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DISSECTING GENE ACTION IN INDIAN MUSTARD (*Brassica juncea* L. Czern & Coss) USING HAYMAN'S NUMERICAL AND GRAPHICAL METHODS IN NORMAL (E_1) AND LATE SOWN (E_2) ENVIRONMENTS

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ABSTRACT

The present investigation was undertaken to elucidate the nature of gene action governing seed yield and related traits in Indian mustard [*Brassica juncea* (L.) Czern & Coss] through Hayman's diallel analysis under normal (E_1) and late-sown (E_2) environments. Eight diverse parental lines were crossed in a half-diallel mating design excluding reciprocals to generate 28 F_1's. The parents and F_1's were evaluated for days to 50% flowering, days to maturity, plant height, primary and secondary branches, siliquae per plant, siliqua density, siliqua length, seeds per siliqua, test weight, seed yield per plant, SPAD value, relative water content, membrane stability index and oil content. Full validity of the additive-dominance model was observed for siliqua density and seeds per siliqua under E_2, whereas partial validity was observed for several traits in both environments. The analysis revealed significant H_1 and H_2 components for most traits, indicating the predominance of non-additive gene action. In contrast, additive genetic effects (D) were significant only for days to maturity, siliqua density and seeds per siliqua under E_2. The $H_2/4H_1$ ratio was less than 0.25 for all traits, suggesting an asymmetrical distribution of positive and negative alleles among parents. Positive F values and KD/KR ratios greater than unity for most traits indicated a higher frequency of dominant alleles. The degree of dominance $[(H_1/D)^{0.5}]$ exceeded unity for nearly all traits, demonstrating the prevalence of overdominance, while partial dominance was observed only for SPAD value. Narrow-sense heritability estimates were generally low, indicating limited effectiveness of direct selection in early generations. Graphical Wr–Vr analysis further confirmed overdominance for days to maturity, plant height, test weight, secondary branches, siliqua length and seeds per siliqua, whereas complete dominance was observed for siliqua density and partial dominance for SPAD value. The results demonstrated considerable genetic diversity among parents and highlighted predominant role of non-additive genetic effects in the inheritance of seed yield and its associated traits. Therefore, the exploitation of heterosis and the development of hybrid breeding strategies may be effective approaches for enhancing productivity in Indian mustard.

Keywords **:** Indian mustard [*Brassica juncea* (L.) Czern & Coss], Hayman's diallel analysis, Non-additive gene action.

Introduction

Indian mustard [*Brassica juncea* (L.) Czern & Coss] is one of the most important oilseed crops cultivated worldwide and serves as a major source of edible oil and protein-rich meal. Globally, rapeseed-mustard ranks as the third most important vegetable oil crop, contributing about 12 per cent of total vegetable oil production after palm oil (36%) and soybean oil (26%). Owing to its adaptability to diverse agro-climatic conditions, lower input requirements and wide industrial applications, mustard plays a significant role in ensuring nutritional and economic security in many countries.

India is the world's fourth-largest producer of oilseeds after the United States, China and Brazil, accounting for nearly 19 per cent of the global oilseed cultivation area and about 2.7 per cent of total production (Thapa *et al*., 2019). The country's oilseed sector comprises nine major crops, among which soybean, rapeseed-mustard and groundnut dominate both area and production. During 2024–25, rapeseed-mustard occupied about 8.65 million hectares, representing 28.44 per cent of the total oilseed area, and contributed nearly 32 per cent of total oilseed production in the country (DA & FW, 2024–25).

India has emerged as the third-largest producer of Brassica oilseeds in the world, cultivating approximately 8.66 million hectares with a production of 12.67 million tonnes during 2024–25. Despite its vast cultivation area, the average productivity remains relatively low (1463 kg ha^{-1}) compared with the attainable yield potential. Rajasthan is the leading rapeseed-mustard producing state in India, accounting for about 3.49 million hectares with a production of 5.42 million tonnes and an average productivity of 1552 kg ha^{-1}. The crop is also extensively grown in Uttar Pradesh, Haryana, Madhya Pradesh, West Bengal, Gujarat, Jharkhand, Assam, Bihar and Punjab (DA & FW, 2024–25).

Although India possesses the largest area under oilseed cultivation, the productivity of most oilseed crops remains below the global average. Furthermore, the demand for edible oils is increasing rapidly owing to population growth, urbanization and changing dietary habits. The country's edible oil requirement is projected to reach 28.40 million tonnes by 2030 and 41.6 million tonnes by 2050 (Kumar, 2017). Therefore, enhancing the productivity of mustard through the development of superior cultivars is essential to reduce import dependence and achieve self-sufficiency in edible oils.

The success of any crop improvement programme depends on the availability of genetically diverse parental lines and a thorough understanding of the inheritance of economically important traits. Among the various mating designs employed in plant breeding, diallel analysis is one of the most effective approaches for investigating the genetic architecture of quantitative traits. It facilitates the evaluation of parental genotypes and their hybrid progenies, enabling the estimation of genetic parameters and the elucidation of the nature of gene action governing trait expression. Knowledge of the relative importance of additive and non-additive genetic effects, as well as the distribution of favourable alleles among parents, is essential for formulating efficient breeding strategies. Furthermore, an understanding of gene behaviour assists breeders in identifying superior parents, eliminating undesirable genotypes at early stages and developing effective cross combinations for the genetic improvement of complex traits. Therefore, diallel analysis serves as a valuable tool for dissecting the inheritance pattern of quantitative traits and accelerating cultivar development.

Materials and Methods

The present investigation was conducted using eight genetically diverse Indian Mustard [*Brassica juncea* (L.) Czern & Coss] genotypes, namely IC 491584, IC 267538, EC 766136, RH 406, DRMR-1165-40, NRCHB-101, DRMR-2017-15 (RADIKA) and BRIJRAJ, obtained from the ICAR-Indian Institute of Rapeseed-Mustard Research, Bharatpur. These parental lines were crossed in a half-diallel mating design during *Rabi*, 2023–24 and resulting 28 F_1's, along with their eight parents, were evaluated during *Rabi*, 2024–25 under two contrasting environments created by sowing on 16 October 2024 (E_1, normal sowing) and 11 November 2024 (E_2, late sowing). A total of 36 genotypes were tested in each environment in a randomized block design with three replications. Each genotype was sown in two rows of 3 m length, with a spacing of 45 cm between rows and 20 cm between plants within a row. All recommended agronomic practices were followed to ensure uniform crop establishment and optimum plant growth.

