Estimation of Genetic Parameters and Character Association in Indian Mustard (*Brassica juncea* L.)

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Authors' contributions

This work was carried out in collaboration among all authors. Author HK did the conceptualization. Author AK did the data curation. Authors HK and AK performed Methodology. Authors SG and AK did a Software analysis. Authors HK, AK and AKS wrote the original draft of the manuscript. Authors SG, VG and AKS wrote & edited the manuscript. All authors have read and approved the final version of the manuscript.

Article Information

Original Research Article

ABSTRACT

An experiment was undertaken to examine the yield potential and genetic parameters of Indian mustard through yield and yield contributing traits in the Bundelkhand region of Uttar Pradesh. Twenty-five mustard genotypes were assessed for nine agro-morphological traits during Rabi 2018-19. Phenotypic data were subjected to analysis of variance, pairwise mean comparison, genetic parameter studies, and association analysis using R-Packages 1.5, STAR 2.0.1, and SPAR 2.0 Package. The evaluated germplasm had ample genetic variability for studied traits and trait-specific genotypes have been identified. The trait seed yield showed higher heritability coupled with higher

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genetic advance as percent of the mean (99% and 70.41) followed by the number of SB (98% and 65.57) and TSW (100% and 62.50) are more authentic for selecting the leading genotype. The association studies revealed a significant and positive correlation of seed yield with the number of siliquae per plant (0.346), siliquae length (0.333), and 1000 seed-weight (0.237) at both genotypic and phenotypic levels. The lines Maya, RH 119, IC 571649, Durgamini, and IC 447111 showed better performance and produced higher seed yields in the Bundelkhand region. These identified genotypes having desirable trait combinations may be utilized for creating variability to develop location-specific cultivars.

1. INTRODUCTION

Indian mustard (*Brassica juncea* L. 2n=36) belonging to the family *Brassicaceae* is an important oilseed *rabi* season crop. It is a natural allopolyploid (2n=36), believed to be originated through interspecific hybridization between *B. rapa* (2n=20) and *B. nigra* (2n=16). Globally, Canada is the largest producer which contributes 28% of the world's production followed by China. In India, mustard harbors the largest acreage amongst different *Brassica* species. It is cultivated in an area of 6.34 million ha with a production of 7.82 million tons and productivity of 1233 kg/ha in 2012-13 [1]. The major mustard growing states are Rajasthan, Haryana, Madhya Pradesh, and Uttar Pradesh contributing about 76.8% of the total mustard production in the country [2]. The highest mustard producing state is Rajasthan (3.40 mt) followed by Madhya Pradesh (0.98 mt). The area, production, and productivity of mustard in Uttar Pradesh are 0.68 ha, 0.95 mt, and 1392 kg/ha, respectively (Directorate of Economics & Statistics, DAC&FW 2017). At the national level, the average production of Indian mustard is low which can be attributed to various reasons like lack of high-yielding varieties, resistance to diseases and pests, response to higher inputs, and other management practices [3]. To overcome these issues, it is of utmost importance to evaluate the limiting factors contributing to the growth and yield of Indian mustard. Therefore, the selection of improved genotypes is essential by estimating variability among the germplasm in this region.

The grain yield is a complex character and is influenced by several yields contributing traits and is also influenced by environmental variations [4,5]. Thus, understanding the interrelationship between yield and its contributing factors would assist in formulating the selection criterion for any crop improvement programme by indirect selection. For selection purposes, we need to know the magnitude of genetic variability in the breeding material. Also, the nature of component traits on which selection would be effective and the influence of environmental factors on each trait need to be known [3].

The various parameters like the phenotypic coefficient of variation, genotypic coefficient of variation, heritability, and genetic advance are used to measure the variability present in any plant population and help to ascertain the real potential of the genotype [6]. This variability is essential for a plant breeder to initiate a crop breeding program because a hybrid originated from parents of diverse origin provides greater heterosis than those of closely related parents [7]. Thus, the present investigation was carried out to assess the genetic parameters *viz.* genetic variability, heritability, and genetic advance to estimate the direct and indirect effects of different agronomical characters on seed yield and to determine the genotypic and phenotypic correlation between seed yield and its contributing characters.

