



ISSN (E): 2277-7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2022; 11(11): 2401-2406
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www.thepharmajournal.com
Received: 19-08-2022
Accepted: 25-09-2022

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Genetic variability, correlation, path coefficient and cluster analysis in Indian mustard (*Brassica juncea* L.)

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Abstract

A field experiment was conducted at Genetics and Plant Breeding Research Farm of Kisan (P.G.) College, Simbhaoli, Hapur (UP), India during *Rabi* 2021-22 with 20 diverse genotypes of Indian mustard to assess the genetic variability, correlation, path coefficient and cluster analysis for yield and yield related traits. The genotypes were evaluated for thirteen quantitative characters *viz.*, days to 50% flowering, days to maturity, plant height (cm), number of primary branches plant⁻¹, number of secondary branches plant⁻¹, length of main raceme (cm), silique on main raceme (cm), seeds silique⁻¹, 1000-seed weight (g), biological yield plant⁻¹ (g), harvest index (%), oil content (%) and seed yield plant⁻¹ (g). The analysis of variance showed highly significant differences among the genotypes for all the characters. The highest estimates of the phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were observed for seed yield plant⁻¹, biological yield plant⁻¹, Secondary Branches Plant⁻¹ and Primary Branches Plant⁻¹. Seed yield plant⁻¹, Biological yield plant⁻¹ and harvest index showed high heritability coupled with high genetic advance as percent of mean indicating the influence of additive gene effects. Seed yield plant⁻¹ showed highly significant and positive association with biological yield plant⁻¹ followed by Length of main raceme, Silique on main Raceme, Secondary Branches Plant⁻¹, harvest index and plant height. Path analysis identified biological yield plant⁻¹ (both at genotypic and phenotypic level) followed by silique on main raceme (at genotypic level) and harvest index (at phenotypic level), as major direct contributors towards seed yield plant⁻¹. Secondary branches plant⁻¹ followed by length of main raceme, plant height, silique on main raceme, seeds silique⁻¹, days to maturity, 1000-seed weight, and primary branches plant⁻¹ showed maximum positive indirect effect on seed yield plant⁻¹ *via.*, biological yield plant⁻¹. The characters mentioned above should be given due consideration at the time of selection to develop stable high yielding genotypes in Indian mustard to sustain the production and productivity. Based on D² values, all the 20 genotypes were grouped in 5 clusters. Cluster II possessing maximum (8) genotypes followed by cluster III, IV, I and V. The maximum intra-cluster distance was found for cluster IV and minimum for cluster V. The highest inter-cluster distance was observed between cluster V and IV whereas lowest inter-cluster distance was observed between cluster II and III. The results clearly showed crossing between the entries belonging to cluster pairs having large inter-cluster distances and possessing high cluster means for one or other characters to be improved may be recommended for isolating desirable recombinants in the segregating generations in Indian Mustard.

Keywords: Indian mustard, correlation, path coefficient, genetic variability, and cluster analysis

Introduction

Indian mustard is the second most important oilseed crop of the world as well as India after groundnut. It is popularly known as rai, raya or laha. It belongs to the family *Cruciferae* (*Brassicaceae*) under the genus *Brassica*, and it is the major *rabi* oilseed crop of northern India. Indian mustard is an amphidiploid species with a chromosome number of 2n = 36. It has 38 to 42% oil and 24% protein. During the 2018-19 crop seasons, Indian mustard accounts for around 75-80 percent of the 6.23 million ha. During the *Rabi* season, in India about 7.40 million hectares of rapeseed-mustard are planted, yielding 9.77 million tons of seeds with an average productivity of 1.04 million tons per hectare. The magnitude of genetic variability present in a population is essential for effective genetic improvement. Correlation and path coefficient analysis provide a better understanding of the association of different characters with seed yield. Cluster analysis helps to understand the genetic relation between the genotypes and facilitate the selection of genetically diverse parents in hybridization programme. Hence, the present investigation was carried out to determine the genetic variability, heritability, genetic diversity, and direct and indirect effects of various characters on seed yield in Indian Mustard.