Statistical Analysis

The diallel data were subjected to combined graphical and numerical analyses according to the methods proposed by Hayman (1954a, 1954b) and Jinks (1954) to elucidate the nature of gene action governing seed yield and related traits in Indian mustard [*Brassica juncea* (L.) Czern & Coss]. The analysis was based on the assumptions of diploid segregation, homozygous parents, absence of maternal effects, independent distribution of genes among parents, absence of epistasis, linkage and multiple allelism.

The adequacy of the additive-dominance model was tested through the t^2 test and regression analysis of covariance (Wr) on variance (Vr) as follows:

Testing of the Adequacy of Hayman's Additive–Dominance Model

I. t^2 Test for Uniformity of Wr–Vr

$$t^2 = \frac{n-2}{4}\left[\frac{[Var_{(Vr)} - Var_{(Wr)}]^2}{[Var_{(Vr)}\ x\ Var_{(Wr)}] - Cov^2(Vr, Wr}\right]$$

where,

n= number of parents,

Var (V_r) = variance of array variances,

Var (W_r) = variance of array covariances, and

Cov (V_r,W_r) = covariance between V_r and W_r.

The calculated t^2 value was compared with the tabulated value of t at 4 and (n-2) degrees of freedom to test the adequacy of the additive-dominance model. A non-significant t^2 value indicated conformity of the assumptions of Hayman's diallel analysis, whereas a significant t^2 value suggested violation of one or more assumptions.

II. The regression coefficient (b) of W_r on V_r was estimated as:

$b = \frac{\sum(V_r - \bar{V}_r)(W_r - \bar{W}_r)}{\sum(V_r - \bar{V}_r)^2}$ equation was:

$$W_r = a + bV_r, a = \bar{W}_r - b\bar{V}_r$$

The regression coefficient (b) was tested against H_0: b = 0 and H_0: b = 1. A value significantly different from zero but not from unity indicated no epistasis and adequacy of the additive-dominance model, while deviation from unity suggested non-allelic interactions. For traits satisfying the assumptions of Hayman's model, genetic parameters including additive genetic variance (D), dominance variance (H_1 and H_2), covariance of additive and dominance effects (F), environmental variance (E), net dominance effect (h^2), average degree of dominance [$(H_1/D)½$], proportion of positive and negative alleles [$H_2/4H_1$], ratio of dominant to recessive genes (KD/KR) and narrow-sense heritability were estimated. Graphical analysis was carried out through Wr–Vr regression graphs to determine the degree of dominance and the distribution of dominant and recessive alleles among the parents.

Results and Discussion

The validity of the additive-dominance model was evaluated by examining the regression of W_r on V_r and the corresponding t^2 value according to Hayman's criteria. In the late sown environment (E_2), the model showed full validity for siliqua density and seeds per siliqua, as the regression coefficient did not differ significantly from unity but differ significantly from zero and t^2 was non-significant; therefore, both numerical and graphical analysis were carried out for these traits. In the normal sown environment (E_1), for days to 50% flowering, primary branches, secondary branches, siliquae per plant, seed yield per plant, SPAD value, relative water content, membrane stability index and for primary branches, seed yield per plant, relative water content and oil content in E_2, the model showed partial validity, because t^2 non-significant, although the regression coefficient deviated significantly from unity; hence, only numerical analysis was performed for these traits. However, for secondary branches, siliqua length and SPAD value in E_2, the regression coefficient differed significantly from unity and t^2 was also significant, indicating non-validity of the additive-dominance model; consequently, the genetic components estimated from Hayman's diallel analysis were not considered reliable and only graphical analysis was used. Similarly, for days to maturity, plant height and test weight in both E_1 and E_2, t^2 was non-significant, but the regression coefficient did not deviate significantly from either zero or unity, indicating inadequacy of Hayman's assumptions; therefore, graphical analysis was also conducted for these traits. The failure or inadequacy of Hayman's assumptions may be attributed to epistatic interactions, correlated gene distribution or linkage disequilibrium. The data presented in Table 1 indicated the following results.

Days to 50% flowering

For days to 50% flowering, numerical analysis indicated that D component was non-significant while both H_1 and H_2 were significant in both environments, demonstrating the predominance of non-additive gene effects. The observation $H_1 > H_2$, together with the ($H_2/4H_1$) ratio being less than 0.25 in E_1 and E_2, indicated an asymmetric distribution of genes among the parents. A positive F parameter, along with KD/KR ratio greater than one, further suggests a higher frequency of dominant genes in the parents. The positively significant h^2 value indicated unidirectional dominance at heterozygous loci. The nonsignificant E component implies a relatively small environmental influence on the trait in both environments. The degree of dominance, expressed as $(H_1/D)^{0.5}$, exceeded unity in E_1 and E_2, indicating overdominance. The ratio h^2/H_2 was less than one, suggesting control primarily by a single gene group. Narrow-sense heritability was low, estimated at 0.15 in E_1 and 0.17 in E_2.

Days to maturity

The regression coefficient (b) exhibited non-significant deviation from zero as well as from unity in both E_1 and E_2. However, the assumptions of the additive–dominance model were not completely satisfied for this trait indicating inadequacy of the model and the interpretation was limited only to the Wr–Vr graphical analysis.

In the Wr–Vr graph (Fig. 1), the regression line intercepted the Wr-axis below the point of origin in both environments, indicating the presence of over-

dominance for days to maturity. The scattering of parental array points in the graph suggested the existence of considerable genetic diversity among the parents for this trait.

The distribution of array points revealed that parents P_7 in E_1 and P_5, P_7 in E_2, which were positioned close to the point of origin, possessed a higher proportion of dominant alleles governing the trait. In contrast, parents P_2 in E_1 and P_1 in E_2, which were located farther away from the origin, were inferred to possess a higher frequency of recessive alleles. Parents P_3, P_6 in E_1 and P_3, P_4, P_6 and P_8 in E_2 were occupying an intermediate position on the regression line, appeared to carry dominant and recessive alleles in nearly equal proportion.

Plant height (cm)

The regression coefficient (b) exhibited non-significant deviation from zero as well as from unity in both E_1 and E_2. However, the assumptions of the additive–dominance model were not fully satisfied, indicating inadequacy of the model and the interpretation was limited only to the Wr–Vr graphical analysis.

In the Wr–Vr graph (Fig. 2), the regression line intercepted the Wr-axis below the point of origin in both environments, indicating the presence of over-dominance for plant height. The scattering of parental array points in the graph suggested the existence of considerable genetic diversity among the parents for this trait.

The distribution of array points revealed that parents P_5 in E_1 and E_2, which were positioned close to the point of origin, possessed a higher proportion of dominant alleles governing the trait. In contrast, parents P_1 in E_1 and P_4 in E_2, which were located farther away from the origin, were inferred to possess a higher frequency of recessive alleles.

