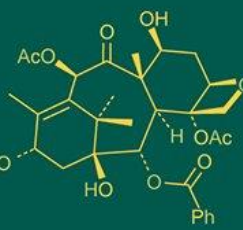
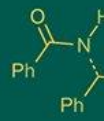


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Genetic variability and path coefficient analysis in Indian mustard (*Brassica Juncea* L.) for seed yield and its component traits

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Abstract

The present investigation entitled “Genetic variability and path coefficient analysis in Indian mustard (*Brassica Juncea* L.) For seed yield and its component traits” was carried out at research farm of faculty of agricultural sciences and allied industries, Rama University, Kanpur-209217 during Rabi season of 205-26 on 40 elite germplasm lines, which were evaluated in a Randomized Complete Block Design with three replications. All recommended agronomic practices have been followed to raise the good crop. High estimates (more than 20%) of phenotypic and genotypic coefficients of variation were recorded for grain yield per plant and biological yield per plant. Moderate estimates (10-20%) were observed for siliqua length, harvest index, number of secondary branches per plant. These results suggest considerable scope for genetic improvement through selection based on these traits. High heritability estimates (> 60%) were observed for biological yield per plant, grain yield per plant, number of siliquae on main shoot, harvest index, length of main shoot, number of secondary branches per plant, siliqua length (cm), and days to 50% flowering. The high heritability of these traits indicates that they are predominantly governed by genetic factors with minimal environmental influence. Furthermore, high heritability coupled with high genetic advance was recorded for number of secondary branches per plant, length of main shoot, number of siliquae on main shoot, siliqua length (cm), harvest index, biological yield per plant, and grain yield per plant, suggesting the predominance of additive gene action and the effectiveness of direct selection for improvement. Correlation analysis revealed that genotypic correlation coefficients were generally higher than phenotypic correlations, indicating strong inherent associations among traits. Grain yield per plant exhibited significant and positive correlations with plant height, number of secondary branches per plant, length of main shoot, number of siliquae on main shoot, siliqua length, and number of seeds per siliqua, harvest index, and biological yield per plant at both genotypic and phenotypic levels. Path coefficient analysis demonstrated that biological yield per plant and harvest index exerted strong positive direct effects on grain yield. Biological yield contributed indirectly through traits such as days to 50% flowering, days to maturity, plant height, number of secondary branches per plant, length of main shoot, siliqua length, number of seeds per siliqua, and test weight. Therefore, improvement in grain yield can be effectively achieved by selecting for biological yield per plant, days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, length of main shoot, siliqua length, number of seeds per siliqua, and test weight. Therefore, crosses involving genotypes such as DRMRHT-18-141, Kranti, RH-2187, PDZ-1, and IJ-19R-5004 are recommended. Such hybridization is expected to generate greater genetic variability in segregating generations, facilitating the selection of superior plant types for yield and its contributing traits.

Keywords: *Brassica Juncea* L., seed yield, genetic variability, GCV, PCV, path analysis, correlation

Introduction

Rapeseed-mustard is the third most important oilseed crop in the world after soybean and oil palm, and in India it ranks second after soybean. Among the cultivated Brassica species, Indian mustard (*Brassica juncea* L.) occupies a dominant position due to its wide adaptability, drought tolerance, and higher productivity under semi-arid conditions. The crop is believed to have originated in the Middle East through natural hybridization between B.

