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Short Communication

Studies on genetic components in Indian mustard (*Brassica juncea* L)

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Abstract

The current study focused on Indian mustard (*Brassica juncea* L.) and aimed to investigate variations and induce variability through hybridization. Additionally, the study aimed to gather genetic information concerning specific yield-related attributes for selection in segregating generations. Seven promising genotypes, namely Azad Mahak, Surekha, NDR 8501, PR-21, PR-20, Kranti, and Ashirwad, were carefully selected and subjected to controlled crosses in all possible combinations, excluding reciprocals, under a diallel system, resulting in 28 treatments (comprising 7 parents and 21 crosses). Statistical analysis of variance revealed significant differences in all these traits, prompting further investigation using Hayman's approach, which indicated the presence of both additive and dominance gene effects governing these characteristics. Furthermore, estimates for the genetic component of variance indicated significant values for both additive and dominance components across all the measured traits. Notably, the degree of dominance exhibited over-dominance for specific traits, including the length of the primary raceme, plant height, number of secondary branches, average number of seeds per siliqua, oil content and seed yield per plant.

Keywords: *Brassica juncea, diallel, genetic advance, heritability, variability*

Introduction

Indian mustard [*Brassica juncea* (L.) Czern. & Coss.], a well-known oilseed crop, has been cultivated in India for centuries and holds great economic significance due to its versatility. One of its primary uses is the extraction of oil from its seeds. Mustard oil, a common and widely consumed product in India and other Asian countries, is renowned for its savory flavor and numerous health benefits. In regions like Punjab and Bengal, Indian mustard leaves are also enjoyed as a leafy vegetable, rich in vitamins A, C, and K, as well as calcium, iron, and other essential nutrients. One of the earliest plants cultivated by humans belongs to the Brassicaceae (Cruciferae) family. The Brassicaceae family, comprising approximately 3,709 species and 338 genera (Warwick *et al.,* 2006), ranks among the ten most commercially significant plant families (Rich, 1991). Despite being the third-largest global producer of oilseed brassicas (rapeseed-mustard) after Canada and China, accounting for 11.3% of production, India still imports 57% of its required edible oils, making it the seventh-largest edible oil importer worldwide (Jat *et al*., 2019). This particular crop is predominantly cultivated in the country under rainfed as well as in irrigated conditions. To meet the demands of our growing population, we continue to import around 50-60% of vegetable oils, totaling Rs. 82,123 crores during 2020-21 (Choudhary *et al.,* 2023).

The success of breeding efforts hinges on two critical and challenging factors: the level of accessible genetic variability and the potential of the parent plants involved in hybridization. The traditional practice of selecting parents based solely on their individual performance does not always yield positive results (Allard, 1960). Plant breeding frequently relies on combining ability analysis, a method developed by Sprague and Tatum in 1942, to assess the performance of parental lines in hybrid combinations. Heterosis, or hybrid vigor, can only occur when the gene frequencies of the parental cultivars used for F1 production differ. Evaluating their combining potential is an effective way to determine if a pair of parental lines will produce superior offspring. In both self-pollinated and cross-pollinated species, the diallel mating design is widely employed to investigate gene action and quantitative traits. It yields valuable data on variance components, general combining ability (GCA), specific combining ability (SCA), and their effects, aiding in breeding strategies and hybrid selection. Moreover, diallel approaches provide insights into gene interactions, enhancing researchers' ability to analyze and interpret dial-cross data.

Materials and Methods

The field experiments were conducted at Oilseed Research Farm, Chandra Shekhar Azad University of Agriculture & Technology, Kalyanpur, Kanpur, Uttar Pradesh, India during the *Rabi* seasons of 2021-22 and 2022-23. The experimental material comprised of a total of seven promising genotypes of Indian mustard, namely

Azad Mahak, Surekha, NDR 8501, PR-21, PR-20, Kranti and Ashirwad obtained from Chandra Shekhar Azad University of Agriculture & Technology (CSAUAT), Kanpur, Uttar Pradesh .

