Estimation of Genetic Variances in Indian mustard (*Brassica juncea* L.)

ABSTRACT

The current investigation on *Brassica juncea* L. genotypes focuses on exploring variations through hybridization to enhance genetic diversity. Additionally, it aims to gather genetic insights into yield and related traits essential for selecting superior varieties in subsequent generations. Using a half diallel design, eight potential genotypes were selected and crossed in every imaginable way. All of the qualities had substantial differences according to analysis of variance; these differences were further examined using Hayman's technique, which revealed that all of the traits are dominated by both additive and dominant gene effects. The findings suggested that dominance and additive genetic variations play a significant role in regulating these features. The magnitude of dominance (H_1 and H_2) was highly significant higher than additive components (D) for all traits. Positive alleles were not equally distributed among parents ($H_2/4H_1 \neq 0.25$) for all the studied traits. The estimates of environmental variance (E) were significantly positive for all studied traits, except for biological yield per plant suggests that environmental factors exert a notable influence on all examined traits. Narrow sense heritability was less than (0.50) for all traits. The graphical analysis Wr/Vr indicated the importance of over dominance gene effects in controlling all traits. Thus suggesting that selection could be effective in latter generations.

Key words: Indian Mustard, Genetic Components, Gene Action, Diallel and Hayman's Approach.

1. INTRODUCTION

Rapeseed-mustard is one of the most important winter oilseed crops in India. The genus *Brassica* includes several species such as *Brassica nigra* (n=8), *Brassica oleracea* (n=9) and *Brassica rapa* (n=10). *Brassica juncea* is a tetraploid species with a chromosome number of 2n=36 resulting from the hybridization of two diploid species *Brassica nigra* and *Brassica rapa* (Nagaharu, 1935). It is primarily a self-pollinated crop known for its extensive genetic diversity encompassing 310 genera and approximately 3500 species.

Among the seven edible oilseed crops grown in India, rapeseed-mustard holds the second position in terms of both area under cultivation and production after groundnut. It contributes significantly to India's oilseed economy accounting for 27.80% of the total production and globally it represents 28.60% of total oilseeds production (Shekhawat *et al*. 2012). “The seeds of Indian mustard typically contain approximately 38 to 42% oil and 24% protein. Indian mustard is primarily cultivated in the states of Rajasthan, Uttar Pradesh, Haryana, Madhya Pradesh and Gujarat. India with an area of 8.06 million hectares, 11.75 million tonnes production and 1458 kg/ha productivity ranks second in area and third in production in rapeseed-mustard scenario of the world” (Anonymous, 2022-23). “Rajasthan is the largest producer of rapeseed-mustard followed by Uttar Pradesh, Haryana, Madhya Pradesh, West Bengal, Gujarat and Assam. Rajasthan state ranks first both in area and production *i.e.* 3.37 million hectares and 5.48 million tonnes, respectively with an average productivity of 1627 kg/ha” (Anonymous, 2022-23).

Indian mustard is not only used in cooking but also finds extensive applications in the food industry, chemical sector, and as bio-fertilizers. India has emerged as the world's leading exporter of mustard seed meal, valued for its nutritional benefits for poultry animals (Sharma *et al.*, 2022).

Extreme temperatures pose significant challenges to the productivity of Indian mustard crops. While the crop can tolerate temperatures ranging from 6 to 27 °C, it optimally responds to light at temperatures between 15-20 °C. During this range, the plant achieves its maximum CO_2 exchange rate, which subsequently declines outside this optimal range (Kaushal *et al.*, 2016).

“There is significant potential for enhancing seed yield in mustard crop, although considerable time is necessary to develop varieties with increased yield per unit area. It is primarily the genetic stability, yield potential, and quality of the marketable product that dictate the cultivation and utilization of a particular oilseed crop” (Wittkop *et al.* 2009). Diallel analysis provides valuable insights into additive and dominance genetic variance, environmental variation components, distribution of genes among parental lines, maternal

and reciprocal effects, proportion of positive and negative genes, ratio of dominant and recessive genes and the average degree of dominance.