2. MATERIALS AND METHODS

2.1 Plant Materials

The field experiment was conducted at the experimental research farm, Department of Genetics and Plant Breeding, Banda University of Agriculture and Technology, Banda (24^{0}53' and 25^{0}55'N, and 80^{0}07' and 81^{0}34'E 123 m ASL), Uttar Pradesh during rabi 2018-19. The experimental material comprised 25 diverse Indian mustard (*B. juncea* L.) genotypes. All the accessions were collected from NBPGR, New Delhi, and State Agricultural Universities. Each accession was planted in a 4-row plot of 4-m length, maintaining a distance of 30 cm between rows and 15 cm between plant to plant following a randomized complete block design with two replications. The recommended package of practices was followed for raising a healthy crop

from germination to maturity stage. The experiment was planted in the third week of October and harvesting was carried out in March. The per-day meteorological observations *viz*: temperature, humidity, and rainfall were recorded at the meteorology observatory unit of the university from October to March 2018-19. The mean of each parameter was averaged weekly and is represented in Fig. 1.

2.2 Phenotypic Evaluation of Studies Traits

The agro-morphological data were recorded on days to 50% flowering (DTF), days to 95% maturity (DTM), plant height (PH), primary branches (PB), secondary branches (SB), number of pods per plant (NPP), pod length (PL), thousand seed weight (TSW) and seed yield per hectare (SY) for all test genotypes. The DTF and DTM were counted from the date of sowing to the days of flowering completed in 50% of plants and days to physiological maturity completed, respectively. Plant height (cm) was measured from the base of the plants adjoining soil surface to the terminal bud on five randomly selected plants from each plot. The PB counted branches emerged from the main stem and SB counted branches emerged from primary branches on the five randomly selected plants. The NPP counted as a total number of seed-filled siliquae of five selected plants in each plot. The PL was measured in centimeters from base to top of the siliqua on five pods taken from the mid part of the plant. For a thousand seed weight, a random sample of 1000-grains was counted with an automatic seed counter from each plot and weighed by electronic weighing balance. The total seed yield of each plot was measured from all four rows of 4 m length for each genotype and transformed into seed yield (kg/ha).

2.3 Statistical Analysis

The average trait values on genotypes were used for statistical analysis. Firstly, experimental data were subjected to analysis of variance (ANOVA). The pairwise mean comparison of all agronomic traits was estimated using Tukey's method initially called 'Honestly significant difference' test using R-Packages 1.5 and Statistical Tool for Agricultural Research (STAR) 2.0.1 [8] software package. The principal component analysis (PCA) was calculated with a correlation matrix among yield and yield component traits. The phenotypic and genotypic coefficient of variation, heritability (Broad Sense),

genetic advance, genotypic and phenotypic correlation coefficients, and path coefficient analysis was estimated using the SPAR 2.0 Package [9].