Primary Branches

The numerical analysis for primary branches revealed that the D component was non-significant in both environments (0.05 in E_1 and 0.14 in E_2), whereas H_1 was highly significant (0.75** and 1.12**) indicating the predominance of non-additive gene effects. The observation $H_1 > H_2$ (0.75 > 0.73 in E_1 and 1.12 > 0.87 in E_2), together with $H_2/4H_1$ values of 0.24 and 0.19, indicates an asymmetric distribution of positive and negative alleles among the parents. The F parameter was negative in E_1 (-0.07) but positive in E_2 (0.12), while the KD/KR ratio was less than unity in E_1 (0.70) and greater than unity in E_2 (1.35), suggesting a higher frequency of recessive genes in E_1 and dominant genes in E_2. The h^2 values were non-significant (0.17 and 0.06), indicating the absence of marked directional dominance. The environmental component (E) was non-significant in both environments (0.05 and 0.03), suggesting limited environmental influence. The degree of dominance $[(H_1/D)^{0.5}]$ exceeded unity in both environments (4.06 and 2.81), indicating overdominance. The h^2/H_2 ratios were below one (0.23 and 0.07), suggesting control by approximately one major gene group. Narrow-sense heritability was moderate, estimated at 0.22 in E_1 and 0.35 in E_2.

Secondary Branches

The D component for secondary branches was non-significant (0.46), whereas H_1 (4.95**) and H_2 (4.38**) were highly significant, indicating the predominance of non-additive gene action. The relationship $H_1 > H_2$ and the $H_2/4H_1$ ratio of 0.22 indicate an unequal distribution of alleles among parental lines. The negative F value (-0.54) and KD/KR ratio below unity (0.70) suggest a greater proportion of recessive alleles in the parents. The positively significant h^2 estimate (3.87**) indicates directional dominance. The environmental component was low and non-significant (0.27). The degree of dominance $[(H_1/D)^{0.5} = 3.28]$ was greater than one, revealing overdominance. The h^2/H_2 ratio of 0.88 indicates involvement of nearly one major gene group. Narrow-sense heritability was moderate (0.37).

In the Wr–Vr graph (Fig. 3), the regression line intercepted the Wr-axis below the point of origin in E_2, indicating the presence of overdominance. The scattering of parental array points in the graph suggested the existence of considerable genetic diversity among the parents for this trait.

The distribution of array points revealed that parent P_6 in E_2, which was positioned close to the point of origin, possessed a higher proportion of dominant alleles governing the trait. In contrast, parent P_3 and P_1 in E_2, which were located farther away from the origin, were inferred to possess a higher frequency of recessive alleles. Parent P_7 in E_2 was occupying an intermediate position on the regression line, appeared to carry dominant and recessive alleles in nearly equal proportion.

Siliquae per Plant

For siliquae per plant, the D component was non-significant at 529.94, whereas H_1 (7059.20**) and H_2 (6121.04**) were highly significant, showing that non-additive gene action was predominant. The fact that H_1 exceeded H_2, along with an $H_2/4H_1$ ratio of 0.22,

indicates an asymmetrical distribution of genes among the parents. The positive F estimate of 371.43 and the KD/KR ratio of 1.21 suggest an excess of dominant alleles in the parental lines. The significant positive h^2 value of 5005.65** points to directional dominance. The E component was non-significant at 129.60, implying that environmental influence on this trait was relatively limited. The degree of dominance $(H_1/D)^{0.5}$ was 3.65, which is greater than unity and therefore indicates overdominance. The h^2/H_2 ratio of 0.82 suggests that approximately one major gene group was involved in controlling this trait. Narrow-sense heritability was low to moderate at 0.25.

Siliqua density

The numerical analysis indicated that the D component was non-significant in E_1 (0.002) but significant in E_2 (0.00**), whereas both H_1 and H_2 were highly significant in both environments (H_1 = 0.01** and 0.003**; H_2 = 0.00** and 0.003**), demonstrating the predominance of non-additive gene effects. The observation $H_1 > H_2$, together with the $H_2/4H_1$ ratio being less than 0.25 in E_1 (0.20) and E_2 (0.23), indicated an asymmetric distribution of genes among the parents. The F parameter was nearly zero in both environments, while the KD/KR ratio was greater than one in E_1 (1.25) and less than one in E_2 (0.77), suggesting a higher frequency of dominant genes in E_1 and recessive genes in E_2. The positively significant h^2 value in E_1 (0.00**) and E2 (0.001*) indicated unidirectional dominance at heterozygous loci. The environmental component of variance (E) was negligible, though significant in E_2 (0.0003*), indicating a minor environmental influence on the trait. The degree of dominance $[(H_1/D)^{0.5}]$ exceeded unity in both E_1 (2.49) and E_2 (1.42), indicating overdominance. The h^2/H_1 ratio was less than one in both environments (0.93 and 0.44), suggesting control primarily by a single gene group. Narrow-sense heritability was very low, estimated at 0.38 in E_1 and 0.54 in E_2.

In the Wr–Vr graph (Fig. 4), the regression line intercepted the Wr-axis from the point of origin in E_2 environment, indicating the presence of complete dominance for siliqua density. The scattering of parental array points in the graph suggested the existence of considerable genetic diversity among the parents for this trait.

The distribution of array points revealed that parents P_2, P_4 in E_2, which were positioned close to the point of origin, possessed a higher proportion of dominant alleles governing the trait. In contrast, parents P_3, P_8 in E_2, which were located farther away from the origin, were inferred to possess a higher frequency of recessive alleles.

Siliqua length (cm)

In the Wr–Vr graph (Fig. 5), the regression line intercepted the Wr-axis below the point of origin in E_2 environment, indicating the presence of over-dominance for siliqua length. The scattering of parental array points in the graph suggested the existence of considerable genetic diversity among the parents for this trait.

