solids and vitamin- c). This recommended that additive-dominance model was adequate for all the traits except above listed.

The non-significant estimate of 'E' for all the traits (except days to first picking, days to last picking and number of picking) point out that there was no considerable environmental influence

modifying their expression.

The average degree of dominance (H_1/D)^{1/2} was found to be more than unity for all the traits indicating over dominance type of gene action, which suggested that heterosis breeding might be advantageous to get higher gain in brinjal. Asymmetrical distribution of positive and negative genes in the parental lines was revealed from the estimate, $H_2/4H_1$ for all the characters under studied.

The KD/KR ratio showed an excess of dominant genes in the parent than recessive genes for all the characters except days to first flowering, number of fruits per plant, number of primary branches per plant, shoot borer infestation and total anthocyanin pigment. All the traits show moderated heritability (except days to first flowering, number of fruits per plant, number of primary branches per plant and shoot borer infestation shows high heritability, where in case, of vitamin-c had low heritability). (Table 1)

In general, narrow sense heritability was found to be less than 50 per cent for days to first flowering, days to first picking, fruit length, average fruit weight, fruit girth, number of primary branches per plant, number of fruits per plant, days to last picking, number of pickings, plant height, total fruit yield per plant, total soluble solids, vitamin-c and fruit and shoot borer infestation suggesting major role of dominance gene action in the expression of this trait. High narrow sense heritability for total anthocyanin pigment indicated that major part of phenotypic variability was due to addictiveness and possibility of fixing these traits by simple selection. (Table 1)

These findings are in concurrence with results of These findings are in concurrence with results of ⁶Yadav *et al.* (2017), ⁵Sujin *et al.* (2019), ²Datta *et al.* (2024), ¹Anvesh *et al.* (2025).

For days to first flowering, the dominance components (H_1 and H_2) were found significant, indicating the importance of dominance effects in its inheritance. The non-significant h^2 value suggested ambidirectional dominance. The average degree of dominance (H_1/D)^{1/2} was greater than unity (2.92), indicating over-dominance. The $H_2/4H_1$ ratio (0.24) revealed nearly symmetrical distribution of positive and negative alleles among the parents. The KD/KR ratio (0.83) along with negative F value (-0.54) indicated a higher proportion of recessive alleles. Narrow sense heritability was moderate (22.20%), suggesting limited effectiveness of selection for this trait.

In contrast, days to first picking exhibited significant dominance components (H_1 and H_2) with values exceeding the additive component (D), indicating predominance of over-dominance. The significant h^2 value reflected directional dominance, while the significant environmental component (E) suggested considerable environmental influence. The degree of dominance (H_1/D)^{1/2} was 3.51, further confirming over-dominance. The $H_2/4H_1$ ratio (0.20) indicated asymmetrical distribution of alleles, whereas the KD/KR ratio (1.56) along with a positive F value (2.19) suggested a higher frequency of dominant alleles. The h^2/H_2 ratio (0.38) indicated that the number of gene groups could not be precisely estimated and the narrow sense heritability was moderate (16.70%), indicating limited effectiveness of direct selection.

For number of fruits per plant, the dominance components (H_1 and H_2) were found to be significant, indicating the major role of non-additive gene effects in the inheritance of this trait. The higher magnitude of dominance variance compared to the additive component (D) suggested the prevalence of over-dominance. The significant h^2 value indicated the presence of directional dominance. The non-significant environmental component (E) implied that environmental influence on this trait

was minimal. The average degree of dominance (H_1/D)^{1/2} was 8.14, confirming strong over-dominance. The $H_2/4H_1$ ratio (0.24) indicated a nearly symmetrical distribution of positive and negative alleles among the parents. The K_D/K_R ratio (0.96) along with the negative F value (-0.53) suggested a relatively higher proportion of recessive alleles. The h^2/H_2 ratio (0.16) indicated that the number of effective gene groups governing the trait could not be precisely estimated. The narrow sense heritability was low (6.80%), suggesting limited scope for improvement through direct selection.