Materials and Methods

The present investigation was carried out at Research farm of Genetics and Plant Breeding, Kisan (P.G.) College, Simbhaoli, Hapur (UP), India during *Rabi* 2021-22. Twenty diverse genotypes of Indian mustard were taken for study obtained from Oilseed Section of Department of Genetics & Plant Breeding, SVPUA&T Campus, Modipuram (Meerut). These genotypes were grown in a Randomized Block Design using three replications each. Each plot consisted of single row of 3-meter length, spaced at 45 cm apart. The distance between plant to plant 15 cm was maintained by thinning. All the recommended cultural practices were adopted for raising a good crop. Data were recorded on five randomly selected plants from each plot for thirteen characters *viz.*, days to 50% flowering, days to maturity, plant height (cm), number of primary branches plant⁻¹, number of secondary branches plant⁻¹, length of main raceme (cm), silique on main raceme (cm), seeds silique⁻¹, 1000-seed weight (g), biological yield plant⁻¹ (g), harvest index (%), oil content (%) and seed yield plant⁻¹ (g), except days to 50% flowering and days to maturity where data were recorded on line basis. Data recorded on the above characters were subjected to estimation of Analysis of variance, correlation coefficient (Al-jibouri *et al.*, 1958) [2], Path-coefficient analysis (Dewey and Lu, 1959) [6] and genetic divergence (D²) (Mahalanobis, 1936) [13].

Results and Discussion

Analysis of variance and coefficient of variation

The analysis of variance for different characters is presented in Table 1 indicating significant differences among the genotypes for all the characters under study. The estimates of mean, range, genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for various characters studied are presented in Table 2. The PCV values were higher than GCV values for all the characters indicating the influence of environment on the expression of characters. High PCV and GCV values were observed for seed yield plant⁻¹ (29.65) and (29.25), Biological yield plant⁻¹ (24.30) and (24.10), Secondary Branches Plant⁻¹(20.18) and (18.57), Primary Branches Plant⁻¹(18.13) and (16.23) indicating better opportunity for improvement in these traits through selection. However, moderate PCV and GCV was observed for Silique on main Raceme (14.95) and (13.99), Harvest Index (14.79) and (13.95), Length of main raceme (13.17) and (12.64), 1000 Seed Weight (11.57) and (10.97). The magnitude of PCV ranged from 1.52 for Oil Content to 29.65 for seed yield plant⁻¹. The characters with high phenotypic coefficient of variation indicated more influence of environmental factors. Similar results on variability for different characters were reported by Chowdhary and Goswami (1991) [4], Pant and Singh (2001) [20], Rai *et al.* (2005) [23], Sharma *et al.* (2014) [24], Akabari and Niranjana (2015) [1] and Yadav *et al.* (2022) [30].

Heritability and expected genetic advance

The estimates of heritability and expected genetic advance for various characters studied are shown in Table 2. Heritability estimates were highest for biological yield plant⁻¹ (98.36), followed by Seed yield plant⁻¹ (97.38), Plant Height (95.50) and Length of main raceme (92.14). High heritability indicated that the characters were least influenced by environmental factors. Lowest heritability was observed for days to maturity (71.54). High value of expected genetic advance expressed as percent of mean was observed for seed

yield plant⁻¹ (59.47), biological yield plant⁻¹ (49.23), Secondary Branches Plant⁻¹ (35.20) and harvest index (27.09). High heritability coupled with high genetic advance (per cent of mean) was observed for seed yield plant⁻¹, biological yield plant⁻¹ and harvest index which suggested that these characters can be considered as favourable for improvement through selection. Plant Height and Length of main raceme showed high heritability coupled with moderate genetic advance while high heritability with low genetic advance was observed for oil content and days to maturity. Similar findings were also reported by Kulbe *et al.* (2000) [10], Mahla *et al.* (2003) [14], Priyamedha *et al.* (2013) [21], Pandey and Pandey (2014) [18], and Vanukuri and Pandey (2022) [29].

