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GENETIC DIVERSITY, VARIABILITY AND HERITABILITY STUDIES IN INDIAN MUSTARD (*Brassica juncea* L. Czern and Coss)

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ABSTRACT

The present investigation was carried out during *rabi* season of 2022-23 at the experimental farm of Department of Agriculture, Himgiri Zee University, Dehradun, Uttarakhand to determine the selection criteria for yield improvement in selected genotypes of Indian mustard (*Brassica juncea* L.). In this investigation, 25 genotypes were sown to evaluate genetic diversity, component of variability, mean, heritability and genetic advance for yield and yield attributing components. Genetic divergence analysis in 25 genotypes of Indian mustard by applying Mahalanobis's D^2 statistics indicated the presence of wider genetic diversity among the genotypes for characters. The genotypes were grouped into seven clusters by Euclidean's method. Clusters II and cluster III were the largest group with 5 genotypes followed by cluster IV and cluster VI with 4 genotypes, cluster V with 3 genotypes and cluster I and cluster VII with 2 genotypes. The highest intra-cluster distance was found for cluster VI (301.732), the maximum inter-cluster distance observed between cluster IV and cluster VII (1713.25*).The maximum contribution to divergence was from days to maturity (35.67). In our present findings, it may be inferred that there was a broad range of variation seen for all characters among genotypes, indicating the substantial possibility for improving Indian mustard cultivars by even selection. Genotypes PM-26, NDRE-4, KRANTI, and PM-21 had the highest yielding genotypes which may be suggested for large-scale cultivation among farmers and employed as donors in any breeding programs.**

(Key words: Genetic advance, genetic diversity, Indian *Brassica*, PCV, GCV, heritability)

INTRODUCTION

Brassica juncea, commonly known as brown mustard, Chinese mustard and Indian mustard (Raut *et al.,* 2021, Sapkal *et al.*, 2021 and Hrishikesh *et al.*, 2021) belongs to the family Brassicaceae (Crucifereceae). It is an amphidiploid with diploid chromosome number 36 derived from natural interspecific hybridization between *Brassica nigra* (n=8) and *Brassica rapa* (n=10).In crop development, genetic diversity is required to create hybrids between genotypes of different origin with stronger heterosis (Aditi *et al.*, 2021), a broader spectrum of variability, and the possibility to acquire acceptable recombinants in segregating generations than between closely related parents. To develop new cultivars with higher yield, wider adaptability and acceptable quality than existing ones, the breeder must have extensive knowledge of the diversity of accessible material (Bocianowski *et al.*, 2017, Li *et al.*, 2023). The availability of sufficient genetic variability is vital for crop improvement programs (Körber *et al.*, 2016). Due to its better production and relative resilience to a variety of biotic and abiotic challenges, Indian mustard is more well-liked by farmers than rapeseed. The foundation for supplying priceless genetic material is having genetically diverse contributors (Lopaty´nska *et al.*, 2021). Since yield is a multi-dimensional characteristic, evaluating yield and the qualities that contribute to it is important for crop development (Kumar *et al.,* 2015). In most cases, genetically dissimilar parents are used to produce desirable recombinants in segregating generations. Genetic diversity also aids in finding genetically potential genotypes, which can subsequently be used to create important selectable variation (Chen *et al.*, 2017).

MATERIALS AND METHODS

The experiment was performed at an experimental farm of Crop Research Centre (CRC) of the Department of Agriculture, Himgiri Zee University, Dehradun, Uttarakhand during the *rabi* season 2022- 2023. The experimental material for the study consisted of 25 genotypes of Indian mustard were sown in randomized block design (RBD) with 3 replications. Each replication had 25 treatments (PM-21, PUSA-JAIKISHAN, RH-725, VARUNA, EC-764646, RH-749, EC-206723, PUSA-BOLD, PM-24, PR-21, RH-0119, EC-765451, EC-491579, EC765865, KRANTI, PM-26, PM-22, EC-766061, EC-399318, NRCHB-101, NDRE-4, PR-19, DRMRIJ-

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31, EC-33571, DRMR-1165-40). Two rows of each genotype was sown. The observations were recorded on five random selected plants for 12 characters *viz.,* days to emergence, days to 50% flowering, plant height (cm), number of primary branches plant^{-1}, number of secondary branches plant^{-1}, length of main raceme, number of silique on main raceme, length of silique, number of seeds silique^{-1}, days to maturity, 1000 seed weight and seed yield plant^{-1}. D^2 statistics (Figure 1) was performed as per the method given by Mahalanobis (1936). PCV and GCV were calculated by formula given by Hasan and Sarker (2020). Heritability in broad sense (h^2) was estimated by formula given by Burton (1952) and genetic advance was calculated by formula given by Johnson *et al.* (1955).