Development of F_1 hybrids

In the *Rabi* season of 2021-22, seven distinct parent plants were cultivated in five rows each as part of a crossing program. Standard agricultural techniques were applied, and when these seven genotypes reached the flowering stage, they were systematically crossed in all possible combinations, excluding reciprocals. This was achieved through manual emasculation and controlled pollination under a diallel breeding system. The final phase of the experiment was conducted during the *Rabi* season of 2022-23. In this phase, each parent and the resulting F1 hybrid plants were assessed using a randomized compact block design, with three replications. Each genotype was planted in two rows, each measuring 5.0 m in length, with a spacing of 45 cm between plants. The distance between individual plants was maintained at 20 cm by thinning the crop at 15 days after sowing (DAS). All recommended agronomic practices were diligently followed to ensure a successful crop.

Data recording

For each replication, data was collected from five randomly chosen plants of each genotype, and subsequently, the average values were calculated for various parameters including days to 50% flowering, days to maturity, length of the main raceme, plant height, the number of primary branches per plant, the number of secondary branches per plant, the number of siliquae on the main raceme, the total number of siliquae per plant, average seeds per siliquae, 1000-seed weight, oil content in seed, and seed yield per plant. Throughout the experiment, recommended agronomic practices were strictly adhered to in order to ensure the cultivation of a healthy and productive crop.

The data, which encompassed 28 genotypes consisting of 7 parent plants and 21 F1 crosses, underwent an analysis of variance following the method outlined by Panse and Sukhatme (1967). The objective was to ascertain the significance of differences among the various genotypes.

Results and Discussion

As data presented in Table 1 of the study, a broad spectrum of variation was evident among both the parent plants and the F1 hybrids across 12 distinct traits. Notably, variance in yield and its associated attributes was detected, indicating the diverse nature of the parent plants. This suggests the potential for generating substantial variation in future generations. Importantly, the analysis revealed significant differences between the parent plants and the F1 crosses, underscoring the diversity among the hybrid combinations.

Estimate of genetic components (Table 2) fo variation indicated that dominant components ware important for all the traits as value of $\hat{H}_1$ and $\hat{H}_2$ were greater than $\hat{D}$ component, where $\hat{H}_1$ is the dominance effect, $\hat{H}_2$=$H_1 1[1-(u-v)^2]$ where u and v are the proportions of positive and negative genes respectively in the parents and $\hat{D}$ is the additive effect. The components of $\hat{H}_1$ and $\hat{H}_1$ indicated that there was pre-dominance of dominant gene action for all traits. Relative magnitude of $\hat{H}_1$ component was higher than that $\hat{D}$ component for most of the traits under study except days to 50% flowering, days to maturity, number of primary branches, number of siliquae on main raceme, number of siliquae per plant, and 1000-seed weight indicating the role of both additive and dominance gene action with prevalence of dominant gene action. The positive and significant values of environmental component was found for all the characters except length of main raceme, plant height and 1000-seed weight. The ratio of mean degree of dominance revealed over dominance for the characters such as length of main raceme, plant height, number of secondary branches, average seeds per siliquae, oil content and seed yield per plant while the characters which showed partial dominance are days to 50% flowering, days to maturity, number of primary branches, number of siliquae on main raceme, number of siliquae per plant and 1000-seed weight. Value of $\hat{H}_1$ was greater than H_2 for most of the traits indicating frequency of gene distribution in the parents was unequal, and it was supported by the ratio of $\hat{H}_2/4\hat{H}_1$ (<25) for all the traits except days to 50% flowering, days to maturity, plant height and number of siliquae on main raceme showing asymmetrical gene distribution at the loci in the parents showing dominance for the traits. The F value was negative for most of the traits reflecting presence of higher number of recessive genes than dominant genes. Favourable situation of preponderance of dominant alleles for the characters days to maturity and 1000-seed weight from proportion of dominant and recessive effects in parents i.e. $[(\hat{D}\hat{H}_1)^{0.5}+$ reflects that recessive alleles were more frequent as compare with dominant alleles and directional selection may help breeder for better improvement for the character under consideration. This would be more helpful in getting the higher gain for direct selection in the advanced generations.

Ratio of $\hat{h}$/was less than unity for 1000-seed weight and average seeds per siliquae which revealed the presence of only one gene group was responsible for inheritance of this characters while the remaining characters which showed the ratio more than one indicated that these characters were governed by more than one major gene group. Characters such as number of secondary branches per plant, days to 50% flowering, number of siliquae on main raceme, number of siliquae per plant, length of main raceme, plant height, oil content and 1000-seed weight recorded high values for heritability (bs) indicating good potential of the genotypes for selection of these traits.