The distribution of array points revealed that parents P_7 and P_8 in E_2, which were positioned close to the point of origin, possessed a higher proportion of dominant alleles governing the trait. In contrast, parent P_2 in E_2, which was located farther away from the origin, inferred to possess a higher frequency of recessive alleles. Parent P_5 in E_2 occupying an intermediate position on the regression line, appeared to carry dominant and recessive alleles in nearly equal proportion

Seeds per Siliqua

The numerical analysis indicated that the D component was non-significant in both environments (0.18 in E_1 and 0.66 in E_2), whereas both H_1 (2.86** and 1.64**) and H2 (2.70** and 1.48**) were highly significant, demonstrating the predominance of non-additive gene effects. The observation $H_1 > H_2$, together with the $H_2/4H_1$ ratio being less than 0.25 in E_1 (0.24) and E_2 (0.23), indicated an asymmetric distribution of genes among the parents. A positive F parameter (0.09 and 0.38), along with KD/KR ratios greater than one (1.13 and 1.45), suggested a higher frequency of dominant genes in the parental lines. The h^2 value was non-significant in E_1 (0.88) but significant and positive in E_2 (1.80**), indicating unidirectional dominance mainly under E_2 conditions. The environmental component was significant in both environments (0.25* and 0.19**), indicating some environmental influence on the expression of the trait. The degree of dominance $[(H_1/D)^{0.5}]$ exceeded unity in both E_1 (3.94) and E_2 (1.58), indicating overdominance. The h^2/H_2 ratio was less than one in E_1 (0.32) but slightly greater than one in E_2 (1.21), suggesting involvement of approximately on major gene group in E_1 and more than one effective gene group in E_2. Narrow-sense heritability was low, estimated at 0.12 in E_1 and 0.28 in E_2.

In the Wr–Vr graph (Fig. 6), the regression line intercepted the Wr-axis below the point of origin in E_2, indicating the presence of overdominance for seed per siliqua. The scattering of parental array points in the

graph suggested the existence of considerable genetic diversity among the parents for this trait.

The distribution of array points revealed that parents P_5, P_7 in E_2, which were positioned close to the point of origin, possessed a higher proportion of dominant alleles governing the trait. In contrast, parent P_2 in E_2, which was located farther away from the origin, were inferred to possess a higher frequency of recessive alleles. Parents P_6, P_4 in E_2 were occupying an intermediate position on the regression line, appeared to carry dominant and recessive alleles in nearly equal proportion.

Test weight (g)

The regression coefficient (b) exhibited non-significant deviation from zero as well as from unity in both E_1 and E_2. However, the assumptions of the additive–dominance model were not completely satisfied, indicating inadequacy of the model. and the interpretation was limited only to the Wr–Vr graphical analysis

In the Wr–Vr graph (Fig. 7), the regression line intercepted the Wr-axis below the point of origin in both environments, indicating the presence of over-dominance for 1000-seed weight. The scattering of parental array points in the graph suggested the existence of considerable genetic diversity among the parents for this trait.

The distribution of array points revealed that parent P_8 in E_1 which positioned close to the point of origin, possessed a higher proportion of dominant alleles governing the trait. In contrast, parents P_7 in E_1 and P_6 in E_2, which were located farther away from the origin, were inferred to possess a higher frequency of recessive alleles. Parents P_2 in E_1 occupying an intermediate position on the regression line, appeared to carry dominant and recessive alleles in nearly equal proportion.

Seed Yield per Plant (g)

The numerical analysis for seed yield per plant showed that the D component was non-significant in both environments (2.55 in E_1 and 1.29 in E_2), whereas H_1 (28.21** and 25.22**) and H_2 (23.19** and 21.80**) were highly significant, indicating the predominance of non-additive gene effects. The H_1 values exceeded H_2 values and $H_2/4H_1$ ratios (0.21 and 0.22) were less than 0.25, indicating asymmetrical distribution of alleles among the parents. The positive F estimates (4.45 and 2.33) along with KD/KR ratios greater than one (1.71 and 1.51) suggest an excess of dominant alleles. The positively significant h^2 values (29.70** and 11.71**) indicate directional dominance. The E component was non-significant in both environments (0.45 and 0.23), indicating little environmental influence. The degree of dominance $[(H_1/D)^{0.5}]$ was greater than unity in both E_1 (3.33) and E_2 (4.42), indicating overdominance. The h^2/H_2 ratios were 1.28 and 0.54, suggesting involvement of one to two effective gene groups. Narrow-sense heritability was low (0.20 in E_1 and 0.17 in E_2).

SPAD value

For SPAD value, the D component was non-significant (6.88), while H_1 (44.56**) and H_2 (32.86**) were highly significant, indicating the predominance of non-additive gene action. The H_1 value exceeded H_2 and the $H_2/4H_1$ ratio (0.18) was below 0.25, suggesting asymmetrical gene distribution among parents. The positive F estimate (10.65) and KD/KR ratio greater than unity (1.87) indicate a higher frequency of dominant alleles. The h^2 value (5.28) was non-significant, suggesting the absence of strong directional dominance. The environmental component was non-significant (1.84). The degree of dominance $[(H_1/D)^{0.5} = 2.54]$ exceeded unity, indicating overdominance. The h^2/H_2 ratio (0.16) suggests control by approximately one major gene group. Narrow-sense heritability was low (0.28).

In the Wr–Vr graph (Fig. 8), the regression line intercepted the Wr-axis above the point of origin in E_2 indicating the presence of partial-dominance for chlorophyll content (SPAD value). The scattering of parental array points in the graph suggested the existence of considerable genetic diversity among the parents for this trait.

The distribution of array points revealed that parent P_4 in E_2, which was positioned close to the point of origin, possessed a higher proportion of dominant alleles governing the trait. In contrast, parent P_2 in E_2, which was located farther away from the origin, were inferred to possess a higher frequency of recessive alleles. Parent P_3 in E_2 occupying an intermediate position on the regression line, appeared to carry dominant and recessive alleles in nearly equal proportion.

Relative Water Content (%)

The D component for relative water content was non-significant in both environments (5.57 and 1.18), while H_1 (61.24** and 49.43**) and H_2 (51.16** and 47.59**) were highly significant, indicating predominance of non-additive gene effects. The H_1 values exceeded H_2 values and the $H_2/4H_1$ ratios (0.21 and 0.24) were less than 0.25, suggesting asymmetrical distribution of alleles. The F value was positive in E_1 (13.44) and slightly negative in E_2 (-0.80), whereas

KD/KR ratios were 2.14 and 0.90, indicating an excess of dominant alleles in E_1 and nearly equal distribution in E_2. The h^2 values (-1.03 and 1.98) were non-significant, indicating absence of directional dominance. The E component was non-significant in both environments (2.45 and 2.59). The degree of dominance $[(H_1/D)^{0.5}]$ exceeded unity in both E_1 (3.32) and E_2 (6.48), indicating overdominance. The h^2/H_2 ratios were close to zero (-0.02 and 0.04), suggesting involvement of very few effective gene groups. Narrow-sense heritability was low (0.07 in E_1 and 0.12 in E_2).