Nigra and *B. campestris* (Olson, 1960; Mizushima and Tsunoda, 1967) [2]. Later, it spread to different parts of Asia, Europe, and Africa, leading to the development of diverse geographical races (Hemingway, 1976; Prakash and Hinata, 1980) [3, 4]. The interspecific relationships among *Brassica* species are well explained by the “U triangle” proposed by Nagaharu. Indian mustard is an important Rabi oilseed crop grown extensively in Rajasthan, Uttar Pradesh, Haryana, Madhya Pradesh, and Gujarat. During 2020-21, it occupied about 6.70 million hectares with a production of 10.21 million tonnes in India (Anonymous, 2021-22) [5]. Despite its economic importance, the productivity of mustard in India remains comparatively low due to biotic and abiotic stresses, lack of high-yielding varieties, poor agronomic practices, and quality concerns related to erucic acid and glucosinolates (Sharma, 2018) [7]. Since India imports a major share of its edible oil requirement, improving the productivity and quality of Indian mustard has become essential. Mustard seeds contain about 36-40% oil and 38-41% protein, making the crop economically important for edible oil extraction and animal feed purposes (Tomar, 2019) [8]. The crop performs well under cool and dry climatic conditions and is suitable for rainfed farming because of its low water requirement (Chauhan, 2011) [9]. However, under late-sown conditions, yield reduction is common; therefore, identification of superior genotypes with better adaptability and yield potential is necessary. The success of any breeding programme depends upon the availability of sufficient genetic variability in the germplasm. Parameters such as genotypic coefficient of variation, phenotypic coefficient of variation, heritability, and genetic advance help in assessing the extent of variability and effectiveness of selection. Correlation analysis provides information regarding the association among yield and its component traits, while path coefficient analysis, proposed by Sewall Wright, helps in partitioning direct and indirect effects of different characters on yield. In addition, Mahalanobis D^2 statistics (Mahalanobis, 1936) [10] is widely used to assess genetic divergence and identify suitable parents for hybridization (Nair and Mukherjee, 1960; Maurya and Singh, 1977) [11, 12, 24]. Keeping these facts in view, the present investigation entitled “Genetic variability and divergence studies for seed yield and its component traits under late sown Indian mustard” was undertaken to evaluate genetic variability, character association, heritability, and genetic divergence among mustard genotypes for the development of efficient selection strategies aimed at improving seed yield and related traits.

Materials and Methods

The present investigation titled “Genetic variability and path coefficient analysis in Indian mustard (*Brassica Juncea* L.) for seed yield and its component traits” was carried out at research farm of FASAI, Rama University, Kanpur-209217. During the Rabi 2025-26. The experimental material comprised 40 germplasm lines, which were evaluated in a Randomized Complete Block Design (RCBD) with three replications. Each genotype was sown in five rows of 5.0 meters length, maintaining a spacing of 45 cm between rows and 15 cm between plants. Proper thinning was carried out to ensure uniform plant-to-plant spacing. All the recommended agronomic practices were adopted to raise a healthy and uniform crop.

Experimental findings

Analysis of variance for fourteen-character Indian mustard genotypes

The analysis of variance (ANOVA) revealed the presence of highly significant differences among the 40 Indian mustard genotypes for all the characters studied, indicating the existence of substantial genetic variability in the experimental material (Table 1). The mean sum of squares due to treatments was highly significant for days to 50% flowering (40.04), days to maturity (9.54), plant height (401.53), primary branches per plant (2.00), secondary branches per plant (16.78), main shoot length (293.54), number of siliques on main shoot (152.69), silique length (2.58), seeds per silique (5.37), test weight (1.83), oil content (9.87), harvest index (53.66), biological yield per plant (1326.93), and seed yield per plant (108.13). The comparatively lower error mean squares for most of the traits indicated good experimental precision and reliability of the observations recorded during the trial. The significant variation observed among genotypes for yield and its contributing traits suggests ample scope for effective selection and genetic improvement in Indian mustard breeding programmes.

Mean performance of Genotypes

The mean performance of 40 Indian mustard germplasm lines for fourteen quantitative traits revealed considerable variability among the genotypes, indicating good scope for selection and crop improvement (Table 2). Days to 50% flowering ranged from 51.33 days (IMG-2) to 68.00 days (IMG-10) with a general mean of 57.27 days, while days to maturity varied from 139.33 days to 147.33 days with an average of 144.19 days. Plant height ranged between 162.80 cm (IMG-3) and 208.33 cm (IMG-38), showing substantial diversity for growth habit. Among yield contributing traits, primary branches per plant ranged from 5.13 to 8.40, whereas secondary branches per plant varied from 10.47 to 22.07, with IMG-26 recording the maximum value. Main shoot length varied from 51.00 cm to 96.73 cm, while number of siliques on main shoot ranged widely from 19.07 to 62.87. Silique length showed variation from 3.37 cm to 8.40 cm, and seeds per silique ranged from 12.40 to 16.83. Test weight varied between 4.20 g and 7.17 g, indicating noticeable differences in seed boldness among the genotypes. Oil content ranged from 36.20% to 43.57%, with IMG-33 exhibiting the highest oil percentage. Harvest index ranged from 18.30% to 38.86%, while biological yield per plant varied from 53.37 g to 148.97 g. Seed yield per plant, the most important economic trait, ranged from 13.42 g to 37.69 g, with IMG-39 and IMG-27 emerging as superior yielders. Overall, the wide range observed for most characters reflected the presence of sufficient genetic variability among the mustard germplasm lines, which can be effectively utilized in future breeding programmes.