RESULTS AND DISCUSSION

The analysis of variance for randomized block design (RBD) for 12 characters revealed that mean sum of squares due to genotype showed significant differences for the characters plant height (cm) (992.3**), followed by days to maturity (279.1**),days to 50 % flowering (162.9**),length of main raceme (138.8**),seed yield plant^{-1} (5.32**),number of primary branches (2.12**), etc. This indicated the presence of variability, which can be exploited through selection for further breeding programs (Table 1). The mean performance of days to emergence ranged from 6.33 to 8.66 days, days to 50% flowering ranged from 53.33 to 72 days, minimum mean value for plant height was 103.36 cm and maximum was 172.26. Highest number of primary branches plant^{-1} was 7.37 and lowest number was 3.55. Maximum number of secondary branches was 18.03 and minimum was 6.39. Maximum length of main raceme was 73.70 cm and minimum was 46.30 cm. The maximum number of silique on main raceme was 40.60 and minimum number of silique on main raceme was 14.33. The maximum length of silique was 5.43 cm and minimum length was 4.06 cm. The highest value of seeds silique^{-1} was 13.46 and lowest value of seeds silique^{-1} was 10.18. Maximum days to maturity was 142.60 and minimum days was 113.66 days. Maximum 1000 seed weight plant^{-1} was 5.13 g and the minimum was 2.26 g. Maximum value of seed yield plant^{-1} was 7.26 g and minimum seed yield was 2.86 g (Table 2).

The data regarding estimates of GCV, PCV, heritability and genetic advance as per mean are presented in Table 2. Due to the influence of the environment, the phenotypic coefficients of variation (PCV) were slightly larger than the associated genotypic coefficients of variation for all the seed quality criteria. The highest phenotypic coefficient of variation was observed in case of seed yield (29.27%) and the lowest were observed in days to maturity (7.41%). The highest GCV was observed in seed yield (25.65%) and the lowest GCV was recorded in length of silique (3.89). The observed high estimates of phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) were recorded in case of seed yield plant^{-1} (PCV=29.27%, GCV=25.65%) followed by 1000 seed weight (PCV=23.36%, GCV=22.82 %). Number of silique on main raceme (PCV= 21.79%, GCV=21.40%), number of secondary branches (PCV=21.32%, GCV=20.89%), and number of primary branches (PCV= 17.48%, GCV= 16.76%), were considered as high. Plant height (cm) (PCV= 13.24%, GCV =13.03%), days to 50% flowering (no.) (PCV= 12.24%, GCV= 12.13%) and length of main raceme (PCV= 11.82%, GCV= 10.91%), were considered as average.

In our finding, the lowest estimates (less than 10%) were observed in number of seeds silique^{-1} (PCV= 8.78%, GCV= 7.06%), days to maturity (PCV= 7.41%, GCV= 7.35%), days to emergence (in number) (PCV= 13.18%, GCV=6.19 and length of silique (cm) (PCV=11.18%, GCV=3.89%). According to Wang *et al.* (2016), the primary photosynthetic organs to support the development of the pericarp and seed at the post-flowering stage is siliques. Thus, these traits can play a dual roles in the source-sink relationship during seed development, and the translocation of dry matter from the pericarp to the seed largely which determines the seed yield and yield attributes in Brassica which was said by Habibi *et al.* (2016). Now, in support of these, our present findings were also closely parallel to the reports of Mishra *et al*. (2009), according to their findings, the high estimates of heritability coupled with higher genetic advance were expressed as per cent of mean for seed yield plant^{-1}, number of silique plant^{-1} and number of secondary branches plant^{-1} indicated that heritability of these traits is mainly due to additive gene effects and phenotypic selection in brassica on the basis of these characters may be effective for yield improvement.