3. RESULTS AND DISCUSSION

3.1 Genetic Variation

The analysis of variance (ANOVA) indicated significant differences among the genotypes for the traits studied indicating the presence of wider genetic variability to be used for the genetic improvement of the desired trait(s) (Table 1). The genotypes were grouped for each trait using pairwise mean comparison analysis based on the least significant differences (Table 2). The genotypes confirm distinct grouping patterns for each trait, where genotypes with the unique single letter are significantly different from another genotype, and means with the same letter are not significantly different. The descriptive statistics and the box plots depicting variability for all the traits are presented in Table 2 & Fig. 2. In attaining 50% flowering, the tested germplasm ranged from 44 (IC-597879) to 68 (IC-571649, IC-58968) days with an average of 53.98±0.81. The plants attained an average height of 179.49 cm wherein the tallest genotype was IC-58968 with a mean height of 226.10 cm whereas the shortest was CS-54 (127.25cm). The average time taken to attain maturity was 125 days with a maximum of 132 days (CS-54) whereas the minimum days were taken by Durgamini (116 days). The number of primary branches ranged from 3.50 (Jagannath) to 9.50 (IC-589690) with a mean value of 5.60±0.13, whereas several secondary branches varied from 6.50 (Kanti) to 21.00 (IC-58968) with a mean of 13.08±0.40. Jagannath had a minimum number of siliquae per plant (138) whereas IC-589690 harbored the maximum number of siliquae (622). The average pod length observed in the test material was 4.83 cm. Thousand seed weight ranged from 1.30 (IC-589690) to 5.46g (IC-571678) with an average of 3.47±1.00. Grain yield varied from 683 (IC-405235) to 2729 kg/ha (Maya) with a mean value of 1764 kg/ha. The number of siliquae plant[-1] revealed a maximum coefficient of variance (28.35), followed by the number of secondary branches (4.29), number of primary branches (3.23), seed yield (2.66), and days to 50% flowering (2.12). The analysis showed wide variation for all the traits studied, thus suggesting a wide spectrum of variability amongst germplasm lines.
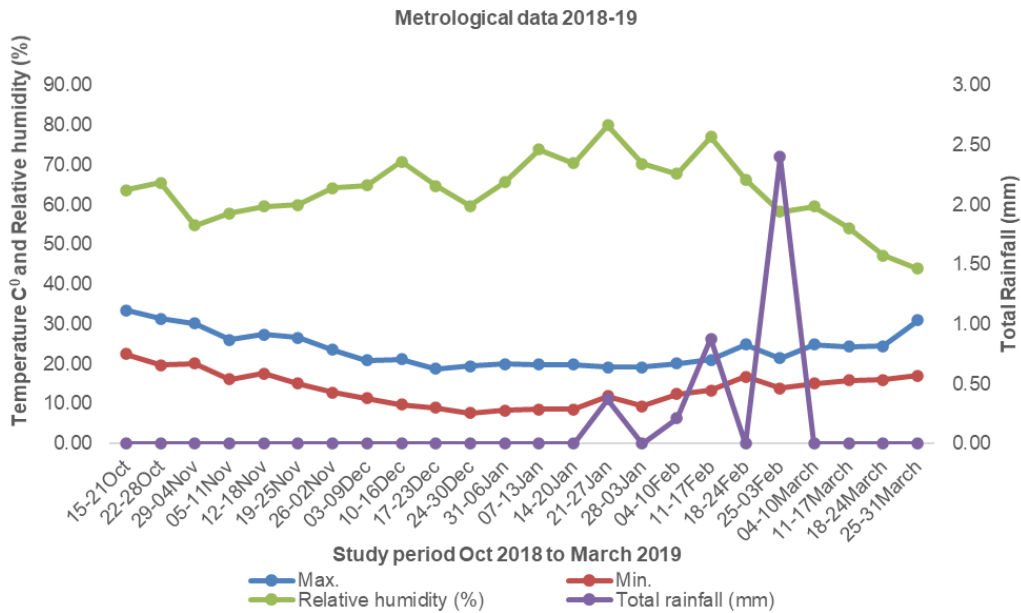
Fig. 1. Weekly temperature (Max. Min.), relative humidity and rainfall during study period in rabi 2018-19
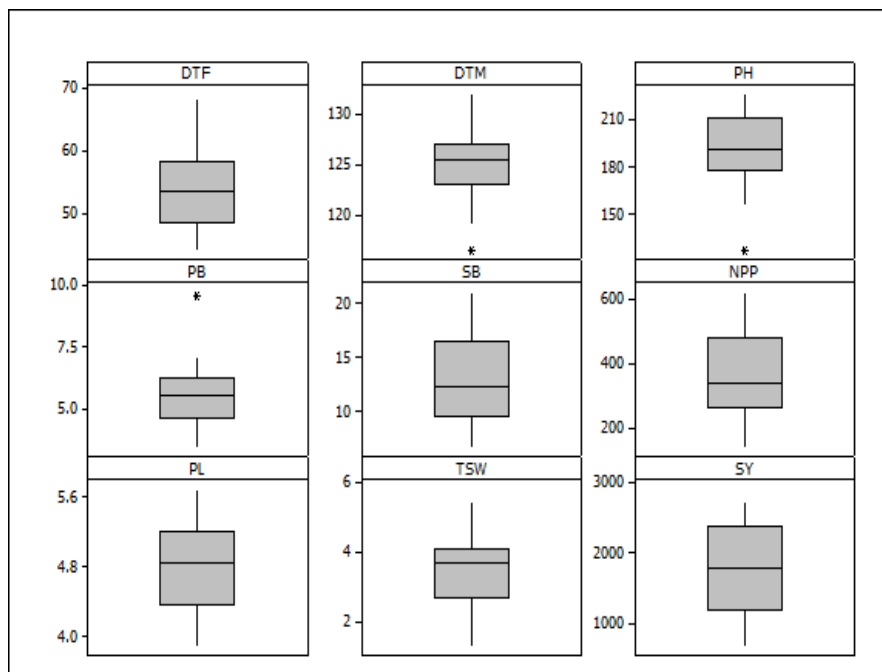
Fig. 2. Box plots depicting variations for; DTF = days to 50% flowering; DTM = days to 95% maturity; PH = plant height; PB= primary branches; SB = secondary branches; NPP = number of pods per plant; PL = pod length; TSW = thousand seed weight; SY = seed yield per hectare