Genetic variability parameters estimate for fourteen characters of Indian mustard

The estimates of variability, heritability, and genetic advance revealed the presence of substantial genetic variability among the mustard genotypes for most of the traits studied. In all fourteen characters, the phenotypic coefficient of variation (PCV) was slightly higher than the genotypic coefficient of variation (GCV), indicating minor

environmental influence on trait expression. High PCV and GCV values were observed for grain yield per plant (25.11 and 24.48, respectively) and biological yield per plant (22.36 and 22.13), suggesting the existence of wide genetic variability for these economically important traits (Table 3.). Moderate estimates of both PCV and GCV were recorded for siliqua length, harvest index, number of secondary branches per plant, number of siliquae on main shoot, test weight, primary branches per plant, and main shoot length, whereas low GCV values were observed for days to maturity (1.14), oil content (4.29%), plant height (5.78), and days to 50% flowering (6.15). Heritability estimates ranged from moderate to high, with the highest values recorded for biological yield per plant (97.94%), grain yield per plant (94.97%), number of siliquae on main shoot (89.12%), and harvest index (87.84%), indicating strong genetic control over these traits. High heritability coupled with high genetic advance as percent of mean was observed for grain yield per plant (49.14%), biological yield per plant (45.12%), siliqua length (33.73%), harvest index (30.90%), and number of siliquae on main shoot (29.35%), suggesting the predominance of additive gene action and the possibility of effective selection for improvement of these traits. In contrast, low genetic advance was observed for days to maturity (1.88%) and oil content (7.13%), indicating comparatively limited scope for improvement through direct selection.

Corelation coefficient analysis estimates

Correlation analysis at both genotypic and phenotypic levels revealed that grain yield per plant had significant positive associations with several important yield contributing traits, indicating their direct role in yield improvement of Indian mustard (Table 4). At the genotypic level, grain yield per plant showed the highest positive correlation with biological yield per plant (0.751), followed by number of seeds per siliqua (0.559), harvest index (0.527), plant height (0.509), number of secondary branches per plant (0.458), and length of main shoot (0.417). Similar trends were observed at the phenotypic level where biological yield per plant (0.730), harvest index (0.498), number of seeds per siliqua (0.487), number of secondary branches per plant (0.409), plant height (0.399), and length of main shoot (0.379) maintained strong positive correlations with grain yield. Siliqua length also exhibited positive associations with grain yield at both genotypic (0.356) and phenotypic (0.319) levels, while number of siliquae on main shoot showed moderate positive correlations of 0.300 and 0.267, respectively (Table 5). Plant height was positively associated with length of main shoot (0.617 genotypic and 0.520 phenotypic), number of siliquae on main shoot (0.501 and 0.402), and biological yield per

plant (0.459 and 0.383), indicating the importance of vigorous plant growth in enhancing productivity. Number of secondary branches per plant also showed strong positive associations with biological yield per plant (0.451 and 0.416), siliqua length (0.407 and 0.342), and seeds per siliqua (0.366 and 0.321). In contrast, oil content exhibited negative correlations with grain yield (-0.132 genotypic and -0.111 phenotypic), siliqua length (-0.394 and -0.292), and test weight (-0.337 and -0.249), suggesting a possible trade-off between oil percentage and yield related traits. Overall, the study indicated that biological yield per plant, seeds per siliqua, harvest index, plant height, and number of secondary branches, main shoot length, and siliqua length are the most important characters for effective selection aimed at improving seed yield in Indian mustard breeding programmes.