This study aimed to explore the genetic mechanisms governing the inheritance of diverse traits in Indian mustard (*B. juncea* L.) using diallel crosses. The diallel analysis technique was utilized to clarify the inheritance patterns of various plant characteristics and to assess the genetic foundation of their variability. This method provides insights into gene actions and genetic variance components aiding in effective selection in future generations.

2. Materials and Methods

The study utilized eight genotypes and encompassed all 28 possible cross combinations of their F_1's. The experiment was conducted using a randomized block design with three replications during the *Rabi* season of 2022-23 at the Agronomy Farm, S.K.N. College of Agriculture, Jobner (Jaipur, Rajasthan). The spacing between rows and plants was maintained at 30 cm and 10 cm, respectively. The recommended agricultural package of practices was adhered to in order to cultivate a healthy crop. The observations were recorded for fourteen traits namely plant height (PH), primary branches per plant (PB), secondary branches per plant (SB), siliquae per plant (SP), siliqua length (SL), seeds per siliqua (SS), seed yield per plant (SY), biological yield per plant (BY) and harvest index (HI) from ten randomly selected plants. Data on days to 50 % flowering (DF), days to maturity (DM), 1000-seed weight (TW), protein content (PC) and oil content (OC) were recorded on whole plot basis. The analysis of variance was carried for fourteen traits following the procedure given by Panse and Sukhatme (1985). Testing of validity of the hypothesis regarding diallel analysis assumptions proposed by Hayman (1954a). Components of variances in the diallel crosses were computed using formula suggested by Hayman (1954a).

3. RESULTS AND DISCUSSION

An analysis of variance was conducted on fourteen characteristics to assess the significance of differences among genotypes (Table-1). The results indicate highly significant variations among treatments across all traits. The analysis of variance revealed highly significant differences among the parent genotypes. Similarly, significant

differences were observed among the F_1's for all fourteen traits. Additionally comparisons between parents and F_1's have showed highly significant differences across all the traits. Similar results were also recorded by Dubey *et al*. (2014) and Tiwari (2019).

To validate the coherence and integrity of (Wr -Vr) and conduct regression analysis under the genetic model (Table 2). The regression coefficients were significantly different from zero to unity for all studied traits. This analysis highlighted highly significant differences among the 36 genotypes indicated the broad genetic diversity of traits present among the parent lines. This diversity among the parent genotypes suggests that these traits could be inherited by the offspring, thus enabling a comprehensive genetic analysis of the data. The non-significance of the appropriateness apply a simple additive-dominance model for the genetic analysis of all studied traits during the 2022-2023 mustard growing season.

3.1. Hayman analysis

Hayman's Diallel Analysis is employed to estimate the genetic component (Tables-3). The dominance component (H_1/H_2) exhibited significantly higher values than the additive component (D) across all traits. The F values and KD/KR ratios were greater than one for all traits, except for plant height and oil content indicating a higher frequency of recessive alleles compared to dominant alleles in the genetic makeup of the parental genotypes for these traits. The estimates of environmental variance (E) were significantly positive for all studied traits, except for biological yield per plant. This suggests that environmental factors exert a notable influence on all examined traits. The average degree of dominance overall loci, as estimated by $(H_1/D)^{1/2}$ indicating the role of over dominance gene effects in the inheritance of these traits. The average degree of dominance overall loci $(H_1/D)^{1/2}$ indicate that over-dominance genes contribute to the inheritance of these traits. The narrow-sense heritability for all traits was below 0.50 indicating that additive gene effects play a significant role in controlling these traits. Positive alleles were unevenly distributed among parents ($H_2/4H_1 \neq 0.25$) across all studied traits. Similar findings were reported by Singh and dixit (2008); Arifullah *et al.* (2013); Chaurasiya *et al.* (2018); Tomar (2019); Singh *et al*. (2020) and Kumar *et al*. (2022).