For fruit length, the dominance variance components (H_1 and H_2) were significant, indicating the prominent role of dominance effects in its inheritance. The magnitude of dominance components exceeding the additive component (D) suggested the prevalence of over-dominance for this trait. The non-significant h^2 value indicated the absence of clear directional dominance. The environmental component (E) was non-significant, implying minimal environmental influence on trait expression. The average degree of dominance (H_1/D)^{1/2} was 3.35, confirming over-dominance. The $H_2/4H_1$ ratio (0.22) indicated an asymmetrical distribution of positive and negative alleles among the parents. The K_D/K_R ratio (1.52) along with a

positive F value (0.93) suggested a higher proportion of dominant alleles in the parental lines. The h^2/H_2 ratio (0.00) indicated that the number of effective gene groups controlling the trait could not be reliably estimated. The narrow sense heritability was low (13.70%), indicating limited effectiveness of direct selection for improvement of this trait.

Analysis of genetic components for average fruit weight revealed that both additive (D) and dominance (H_1 and H_2) variances were significant, indicating the involvement of both gene effects in its inheritance. The non-significant h^2 value suggested ambidirectional dominance, while the non-significant environmental component (E) indicated negligible environmental influence on this trait. The average degree of dominance (H_1/D)^{1/2} was 2.20, indicating over-dominance. The $H_2/4H_1$ ratio (0.22) reflected an asymmetrical distribution of positive and negative alleles among the parents. The K_D/K_R ratio (1.16), along with a positive F value (32.44), suggested a higher proportion of dominant alleles. The h^2/H_2 ratio (-0.008) indicated that the number of effective gene groups controlling the trait could not be reliably estimated. The narrow sense heritability was moderate (34.20%), suggesting moderate scope for improvement through selection.

Table 1: Estimation of genetic components of variation with their standard error and ratios for different characters in brinjal

Components / Ratios	Days to first flowering	Days to first picking	Number of fruits per plant	Fruit length (cm)	Average Fruit weight (g)	Fruit girth (cm)	Number of primary branches per plant	Plant height (cm)
D	1.04 ± 0.74	1.42 ± 2.19	1.76 ± 6.86	0.66 ± 0.49	98.57* ± 48.25	0.34* ± 0.11	0.01 ± 0.22	101.39 ± 63.54
H_1	8.93* ± 1.64	17.55* ± 4.83	117.05* ± 15.14	7.51* ± 1.10	479.90* ± 106.50	1.42* ± 0.25	4.36* ± 0.48	717.94* ± 140.25
H_2	8.90* ± 1.41	14.70* ± 4.15	114.96* ± 13.02	6.69* ± 0.94	425.68* ± 91.55	1.12* ± 0.21	4.16* ± 0.42	618.38* ± 120.56
h^2	-0.23 ± 0.94	5.59* ± 2.78	19.05 ± 8.72	-0.002* ± 0.63	-3.45 ± 61.33	1.32* ± 0.14	1.28* ± 0.28	-1.59 ± 80.77
F	-0.56 ± 1.74	2.19 ± 5.11	-0.53 ± 16.01	0.93 ± 1.16	32.44 ± 112.57	0.56* ± 0.27	-0.05 ± 0.51	57.93 ± 148.23
E	0.60 ± 0.23	1.47* ± 0.69	1.44 ± 2.17	0.078 ± 0.15	9.52 ± 15.25	0.030 ± 0.036	0.05 ± 0.07	7.05 ± 20.09
(H_1/D) ^{1/2}	2.92	3.51	8.14	3.35	2.20	2.03	1.94	2.66
$H_2/4H_1$	0.24	0.20	0.24	0.22	0.22	0.19	0.23	0.21
K_D/K_R	0.83	1.56	0.96	1.52	1.16	2.37	0.78	1.24
h^2/H_2	-0.02	0.38	0.16	0.00	-0.008	1.17	0.30	-0.003
Heritability(ns)%	22.20	16.70	6.80	13.70	34.20	10.20	11.10	30.70
T_2	2.75	0.027	4.87	18.34*	0.27	4.63*	6.10*	1.82

Table 1: Cont.