Membrane Stability Index (%)

For membrane stability index, the D component was non-significant (14.67), whereas H_1 (119.95**) and H_2 (83.64**) were highly significant, indicating predominance of non-additive gene action. The H_1 value exceeded H_2 and the $H_2/4H_1$ ratio (0.17) was less than 0.25, indicating asymmetrical distribution of genes among parents. The positive F estimate (34.24) and KD/KR ratio greater than unity (2.38) suggest a higher frequency of dominant alleles. The h^2 value (28.13) was non-significant, indicating weak directional dominance. The environmental component was non-significant (0.84), suggesting limited environmental influence. The degree of dominance $[(H_1/D)^{0.5} = 2.86]$ exceeded unity, indicating overdominance. The h^2/H_2 ratio (0.34) suggests control by approximately one major gene group. Narrow-sense heritability was low (0.28).

Oil Content (%)

The numerical analysis for oil content under E_2 revealed that the D component was non-significant (3.24), whereas both H_1 (23.41*) and H_2 (20.12*) were significant, indicating the predominance of non-additive gene effects. The observation $H_1 > H_2$, together with the $H_2/4H_1$ ratio of 0.21, indicates an asymmetric distribution of genes among the parents. The positive F parameter (4.78) and KD/KR ratio greater than unity (1.76) suggest a higher frequency of dominant alleles in the parental lines. The h^2 value (3.42) was non-significant, indicating absence of marked directional dominance. The E component was non-significant (0.63), suggesting a relatively small environmental influence. The degree of dominance $[(H_1/D)^{0.5} = 2.69]$ exceeded unity, indicating overdominance. The h^2/H_2 ratio (0.17) suggests control primarily by a single major gene group. Narrow-sense heritability was low (0.13).

Conclusion

The D component was significant for days to maturity, siliqua density, and seeds per siliqua in E_2, indicating the importance of additive gene effects in the inheritance of these traits. In contrast, the H_1 and H_2 components were significant for all traits in both environments, demonstrating that non-additive gene effects played a predominant role in trait inheritance. Since H_1 was greater than H_2 for all traits, the results suggest an asymmetrical distribution of positive and negative alleles among the parental lines. The degree of dominance $(H1/D)^{0.5}$ exceeded unity for almost all traits in both environments, indicating the prevalence of overdominance, whereas siliqua length recorded a value below unity, suggesting partial dominance. The h^2 component, which represents dominance effects due to heterozygous loci, was significant for most traits, indicating unidirectional dominance in their expression. However, non-significant h^2 estimates were observed for primary branches, relative water content, and oil content in both environments, as well as for SPAD value and membrane stability index in E_1, suggesting bidirectional dominance effects for these traits. The F parameter was positive for most traits in both environments, indicating a higher frequency of dominant alleles in the parental lines and this was further supported by KD/KR ratios greater than unity. Conversely, primary branches, secondary branches, and siliqua length in E_1, as well as relative water content in E_2, showed negative F values with KD/KR ratios below unity, suggesting a greater frequency of recessive alleles. The h^2/H_2 ratio, which indicates the number of effective gene groups controlling a trait, was less than unity for most traits, implying the involvement of a single major gene group; however, values above unity were recorded for seeds per siliqua in E_2, test weight in both environments and seed yield in E_1, suggesting the involvement of more than one gene group in controlling these traits. The $H_2/4H_1$ ratio was below 0.25 for all traits in both environments, confirming an asymmetrical distribution of alleles among the parental lines. The environmental component of variance (E) was significant for days to maturity, seeds per siliqua, and test weight in both environments, for plant height and siliqua density in E_2, and for siliqua length in E_1, indicating that environmental factors influenced the expression of these traits. All traits exhibited low narrow-sense heritability, except siliqua density in E_2, which showed moderate heritability and therefore greater potential for transmission to the progeny.

Hayman's graphical analysis indicated that, for days to maturity, plant height, and test weight in both E_1 and E_2, the regression line passes below the point of origin indicating the presence of over dominance. In E_2, the regression line for secondary branches, siliqua length, and seeds per siliqua passed below the point of

origin, indicating the presence of overdominance. For siliqua density in E_2, the regression line passed through the point of origin, suggesting complete dominance. In the case of SPAD value in E_2, the regression line passed above the point of origin, indicating partial dominance gene action. Hayman's analysis revealed the predominance of non-additive gene action for most of the traits, indicating the potential utility of heterosis breeding for improving seed yield and overall productivity in Indian mustard.

These findings are consistent with earlier reports by Arifullah *et al.* (2013), Shrimali *et al.* (2017), Chaurasiya *et al.* (2018), Avtar *et al*. (2019), Ashish *et al*. (2019), Singh *et al*. (2019), Kumar and Singh (2021), Singh *et al*. (2024) and Anita *et al*. (2025).

Table 1 : Estimates of Genetic Variance Components, Degree of Dominance and Heritability for Different Traits in Indian Mustard

Characters	DFF		DTM		PH (cm)		PB		SB		SPP		SD		SL (cm)	
Env.	E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2
T^2	3.89	1.80	0.04	0.34	3.10	0.24	4.33	3.68	3.26	36.65**	0.30	0.52	2.56	0.48	0.67	53.48**
b (w_r,v_r)	0.12	0.65	0.44	0.49	0.30	0.01	-0.09	-0.05	0.2	0.07	-0.14	0.78	0.22	0.69	0.43	0.27
t_{b-0}	0.60	1.06	1.32	1.80	0.39	0.01	0.5	0.24	0.98	0.91	0.43	1.96	1.02	3.45*	1.70	4.31**
T_{1-b}	4.57**	0.58	1.66	1.87	0.89	1.99	5.83**	5.28**	4.02**	11.74**	3.54**	0.54	3.68*	1.53	2.21	11.84**
D	5.06	14.44	1.1	7.90*	58.8	5.28	0.05	0.14	0.46	-	529.94	291.15	0	0.002**	-0.02	-
H_1	96.72**	84.61**	23.44**	25.71**	430.25**	356.95**	0.75**	1.12**	4.95**	-	7059.20**	3154.17**	0.01**	0.003**	0.29**	-
H_2	88.29**	75.41**	22.28**	22.11**	348.59**	309.14**	0.73**	0.87**	4.38**	-	6121.04**	2472.72**	0.00**	0.003**	0.27**	-
F	4.68	15.09	2.1	4.12	107.97	43.33	-0.07	0.12	-0.54	-	371.43	506.56	0	-0.001	-0.06	-
h^2	72.64**	29.61*	8.37*	17.88**	189.29**	207.61**	0.17	0.06	3.87**	-	5005.65**	1324.44**	0.00**	0.001*	0.24**	-
E	2.36	2.26	3.95**	2.88**	28.64	25.22*	0.05	0.03	0.27	-	129.6	87.17	0	0.0003*	0.05**	-
$(H_1/D)^{1/2}$	4.37	2.42	4.63	1.8	2.71	8.22	4.06	2.81	3.28	-	3.65	3.29	2.49	1.42	0	-
H_2/ 4 H_1	0.23	0.22	0.24	0.21	0.2	0.22	0.24	0.19	0.22	-	0.22	0.2	0.2	0.23	0.23	-
h^2/ H_2	0.82	0.39*	0.38*	0.81	0.54	0.67	0.23*	0.07*	0.88	-	0.82	0.54*	0.93	0.44	0.9	-
KD/KR	1.24	1.55	1.52	1.34	2.03	2.99	0.7	1.35	0.7	-	1.21	1.72	1.25	0.77	0	-
h^2 (NS)	0.15	0.17	0.01	0.31	0.12	0.05	0.22	0.35	0.37	-	0.25	0.25	0.38	0.54	0.21	-

