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Studies on Genetic Components for Seed Yield in Indian Mustard [*Brassica juncea* (L.) Czern. and Coss.]

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ABSTRACT: The current study was carried out by performing half diallel analysis on 28 treatments [7 genotypes (KMR(E)18-2, TM188, KMR(E)18-1, KMR(E)16-1, KMR(E)17-2, KMR(E)16-2 (Surekha), KMR(E)17-1] and their 21 crosses in order to conduct a study on Components of Genetic variance of metric traits contributing to seed yield in Indian Mustard [*Brassica juncea* (L.) Czern. and Coss.]. Twelve quantitative characters were used to record the observations. With the exception of seed yield per plant (g), genetic analysis showed that both the additive and dominance components were significant for all the traits. However, for all the traits with the exception of days to maturity and length of main raceme (cm), the dominance component values were found to be higher than the additive component values. The estimates of the average degree of dominance showed the presence of over-dominance for all features except days to maturity and the length of the main raceme (in cm) which showed presence of partial dominance. The estimates of H2/4H1 showed a symmetrical distribution of positive and negative genes in the parents for days to maturity, plant height, and length of main raceme, whereas the distribution of other characters was asymmetrical. For nearly every attribute, the values of component KD/KR showed an unequal frequency of dominant and recessive genes, with a larger frequency of recessive genes, and the values of h^2/H_2 showed that more than one gene groups were in charge of governing all characters under investigation.

Keywords: *Brassica juncea,* Indian Mustard, Quantitative traits, Genetic Variance, Diallel Mating.

INTRODUCTION

One of the first domesticated crop plants that humans tamed was *Brassica juncea* (L.) Czern. and Coss., also referred to as Indian mustard, brown mustard, Chinese mustard, or Oriental mustard, Rai, Raya, and Laha. There are six cultivated species in the genus Brassica of them, three are diploids: *Brassica nigra* (n = 8), *B. oleracea* (n = 9), and *B. rapa* (n = 10) while remaining three are amphidiploids: *B. carinata* (n=17), *B. napus* (n=19), and *B. juncea* (n=18) (Nagaharu, 1935). A hybrid between two diploid species, *B. campestris* (L.) (2n = 20, AA) and *B. nigra* (L.) (2n = 16, BB), produced the Indian Mustard (2n = 36; AABB). 85–90% of the crop is self-pollinated. However, the degree of cross-pollination varies from 4.0 to 16.6% because of insects, particularly honeybees (Bhajan *et al.,* 1991). India maintains third place in terms of area and output after China and Canada (Jat *et al*., 2019). It is a highly diverse and significant source of edible oil in the nation. Although it is grown all over the nation, eight states account for approximately 97.2% of the nation's rapeseed-mustard production namely, Rajasthan (48.3%), Madhya Pradesh (14.1%), Haryana (11.4%), Uttar Pradesh (8.6%), West Bengal (6.2%), Gujarat (4.2%), Jharkhand (2.8%), and Assam (1.6%) (DRMR, 2022). Most of it is grown in the Rajasthani districts of Alwar, Bharatpur, Sri Ganganagar, Kota, Bikaner, and Jaipur (Shekhawat *et al*., 2022). India imported 131.3 lakh tonnes of edible oils for Rs. 1.17 trillion during the 2020–21 oil year (November–October), according to the Solvent Extractors Association of India (SEA). This resulted in a significant loss of foreign exchange due to agricultural imports into the nation. Therefore, in order to achieve self-sufficiency, mustard seed output and oil quality must be increased. Indian mustard has a productivity ceiling that can be overcome by creating high-yielding hybrids and types through hybridization, which reorganizes the genes of suitable, diverse parents (Monpara and Dobariya 2007). The nature of gene activity involved in the production of quantitative features in self- and cross-pollinated crop plants has been extensively explained by the half-diallel mating system. It has been discovered that the half diallel mating design offers the plant breeder significant advantages in terms of comprehending the genetic composition of the parents. It offers trustworthy data on variance components as well as the effects of gca and sca variances. As a result, it helps choose appropriate parents for hybridization as well as efficient breeding procedures (Hayman, 1954a; Griffing, 1956) keeping these in view the present investigation was undertaken

to make an assessment of components of genetic variance to understand the nature of gene action involved in the expression of the metric traits contributing to the seed yield in Indian Mustard [*Brassica juncea* (L.) Czern. and Coss.]