In continuation, magnitude of heritability in broad sense varied between 22.1% to 98.5%. The high estimates of heritability (h^2b) (>50%) were noted in case of days to maturity (98.5%), days to 50% flowering (98.2%), plant height (96%), number of secondary branches (96%), number of silique on main raceme (96%), 1000 seed weight (95%), number of primary branches (91%), length of main raceme (85%), seed yield plant^{-1} (76%), number of seeds silique^{-1} (64%). The lowest estimates of heritability (h^2b) (less than 50%) observed in days to emergence (22%) and length of silique (12%).Akkenapally and Chetaria (2022) reported high heritability for number of secondary branches plant^{-1}, plant height, 1000 seed weight, and number of silique on main raceme, number of silique plant^{-1} and length of main raceme. Other researcher like Singh *et al.* (2022), also reported high heritability for silique plant^{-1}, 1000 seed weight and seed yield plant^{-1}, silique plant^{-1} and seed yield plant^{-1}. They detected high heritability for seed yield plant^{-1} and days to 50% flowering. The genetic advance in per cent over mean ranged from (2.79%) length of silique to (46.31%) seed yield plant^{-1}. The very high estimates of genetic advance (>15%) were recorded for seed yield plant^{-1} (46.31%), 1000 seed weight (45.94%), number of silique on main raceme (43.31%), number of secondary branches (42.19%), number of primary branches (33.10%), plant height (26.42%). Lowest estimate of genetic advance was recorded in length of silique (2.79%).

Table 1. Analysis of variance (ANOVA) of genotypes for 12 characters of Indian mustard (*Brassica juncea* L.)

S.no.	Characters	Mean sum of squares			CV (%)
		Treatment (df=24)	Replication (df=2)	Error (df=48)	
1.	Days to emergence	1.47*	2.57*	0.79	11.63
2.	Days to 50 % flowering	162.9**	0.16	0.96	1.62
3.	Plant height (cm)	992.3**	49.4*	10.5	2.33
4.	No. of primary branches plant^{-1}	2.12**	0.09	0.06	4.96
5.	No. of secondary branches plant^{-1}	21.52**	0.43	0.28	4.22
6.	Length of main raceme	138.8**	4.87	7.57	4.54
7.	No. of silique on main raceme	99.42**	0.32	1.19	4.08
8.	Length of silique	0.37	0.38	0.26	10.48
9.	No. of seeds silique^{-1}	2.5**	0.86	0.38	5.22
10.	Days to maturity	279.1**	0.69	1.42	0.91
11.	1000 seed weight	1.37**	0.02	0.021	4.97
12.	Seed yield plant^{-1}	5.32**	1.17	0.48	14.09

df =Degrees of freedom, *=significant at 5% probability level, CV= Coefficient of Variation