DFF=days to 50% flowering, DTM=days to maturity, PH=plant height, PB=primary branches, SB=secondary branches, SPP=siliquae per plant, SD=siliqua density, SL=siliqua length,

Table1.contd…

Characters	SPS		TW (g)		SYPP (g)		SPAD		RWC (%)		MSI (%)		OC (%)	
Env.	E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2
T^2	0.06	1.05	0.07	0.05	1.31	0.17	3.24	12.07*	0.26	3.51	3.05	0.41	1.32	4.60
b (w_r,v_r)	-0.33	0.67	0.74	0.14	0.15	-0.17	0.21	-0.1	-0.12	-0.18	0.14	0.31	0.47	0.12
t_{b-0}	0.96	3.78**	2.29	0.31	0.57	0.52	1.07	0.81	0.35	0.92	0.70	0.60	2.18	0.65
T_{1-b}	3.84**	1.87	0.81	1.95	3.34*	3.47*	3.95**	8.61**	3.38*	6.01**	4.13**	1.36	2.44	4.82**
D	0.18	0.66**	0.05	0.02	2.55	1.29	6.88	-	5.57	1.18	14.67	11.48	1.83	3.24
H_1	2.86**	1.64**	0.51**	0.50**	28.21**	25.22**	44.56**	-	61.24**	49.43**	119.95**	135.70**	15.29**	23.41*
H_2	2.70**	1.48**	0.41**	0.43**	23.19**	21.80**	32.86**	-	51.16**	47.59**	83.64**	114.85**	14.52**	20.12*
F	0.09	0.38	0.06	0.02	4.45	2.33	10.65	-	13.44	-0.8	34.24	10.39	0.71	4.78
h^2	0.88	1.80**	0.56**	0.54**	29.70**	11.71**	5.28	-	-1.03	1.98	28.13	89.93**	1.38	3.42
E	0.25*	0.19**	0.03**	0.04**	0.45	0.23	1.84	-	2.45	2.59	0.84	0.52	0.71	0.63
$(H_1/D)^{1/2}$	3.94	1.58	3.29	4.64	3.33	4.42	2.54	-	3.32	6.48	2.86	3.44	2.89	2.69
H_2/ 4 H_1	0.24	0.23	0.2	0.22	0.21	0.22	0.18	-	0.21	0.24	0.17	0.21	0.24	0.21
h^2/ H_2	0.32*	1.21	1.36*	1.25	1.28	0.54*	0.16*	-	-0.02**	0.04**	0.34	0.78	0.10**	0.17
KD/KR	1.13	1.45	1.47	1.25	1.71	1.51	1.87	-	2.14	0.9	2.38	1.3	1.14	1.76
h^2 (NS)	0.12	0.28	0.24	0.19	0.2	0.17	0.28	-	0.07	0.12	0.28	0.27	0.18	0.13

SPS=seeds per siliqua, TW=test weight, SYPP= seed yield per plant, RWC=relative water content, MSI=membrane stability index, OC=oil content

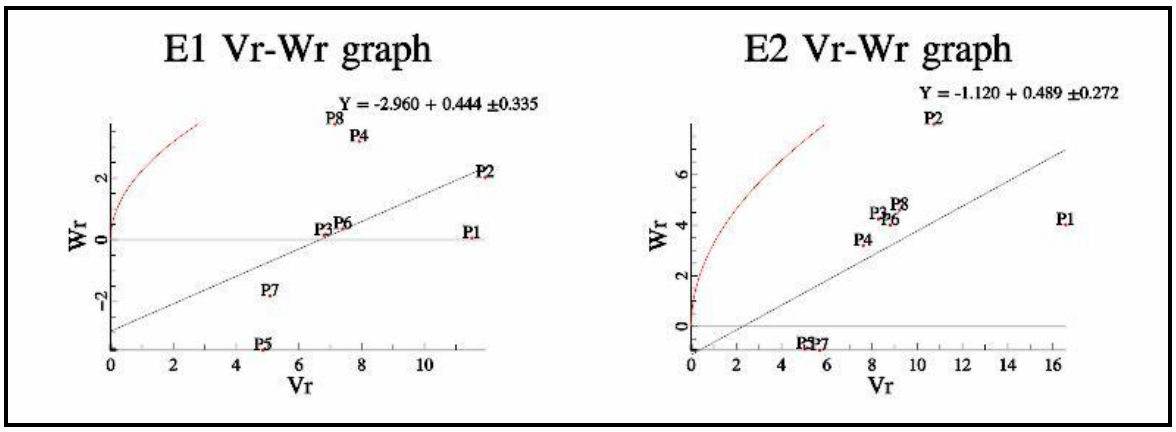

Fig. 1: Wr -Vr graph for days to maturity in E_1 and E_2 environment.