3.2 Genetic Parameters

The study revealed higher phenotypic variance than the corresponding genotypic variance for days to maturity and the number of siliquae per plant. Higher phenotypic variance suggested more influence of environmental factors on these traits [10,3,2]. For all other traits, PCV and GCV were almost at par with each other. The maximum genotypic coefficient of variance (GCV) was observed for SY (34.28%), followed by NPP (32.33%). Our results are in agreement

with previous studies [11,12,13], which reported high GCV for seed yield per plant. The phenotypic coefficient of variance (PCV) was highest for the number of NPP (43.00%), followed by SY (34.38%), number of SB (32.36%), and number of PB (23.61%). Traits with high GCV and PCV suggested yield improvement can be achieved through selection. The least genotypic, as well as phenotypic variability, was observed for DTM (2.60 & 3.01%, respectively) (Table 3). The higher magnitude of variability has been reported previously in different studies for days to 50% flowering, days to maturity, plant height, total siliquae/plant, 1000-seed weight, and seed yield in Indian mustard [14, 4,15].

3.3 Heritability and Genetic Advance

The efficiency of selection depends upon the magnitude of heritability of traits because it measures the transmissibility of characters from parents to offspring [3]. The highest heritability was observed for TSW (100%) followed by SY and PH (99%), PL, PB and SB (98%), and DTF (97%) whereas, the traits like DTM and NPP recorded moderate heritability (55-75%) (Table 3). Higher estimates of heritability for thousand seed weight, seed yield, and plant height were also reported in many previous studies [16,17,18,19]. Improvement in the mean

genotypic value of selected plants over the parental population is known as genetic advance. Three factors determine the genetic advance under selection, i.e. genetic variability, heritability, and selection intensity. In the present study, a higher magnitude of genetic advance was observed for SY (576.43) and NPP (178.44), suggesting direct selection for these traits would be beneficial for seed yield improvement (Singh et al., 2018). The genetic advance in percent of mean ranged from 4.61% for DTM to 70.41% for SY. The number of SB, TSW, NPP, PB, PH, DTF, and PL showed intermediate values for genetic advance as percent of the mean. The heritability estimates together with genetic advances are more authentic for selecting the leading genotype [20]. The higher heritability coupled with higher genetic advance as percent of mean was observed for SY (99% and 70.41) followed by the number of SB (98% and 65.57) and TSW (100% and 62.50) (Table 2). The high heritability coupled with high genetic advance has earlier been reported for the number of siliqua per plant [21], seed yield, and thousand seed weight [11, 22,23] This cumulative response of high heritability with high genetic advance indicates the pronounced additive gene control in expression of studied traits, so early generation selection for these traits would be effective in breeding programmes [19,10,3].
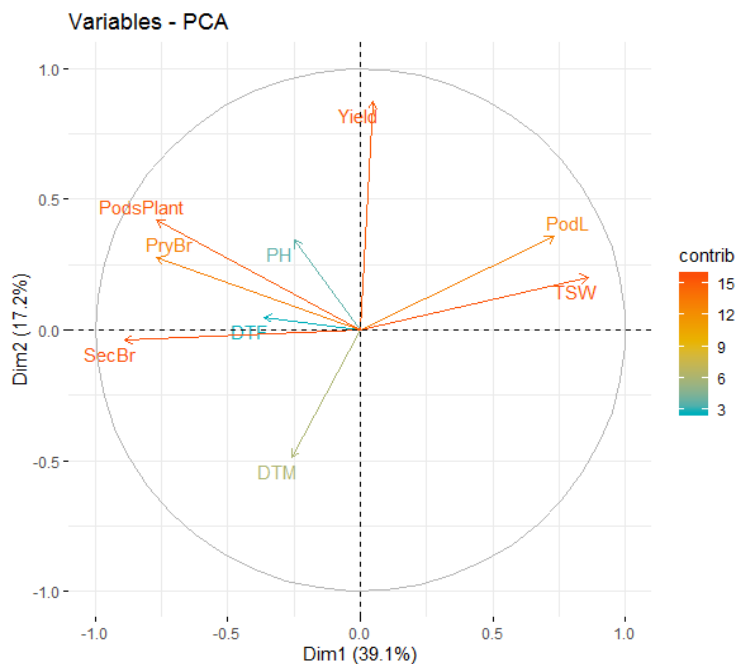