Correlations

Correlation analysis estimates the degree and direction of the relationship between variables and are widely used in breeding selection programs. The phenotypic and genotypic correlation for all the characters is presented in Table 3. Simple correlation coefficients computed among the thirteen characters indicated that there are significant associations between the investigated traits. The strongest positive correlations were formed between biological yield plant⁻¹ and seed yield plant⁻¹ and between Length of main raceme and seed yield plant⁻¹. The seed yield plant⁻¹ exhibited highly significant and positive correlation with biological yield plant⁻¹ (0.853), Length of main raceme (0.567), Silique on main Raceme (0.456), Secondary Branches Plant⁻¹ (0.446), harvest index (0.441), and plant height (0.357). Thus, these characters emerged as most important factors influencing seed yield in Indian mustard. The seed yield plant⁻¹ also exhibited highly significant and negative correlation with Days to 50% Flowering (-0.511). Seed yield plant⁻¹ showed significant and positive correlation with Seeds silique⁻¹ (0.326), 1000 Seed Weight (0.325) and Days to Maturity (0.306). Seed yield plant⁻¹ showed non-significant and positive correlation with Primary Branches Plant⁻¹ (0.078); besides, non-significant and negative correlation with Oil Content (-0.094). Days to 50% flowering showed highly significant and positive correlation with oil content (0.336) while highly significant and negative correlation with biological yield plant⁻¹ (-0.520), plant height (-0.404) and 1000 Seed Weight (-0.404). Days to maturity exhibited highly significant and positive correlation with silique on main raceme (0.394) while significant and positive correlation with Secondary Branches Plant⁻¹ (0.259) and biological yield plant⁻¹(0.256). It also showed significant and negative correlation with Primary Branches Plant⁻¹(-0.255). Plant height showed highly significant and positive correlation with Silique on main Raceme (0.480), Length of main raceme (0.444) and biological yield plant⁻¹ (0.432). Secondary branches plant⁻¹ showed highly significant and positive correlation with biological yield plant⁻¹ (0.574) and Length of main raceme (0.350). Length of main raceme showed highly significant and positive correlation with silique on main raceme (0.619) and biological yield plant⁻¹ (0.477). Silique on main raceme showed highly significant and positive correlation with biological yield plant⁻¹ (0.421) while significant and positive correlation with Seeds silique⁻¹ (0.265). Seeds Silique⁻¹ showed highly significant and positive correlation with biological yield plant⁻¹ (0.361). Test weight showed highly significant and positive correlation with Harvest Index (0.359). These findings are broadly in agreement with some earlier reports Tyagi *et al.* (1996) [28],

Srivastava and Singh (2002) ^[27], Sirohi *et al.* (2004) ^[26], Gangapur *et al.* (2009) ^[7], Lodhi *et al.* (2014) ^[12], Davar *et al.* (2018) ^[5], Pal *et al.* (2019) ^[16] and Nandi *et al.* (2021) ^[15].

Path Coefficient

The genotypic and phenotypic correlation coefficients of seed yield plant⁻¹ with remaining traits under study were further partitioned into direct and indirect effects using path coefficient analysis and are presented in Table 4. Path coefficient analysis showed that biological yield plant⁻¹ exhibited maximum direct effect (1.3263) on seed yield plant⁻¹ followed by siliques on main raceme (1.2366), harvest index (1.0965), secondary branches plant⁻¹ (0.5605) and oil content (0.4801) at genotypic level; and at phenotypic level biological yield plant⁻¹ possessed maximum direct effect (0.9307) on seed yield plant⁻¹ followed by harvest index (0.5345), oil content (0.0572), length of main raceme (0.0266) and secondary branches plant⁻¹ (0.0057). Other traits *viz.*, days to 50% flowering, primary branches plant⁻¹, plant height, days to maturity, 1000-seed weight and seeds siliques⁻¹ had negative direct effect on seed yield plant⁻¹ at both genotypic and phenotypic levels. On the other hand, length of main raceme showed negative direct effect on seed yield plant⁻¹ only at genotypic level whereas siliques on main raceme had negative direct effect on seed yield plant⁻¹ only at phenotypic level. Therefore, it is suggested that the traits which exhibited maximum direct effects on grain yield and oil content should be considered in selection programme for enhancing yield potential. Similar findings were also reported by Srivastava and Singh (2002) ^[27], Sirohi *et al.* (2004) ^[26], Kumar and Pandey (2014) ^[18], Davar *et al.* (2018) ^[5], and Pal *et al.* (2019) ^[16]. The maximum positive indirect effect on seed yield plant⁻¹ *via.*, biological yield plant⁻¹ was observed for secondary branches plant⁻¹ followed by length of main raceme, plant height, siliques on main raceme, seeds siliques⁻¹, days to maturity, 1000-seed weight, and primary branches plant⁻¹ whereas negative indirect effect was observed for days to 50% flowering *via.*, biological yield plant⁻¹ both at genotypic and phenotypic levels. Therefore, the characters exhibited positive direct effects on seed yield should be preferred while making selection for improvement of seed yield and more emphasis should be given to these traits with greater magnitude of positive direct effect than those with smaller magnitude.