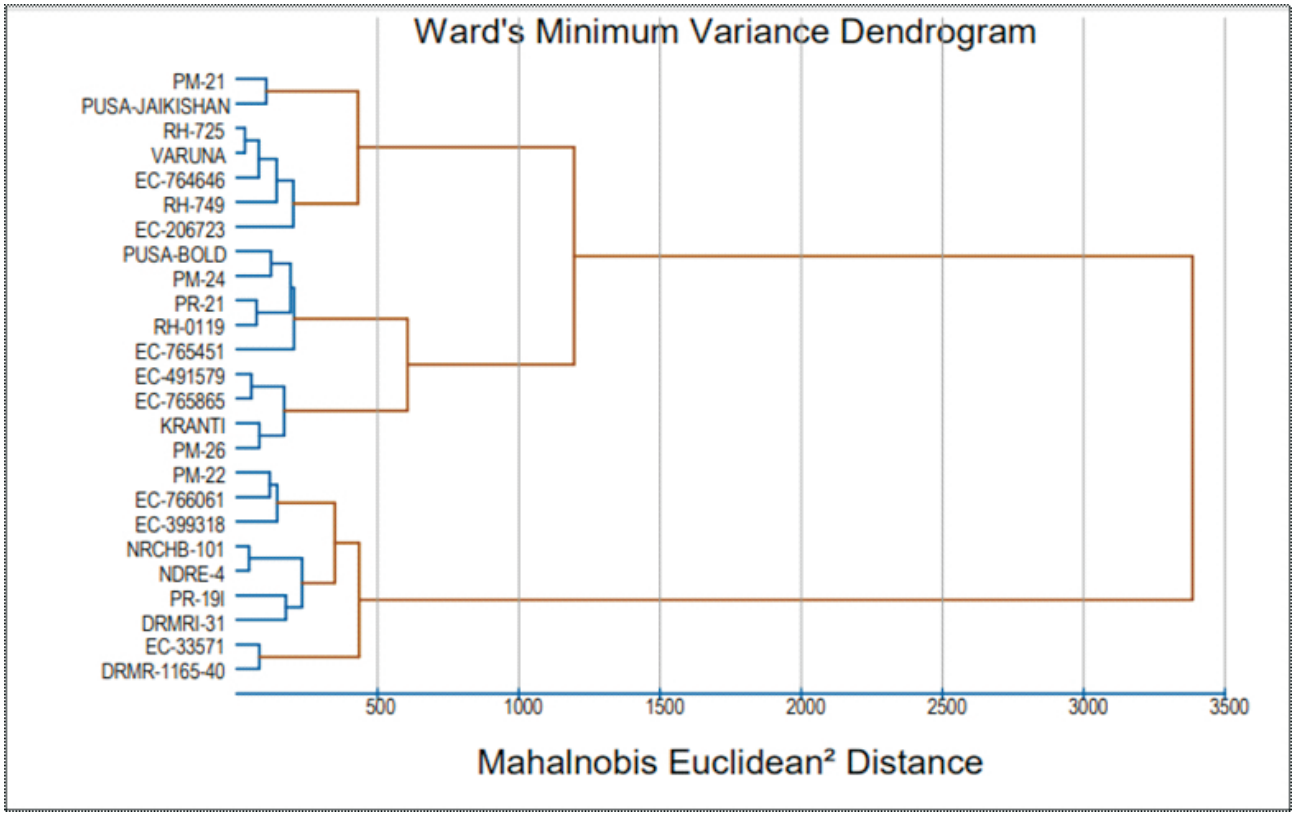

Figure 1. D^2 statistics of 25 genotypes of Indian mustard performed as per the method given by Mahalanobis (1936)

Table 2. Estimates of mean, range, variance components, coefficients of variability, heritability and genetic advance as per cent of mean for 12characteristics of Indian mustard (*Brassica juncea* L.)

Sr. no.	Characters	Mean	Range		Ve	Vg	Vp	ECV(%)	GCV(%)	PCV(%)	C.V.	SE±	h^2	GAM5%	GA(5%)
			Min	Max											
1.	Days to emergence(no.)	7.66	6.33	8.66	0.76	0.22	1.02	11.64	6.19	13.18	11.63	0.51	22.1	5.99	0.46
2.	Days to 50% flowering(no.)	60.56	53.33	72.00	0.96	54.00	54.90	1.62	12.13	12.24	1.62	0.56	98.2	24.77	15.00
3.	Plant height(cm)	138.79	103.36	172.26	10.51	327.20	337.70	2.33	13.03	13.24	2.33	1.87	96.9	26.42	36.68
4.	No. of primary branches	4.94	3.55	7.37	0.06	0.68	0.74	4.96	16.76	17.48	4.96	0.14	91.9	33.10	1.63
5.	No. of secondary branches	12.73	6.39	18.03	0.28	7.07	7.36	4.22	20.89	21.32	4.22	0.31	96.1	42.19	5.37
6.	Length of main raceme	60.57	46.30	73.70	7.57	43.70	51.31	4.54	10.91	11.82	4.54	1.58	85.2	20.76	12.57
7.	No. of silique on main raceme	26.73	14.33	40.60	1.19	32.74	33.93	4.08	21.40	21.79	4.08	0.63	96.5	43.31	11.57
8.	Length of silique (cm)	4.91	4.06	5.43	0.26	0.03	0.30	10.48	3.89	11.18	10.48	0.29	12.1	2.79	0.57
9.	No. of seeds silique^{-1}	11.92	10.18	13.46	0.38	0.70	1.09	5.23	7.06	8.78	5.22	0.36	64.6	11.68	1.39
10.	Days to maturity	130.78	113.33	143.33	1.42	92.50	93.98	0.91	7.35	7.41	0.91	0.69	98.5	15.03	19.66
11.	1000 seed weight (g)	2.94	2.26	5.13	0.02	0.45	0.47	4.93	22.82	23.36	4.97	0.08	95.5	45.94	1.35
12.	Seed yield plant^{-1} (g)	4.95	2.86	7.43	0.48	1.61	2.10	14.09	25.65	29.27	14.09	0.40	76.8	46.31	2.29