3.2. Graphical analysis

"Hayman's graphical analysis of parent-offspring array covariance (Wr) and variance (Vr) along with related statistical analyses was done to provide a clear cut picture about inheritance patterns of all studied traits (Figures 1-8). A graphical analysis of Wr-Vr indicated that over-dominance gene effects determine the outcome of all traits. The presence of complementary non-allelic interactions which distorted the (Wr-Vr) graphs and inflated the ratios of $(H_1/D)^{1/2}$" (Hayman 1954b and Mather and Jinks, 1982). The array points of the tested parents were scattered widely for all traits studied indicating genetic diversity. The distribution of eight parental mustard varieties along the regression lines showed that the parental varieties, P_1, P_2, P_3, P_5, P_6 and P_7 for days to maturity; P_4, P_6 and P_2 for plant height; P_5 for primary branches per plant; P_1 and P_8 for secondary branches per plant; P_1 and P_4 for siliquae per plant; P_3, P_4, P_5 and P_1 for seed yield per plant; P_8 for biological yield per plant and P_1, P_2, P_3, P_4, P_7 and P_8 for oil content appeared to possess a higher presence of dominant genes responsible for trait expression which being closer to the origin of regression graph.

4. Conclusion

Based on prior research, it was determined that hybridization represented the most effective approach for enhancing yield and its constituents in mustard. Analysis of variance indicated highly significant variations among treatments across all traits. Graphical analysis using Wr-Vr highlighted the significant role of over-dominance gene effects in regulating all traits. The ratio of dominance (H_1 & H_2) was notably highly significant as compare to additive components (D) for all studied traits.

Disclaimer (Artificial intelligence)

Option 1:

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of manuscripts.

Reference

Anonymous (2022-23). Agricultural Statistics at a Glance, Ministry of Agriculture, Directorate of Economics and Statistics, Department of Agriculture, Cooperation and Farmers Welfare, Ministry of Agriculture and Farmer Welfare, Govt. of India.

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 & Coss]. *African Journal of Plant Science* 7(6): 219-226.

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 & Coss]. *The Pharma Innovation Journal* 7(2): 104-107.

Dubey, A., Krishna, R., Singh, M., Tomar, A. and Yadav, R.K. (2014). Combining ability and heterosis analysis in Indian mustard (*Brassica juncea*). 2nd National Brassica Conference on *Brassicas* for addressing edible oil and nutritional security held at PAU, Ludhiana from 14th-16th Feb., 39 pp.

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

Hayman, B.I. (1954b). The analysis of variance of diallel tables. *Biometrics* **10**: 235-244.

Kaushal, N., Bhandari, K., Siddique, K.H. and Nayyar, H. (2016). Food crops face rising temperatures: an overview of responses, adaptive mechanisms, and approaches to improve heat tolerance. *Cogent food & agriculture*, 2(1): 1134380.

Kumar, R., Singh, M. and Tomar, A. (2022). Genetic analysis for estimates components of genetic variance in Indian mustard [*Brassica juncea* (L.) Czern & Coss]. *Journal of Pharmacognosy and Phytochemistry*, 6(1): 352-355.

Mather, K. and Jinks, J.L. (1982). Introduction to biometrical genetics. Chapman and Hall Ltd., London.

Nagaharu, U., and Nagaharu, N. (1935). Genome analysis in Brassica with special reference to the experimental formation of *B. napus* and peculiar mode of fertilization. *Japan Journal of Botany* **7**(7): 389-452.

Panse, V.G. and Sukhatme, P.V. (1985). Statistical Methods for Agricultural Workers. *Indian Council of Agricultural Research,* New Delhi: 381 pp.

Sharma, S., Bala, M., Kaur, G., Tayyab, S. and Feroz, S.R. (2022). Chemical composition of oil and cake of *Brassica juncea*: Implications on human and animal health. In: J. Smith (Ed.), *The Brassica juncea Genome* (*pp.* 29-55), Academic Press.

Shekhawat, K., Rathore, S.S., Premi, O.P., Kandpal and Chauhan, J.S. (2012.) Advances in agronomic management of Indian mustard [*Brassica juncea* (L.) Czern. Coss.]. *International Journal of Agronomy*, https://doi.org/10.1155/2012/408284.