Genetic Divergence

Based on D² values, all the 20 genotypes were grouped in 5 clusters (Table 5). Among the five clusters, cluster II was the largest, comprising of 8 genotypes followed by cluster III with 5 genotypes, cluster IV with 3 genotypes and cluster I&V with 2 genotypes each. The clustering pattern revealed that the groups of genotypes which were together in a cluster

also indirectly proved their stable performance.

The inter and intra cluster distance among the genotypes is presented in Table 6. The maximum intra-cluster distance was observed in cluster IV (2.769) followed by cluster III (2.756) and cluster II (2.447) indicating differences in genotypes within the cluster. The least intra-cluster distance was found in cluster V (0.629) indicating close resemblance between the genotypes presented in this cluster. The highest inter-cluster distance was observed between cluster V and IV (6.614) indicating a high degree of genetic diversity. The lowest inter-cluster distance was observed between cluster II and III (2.872) followed by cluster I and II (3.420) indicating that these clusters were relatively less divergent. Presence of substantial genetic diversity among the varieties/lines screened in the present study indicated that these materials may serve as good source for selecting the diverse parents for hybridization programme aimed at isolating desirable segregates for seed yield as well as other important characters. The cluster mean for each character is tabulated in Table 7. Highest mean values for Days to Maturity (128.33), Plant Height (178.53), Secondary Branches Plant⁻¹ (12.38), Length of main raceme (67.57), Siliques on main Raceme (48.51), 1000 Seed Weight (4.77), Biological yield plant⁻¹ (49.39) and Seed yield plant⁻¹ (13.33) whereas lowest mean value for Days to 50% Flowering (55.78) was observed in cluster IV. Cluster I exhibited the highest mean values for Primary Branches Plant⁻¹ (7.80) and Seeds Siliques⁻¹ (13.62) whereas highest mean values for Harvest Index (28.07) and Oil Content (40.06) was found in cluster V. Cluster II showed highest mean values for Days to 50% Flowering (63.46) whereas lowest mean value for 1000 Seed Weight (4.06). Cluster I exhibited lowest mean values for Days to Maturity (119.67), Length of main raceme (46.08), Siliques on main Raceme (34.10), Harvest Index (19.86) and Oil Content (39.53). Lowest mean values for Plant Height (144.35), Primary Branches Plant⁻¹ (6.10) and Seeds siliques⁻¹ (11.93) was found in cluster III while cluster V exhibited Lowest mean values for Secondary Branches Plant⁻¹ (5.92), Biological yield plant⁻¹ (20.93) and Seed yield plant⁻¹ (5.87). The above discussion clearly shows wide variation from one cluster to another in respect of cluster means for 13 characters, indicating that genotypes having distinctly different mean performance for various characters were separated into different clusters. The crossing between the entries belonging to cluster pairs having large inter-cluster distances and possessing high cluster means for one or other characters to be improved may be recommended for isolating desirable recombinants in the segregating generations in mustard. Similar findings were also reported by Goswami and Behl (2006) ^[8], Binesh Goyal *et al.* (2012) ^[9], Ratnesh Pandey *et al.* (2013) ^[17], Shekhawat *et al.* (2014) ^[25], Bind *et al.* (2015) ^[3], and Priyanka and Pandey (2021) ^[22].

Table 1: Mean squares from analysis of variance (ANOVA) of thirteen characters in twenty genotypes of Indian Mustard

Source of variation	DF	Days to 50% Flowering	Days to Maturity	Plant Height (cm)	Primary Branches/Plant	Secondary Branches/Plant	Length of main raceme (cm)	Silique on main Raceme	Seeds/Silique	1000 Seed Weight (gm)	Biological yield/plant (g)	Harvest Index (%)	Oil Content (%)	Seed yield/plant (gm)
Replication	2	6.35	3.20	10.52	0.83	0.04	0.10	12.68	0.63	0.05	5.35	0.12	0.04	0.26
Treatment	19	50.22**	38.72**	605.17**	3.99**	12.64**	157.80**	98.52**	2.54**	0.73**	216.56**	36.35**	0.89**	19.06**
Error	38	2.63	4.53	9.37	0.31	0.72	4.36	4.46	0.28	0.03	1.19	1.45	0.10	0.17