Fig. 3. Phenotypic correlation between seed yield (Yield) and its component traits

Table 1. Analysis of variance (ANOVA) for grain yield and yield components in 25 germplasm lines of Indian mustard

Characters	Mean Sum of Square (df)		
	MSr **(1)**	MSg **(24)**	MSe**(24)**
Days to 50% flowering (Days)	0.9800	79.436***	1.3133
Plant height (cm)	3.5378	1071.807***	5.4420
Days to maturity (Days)	0.9800	24.750***	3.6467
Number of primary branches	0.0512	3.429***	0.0325
Number of secondary branches	0.7688	35.613***	0.3157
Number of siliquae per plant	8549.0888	36763.153**	10211.9221
Siliquae length (cm)	0.0031	0.500***	0.0047
1000 seed weight (g)	0.0924	2.1927***	0.0224
Seed yield (gm/plot) Kg/ha	10863.380	158017.583***	474.4633

*** Significance at P=0.01, *** Significance at P=0.001*
MSr = mean square for replication, MSe = mean square for error; MSg = mean square for genotype.

3.4 Correlation Studies

A higher genotypic correlation coefficient as compared to the phenotypic correlation coefficient revealed that the association between these characters is mainly due to genetic effects [10]. Grain yield is a complex character with several component traits and knowledge of correlation will be beneficial to design breeding methodology. As the environmental effects are also very prominent on yield, so the selections based only on yield is not effective. The correlation studies and path co-efficient analysis would pave way for plant selection to use in breeding programmes. Associations between seed yield and related traits were estimated by correlation coefficients, both genotypic as well as phenotypic. Amongst genotypic and phenotypic correlation, higher genotypic correlation than phenotypic indicates the inherent associations among the traits [2]. The correlations of yield with yield component traits are presented in Table 4, Fig. 3. Traits like NPP (0.346), PL (0.333), and TSW (0.237) revealed a significant and positive correlation with SY.

Similar results were also reported by Rauf and Rahim [10] which supports the findings of the present study, and also indicates that grain yield can be enhanced by NPP, PL, and TKS. Additionally, the number of primary branches (0.197) also exhibited a significant positive correlation at the phenotypic level. All these parameters could be used as marker traits for improvement in the seed yield of mustard. Among other traits, TSW was positively and significantly correlated top at both genotypic (0.690) and phenotypic (0.684) level whereas, negatively correlated to the number of PB (-0.479, -0.474), number of SB (-0.789, -0.782), and NPP (-0.628, -0.472) at both genotypic and phenotypic level, respectively. Pod length exhibited a significant and negative correlation with the number of SB (-0.713) at the genotypic level and with the number of NPP at both genotypic (-0.405) and phenotypic level (-0.700). The NPP per plant was associated positively with the number of PB (0.858, 0.649), SB (0.718, 0.503) at the genotypic and phenotypic levels, respectively. The number of SB exhibited a positive and significant correlation with the number of PB (0.567, 0.554) at both levels (genotypic and phenotypic). At the genotypic level, DTM showed a significant and positive correlation with DTF (0.390) (Table 4).

3.5 Path Analysis

Path coefficient analysis estimates the direct and indirect effects of several yield component traits on SY. Seed yield was used as a dependent variable (effect) and the rest of the traits were treated as independent variables (causes). The highest positive direct effect on SY was showed by siliquae length (0.438) followed by the number of NPP (0.407), TSW (0.364), PB (0.211), SB (0.210) and DTF (0.131) in the present study. The negative direct effect was shown in DTM (-0.416) and PH (-0.160) on SY. The positive indirect effect was recorded by PL (0.302) *via* TSW; TSW (0.251) and DTM (0.023) *via* PL; PB (0.181), SB (0.151) NPP; PB (0.120), NPP (0.292) *via* SB; NPP (0.349), SB (0.119) *via* NPP; DTF (0.051), PB (0.073) *via* DTM; DTM (0.127) *via* PH; NPP (0.119) *via* DTM (Table5). The positive indirect effect is per results that have been reported earlier [21]. Number of NPP (-0.256), number of SB (-0.165) *via* TSW and PL; TSW (-0.229), PL (-0.177) *via* NPP and SB; DTM (-0.162) *via* DTF; TSW