Path Coefficient Analysis estimates

The genotypic path coefficient analysis revealed that biological yield per plant exerted the highest positive direct effect on grain yield per plant (0.8078), followed by harvest index (0.6811), plant height (0.1123), oil content (0.0977), number of secondary branches per plant (0.0690), test weight (0.0602), and siliqua length (0.0390), indicating that these traits contributed directly towards yield improvement in Indian mustard. In contrast, negative direct effects were observed for days to maturity (-0.0580), length of main shoot (-0.0431), days to 50% flowering (-0.0366), number of siliquae on main shoot (-0.0343), number of seeds per siliqua (-0.0237), and number of primary branches per plant (-0.0212). Among the indirect effects, biological yield per plant contributed positively towards grain yield through number of seeds per siliqua (0.4491), plant height (0.3704), number of secondary branches per plant (0.3639), test weight (0.2840), days to 50% flowering (0.2679), and siliqua length (0.2357). Plant height also exhibited considerable positive indirect effects through days to maturity (0.0786), days to 50% flowering (0.0699), length of main shoot (0.0693), and biological yield per plant (0.0515). Similarly, days to maturity showed positive indirect effects through number of secondary branches per plant (0.0199) and number of seeds per siliqua (0.0074), while negative indirect influences were mainly observed through plant height (-0.0406) and days to 50% flowering (-0.0355). Overall, the path analysis indicated that biological yield per plant, harvest index, plant height, number of secondary branches per plant, test weight, and siliqua length are the most important traits contributing directly and indirectly towards higher seed yield and therefore may be effectively utilized as selection criteria in Indian mustard improvement programmes.

Table 1: Analysis of variance for fourteen characters in Indian mustard (*Brassica juncea* L.)

Source of variation	Df	DFF	DTM	PHT (cm)	PBP	SBP	MSL (cm)	NSMS
Replication	2	5.83	2.01	63.61	0.05	0.65	27.75	7.31
Treatment	39	40.04**	9.54**	401.53**	2.00**	16.78**	293.54**	152.69**
Error	78	2.85	1.47	47.42	0.25	0.85	14.85	5.97
Total	119	15.09	4.12	163.74	0.82	6.07	106.41	54.08
Source of variation	Df	SL (cm)	SPS	TW (g)	OC (%)	H. I. (%)	BYPP (g/plant)	SYPP (g/plant)
Replication	2	0.04	0	0.27	12.26	7.32	17.09	1.58
Treatment	39	2.58**	5.37**	1.83**	9.87**	53.66**	1326.93**	108.13**
Error	78	0.17	0.44	0.18	1.49	2.37	9.23	1.87
Total	119	0.96	2.05	0.72	4.42	19.15	441.53	36.68

Table 2: Mean performance of 40 genotypes for 14 characters in Indian mustard (*Brassica juncea* L.)

Genetic variability	DFE	DTM	PHT (cm)	PBP	SBP	MSL (cm)	NSMS	SL (cm)	SPS	TW (g)	OC (%)	H. I. (%)	BYPP	SYPP
Mean	57.27	144.19	187.97	6.64	15.14	79.86	46.34	4.95	14.4	5.64	38.98	25.84	94.7	24.32
Min	51.33	139.33	162.8	5.13	10.47	51	19.07	3.37	12.4	4.2	36.2	18.3	53.37	13.42
Max	68	147.33	208.33	8.4	22.07	96.73	62.87	8.4	16.83	7.17	43.57	38.86	148.97	37.69
SE(d) ±	1.38	0.99	5.62	0.41	0.75	3.15	2	0.34	0.54	0.35	1	1.21	2.55	1.11
C.D. at 5%	2.75	1.98	11.22	0.81	1.5	6.28	3.98	0.68	1.08	0.69	1.99	2.41	5.08	2.22
C.V. (%)	2.95	0.84	3.66	7.46	6.1	4.83	5.27	8.44	4.6	7.56	3.14	5.73	3.29	5.6

Table 3: Range, coefficient of variation, heritability, genetic advance and genetic advance mean for twelve characters in indian mustard (*brassica juncea* l.)