MATERIALS AND METHODS

The experimental material consisted of seven morphologically diverse but genetically homozygous genotypes/varieties *viz.,* KMR(E) 18-2, TM-188, KMR(E)18-1, KMR(E)16-1, KMR(E)17-2, KMR(E)16-2 (Surekha), KMR(E)17-1 and their 21 direct crosses *i.e.,* the F_1 populations. All the 28 treatments (7 parents and 21 F_1s) were grown in Randomized Block Design with three replications at oil seed research farm of Chandra Shekhar Azad University of Agriculture & Technology (CSAUA&T), Kanpur during *Rabi* 2022-23. The data was recorded on five randomly selected plants of each genotype per replication and the mean data calculated from it for different traits *viz.,* days to 50% flowering, days to maturity**,** plant height (cm), length of main raceme (cm),number of primary branches per plant, number of secondary branches per plant, number of siliquae in main raceme, total siliquae per plant, number of seeds per siliqua,1000-seed weight, oil content (%) and seed yield per plant (g). Oil content of each sample was estimated in percentage by using Nuclear Magnetic Resonance Technology.

The material under present investigation was tested for the agreement with assumptions basic to Hayman diallel analysis (Hayman, 1954a). Mustard is a self-pollinated species. The parents included in the study were homozygous. The maternal effects are assumed to be absent in the present material. The multiple allelism might be present at certain loci controlling quantitative traits, but Hayman (1960) reported that it did not disturb measure of dominance critically. For testing other assumptions, two general tests *i.e.,* t^2 test and regression of Wr on Vr were used.

Genetic component analysis: Genetic component of variance was computed by employing diallel cross method suggested by Hayman (1954a) for the characters where additive – dominance model was fitted well. Adequacy of the additive dominance model was tested with the help of 't^2 ' test as proposed by Hayman (1954a) as follows:

$$t^2 = \frac{n-2}{4} \times \frac{(\text{Var.Vr} \times \text{Var.Wr})^2}{(\text{Var.Vr} \times \text{Var.Wr})\ \text{Cov}^2\ (\text{Vr.Wr})}$$

The values were compared against table value of 'F' at 4 and (n – 2) degrees of freedom. Significant value indicates the failure of hypothesis, *i.e.,* Wr – Vr are not constant over arrays. Where, n=Number of parents.

Estimated genetic components

Following genetic components of variance were estimated according to Hayman (1954b).

$\hat{D}$ = Component of genetic variance due to additive effects of the genes

$\hat{H}_1$ = Component of genetic variance due to dominant effects of the genes

$\hat{H}_2$ = Component of genetic variance due to dominance effects corrected for the gene distribution

$\hat{F}$ = The mean of Fr over the arrays, where Fr is the dominance effects in single array.

h^2 = Overall dominance effects of heterozygous loci.

$\hat{E}$ = The expected environmental component of variation.

$(H_1/D)^{1/2}$: Mean degree of dominance.

$(H_2/4H_1)$: proportion of genes with positive and negative effects in the parents.

$[(4DH_1)^{1/2}+F]/[(4DH_1)^{1/2} -F]$: proportion of dominant and recessive gene.

(h^2/H_2): number of group of genes which control the character and exhibit dominance.

RESULTS AND DISCUSSION

The non-significant value of t^2 for the characters days to maturity (0.024), plant height (0.408), length of main raceme (1.385), number of secondary branches per plant (1.238), number of siliquae in main raceme (0.310) and total siliquae per plant (1.026) indicated the validity of the additive-dominance model for these characters and also these traits did not show significant deviation of regression coefficient 'b' from unity indicating the validity of model for these traits.

Whereas the traits days to 50% flowering (5.543), number of primary branches per plant (7.627), number of seeds per siliqua (8.407) and seed yield per plant(18.516) showed significant deviation from t^2 values and the regression coefficient also showed significant deviation from unity which indicated non validity of the additive-dominance model and involvement of epistasis and/or linkage disequilibrium in these traits and therefore, the genetical parameters of Hayman's diallel were invalid for these traits.

Whereas there were two characters which had significant values for t^2 but their regression coefficient did not show significant deviation from unity.

So, the numerical analysis of the components of genetic variance were carried out for the traits showing validation for the additive – dominance model which are as following:

Days to maturity

The component D, H_1 and H_2 were found significant and the values of H_1 and H_2 were found to be lower than D indicating the role of both additive and dominant gene action with prevalence of additive gene action. The F component was negative and significant indicating the higher proportion of recessive genes than dominant in the parents. The h^2 component was found to be positive & significant indicating presence of dominance effect due to heterozygous loci. $(H_1/D)^{1/2}$(0.39) indicated partial dominance and the value of $H_2/4H_1$ was (0.26) near to (0.25) which indicated equal distribution of positive and negative alleles among the parents. The ratio KD/KR (0.84) indicated presence of higher proportion of recessive genes and the parameter h^2/H_2 (5.07) suggested that more than one gene group was governing the character.

Plant Height (cm)

The component D, H_1 and H_2 were found significant and the values of H_1 and H_2 were higher than D

indicating the predominance of dominant gene action for this character. The F component was negative indicating the higher proportion of recessive genes than dominant in the parents. The h^2 component was found to be positive & significant indicating presence of dominance effect due to heterozygous loci.