Genetic divergence analysis

The study of genetic divergence among 25 genotypes of Indian mustard genotypes was performed by employing Non-hierarchical Euclidean cluster analysis (Table 4) for twelve characters. The 25 genotypes were grouped into seven different non-overlapping clusters as presented in Table 3. Cluster II and cluster III, having 5 genotypes, emerged with highest number of entries followed by cluster IV and cluster VI with 4 genotypes, cluster V with 3 genotypes. Cluster I and cluster VII contained 2 genotypes each. The estimates of intra and inter-cluster distances represented by D^2 values have been depicted in Table 4. The intra-cluster distances ranged from 124.38 (cluster I) to 301.73 (cluster VI). The highest intra-cluster distance was found for cluster VI (301.732**) followed by cluster III (295.338),V cluster (264.768), cluster II (228.573), cluster IV (202.152), cluster VII (164.183). The minimum estimate for the inter-cluster distance was recorded on cluster I (124.383*). The maximum inter-cluster distance (>1000) was observed between cluster IV and cluster VII (1713.25), followed by cluster IV and cluster V (1594.54), cluster IV and VI (1219.96), cluster III and cluster VII (1056.20) and cluster III and cluster V (1052.96). The average inter-cluster distances (<1000) observed between cluster II and cluster V (904.57) followed by cluster II and cluster VII (878.832) cluster III and cluster VI (841.61), cluster II and cluster IV (757.04), cluster I and cluster III (518.52) and so on.

The minimum estimate for inter- cluster distance was recorded between cluster V and cluster VI (405.11) and cluster I and cluster II (446.53). The intra cluster groups means for 12 characters, given in Table 5 revealed marked differences between the clusters in respect of cluster means for different characters. The 2 genotypes of cluster I showed highest cluster mean for length of main raceme (54.31) and lowest cluster mean for days to emergence (8.500) and length of main raceme (54.31).The 5 genotypes of cluster II showed highest cluster mean for number of seeds silique^{-1} (12.25) and the lowest cluster mean observed in number of secondary branches plant^{-1} (9.123) and number of silique on main raceme (24.76). Cluster III having 5 genotypes were responsible for highest cluster mean for days to 50% flowering (67.86) and number of primary branches plant^{-1} (5.819). The 4 genotypes of cluster IV showed highest cluster mean for days to maturity (140.50) and showed lowest cluster mean for plant height (120.10). The 3 genotypes of cluster V showed highest cluster mean for plant height (163.53), number of secondary branches plant^{-1} (16.05), and length of silique (5.210). The lowest cluster mean observed in days to maturity (116.77), 1000 seed weight (2.422) and seed yield plant^{-1} (4.297). Cluster VI having 4 genotypes were responsible for highest cluster for length of main raceme (60.61) and number of silique on main raceme (33.30). 2 genotypes of cluster VII showed highest cluster mean for 1000 seed weight and seed yield plant^{-1} and the lowest cluster mean showed for days to emergence (7.000), days to 50% flowering (54.33) and number of seeds silique^{-1} (11.45).

According to Li *et al.* (2023), positive effect of plant architecture on seed yield derived from the high plant height, long-branch length, low relative branch height, and small branch angle. The data regarding per cent contributions of twelve characters have been presented in Table 6. The character days to maturity contributed highest to the total divergence (35.67 %) followed by days to 50 % flowering (19.33 %) and 1000 seed weight (15.67 %), whereas days to emergence, length of silique, number of seeds silique^{-1} and seed yield plant^{-1} showed very low contribution (0.00 %) followed by length of main raceme (0.67%). According to Ratnesh *et al.* (2013), the maximum character contribution towards divergence was observed for 1000 seed weight followed by biological yield plant^{-1} and oil content in timely sown. Under late sown condition maximum character contribution towards divergence was observed for biological yield plant^{-1} followed by oil content and length of main raceme. However, plant height, 1000 seed weight and harvest index showed moderate character contribution in their findings. Neelam *et al.* (2014), also found that phenotypic coefficient of variation (PCV) was higher than the corresponding genotypic coefficient of variation (GCV) for all the observed characters in *Brassica juncea* and thus suggested such variation will help to measure the range of genetic variability present in the particular character.