Characters	Mean	Range	Heritability (%)	GA	GA% mean	GCV (%)	PCV (%)
Days to 50% flowering	57.27	51.33- 68.00	81.30	6.54	11.42	6.15	6.82
Days to maturity	144.19	139.33-147.33	64.66	2.72	1.88	1.14	1.41
Plant height (cm)	187.97	162.80-208.33	71.34	18.90	10.06	5.78	6.84
Primary branches/plant	6.64	5.13-8.40	70.37	1.32	19.88	11.50	13.71
Secondary branches/plant	15.14	10.47-22.07	86.16	4.41	29.11	15.22	16.40
Length of main shoot (cm)	79.86	51.00-96.73	86.22	18.44	23.08	12.07	13.00
No. siliquae on main shoot	46.34	19.07-62.87	89.12	13.60	29.35	15.09	15.98
Silique length (cm)	4.95	3.37-8.40	82.09	1.67	33.73	18.07	19.95
No. of seeds/ siliqua	14.40	12.40-16.83	78.92	2.35	16.29	8.90	10.02
Test weight (g)	5.64	4.20-7.17	75.13	1.32	23.45	13.13	15.15
Oil content (%)	38.98	36.20-43.57	65.15	2.78	7.13	4.29	5.31
Harvest index (%)	25.84	18.30-38.86	87.84	7.98	30.90	16.00	17.08
Biological yield/plant (g)	94.70	53.37-148.97	97.94	42.73	45.12	22.13	22.36
Grain yield/plant (g)	24.32	13.42-37.69	94.97	11.95	49.14	24.48	25.11

Table 4: Genotypic correlation coefficient among fourteen characters in Indian mustard (*Brassica juncea* L.)

Characters	DFE	DTMy	PHT(cm)	PB	SB	LM (cm)	SMS	SL (cm)	SPS	TW (g)	OC (%)	HI (%)	BYPP (g)	GYPP (g)
DFE	1.000	0.612**	0.622**	0.184*	0.091	0.140	0.132	0.232*	-0.153	0.321**	-0.182*	-0.024	0.332**	0.255**
DTM		1.000	0.700**	0.222*	-0.343**	0.231*	0.092	0.154	-0.128	0.378**	0.034	0.127	0.185*	0.228*
PHT(cm)			1.000	0.066	0.065	0.617**	0.501**	0.324**	-0.010	0.306**	-0.187*	0.172	0.459**	0.509**
PB				1.000	0.230*	-0.113	-0.064	-0.035	0.226*	-0.154	0.483**	-0.212*	0.244**	0.073
SB					1.000	-0.017	0.054	0.407**	0.366**	-0.193*	-0.208*	0.047	0.451**	0.458**
LMS (cm)						1.000	0.610**	0.176	0.164	0.363**	-0.129	0.298**	0.265**	0.417**
SMS							1.000	0.025	0.042	-0.057	0.084	0.302**	0.122	0.300**
SL (cm)								1.000	0.281**	0.369**	-0.394**	0.095	0.292**	0.356**
SPS									1.000	0.118	0.102	0.120	0.556**	0.559**
TW (g)										1.000	-0.337**	-0.064	0.352**	0.257**
OC (%)											1.000	-0.175	-0.043	-0.132
HI (%)												1.000	-0.163	0.527**
BYPP (g)													1.000	0.751**
GYPP (g)														1.000

*, ** significant at 5% and 1% level, respectively

Table 5: Phenotypic correlation coefficient among fourteen characters in Indian mustard (*Brassica juncea* L.)