Components / Ratios	Days to last picking	Number of pickings	Total fruit yield per plant (kg)	Total soluble solids (TSS) (°B)	Fruit borer infestation (%)	Shoot borer infestation (%)	Vitamin-C (100 mg)	Total anthocyanin pigment (100 mg)
D	46.05* ± 7.68	0.47* ± 0.20	0.41 ± 0.34	0.49* ± 0.16	2.66* ± 1.20	0.50* ± 0.12	0.65 ± 0.48	140.42* ± 38.83
H_1	139.94* ± 16.96	2.20* ± 0.45	4.62* ± 0.76	1.48* ± 0.37	11.09* ± 2.64	2.34* ± 0.28	4.96* ± 1.08	212.91* ± 85.72
H_2	100.82* ± 14.58	1.81* ± 0.39	4.33* ± 0.66	1.14* ± 0.32	9.46* ± 2.27	2.20* ± 0.24	4.14* ± 0.92	164.18* ± 73.69
h^2	-1.02* ± 9.76	2.55* ± 0.26	0.018 ± 0.44	0.19 ± 0.21	0.89 ± 1.52	2.02* ± 0.16	0.97 ± 0.62	65.36 ± 49.36
F	73.92* ± 17.92	0.74 ± 0.48	0.51 ± 0.81	0.49 ± 0.39	1.42 ± 2.79	-0.05 ± 0.30	1.35 ± 1.14	-50.60 ± 90.60
E	6.33* ± 2.43	0.24* ± 0.06	0.037 ± 0.11	0.014 ± 0.053	0.24 ± 0.37	0.07 ± 0.04	0.10 ± 0.15	1.14 ± 12.28
(H_1/D) ^{1/2}	1.74	2.16	3.35	1.72	2.04	2.16	2.74	1.23
$H_2/4H_1$	0.18	0.20	0.23	0.19	0.21	0.23	0.20	0.19
K_D/K_R	2.70	2.16	1.46	1.80	1.30	0.94	2.19	0.74
h^2/H_2	-0.01	1.40	0.004	0.16	0.09	0.91	0.23	0.39
Heritability(ns)%	15.10	7.10	7.60	36.60	35.40	35.80	5.40	74.00
T_2	7.31*	0.18	0.00	8.10*	0.37	0.08	24.35*	5.73*

Estimates of genetic variance components indicated that both additive (D) and dominance (H_1 and H_2) effects were significant, suggesting their involvement in the inheritance of fruit girth. The higher magnitude of dominance variance compared to additive variance reflected the predominance of over-dominance for this trait. The significant h^2 value pointed towards directional dominance, while the non-significant environmental component (E) indicated minimal environmental influence on its expression. The average degree of dominance $(H_1/D)^{1/2}$ was 2.03, confirming over-dominance. The $H_2/4H_1$ ratio (0.19) revealed an asymmetrical distribution of positive and negative alleles among the parents. The KD/KR ratio (2.37), along with a positive F value (0.56), suggested a greater proportion of dominant alleles. The h^2/H_2 ratio (1.17) indicated the involvement of dominant gene groups controlling the trait. The narrow sense heritability was low (10.20%), suggesting limited effectiveness of selection for improvement.

Variation in genetic parameters showed that dominance components (H_1 and H_2) were significant and exceeded the additive component (D), indicating the predominance of over-dominance in controlling number of primary branches per plant. The significant h^2 value suggested the presence of directional dominance, whereas the non-significant environmental component (E) indicated minimal environmental influence on trait expression. The average degree of dominance $(H_1/D)^{1/2}$ was 1.94, supporting over-dominance. The $H_2/4H_1$ ratio (0.23) indicated an asymmetrical distribution of positive and negative alleles among the parents. The KD/KR ratio (0.78), along with a negative F value (-0.05), suggested a relatively higher proportion of recessive alleles. The h^2/H_2 ratio (0.30) indicated that the number of effective gene groups governing the trait could not be precisely estimated. The narrow sense heritability was low (11.10%), indicating limited scope for improvement through direct selection.

Estimates of genetic variance components indicated that dominance effects (H_1 and H_2) were significant, highlighting the importance of non-additive gene action in the inheritance of plant height. The non-significant h^2 value suggested ambidirectional dominance, while the non-significant environmental component (E) indicated minimal environmental influence on this trait. The average degree of dominance $(H_1/D)^{1/2}$ was 2.66, suggesting over-dominance. The $H_2/4H_1$ ratio (0.21) revealed an asymmetrical distribution of positive and negative alleles among the parents. The KD/KR ratio (1.24), along with a positive F value (57.93), indicated a higher proportion of dominant alleles. The h^2/H_2 ratio (-0.003) suggested that the number of effective gene groups controlling the trait could not be reliably estimated. The narrow sense heritability was relatively high (30.70%), indicating better prospects for improvement through selection.