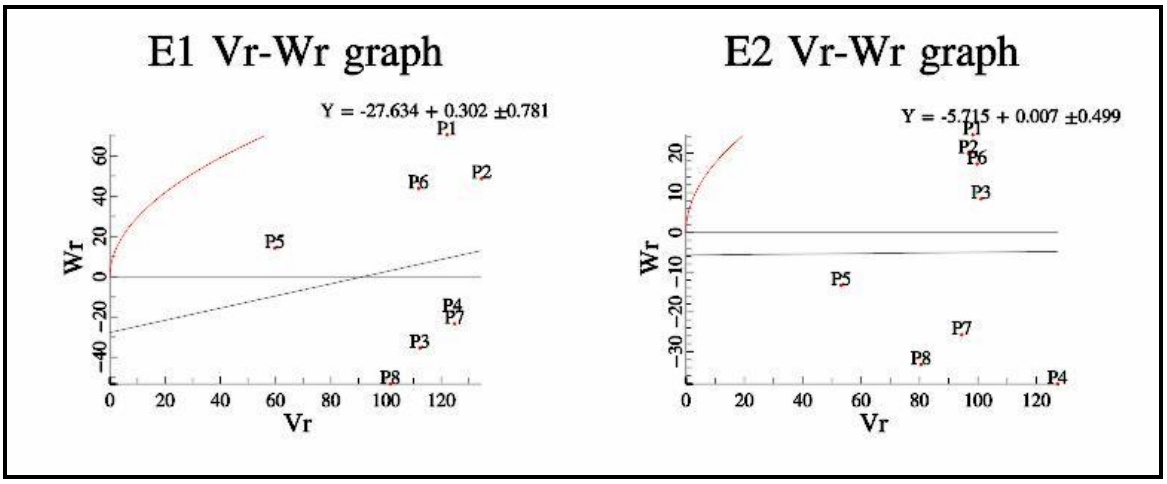

Fig. 2: Wr -Vr graph for plant height (cm) in E_1 and E_2 environment

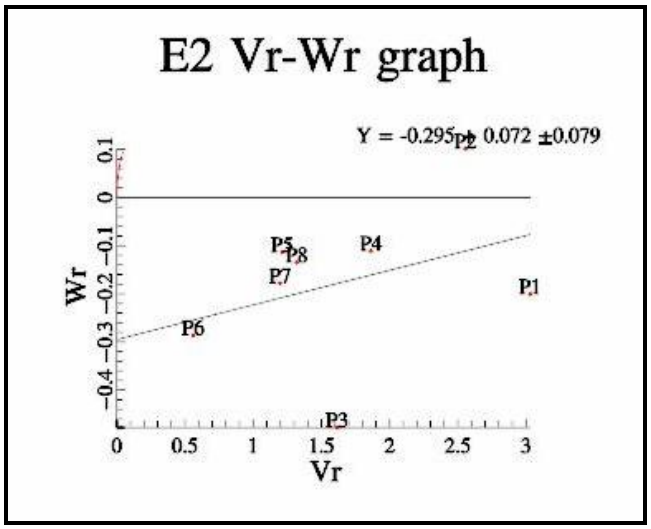

Fig. 3: Wr -Vr graph for secondary branches per plant in E_2 environment.

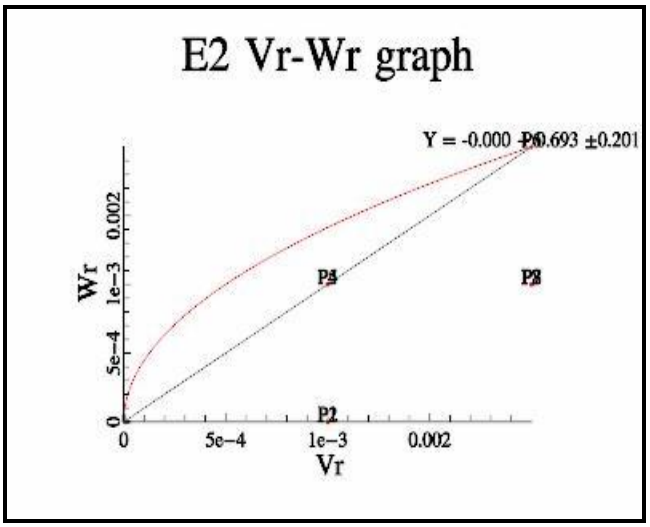

Fig. 4: Wr -Vr graph for siliqua density in E_2 environment.

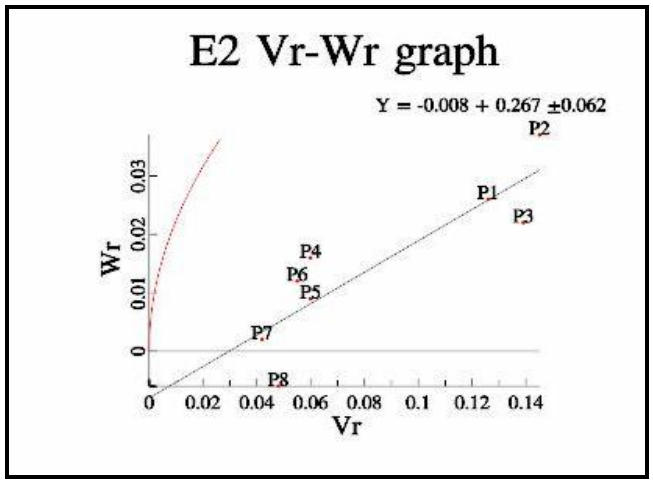

Fig. 5: Wr -Vr graph for siliqua length (cm) in E_2 environment.

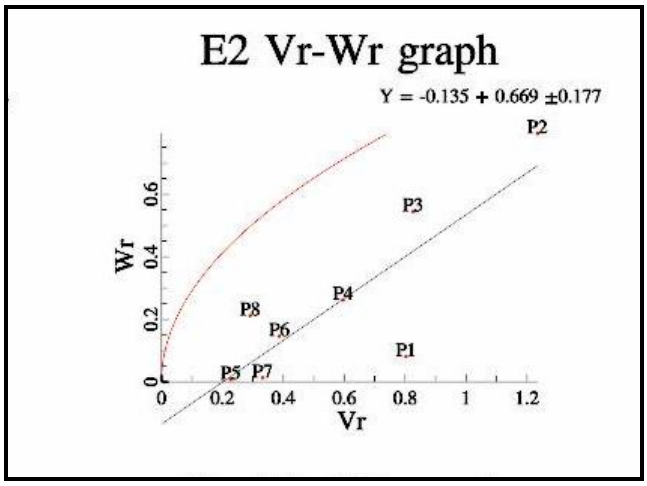

Fig. 6: Wr -Vr graph for seeds per siliqua in E_2 environment.