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

Table 2: Mean, range, GCV, PCV, Heritability and genetic advance for thirteen characters of Indian mustard

Characters	Mean	Min	Max	Heritability (%)	Genetic advance (GA)	GA as% mean	GCV (%)	PCV (%)
Days to 50% Flowering	61.45	49.67	67.00	85.78	7.60	12.37	6.48	7.00
Days to Maturity	124.40	119.00	131.33	71.54	5.88	4.73	2.71	3.21
Plant Height (cm)	156.37	136.54	188.26	95.50	28.37	18.14	9.01	9.22
Primary Branches/Plant	6.83	5.45	10.25	80.09	2.04	29.92	16.23	18.13
Secondary Branches/Plant	10.74	5.76	13.34	84.69	3.78	35.20	18.57	20.18
Length of main raceme (cm)	56.56	42.81	70.28	92.14	14.14	25.00	12.64	13.17
Silique on main Raceme	40.02	30.78	50.35	87.55	10.79	26.97	13.99	14.95
Seeds/Silique	12.83	10.24	14.13	72.92	1.53	11.90	6.77	7.93
1000 Seed Weight (gm)	4.42	3.45	5.31	89.97	0.95	21.44	10.97	11.57
Biological yield/plant (g)	35.16	20.42	50.96	98.36	17.31	49.23	24.10	24.30
Harvest Index (%)	24.45	19.81	31.06	88.91	6.62	27.09	13.95	14.79
Oil Content (%)	39.79	38.48	40.48	71.82	0.90	2.25	1.29	1.52
Seed yield/plant (gm)	8.58	5.83	15.83	97.38	5.10	59.47	29.25	29.65

Table 3: Genotypic (G) and phenotypic (P) correlation coefficients for different characters in Indian mustard

Characters		Days to 50% Flowering	Days to Maturity	Plant Height (cm)	Primary Branches/Plant	Secondary Branches/Plant	Length of main raceme (cm)	Silique on main Raceme	Seeds/Silique	1000 Seed Weight (gm)	Biological yield/plant (g)	Harvest Index (%)	Oil Content (%)	Seed yield/plant (gm)
Days to 50% Flowering	G	1.000	-0.097	0.454**	0.094	-0.072	-0.238	-0.071	-0.258*	0.516**	-0.557**	-0.144	0.418**	-0.556**
	P	1.000	-0.001	0.404**	0.087	-0.033	-0.202	-0.068	-0.197	0.404**	-0.520**	-0.115	0.336**	-0.511**
Days to Maturity	G		1.000	0.208	-0.320*	0.344**	0.186	0.528**	-0.340**	0.002	0.287*	0.201	0.027	0.356**
	P		1.000	0.182	-0.255*	0.259*	0.128	0.394**	-0.218	0.055	0.256*	0.148	0.126	0.306*
Plant Height (cm)	G			1.000	-0.236	-0.016	0.447**	0.524**	0.246	-0.008	0.452**	-0.049	-0.042	0.376**
	P			1.000	-0.210	0.018	0.444**	0.480**	0.190	0.017	0.432**	-0.043	-0.019	0.357**
Primary Branches/Plant	G				1.000	0.312*	0.065	0.028	0.116	0.063	0.169	-0.149	0.016	0.076
	P				1.000	0.249	0.055	0.037	0.065	0.047	0.129	-0.052	-0.033	0.078
Secondary Branches/Plant	G					1.000	0.374**	0.195	-0.057	0.222	0.642**	-0.179	0.014	0.499**
	P					1.000	0.350**	0.183	-0.045	0.204	0.574**	-0.153	0.010	0.446**
Length of main raceme (cm)	G						1.000	0.658**	0.172	0.035	0.509**	0.251	0.064	0.606**
	P						1.000	0.619**	0.161	0.069	0.477**	0.227	0.033	0.567**
Silique on main Raceme	G							1.000	0.278*	-0.240	0.451**	0.128	0.125	0.477**
	P							1.000	0.265*	-0.207	0.421**	0.148	0.053	0.456**
Seeds/Silique	G								1.000	0.110	0.403**	0.116	0.199	0.381**
	P								1.000	0.114	0.361**	0.066	0.224	0.326*
1000 Seed Weight (gm)	G									1.000	0.205	0.402**	0.002	0.346**
	P									1.000	0.191	0.359**	0.048	0.325*
Biological yield/plant (g)	G										1.000	-0.076	-0.161	0.862**
	P										1.000	-0.079	-0.120	0.853**
Harvest Index (%)	G											1.000	-0.010	0.430**
	P											1.000	-0.029	0.441**
Oil Content (%)	G												1.000	-0.120
	P												1.000	-0.094
Seed yield/plant (gm)	G													1.000
	P													1.000