Characters	DFE	DTMy	PHT (cm)	PB	SB	LMS (cm)	SMS	Sq. L (cm)	SPS	TW (g)	OC (%)	HI (%)	BYPP (g)	GYPP (g)
DFE	1.000	0.479**	0.509**	0.097	0.103	0.146	0.138	0.220*	-0.158	0.276**	-0.150	-0.015	0.307**	0.220*
DTM		1.000	0.474**	0.145	-0.249**	0.196*	0.076	0.176	-0.076	0.271**	0.076	0.092	0.152	0.173
PHT (cm)			1.000	0.067	0.114	0.520**	0.402**	0.227*	-0.075	0.224*	-0.135	0.110	0.383**	0.399**
PB				1.000	0.221*	-0.106	-0.082	-0.085	0.156	-0.106	0.315**	-0.170	0.200*	0.070
SB					1.000	0.000	0.025	0.342**	0.321**	-0.143	-0.166	0.038	0.416**	0.409**
LMS (cm)						1.000	0.559**	0.134	0.125	0.303**	-0.095	0.254**	0.244**	0.379**
SMS							1.000	0.022	0.042	-0.069	0.044	0.254**	0.112	0.267**
SL (cm)								1.000	0.261**	0.306**	-0.292**	0.077	0.262**	0.319**
SPS									1.000	0.072	0.106	0.110	0.481**	0.487**
TW (g)										1.000	-0.249**	-0.036	0.315**	0.213*
OC (%)											1.000	-0.110	-0.029	-0.111
HI (%)												1.000	-0.157	0.498**
BYPP (g)													1.000	0.730**
GYPP (g)														1.000

Traits detail name:

Days to 50% flowering (DFF)	Number of Primary branches/plant (PB)	Length of main shoot (cm) (LMS)	Siliqua length (cm) (SL)	Test weight (g) (TW)	Plant height (cm) (PHT)	Biological yield/plant (g) (BYPP)
Days to maturity (DTM)	Number of Secondary branches/plant (SB)	Number of siliquae on main shoot (SMS)	No. of seeds/siliqua (SPS)	Oil content (%) (OC)	Harvest Index (%) (HI)	Grain yield/ Plant (g) (GYPP)

Table 6: Genotypic path coefficient analysis for fourteen characters in Indian mustard (*Brassica juncea* L.)

Characters	DFF	DTM	PHT (cm)	PB	SB	LMS (cm)	SMS	SL (cm)	SPS	TW (g)	OC (%)	HI (%)	BYPP (g)	GYPP (g)
DFF	-0.0366	-0.0355	0.0699	-0.0039	0.0063	-0.0061	-0.0045	0.0090	0.0036	0.0193	-0.0178	-0.0164	0.2679	0.255**
DTM	-0.0224	-0.0580	0.0786	-0.0047	-0.0236	-0.0100	-0.0032	0.0060	0.0030	0.0228	0.0033	0.0862	0.1496	0.228*
PHT (cm)	-0.0228	-0.0406	0.1123	-0.0014	0.0045	-0.0266	-0.0172	0.0126	0.0002	0.0184	-0.0183	0.1168	0.3704	0.509**
PB	-0.0067	-0.0129	0.0074	-0.0212	0.0159	0.0049	0.0022	-0.0014	-0.0054	-0.0093	0.0472	-0.1446	0.1970	0.073
SB	-0.0033	0.0199	0.0073	-0.0049	0.0690	0.0007	-0.0019	0.0159	-0.0087	-0.0116	-0.0203	0.0320	0.3639	0.458**
LMS (cm)	-0.0051	-0.0134	0.0693	0.0024	-0.0012	-0.0431	-0.0209	0.0069	-0.0039	0.0218	-0.0126	0.2031	0.2137	0.417**
SMS	-0.048	-0.0053	0.0562	0.0014	0.0037	-0.0263	-0.0343	0.0010	-0.0010	-0.0035	0.0082	0.2058	0.0990	0.300**
SL (cm)	-0.0085	-0.0089	0.0364	0.0007	0.0281	-0.0076	-0.0008	0.0390	-0.0067	0.0223	-0.0385	0.0649	0.2357	0.356**
SPS	0.0056	0.0074	-0.0011	-0.0048	0.0253	-0.0070	-0.0014	0.0110	-0.0237	0.0071	0.0099	0.0818	0.4491	0.559**
TW (g)	-0.0117	-0.0219	0.0343	0.0033	-0.0133	-0.0156	0.0020	0.0144	-0.0028	0.0602	-0.0329	-0.0433	0.2840	0.257**
OC (%)	0.0067	-0.0020	-0.0210	-0.0102	-0.0144	0.0056	-0.0029	-0.0154	-0.0024	-0.0203	0.0977	-0.1189	-0.0346	-0.132
HI (%)	0.0009	-0.0073	0.0193	0.0045	0.0032	-0.0128	-0.0104	0.0037	-0.0029	-0.0038	-0.0171	0.6811	-0.1315	0.527**
BYPP (g)	-0.0121	-0.0107	0.0515	-0.0052	0.0311	-0.0114	-0.0042	0.0114	-0.0132	0.0212	-0.0042	-0.1108	0.8078	0.751**