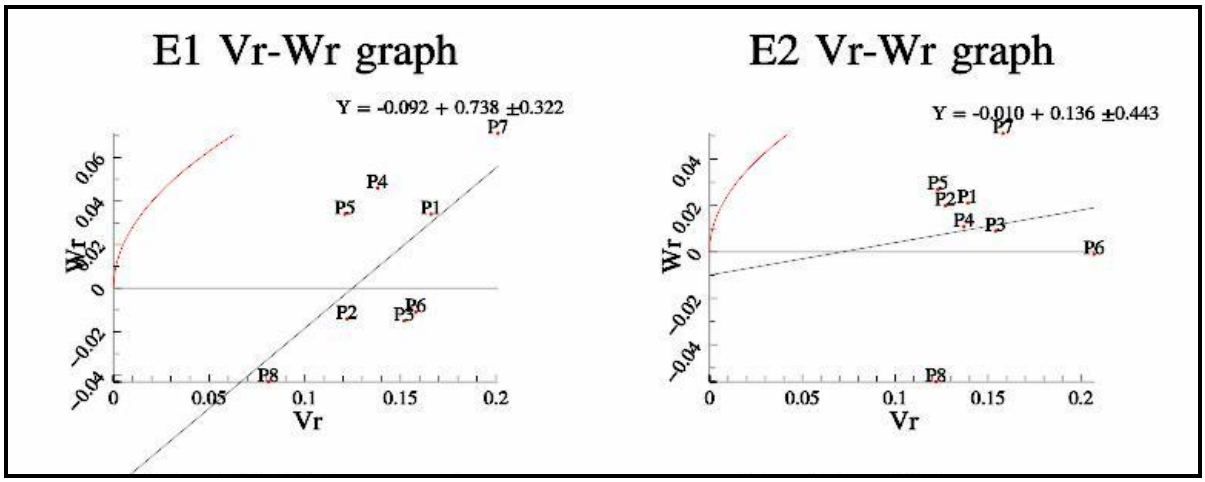

Fig.7: Wr -Vr graph for 1000-seed weight (g) in E_1 and E_2 environment.

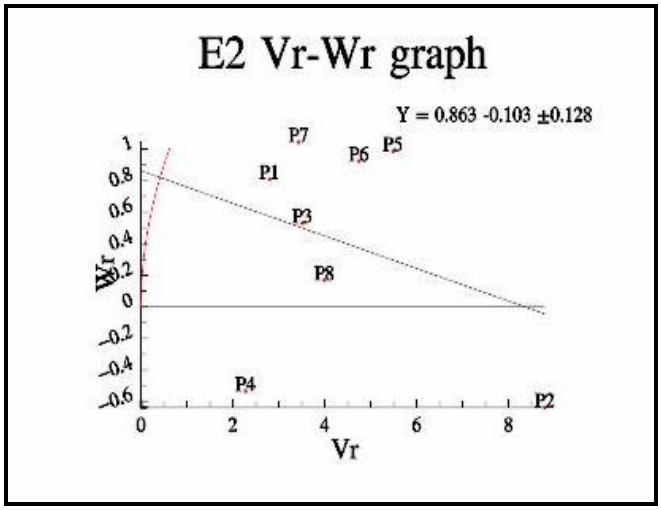

Fig. 8: Wr -Vr graph for chlorophyll content (SPAD value) in E_2 environment.

P1= IC 491584, P2= IC 267538, P3= EC 766136, P4= RH-406, P5= DRMR-1165-40, P6= NRCHB-101, P7= DRMR-2017-15, P8= BRIJRAJ.

References

Anita, G.D., Kumar, A., Sharma, M.K. and Mital, G.K. (2025). Genetic analysis of traits in Indian mustard [*Brassica juncea* (L.) Czern and Coss] using Additive-Dominance model. *Agriculture Association of Textile Chemical and Critical Reviews Journal*, **13**(1), 266-273.

Arifullah, M., Munir, M., Mahmood, A., Ajmal, S.K. and Hassan, F.U. (2013). Genetic analysis of some yield attributes in Indian mustard [*Brassica juncea* (L.) Czern and Coss]. *African Journal of Plant Science*, **7**(6), 219-226.

Ashish, A., Chauhan, M. P., Verma, S. P. and Mishra, S. (2019). Assessing gene action for yield and its contributing traits in Indian mustard [*Brassica juncea* (L.) Czern and Coss] under timely and late sown conditions. *Journal of Agri Search*, **6**(Special), 50-53.

Avtar, R., Singh, M. and Tomar, A. (2019). Genetic components analysis in Indian mustard [*Brassica juncea* (L.) Czern and Coss]. *International Journal of Agricultural Invention*, **4**(2), 175-181

Chaudhari, G. R., Patel, D. A., Kalola, A. D. and Kumar, S. (2023). Use of graphical and numerical approaches for diallel analysis of grain yield and its attributes in bread wheat (*Triticum aestivum* L.) under varying environmental conditions. *Agriculture*, **13**(1), 1-16

Chaurasiya, J.P., Singh, M., Yadav, R.K., Singh, L. and Yadav, H.C. (2018). Genetic analysis for estimates components of genetic variance in Indian mustard [*Brassica juncea* (L.) Czern and Coss]. *The Pharma Innovation Journal*, **7**(2), 104-107.

DA and FW (2024-25). Estimates of production of food grains. Directorate of Economics and Statistics. Ministry of Agriculture and Farmers Welfare, Government of India.

Hayman, B.I. (1954). The theory and analysis of diallel crosses. *Genetics*, **39**, 789–809.

Hayman, B.I. (1960). The theory and analysis of diallel crosses. III. Genetics, **45**, 155–172.

Jinks, J.L. (1954). The analysis of continuous variation in a diallel cross of nicotiana rustica varieties. *Genetics*, **39**, 767–788.

Jinks, J.L. (1956). The F2 and backcross generations from a set of diallel crosses. *Heredity*, **10**, 1–30.

Jinks, J.L.; Hayman, B.I. (1953). The analysis of diallel crosses. *Maize Genet. Newsl.*, **27**, 48–54.

Kumar, A. (2017). Proceedings of 3rd National Brassica Conference held at IARI New Delhi; **11**, 16-18.

Shrimali, T.M., Chauhan, R.M., Gami, R.A. and Patel, P.T. (2016). Diallel analysis in Indian mustard [*Brassica juncea* (L.) Czern and Coss]. *Electronic Journal of Plant Breeding*, **7**(4), 919-924.

Shrimali, T.M., Chauhan, R.M., Gami, R.A. and Patel, P.T. (2017). Components of Genetic Variation and Graphical Analysis (Wr-Vr) in Indian mustard [*Brassica juncea* (L.) Czern and Coss]. *International Journal of Current Microbiology and Applied Science*, **6**(2), 535-545.

Singh, K., Shweta. and Singh, M. (2024). Studies on genetic components in Indian mustard [*Brassica juncea* (L.) Czern and Coss]. *Journal of Oilseed Brassica*, **15(**2), 318-322.

Thapa, S., Baral, R. and Thapa, S. (2019). Status, challenges, and solutions of oil-seed production in India. *Research and Reviews: Journal of Agriculture and Allied Sciences*, **8**(1), 27-34.