The ratio $(H_1/D)^{1/2}$ (2.73) indicated over dominance and the value of $H_2/4H_1$ was 0.24 near to 0.25 which indicated equal distribution of positive and negative alleles among the parents. The ratio KD/KR (0.79) indicated presence of higher proportion of recessive genes and the parameter h^2/H_2 (4.63) which suggested that more than one gene group was governing the character.

Length of main raceme (cm)

The component D, H_1 and H_2were found significant and the values of H1 and H2 were lower than D indicating the role of both additive and dominant gene action with prevalence of additive gene action. The F component was negative and significant indicating the higher proportion of recessive genes than dominant in the parents. The h^2 component was found to be positive & significant indicating presence of dominance effect due to heterozygous loci.

The ratio $\mathbf{(H_1/D)^{1/2}}$ (0.88) indicated partial dominance and the value of $H_2/4H_1$ was 0.24 near to 0.25 which indicated equal distribution of positive and negative alleles among the parents. The ratio KD/KR (0.75) indicated presence of higher proportion of recessive genes and the parameter h^2/H_2 (4.82) which suggested that more than one gene group was governing the character.

Number of secondary branches per plant

The component D, H_1 and H_2were found significant and the values of H_1 and H_2 were higher than D indicating the predominance of dominant gene action for this character. The F component was positive and significant indicating the higher proportion of dominant genes than recessive in the parents. The h^2 component was found to be positive &significant indicating presence of dominance effect due to heterozygous loci.

The ratio $(H_1/D)^{1/2}$ (1.92) indicated over dominance and the value of $H_2/4H_1$ was 0.13 which was not near to theoretical value (0.25) indicated unequal distribution of positive and negative alleles among the parents. The ratio KD/KR (2.61) indicated presence of higher proportion of dominant genes and the parameter h^2/H_2 (1.95) which suggested that more than one gene group was governing the character.

Number of siliquae in main raceme

The component D, H_1 and H_2 were found significant and the values of H_1 and H_2 were higher than D indicating the predominance of dominant gene action for this character. The F component was positive and significant indicating the higher proportion of dominant genes than recessive in the parents. The h^2 component was found to be positive & significant indicating presence of dominance effect due to heterozygous loci.

The ratio $(H_1/D)^{1/2}$ (2.82) indicated over dominance and the value of $H_2/4H_1$ was 0.20 which was not near to theoretical value (0.25) indicated unequal distribution of positive and negative alleles among the parents. The ratio KD/KR (1.64) indicated presence of higher proportion of dominant genes and the parameter h^2/H_2 (2.05) suggested that more than one gene group was governing the character.

Total siliquae per plant

The component D, H_1 and H_2 were found significant and the values of H_1 and H_2 were higher than D indicating the predominance of dominant gene action for this character. The F component was negative indicating the higher proportion of recessive genes than dominant in the parents. The h^2 component was found to be positive & significant indicating presence of dominance effect due to heterozygous loci.

The ratio $(H_1/D)^{1/2}$ (2.92) indicated over dominance and the value of $H_2/4H_1$ was 0.20 which was not near to theoretical value (0.25) indicated unequal distribution of positive and negative alleles among the parents. The ratio KD/KR (0.93) indicated presence of higher proportion of recessive genes and the parameter h^2/H_2 (1.35) suggested that more than one gene group was governing the character.

Table 1: Estimates of genetic components of variance and other related parameters for various characters in Indian Mustard.

Components	Days to 50% flowering	Days to maturity	Plant height (cm)	Length of main raceme (cm)	No. Of primary branches	No. Of secondary branches	No. of siliqua in main raceme	Total siliqua per plant	Number of seeds per siliqua	1000 seed weight (g)	Oil content (%)	Seed yield per plant (g)
b	0.177	0.981	0.344	1.114	0.173	0.703	0.400	-0.005	0.069	0.828	0.576	0.145
t_{b-0}	1.019	16.220**	1.105	7.363**	1.124	4.238*	1.276	-0.016	0.453	11.937**	4.573*	1.357
t_{1-b}	4.738*	0.310	2.108	-0.755	5.365*	1.794	1.914	3.484	6.135**	2.474	3.363	7.982**
t^2	5.543*	0.024	0.408	1.385	7.627**	1.238	0.310	1.026	8.407**	4.360*	5.453*	18.516**
D	9.94**	37.30**	28.91**	41.41**	0.289*	1.420**	6.21**	267.52**	1.29**	0.245**	0.821**	0.32
F	2.37	-2.47*	-18.27	-10.39**	0.261	2.433**	8.54**	-59.49	1.51**	0.316**	0.276	-0.76
H_1	23.77**	5.57**	215.55**	32.15**	1.202**	5.244**	49.49**	2276.32**	6.83**	0.648**	2.182**	11.29**
H_2	19.09**	5.88**	207.24**	30.74**	0.943**	2.919**	40.06**	1777.34**	5.63**	0.363**	1.721**	9.89**
h^2	56.13**	29.78**	958.78**	148.22**	1.044**	5.700**	82.28**	2399.32**	6.94**	0.697**	0.920**	24.24**
E	0.64	0.88	0.90	0.52	0.016	0.056	0.79	22.43	0.02	0.002	0.019	0.04
$(H_1/D)^{1/2}$	1.55	0.39	2.73	0.88	2.040	1.922	2.82	2.92	2.30	1.625	1.630	5.92
$(H_2/4H_1)$	0.20	0.26	0.24	0.24	0.196	0.139	0.20	0.20	0.21	0.140	0.197	0.22
KD/KR	1.17	0.84	0.79	0.75	1.569	2.610	1.64	0.93	1.68	2.311	1.230	0.67
h^2/H_2	2.94	5.07	4.63	4.82	1.107	1.953	2.05	1.35	1.23	1.919	0.535	2.45