The effectiveness of a plant breeder hinges on the continuous enhancement of the genetic makeup of crop plants, aimed at creating superior genotypes capable of achieving higher production yields per unit of cultivated land. Achieving this goal is only possible through a deep understanding of the genetic mechanisms governing various agricultural parameters and traits. Singh *et al.* (2008) observed that both $\hat{D}$ and $\hat{H}$ components were important in genetic control of plant height. Similar results for additive gene action as well as dominance gene action were observed by Dholu *et al.* (2014) and Meena *et al.* (2017) and Yadav *et al.* (2020). Sohan and Nutan (2010), Kumari *et al.* (2018) and Gadi *et al.* (2020) also reported that the non-additive component was more prominent than additive component for all the traits based on average degree of dominance (more than unity for almost all traits). Chaurasiya *et al.* (2018) and Yadav *et al.* (2020) also reported Ratio of $\hat{h}$/was was less than unity for yield attributing traits. Singh *et al.* (2008) indicated that both the $\hat{D}$ and $\hat{H}$ components were important in genetic control of the number of seeds per siliquae. The findings of our study align with those of Rai *et al.* (2005), who also observed the prevalence of partial dominance, alongside high heritability estimates for traits such as seeds per siliqua. It's worth noting that certain discrepancies in our results are to be expected, as environmental factors inevitably play a role in influencing these traits.

Conclusion

Based on the results obtained in this study, it is evident that both additive and non-additive gene actions play a role in shaping the characteristics of the population across all 12 traits. To harness the maximum yield potential, it is advisable to maintain a certain level of genetic heterozygosity within the population. The wide range of genetic variability and significant variances observed across all traits among the different genotypes suggests that this diversity can be valuable for the

Table 1. ANOVA for parent and F_1s for twelve traits in of Indian mustard

Source of variation	*df*	Days to 50% flowering	Days to maturity	Length of main raceme (cm)	Plant height (cm)	Primary branches	Secondary branches	Siliquae on main raceme	Siliquae/ plant	Seeds per siliquae	1000-seed weight (g)	Oil content (%)	Seed yield per plant (g)
Replications	2	26.0**	11.0	3.1	22.6*	0.0	1.5	7.1	506	6.0**	0.0	0.0	0.7
Treatments	27	39.3**	52.2**	70.9**	242.0**	1.3**	3.7**	129.3**	4939**	2.4**	0.5**	3.0**	4.7**
Parents	6	63.0**	89.6**	64.3**	162.5**	1.9**	2.0**	188.1**	5643**	1.6	0.8**	2.0**	2.4**
F_1s	20	28.8**	31.1**	36.6**	109.0**	0.8**	1.7**	75.7**	3464**	1.5*	0.4**	3.2**	3.9**
Parent vs. F_1s	1	105.4**	232.4**	797.1**	3380.7**	6.3**	54.1**	847.0**	30202**	27.0**	0.2**	5.8**	32.5**
Error	54	4.9	9.5	2.3	7.0	0.3	0.5	10.14	168	0.8	0.0	0.0	0.7

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

Table 2. Estimates of variance components analysis and related parameters for 12 traits in Indian mustard