Table 2. Tukey's pairwise mean comparison and statistical parameters of agronomic traits among 25 Mustard accessions

Genotype	DTF	DTM	PH	PB	SB	NPP	PL	TSW	SY (Kg/ha)
Ashirwad	54^{cde}	126^{abcde}	209.70^{bc}	6^{bcd}	11^{hij}	340^{abc}	5.14^{cde}	2.80^{hi}	1798.50^{fg}
Basanti	58^{bc}	130^{abc}	155.90^{j}	5de	12^{ghi}	259^{abc}	5.30^{bcd}	3.09^{ghi}	869.50^{mn}
BR40	57^{bcd}	121^{def}	174.60^{i}	6^{cd}	14^{efg}	343^{abc}	4.49^{jk}	3.86^{ef}	2217.50^{de}
CS-54	58^{bc}	132^{a}	127.25^{k}	5de	14^{efg}	260^{abc}	4.69^{ghi}	3.59^{fg}	1565.00^{ghi}
Durgamini	47^{ghi}	116^{f}	218.60^{ab}	4^{ef}	11^{hij}	206^{bc}	5.45^{ab}	3.81^{ef}	2442.00^{bcd}
Gita	58^{bc}	122^{def}	196.20^{ef}	5de	15^{def}	247^{abc}	4.70^{ghi}	4.10^{def}	1787.00^{fgh}
IC335858	45^{hi}	122^{def}	213.60^{bc}	6^{cd}	10^{hij}	321^{abc}	4.86^{fgh}	3.91^{ef}	1747.50^{gh}
IC339953	57^{bcd}	126^{abcde}	183.70^{ghi}	6^{bcd}	16^{cde}	503^{abc}	4.33^{klm}	2.62^{hij}	1686.50^{ghi}
IC355856	48^{ghi}	128^{abcd}	190.40^{efg}	6^{bcd}	20^{a}	338^{abc}	4.63^{hij}	2.89^{hi}	1078.00^{klm}
IC405235	51^{efg}	125^{abcde}	198.50^{de}	4^{ef}	9^{ijk}	200^{bc}	4.18^{lm}	3.18^{gh}	682.50^{n}
IC447111	57^{bcd}	125^{abcde}	179.90^{hi}	7^{bc}	17^{bcd}	515^{abc}	5.04^{def}	3.67^{fg}	2427.00^{cd}
IC571630	60^{b}	124^{cdef}	212.20^{bc}	5de	19^{ab}	582^{ab}	4.37^{jkl}	2.02^{jkl}	1260.50^{jk}
IC571649	67^{a}	131^{ab}	211.90^{bc}	7^{b}	16de	536^{abc}	4.92^{efg}	2.59^{hijk}	2568.00^{abc}
IC571678	53^{cde}	123^{bcdef}	178.10^{i}	4^{ef}	8^{jk}	197^{bc}	5.00^{ef}	5.51^{a}	949.00^{lm}
IC58968	68^{a}	124^{bcdef}	226.10^{a}	7^{b}	21^{a}	461^{abc}	4.19^{lm}	2.00^{kl}	1784.50^{fgh}
IC589686	50^{efgh}	127^{abcd}	189.10^{efgh}	5de	10^{hij}	278^{abc}	5.46^{ab}	3.86^{ef}	1800.00^{fg}
IC589690	50^{efgh}	127^{abcd}	216.10^{b}	10^{a}	19^{ab}	622^{a}	3.90^{n}	1.52^{l}	1072.00^{klm}
IC597879	44^{i}	119^{ef}	165.00^{j}	5de	19^{abc}	395^{abc}	4.08^{mn}	2.54^{ijk}	2005.50^{ef}
Narinder Rai	51^{efg}	125^{abcde}	206.40^{cd}	6^{bcd}	10^{hij}	364^{abc}	5.08^{def}	5.20^{ab}	2394.00^{cd}
Jagannath	53^{def}	126^{abcde}	188.90^{fgh}	4^{f}	8^{jk}	138^{c}	5.05^{def}	4.35^{cde}	1459.50^{ij}
Jawahar Mustard	48^{ghi}	126^{abcde}	191.20^{efg}	7^{b}	12^{fgh}	337^{abc}	4.83^{fgh}	4.09^{def}	2396.00^{cd}
Kanti	54^{cde}	124^{bcdef}	209.90^{bc}	4^{ef}	7^{k}	268^{abc}	5.70^{a}	5.04^{ab}	1133.00^{kl}
Kranti	48^{fghi}	127^{abcd}	178.00^{i}	7^{bc}	15^{def}	294^{abc}	4.38^{jkl}	3.86^{ef}	1558.00^{hi}
Maya	48^{fghi}	122^{cdef}	159.30^{j}	6^{bcd}	9^{jk}	590^{ab}	5.38^{bc}	4.66^{bcd}	2728.50^{a}
RH119	61^{b}	125^{abcde}	183.80^{ghi}	6^{bcd}	12^{ghi}	309^{abc}	5.54^{ab}	4.79^{bc}	2678.50^{ab}
Overall Mean+SEM	54±0.81	125±1.35	179.49±1.65	6±0.13	14±0.40	356±71.46	4.83±0.05	3.58±0.149	1763.52±16.38
Max.	68	132	226.1	9.5	21	622	5.7	5.56	2822
Min.	44	116	127.25	4	7	138	3.9	1.3	654
CV (%)	2.12	1.53	1.22	3.23	4.29	28.35	1.42	4.17	3.28
StdDev	6.29	3.73	22.97	1.37	4.22	152.2	0.496	1.04	607.06