*Significant at 5% level; **Significant at 1% level

SUMMARY AND CONCLUSIONS

For all the characters under study except for days to maturity and length of main raceme the magnitude of dominance components (H_1&H_2) was higher than the additive component (D) indicating the predominance of dominant gene action for all the traits except for the two aforesaid traits and that there is predominance of non-additive gene action for all traits except for days to maturity & length of main raceme. The predominance of non-additive gene action for plant height and number of branches per plant was also supported by Shrimali *et al*. (2017).

The F component was found to be negative for four of the characters days to maturity, plant height, length of main raceme, total siliquae per plant indicating higher proportion of recessive genes than dominant in the parents.

The values of ratio $(H_1/D)^{1/2}$ were found to be more than unity for all the traits indicating over dominance except for days to maturity and length of main raceme where it was less than unity. Over dominance for yield contributing traits were also reported by Thakral *et al*. (2000); Arifullah *et al*. (2012).

The values of $H_2/4H_1$ revealed that there was symmetrical distribution of positive and negative genes in the parents for the traits days to maturity, plant height and length of main raceme, while other characters showed asymmetrical distribution. The equal distribution of positive and negative genes in the parents enables the breeder in selecting specific desirable traits without sacrificing any other desirable trait.

The values of component KD/KR indicated unequal frequency of dominant and recessive genes with higher frequency of recessive genes for all the traits except for number of secondary branches per plant and number of siliquae in main raceme.

The knowledge of number of genes/group of genes responsible for particular traits is important for the genetic progress through selection in the present study, the values of h^2/H_2 indicated that more than one gene group were responsible for governance of all the characters under study.

REFERENCES

Arifullah, M., Munir, M., Mahmood, A., Khan, S., Ajmal and Shabbir, G. (2012). Combining ability analysis of some yield attributes in Indian mustard (*Brassica juncea* L). *Pakistan Journal of Agriculture & Research, 25*(2), 104-109.

Bhajan, R., Chauhan, Y. S. and Kumar, K. (1991). Natural cross pollination in Indian mustard. *Cruciferae Newsletter*, *15*, 24-25.

DRMR (2022): www.eands.dacnet.nic.in, www.drmr.res.in .

Griffing, B. (1956). Concept of general and specific combining ability in relationto diallel crossing systems. *Australia Biology Science, 9*, 463-493.

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.

Hayman, B. I. (1960). The separation of epistasis from additive and dominance variation in generation mean II. *Genetica, 31*, 133-146.

Jat, R. S., Singh, V. V., Sharma, P. and Rai, P. K. (2019). Oilseed brassica in India: Demand, supply, policy perspective and future potential. *OCL-Oilseeds and fats, Crops and Lipids*, *26*, 8.

Monpara, B. A. and Dobariya, K. L. (2007). Heterosis and combining ability in Indian Mustard [*Brassica juncea* (L.) Czern&Coss]. *Journal Oilseeds Research, 24* (2), 306-308.

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

Shekhawat, N., Sharma, H. and Chandrawat, K. S. (2022). Heterosis and combining ability analysis for yield and its component traits in Indian Mustard (*Brassica juncea). Indian Journal of Agricultural Sciences, 92*(8), 952- 956.

Shrimali, T. M., Chauhan, R. M., Gami, R. A. and Patel, P .T. (2017). Diallel Analysis in Indian Mustard (*Brassica juncea* (L.) czern. & coss.). *Electronic Journal of plant breeding, 7*(4), 919-924.

Thakral, N. K., Parkash, K., Amit, S. and Rekha, S. (2000). Genetic architecture of yield components in Indian mustard. *International Journal of Tropical Agriculture*, *18*(2), 177-180.

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