Resi = 0.0251

*, ** significant at 5% and 1% level, respectively

Discussion:

The present investigation revealed the existence of considerable genetic variability among the Indian mustard genotypes for all fourteen characters studied, with variability estimates ranging from 1.83 to 1326.93, indicating ample scope for effective selection and crop improvement. The phenotypic coefficient of variation (PCV) was slightly higher than the genotypic coefficient of variation (GCV) for all traits, suggesting limited environmental influence on trait expression. High PCV and GCV values were observed for grain yield per plant and biological yield per plant, while moderate variability was recorded for siliqua length, harvest index, number of secondary branches per plant, number of siliquae on main shoot, test weight, and length of main shoot. Similar findings were reported by Chaurasiya *et al.*, (2019) [13], Tripathi *et al.*, (2019) [14], Gadi *et al.*, (2020) [15], Pradhan *et al.*, (2021) [16], Yadav *et al.*, (2021) [17], Mishra *et al.*, (2022) [18], and Sarkar *et al.*, (2023) [19]. High heritability coupled with high genetic advance was recorded for grain yield per plant, biological yield per plant, siliqua length, harvest index, number of siliquae on main shoot, and number of secondary branches per plant, indicating the predominance of additive gene action and effectiveness of direct selection. These findings are in agreement with Pal *et al.*, (2019), Rout *et al.*, (2019), Kumari *et al.*, (2020), Patel *et al.*, (2021) [23], Singh *et al.*, (2021) [21, 24], Nishad *et al.*, (2022) [25], and Kumar *et al.*, (2023) [22]. Correlation analysis showed that genotypic correlations were generally higher than phenotypic correlations, indicating strong inherent relationships among the traits. Grain yield per plant exhibited significant positive correlations with biological yield per plant, number of seeds per siliqua, harvest index, plant height, number of secondary branches per plant, length of main shoot, siliqua length, and number of siliquae on main shoot at both genotypic and phenotypic levels, suggesting that improvement in these characters would directly contribute towards higher yield. Similar observations were also reported by Swetha *et al.*, (2019) [26], Patel *et al.*, (2019) [20], and Kumar *et al.*, (2019) [27]. Path

coefficient analysis further revealed that biological yield per plant, harvest index, plant height, and number of secondary branches per plant exerted high positive direct effects on grain yield at both genotypic and phenotypic levels, indicating their major role in determining seed yield. Moreover, biological yield and harvest index also contributed indirectly through traits like number of seeds per siliqua, siliqua length, and main shoot length. Similar results were reported by Swetha *et al.*, (2019) [26] and Ray *et al.*, (2019) [28]. Overall, the study indicated that biological yield per plant, harvest index, plant height, number of secondary branches per plant, siliqua length, and number of seeds per siliqua are the most important selection criteria for improving seed yield in Indian mustard breeding programmes.

Conclusion

The analysis of variance confirmed the existence of considerable genetic variability among the studied genotypes, validating their suitability for further genetic analysis. High heritability coupled with high genetic advance for traits such as number of secondary branches per plant, length of main shoot, number of siliquae on main shoot, siliqua length (cm), harvest index, biological yield per plant, and grain yield per plant suggests that direct selection for these traits would be effective for crop improvement.

Correlation and path coefficient analyses further indicated that enhancement of grain yield could be achieved through improvement in days to 50% flowering, days to maturity, plant height, number of secondary branches per plant, length of main shoot, number of siliquae on main shoot, siliqua length (cm), seeds per siliqua, harvest index, and biological yield per plant.

Based on genetic divergence analysis, it is suggested that crosses among the genotypes DRMRHT-18-141, Kranti, RH-2187, PDZ-1, IJ-19R-5004 (Cluster I), and RGN-528, PBR-813-2, RH-1934 (Cluster VI) may prove effective in generating desirable segregants in subsequent generations.

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