Singh, M., Singh, R., Yadav, K. and Chaurasiya, J.P. (2020). Genetic analysis for seed yield and its contributing traits in Indian mustard [*Brassica juncea* (L.) Czern & Coss]. *Journal of Oilseeds Research*, https://doi.org/10.56739/jor.v.

Singh, R.K. and Dixit, P. (2008). Genetics of Quantitative Traits in Indian mustard [*Brassica juncea* (L.) Czern & Coss]. *Journal of Plant Genetic Resource* **21**(1): 89-92.

Tiwari, V.K. (2019). Morphological parameters in breeding for higher seed yield in Indian mustard [*Brassica juncea* (L.) Czern. & Coss.], *Electronic Journal of Plant Breeding* **10**(1): 187-195.

Tomar, A. (2019). Genetic components analysis in Indian mustard (*Brassica juncea* L. Czern & Coss) under Saharanpur districts, *International Journal of Agricultural Invention* **4**(1): 66-700.

Wittkop B, Snowdon RJ, Friedt W. (2009). Status and prospective of breeding for enhanced yield and quality of oilseed crops for Europe. *Euphytica* 170:131-140.

Table 1: Analysis of variance showing mean squares for parents and F_1's for seed yield and its contributing traits in Indian mustard.

Characters	Source of variations					
	Replications (2)	Genotypes (35)	Parents (7)	F_1's (27)	Parents vs F_1's (1)	Error (70)
Days to 50% flowering	1.37	18.68**	19.90**	17.47**	42.67**	2.07
Days to maturity	12.70	99.81**	29.87**	116.74**	134.52**	9.84
Plant height (cm)	26.77	410.90**	228.89*	230.88**	6545.43**	96.63
Primary branches per plant	0.24	1.59**	0.76**	1.35**	13.81**	0.20
Secondary branches per plant	1.24	13.52**	7.10**	8.05**	205.84**	2.20
Siliquae per plant	293.25	4953.04**	2805.91**	5101.87**	15964.65**	384.47
Siliqua length (cm)	0.03	0.42**	0.19*	0.45**	1.13**	0.07
Seeds per siliqua	0.15	1.75**	2.29**	1.42**	6.81**	0.58
1000-seed weight (g)	0.06	0.23**	0.22**	0.13**	2.92**	0.03
Seed yield per plant (g)	0.22	14.06**	3.35*	11.11**	168.92**	1.20
Biological yield per plant (g)	1.50	196.40**	102.73**	112.26**	3123.75**	20.50
Harvest index (%)	1.84	7.64**	2.78*	8.57**	16.68**	1.19
Oil content (%)	0.08	4.40**	2.83**	2.68**	61.87**	0.70
Protein content (%)	0.10	7.59**	3.18**	8.60**	11.10**	0.31

*, ** Significant at 5 % and 1 %, respectively

Table-2. Regression coefficient (b), (b = 0) and (b = 1) for seed yield and yield component traits in mustard.

Characters	Regression coefficient (b)± SE	b-0	b-1
Days to 50% flowering	0.48±0.34	1.40	1.52
Days to maturity	0.21±0.28	0.77	2.85*
Plant height (cm)	0.70±0.14	5.04**	2.11
Primary branches per plant	0.67±0.25	2.69*	1.35
Secondary branches per plant	0.95±0.16	6.11**	0.32
Siliquae per plant	0.61±0.24	2.52*	1.63
Siliqua length (cm)	0.12±0.29	0.41	3.03*
Seeds per siliqua	0.50±0.26	1.90	1.89
1000-seed weight (g)	0.29±0.23	1.26	5.62**
Seed yield Per plant (g)	0.55±0.22	2.47*	2.03
Biological yield per plant (g)	0.52±0.21	2.47*	2.28
Harvest index (%)	0.07±0.14	0.53	7.81**
Oil content (%)	0.62±0.16	3.81**	2.37
Protein content (%)	-0.02±0.08	-0.21	12.14**

Table.3. Estimates of components of genetic variances for seed yield and its contributing traits in Indian mustard.