Table 3. Cluster classification of 25 genotypes of Indian mustard

Clusters	Genotypes
Cluster no. I (2)	PM-21, PUSA-JAIKISHAN
Cluster no. II (5)	RH-725, VARUNA, EC-764646, RH-749, EC-206723
Cluster no. III (5)	PUSA-BOLD, PM-24, PR-21, RH-0119, EC-765451
Cluster no. IV (4)	EC-491579, EC765865, KRANTI, PM-26
Cluster no. V (3)	PM-22, EC-766061, EC-399318
Cluster no. VI (4)	NRCHB-101, NDRE-4, PR-19, DRMRIJ-31
Cluster no. VII (2)	EC-33571, DRMR-1165-40

Table 4. Euclidean^2 distances between 25 genotypes of Indian mustard

	1.Cluster	2.Cluster	3.Cluster	4.cluster	5.Cluster	6.Cluster	7.Cluster
1.Cluster	124.383*	446.535	518.522	493.193	743.999	515.646	993.417
2.Cluster		228.573	573.217	757.049	904.574	636.777	878.832
3.Cluster			295.338	466.603	1052.968	841.615	1056.203
4.Cluster				202.152	1594.549	1219.96	1713.251**
5.Cluster					264.768	405.117*	464.404
6.Cluster						301.732**	478.712
7.Cluster							164.183

Bold figures represent intra-cluster distance. Minimum value*. Maximum value**

Table 5. Cluster means of 25 genotypes for various parameters of Indian mustard by Euclidian's method

	Day to emergence (no.)	Days to 50% flowering (no.)	Plant height (cm)	No. of primary branches	No. of secondary branches	Length of main raceme	No. of silique on main raceme	Length of silique (cm)	No. of seeds silique^{-1}	Days to maturity	1000 seed weight (g)	Seed yield plant^{-1} (g)
1. Cluster	8.500**	59.167	121.615	4.463*	15.270	54.317*	24.967	4.507	11.958	133.333	2.583	4.500
2. Cluster	7.600	55.333	139.496	4.520	9.123*	58.845	24.763*	4.933	12.252**	132.600	2.713	4.410
3. Cluster	8.200	67.867**	145.763	5.819**	13.307	62.115	28.016	4.995	11.783	139.467	3.220	5.147
4. Cluster	7.833	70.917	120.106*	4.933	12.752	61.333	19.263	4.432*	12.082	140.500**	2.617	5.159
5. Cluster	7.111	54.556	163.531**	5.108	16.058**	61.498	29.592	5.210**	12.078	116.778*	2.422*	4.297*
6. Cluster	7.250	55.917	132.732	4.521	12.523	60.617**	33.305**	5.167	11.628	122.750	2.942	5.500
7. Cluster	7.000*	54.333*	149.192	4.933	13.167	64.350	27.708	5.127	11.450*	119.667	4.633**	5.750**

Table 6. Per cent contribution of characters towards divergence in Indian mustard

Characters	Contribution %
1 Days to emergence (nos.)	0%
2 Days to 50 % Flowering (nos.)	19.33 %
3 Plant Height (cm)	11.33 %
4 Number of Primary branches plant^{-1} (nos.)	2.67 %
5 Number of Secondary Branches plant^{-1} (nos.)	7.33 %
6 Length of main raceme (cm)	0.67 %
7 Number of Silique on main raceme(nos.)	7.33 %
8 Length of Silique (cm)	0%
9 Number of seeds silique^{-1} (no.)	0%
10 Days to maturity (nos.)	35.67 %
11 1000 seed weight (g)	15.67 %
12 Seed yield plant^{-1} (g)	0%

Based on the findings, it is possible to conclude that there was a broad range of variation seen for all characters among genotypes, indicating that there is substantial possibility for improving Indian mustard cultivars by even selection. The variability component suggested that phenotypic selection could be a reliable breeding approach for improving mustard genotypes. Genetic characteristics in conjunction with correlation studies revealed that superior genotypes should be selected. Out of twenty-five genotypes, PM-26, NDRE-4, KRANTI, and PM-21 were discovered to have the highest yielding genotypes. As a result, these genotypes may be suggested for large-scale cultivation among farmers and employed as donors in breeding programs.

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