Source of variation	Days to 50% flowering	Days to maturity	Length of main raceme (cm)	Plant height (cm)	Primary branches	Secondary branches	Siliquae on main raceme	Siliquae/ plant	Seeds per siliquae	1000-seed weight (g)	Oil content (%)	Seed yield per plant (g)
$\hat{D}$	19.2**	26.7**	20.7**	51.7**	0.5**	0.5**	59.4**	1821.0**	0.2**	0.3**	0.7**	0.6**
SE±	0.4	1.1	1.7	4.7	0.0	0.1	0.9	39.5	0.0	0.0	0.3	0.3
$\hat{F}$	-4.1	1.6	-4.9	-23.7	-0.0	-0.2	-5.4	-732.8	-0.5	0.0	-0.3	-1.4
SE±	0.8	2.7	4.0	11.2	0.0	0.3	2.1	94.8	0.2	0.0	0.8	0.7
$\hat{H}$	2.0**	7.7**	33.3**	133.6*	0.2**	2.5**	26.4**	1258.4**	1.0**	0.2**	2.6**	1.8**
SE±	0.8	2.7	4.1	11.3	0.0	0.3	2.1	95.1	0.2	0.0	0.8	0.7
$\hat{H}_2$	3.0**	7.7**	32.2**	132.3**	0.2**	2.4**	28.3**	1208.9**	0.9**	0.2**	2.5**	1.5**
SE±	0.8	2.4	3.6	9.9	0.0	0.3	1.9	83.8	0.2	0.0	0.7	0.6
$\hat{h}^2$	18.8**	41.8**	148.4**	629.6**	1.1**	10.0**	156.4**	5606.0**	4.9**	0.0	1.0**	6.0**
SE±	0.5	1.6	2.4	6.7	0.0	0.2	1.3	56.3	0.1	0.0	0.5	0.4
$\hat{E}$	1.9**	3.2**	0.8	2.5	0.0**	0.2**	3.3**	59.9*	0.3**	0.0	0.0**	0.2**
SE±	0.1	0.4	0.6	1.6	0.0	0.0	0.3	14.0	0.0	0.0	0.1	0.1
$(\hat{H}_1/\hat{D})^{½}$	0.3	0.5	1.3	1.6	0.7	2.3	0.7	0.8	2.2	0.8	2.0	1.8
$(\hat{H}_2/4\hat{H}_1)$	0.4	0.2	0.2	0.2	0.2	0.2	0.3	0.2	0.2	0.2	0.2	0.2
$[(4\hat{D}\hat{H}_1)^{½}+\hat{F}]$ $/[4\hat{D}\hat{H}_1)^{½}-\hat{F}]$	0.5	1.1	0.8	0.8	0.9	0.9	0.9	0.6	0.3	1.0	0.8	0.2
Va	11.1	12.6	13.4	38.3	0.3	0.4	31.5	1301.7	0.3	0.1	0.6	1.2
Vd	0.8	1.9	8.0	33.1	0.0	0.6	7.1	302.2	0.2	0.0	0.6	0.4
$\hat{h}^2/\hat{H}_2)$	6.1	5.4	4.6	4.8	5.4	4.1	5.5	4.6	5.1	0.2	0.4	4.0
$\hat{h}^2$	0.8	0.7	0.6	0.5	0.7	0.3	0.8	0.8	0.4	0.8	0.5	0.7
Dominant parent	48.8	106.9	52.6	117.1	7.5	16.6	57.5	-461.6	17.5	4.5	39.8	19.2
Dominant parent	75.4	158.0	82.0	157.8	8.1	16.7	116.8	1745.7	17.6	4.8	39.8	19.2

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

$\hat{D}$ = Additive effect, $\hat{F}$ = Mean Fr over arrays, $\hat{H}_1$ = Dominance effect, $\hat{H}_2$ = H1[1-(u-v)^2] whree u and v are the proportions of positive and negative genes respectively in the parents, $\hat{h}^2$ = Heritability, $\hat{E}$ = Environmental component, SE ± b = Standard error, $(\hat{H}_1/\hat{D})^{½}$ = Mean degree of dominance, $(\hat{H}_2/4\hat{H}_1)$ = proportion of genes with positive and negative effects in the parents, $[(4\hat{D}\hat{H}_1)^{½}+\hat{F}]/[4\hat{D}\hat{H}_1)^{½}-\hat{F}]$ = proportion of dominant and recessive gene, Va = Additive gene effects, Vd = Dominance deviations, $\hat{h}^2/\hat{H}_2$ = No. of gene groups, $\hat{h}^2$ = Heritability in narrow sense identification of superior germplasm. In the context of future use as donor parents, it is crucial to gather information regarding the maximum and minimum presence of dominant and recessive genes in distinct genotypes for specific characteristics. Such insights can be of substantial benefit in breeding programs. Therefore, this study makes a noteworthy contribution by shedding light on the genetic control mechanisms behind various yield-related traits, which in turn can expedite the selection and breeding of high-yielding Indian mustard genotypes in India.

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