Traits Components	Days to maturity	Plant height (cm)	Primary branches/plant	Secondary branches/plant
D	4.72±3.9	40.90**±16.2	0.19**±0.04	1.63**±0.44
H_1	98.52**±8.9	365.38**±37.3	0.93**±0.10	11.88**±1.02
H_2	90.95**±7.8	353.19**±32.4	0.92**±0.09	11.66**±0.89
h^2	3099.78**±5.2	1141.98**±21.7	1.29**±0.06	7.70**±0.59
F	8.78±9.2	17.97±38.3	0.07±0.10	0.08±1.05
E	4.07**±1.3	32.21**±5.4	0.10±0.01	0.73**±0.15
$(H_1/D)^{1/2}$	4.57	2.88	2.21	2.70
$H_2/4H_1$	0.23	0.24	0.25	0.25
KD/KR	1. 51	1.15	1.18	1.02
h^2/H_2	34.08	32.31	1.40	0.66
h^2 (ns)	0.06	0.14	0.19	0.20

Cont…..

Traits Components	Siliquae per plant	Seed yield per plant (g)	Biological yield per plant (g)	Oil content (%)
D	80.15*±41.1	0.72±0.62	27.41*±11.62	0.71**±0.24
H_1	725.08**±94.1	16.54**±1.42	21.06**±11.62	3.06**±0.55
H_2	671.47**±82.2	15.34**±1.23	20.26**±23.25	3.00**±0.48
h^2	671.05**±55.4	0.03±0.83	81.28**±15.59	16.17**±0.32
F	113.77±97.4	0.40±1.46	30.32±27.47	-0.22±0.56
E	12.16±13.0	0.40±0.21	6.84±3.87	0.23**±0.08
$(H_1/D)^{1/2}$	3.00	4.79	2.82	2.08
$H_2/4H_1$	0.23	0.23	0.23	0.25
KD/KR	1.62	1.12	1.49	0.86
h^2/H_2	1.00	0.01	0.40	54.06
h^2 (ns)	0.06	0.15	0.10	0.34