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

Table 4: Direct and indirect effects for different characters on seed yield at genotypic and phenotypic levels in Indian mustard

Chrs		Days to 50% Flowering	Days to Maturity	Plant Height (cm)	Primary Branches/Plant	Secondary Branches/Plant	Length of main raceme (cm)	Silique on main Raceme	Seeds/Silique	1000 Seed Weight (gm)	Biological yield/plant (g)	Harvest Index (%)	Oil Content (%)	Seed yield/plant (gm)
Days to 50% Flowering	G	-0.5579	0.1392	0.0743	-0.0418	-0.0403	0.2321	-0.0880	0.2641	0.1575	-0.7388	-0.1574	0.2006	-0.556**
	P	-0.0184	0.0001	0.0091	-0.0017	-0.0002	-0.0054	0.0005	0.0117	0.0201	-0.4841	-0.0617	0.0192	-0.511**
Days to Maturity	G	0.0542	-1.4318	-	0.1422	0.1930	-0.1814	0.6524	0.3484	-0.0005	0.3806	0.2200	0.0129	0.356**
	P	0.0000	-0.0315	0.0340	0.0049	0.0015	0.0034	-0.0030	0.0129	-0.0027	0.2386	0.0790	0.0072	0.306*
Plant Height (cm)	G	0.2531	-0.2974	-	0.1049	-0.0092	-0.4362	0.6478	-0.2524	0.0026	0.6001	-0.0534	-0.0201	0.376**
	P	0.0075	-0.0057	0.1638	0.0041	0.0001	0.0118	-0.0037	-0.0112	-0.0009	0.4019	-0.0232	-0.0011	0.357**
Primary Branches/Plant	G	-0.0525	0.4580	0.0387	-0.4445	0.1748	-0.0636	0.0349	-0.1189	-0.0194	0.2245	-0.1635	0.0076	0.076
	P	-0.0016	0.0081	0.0047	-0.0194	0.0014	0.0015	-0.0003	-0.0039	-0.0023	0.1198	-0.0279	-0.0019	0.078
Secondary Branches/Plant	G	0.0402	-0.4930	0.0027	-0.1386	0.5605	-0.3653	0.2405	0.0587	-0.0679	0.8509	-0.1966	0.0068	0.499**
	P	0.0006	-0.0082	0.0004	-0.0048	0.0057	0.0093	-0.0014	0.0027	-0.0101	0.5339	-0.0820	0.0006	0.446**
Length of main raceme (cm)	G	0.1327	-0.2660	-	-0.0290	0.2097	-0.9764	0.8141	-0.1761	-0.0108	0.6747	0.2754	0.0306	0.606**
	P	0.0037	-0.0041	0.0732	-0.0011	0.0020	0.0266	-0.0047	-0.0095	-0.0034	0.4440	0.1211	0.0019	0.567**
Silique on main Raceme	G	0.0397	-0.7553	-	-0.0125	0.1090	-0.6428	1.2366	-0.2850	0.0734	0.5985	0.1408	0.0601	0.477**
	P	0.0013	-0.0124	0.0858	-0.0007	0.0011	0.0165	-0.0076	-0.0157	0.0103	0.3917	0.0790	0.0030	0.456**
Seeds/Silique	G	0.1438	0.4867	-	-0.0516	-0.0321	-0.1678	0.3439	-1.0249	-0.0335	0.5344	0.1269	0.0954	0.381**
	P	0.0036	0.0069	0.0403	-0.0013	-0.0003	0.0043	-0.0020	-0.0591	-0.0057	0.3355	0.0350	0.0128	0.326*
1000 Seed Weight (gm)	G	0.2878	-0.0022	0.0014	-0.0282	0.1247	-0.0347	-0.2972	-0.1126	-0.3053	0.2712	0.4403	0.0010	0.346**
	P	0.0074	-0.0017	-	-0.0009	0.0012	0.0018	0.0016	-0.0067	-0.0498	0.1776	0.1919	0.0028	0.325*
Biological yield/plant (g)	G	0.3108	-0.4109	-	-0.0752	0.3596	-0.4967	0.5580	-0.4130	-0.0624	1.3263	-0.0836	-0.0773	0.862**
	P	0.0096	-0.0081	0.0741	-0.0025	0.0033	0.0127	-0.0032	-0.0213	-0.0095	0.9307	-0.0423	-0.0069	0.853**
Harvest Index (%)	G	0.0801	-0.2872	0.0080	0.0663	-0.1005	-0.2452	0.1588	-0.1186	-0.1226	-0.1011	1.0965	-0.0048	0.430**
	P	0.0021	-0.0047	0.0010	0.0010	-0.0009	0.0060	-0.0011	-0.0039	-0.0179	-0.0737	0.5345	-0.0016	0.441**
Oil Content (%)	G	-0.2331	-0.0385	0.0068	-0.0070	0.0079	-0.0622	0.1548	-0.2036	-0.0006	-0.2135	-0.0110	0.4801	-0.120
	P	-0.0062	-0.0040	0.0004	0.0006	0.0001	0.0009	-0.0004	-0.0132	-0.0024	-0.1120	-0.0153	0.0572	-0.094