Evaluation of genetic parameters indicated that both additive (D) and dominance (H_1 and H_2) components were significant, suggesting the involvement of both gene effects in the inheritance of days to last picking, with dominance variance exceeding the additive component and indicating over-dominance. The non-significant h^2 value suggested ambidirectional dominance, while the significant environmental component (E) indicated a considerable influence of environment on trait expression. The average degree of dominance $(H_1/D)^{1/2}$ was 1.74, supporting over-dominance. The $H_2/4H_1$ ratio (0.18) indicated an asymmetrical distribution of positive and negative alleles among the parents. The KD/KR ratio (2.70), along with a positive F value (73.92), suggested a higher proportion of dominant alleles. The h^2/H_2 ratio (-0.01)

indicated that the number of effective gene groups controlling the trait could not be precisely estimated. The narrow sense heritability was moderate (15.10%), indicating limited effectiveness of selection for improvement of this trait.

Assessment of genetic parameters indicated that both additive (D) and dominance (H_1 and H_2) components were significant, suggesting the involvement of both gene effects in the inheritance of number of pickings, with dominance variance showing a relatively greater influence and indicating over-dominance. The significant h^2 value reflected the presence of directional dominance, while the significant environmental component (E) indicated a substantial environmental effect on trait expression. The average degree of dominance $(H_1/D)^{1/2}$ was 2.16, confirming over-dominance. The $H_2/4H_1$ ratio (0.20) indicated an asymmetrical distribution of positive and negative alleles among the parents. The KD/KR ratio (2.16), along with a positive F value (0.74), suggested a higher proportion of dominant alleles. The h^2/H_2 ratio (1.40) indicated the involvement of dominant gene groups controlling the trait. The narrow sense heritability was very low (7.10%), indicating poor scope for improvement through direct selection.

Estimation of genetic parameters indicated that dominance components (H_1 and H_2) were significant, highlighting the major role of non-additive gene effects in the inheritance of total fruit yield per plant, with dominance variance exceeding the additive component (D) and suggesting over-dominance. The non-significant h^2 value indicated ambidirectional dominance, while the non-significant environmental component (E) suggested minimal environmental influence on this trait. The average degree of dominance $(H_1/D)^{1/2}$ was 3.35, confirming over-dominance. The $H_2/4H_1$ ratio (0.23) indicated an asymmetrical distribution of positive and negative alleles among the parents. The KD/KR ratio (1.46), along with a positive F value (0.51), suggested a higher proportion of dominant alleles. The h^2/H_2 ratio (0.004) indicated that the number of effective gene groups controlling the trait could not be reliably estimated. The narrow sense heritability was low (7.60%), indicating limited scope for improvement through direct selection.

In brinjal, estimates of genetic parameters indicated that both additive (D) and dominance (H_1 and H_2) components were significant for total soluble solids, suggesting the involvement of both gene effects in its inheritance, with dominance variance exceeding the additive component and indicating over-dominance. The non-significant h^2 value suggested ambidirectional dominance, while the negligible environmental component (E) indicated minimal environmental influence on the expression of this trait. The average degree of dominance $(H_1/D)^{1/2}$ was 1.72, confirming over-dominance. The $H_2/4H_1$ ratio (0.19) indicated an asymmetrical distribution of positive and negative alleles among the parents. The KD/KR ratio (1.80), along with a positive F value (0.49), suggested a higher proportion of dominant alleles. The h^2/H_2 ratio (0.16) indicated that the number of effective gene groups controlling the trait could not be precisely estimated. The narrow sense heritability was high (36.60%), indicating better prospects for improvement through selection.

Genetic parameter estimates revealed that both additive (D) and dominance (H_1 and H_2) components were significant for fruit borer infestation, indicating the involvement of both gene effects in its inheritance, with dominance variance being relatively higher and suggesting over-dominance. The non-significant h^2 value indicated ambidirectional dominance, while the non-significant environmental component (E) suggested minimal environmental influence on the expression of this trait. The

average degree of dominance (H_1/D)^{1/2} was 2.04, confirming over-dominance. The $H_2/4H_1$ ratio (0.21) indicated an asymmetrical distribution of positive and negative alleles among the parents. The KD/KR ratio (1.30), along with a positive F value (1.42), suggested a higher proportion of dominant alleles. The h^2/H_2 ratio (0.09) indicated that the number of effective gene groups controlling the trait could not be precisely estimated. The narrow sense heritability was high (35.40%), indicating good scope for improvement through selection.