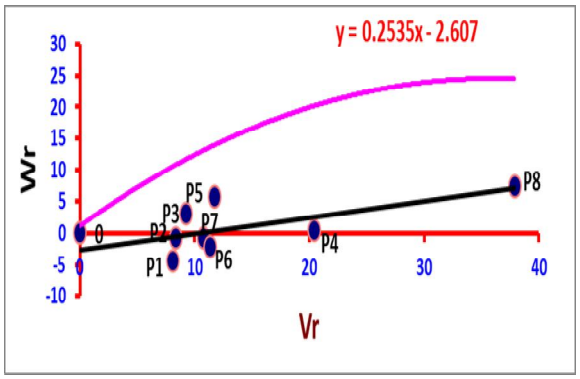

Fig.1: Wr-Vr graph for days to maturity

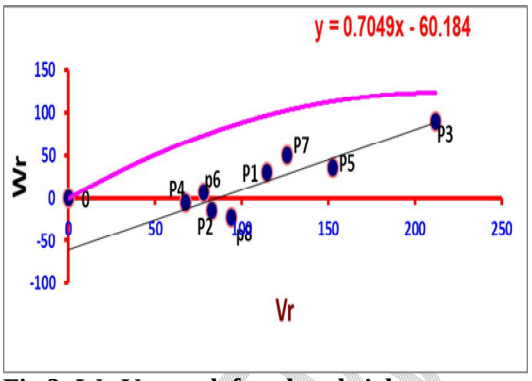

Fig.2: Wr-Vr graph for plant height

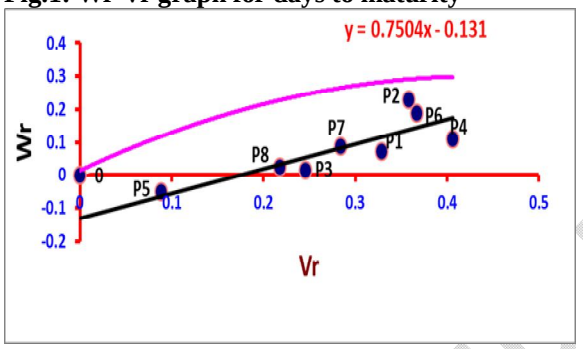

Fig.3: Wr-Vr graph for primary branches/plant

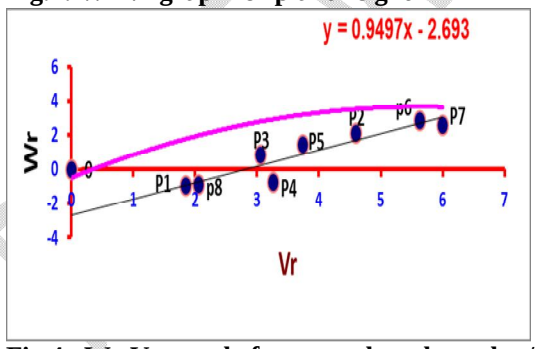

Fig.4: Wr-Vr graph for secondary branches/ plant

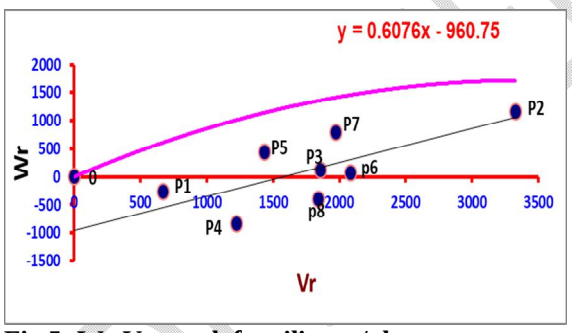

Fig.5: Wr-Vr graph for siliquae/plant

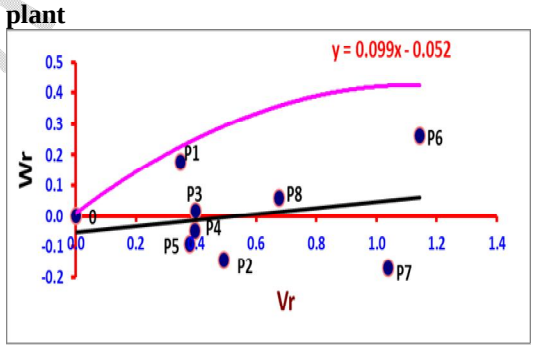

Fig.6: Wr-Vr graph for seed yield/plant

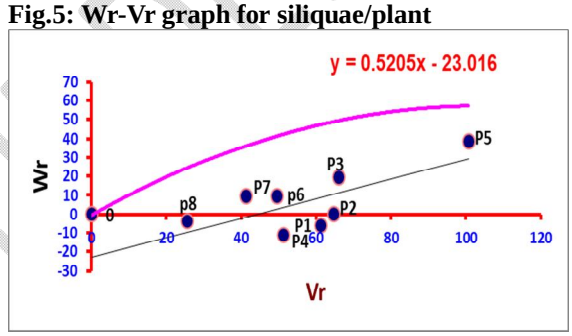

Fig.7: Wr-Vr graph for biological yield/plant

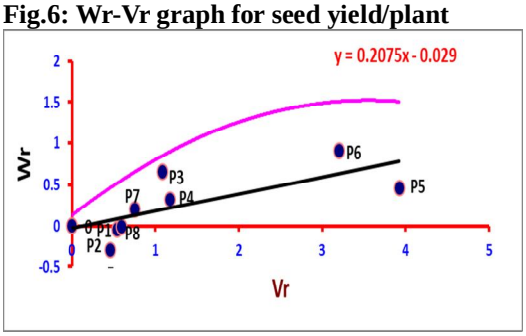

Fig.8: Wr-Vr graph for oil content

P_1=DRMR-150-35, P_2=DRMR-1165-40, P_3=DRMR-2059, P_4=BRIJRAJ, P_5=RH-406, P_6=RH-725, P_7=KRANTI, P_8=BPR-540-6