Bold figure indicates direct effect

Residual effect = 0.0435 (at genotypic level), 0.0271 (at phenotypic level)

*, ** significant at 5% and 1% probability levels, respectively

Table 5: Number of genotypes in each cluster

Clusters	No of genotypes	Genotypes
I	2	Ashirwad, MCN 13-37
II	8	RGN 73, RH 919, JD 6, QM 13-2, QM 13-10, Vardan, QM 13-7, NPJ-112
III	5	Kranti, Varuna, MCN 13-41, RH-0749, MCN 13-38
IV	3	Divya 33, Maya, Pusa Mustard 21
V	2	CS 54, CS 52

Table 6: Inter and intra distances

Clusters	I	II	III	IV	V
I	1.588				
II	3.420	2.447			
III	3.849	2.872	2.756		
IV	6.085	4.765	5.561	2.769	
V	4.768	3.986	3.770	6.614	0.629

Table 7: Cluster mean Mahalanobis D² analysis

Cluster	Days to 50% Flowering	Days to Maturity	Plant Height (cm)	Primary Branches/Plant	Secondary Branches/Plant	Length of main raceme (cm)	Silique on main Raceme	Seeds/Silique	1000 Seed Weight (gm)	Biological yield/plant (g)	Harvest Index (%)	Oil Content (%)	Seed yield/plant (gm)
I	58.17	119.67	154.68	7.80	10.37	46.08	34.10	13.62	4.68	39.04	19.86	39.53	7.75
II	63.46	123.58	154.66	7.31	11.02	59.18	41.47	13.04	4.06	35.09	22.92	39.97	8.06
III	62.67	125.53	144.35	6.10	11.37	52.17	35.01	11.93	4.60	30.88	25.82	39.59	7.97
IV	55.78	128.33	178.53	6.59	12.38	67.57	48.51	13.13	4.77	49.39	26.93	39.66	13.33
V	62.17	123.67	161.70	6.16	5.92	51.06	39.95	13.01	4.62	20.93	28.07	40.06	5.87

Conclusion

From the present study it is concluded that the analysis of variance showed highly significant differences among the genotypes for all the characters studied. PCV values were higher than GCV values. The characters seed yield plant⁻¹, biological yield plant⁻¹, and harvest index were recorded with high heritability and genetic advance values. From correlation and path analysis studies, it is concluded that the traits such as biological yield plant⁻¹, Length of main raceme, Silique on main Raceme, Secondary Branches Plant⁻¹, harvest index and plant height which exhibited highly significant and positive correlation and most of them also had either direct or indirect effects on seed yield both under timely and late sown conditions, emerged as important component contributing to seed yield plant⁻¹ and the selection primarily based on these traits may result in development of high yielding genotypes. Cluster analysis revealed that highest inter- cluster distance was observed between cluster V and IV indicating a high degree of genetic diversity among the genotypes.

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