Estimation of genetic components indicated that both additive (D) and dominance (H_1 and H_2) variances were significant for shoot borer infestation, suggesting the involvement of both gene effects in its inheritance, with dominance variance being relatively higher and indicating over-dominance. The significant h^2 value reflected the presence of directional dominance, while the non-significant environmental component (E) indicated minimal environmental influence on this trait. The average degree of dominance (H_1/D)^{1/2} was 2.16, confirming over-dominance. The $H_2/4H_1$ ratio (0.23) indicated an asymmetrical distribution of positive and negative alleles among the parents. The KD/KR ratio (0.94), along with a negative F value (-0.05), suggested a relatively higher proportion of recessive alleles. The h^2/H_2 ratio (0.91) indicated that the number of effective gene groups controlling the trait could not be precisely estimated. The narrow sense heritability was moderate (35.80%), indicating moderate scope for improvement through selection.

Genetic parameter estimates indicated that dominance components (H_1 and H_2) were significant for vitamin-c content, highlighting the importance of non-additive gene effects in its inheritance. The non-significant h^2 value suggested ambidirectional dominance, while the non-significant environmental component (E) indicated minimal environmental influence on the expression of this trait. The average degree of dominance (H_1/D)^{1/2} was 2.74, indicating over-dominance. The $H_2/4H_1$ ratio (0.20) revealed an asymmetrical distribution of positive and negative alleles among the parents. The KD/KR ratio (2.19), along with a positive F value (1.35), suggested a higher proportion of dominant alleles. The h^2/H_2 ratio (0.23) indicated that the number of effective gene groups controlling the trait could not be precisely estimated. The narrow sense heritability was low (5.40%), indicating limited scope for improvement through direct selection.

In brinjal, estimates of genetic parameters indicated that both additive (D) and dominance (H_1 and H_2) components were significant for total anthocyanin pigment, suggesting the involvement of both gene effects in its inheritance, with dominance variance exceeding the additive component and indicating over-dominance. The non-significant h^2 value suggested ambidirectional dominance, while the negligible environmental component (E) indicated minimal environmental influence on the expression of this trait. The average degree of dominance (H_1/D)^{1/2} was 1.23, indicating over-dominance. The $H_2/4H_1$ ratio (0.19) revealed an asymmetrical distribution of positive and negative alleles among the parents. The KD/KR ratio (0.74), along with a negative F value (-50.60), suggested a higher proportion of recessive alleles. The h^2/H_2 ratio (0.39) indicated that the number of effective gene groups controlling the trait could not be precisely estimated. The narrow sense heritability was high (74.00%), indicating good scope for improvement through selection.

Conclusion

The present investigation revealed the presence of considerable genetic variability among the studied genotypes for yield and its

component traits in brinjal. The estimates of genetic components of variance indicated that dominance components were higher in magnitude than additive components for most of the traits, suggesting the predominance of non-additive gene action. The average degree of dominance further confirmed over-dominance for the majority of characters. The distribution of alleles among parents was found to be asymmetrical for most traits, with a higher proportion of dominant alleles in several cases. Environmental influence was minimal for most traits, indicating stability in expression. Heritability estimates varied from low to high, suggesting differential scope for selection across traits. The predominance of non-additive gene effects indicated that simple selection would be less effective for yield improvement. Therefore, exploitation of heterosis through hybrid breeding is recommended as an efficient approach. The superior performance of certain crosses indicated the presence of desirable gene combinations. Overall, heterosis breeding can be effectively utilized for enhancing fruit yield and quality traits in brinjal.

References

1. Anvesh S, Delvadiya IR, Thota H, Yasaswini M. Analyzing genetic variation and graphical representation (W_r-V_r) in brinjal (*Solanum melongena* L.) using the Hayman approach in the north-western region of India. Indian Journal of Agricultural Research. 2025;59(3):221-248.
2. Datta RD, Rafii MY, Misran A, Jusoh M, Yusuff O, Uddin SM. Estimation of genetic analysis by using half diallel crosses underlying eggplant for tropical climates. Genetika. 2024;56(3):423-442.
3. Hayman BI. The analysis of variation of diallel tables. Biometrics. 1954;10(2):235-244.
4. Hayman BI. The theory and analysis of diallel crosses. Genetics. 1954;39(6):789-809.
5. Sujin GS, Karuppaiah P, Anbuselvam Y, Muraleedharan A. Gene action for determining yield and yield attributing traits in brinjal (*Solanum melongena* L.). Plant Archives. 2019;19(2):2944-2948.
6. Yadav PK, Warade SD, Kumar M, Singh S, Pandey AK. Gene action for determining yield and quality attributing traits in brinjal (*Solanum melongena* L.). International Journal of Current Microbiology and Applied Sciences. 2017;6(6):1475-1480.