Note: Genotypes with a unique single letter are significantly different from another genotype
** Significance at P=0.01, *** Significance at P=0.001, CV = coefficient of variation; SD= standard deviation; DTF = days to 50% flowering; DTM = days to 95% maturity; PH = plant height; PB= primary branches; SB=secondary branches; NPP = number of pods per plant; PL = pod length; TSW = thousand seed weight; ; SY = seed yield per hectare

Table 3. Estimates of GCV, PCV, heritability, genetic advance (GA) & genetic advance as a percent of mean (GAM)

Trait	Coefficient of variation		Heritability (broad sense)	GA	GAM (5%)
	GCV (%)	PCV (%)			
DTF	11.58	11.77	0.97	12.66	23.46
PH	12.12	12.18	0.99	47.33	26.37
DTM	2.60	3.01	0.74	5.77	4.61
PB	23.38	23.61	0.98	2.66	47.47
SB	32.08	32.36	0.98	8.58	65.57
NPP	32.33	43.00	0.57	178.44	50.07
PL	10.33	10.42	0.98	1.01	21.02
TSW	29.85	29.85	1.00	2.17	62.50
SY (Kg/ha)	34.28	34.38	0.99	576.43	70.41
Max.	**34.28**	**43.00**	**1.00**	**576.43**	**70.41**
Min.	**2.60**	**3.01**	**0.57**	**1.01**	**4.61**

Table 4. Estimates of genotypic and phenotypic correlation for different quantitative characters in 25 germplasm lines of Indian mustard

Characters		DTF	PH	DTM	PB	SB	NPP	PL	TSW	SY (Kg/ha)
DTF	rg	1	0.104	0.390*	0.194	0.296	0.292	-0.001	-0.227	0.091
	rp	1	0.100	0.318	0.193	0.290	0.204	0.002	-0.223	0.085
PH	rg		1	-0.305	0.212	0.098	0.201	-0.061	-0.283	-0.002
	rp		1	-0.266	0.209	0.101	0.147	-0.061	-0.281	-0.004
DTM	rg			1	0.347	0.131	-0.017	-0.056	-0.185	-0.314
	rp			1	0.287	0.089	0.137	-0.026	-0.160	-0.259
PB	rg				1	0.567***	0.858***	-0.355	-0.479**	0.197
	rp				1	0.554***	0.649***	-0.345	-0.474**	0.192
SB	rg					1	0.718***	-0.713***	-0.789***	-0.009
	rp					1	0.503**	-0.700***	-0.782***	-0.007
NPP	rg						1	-0.405*	-0.628***	0.346
	rp						1	-0.298	-0.472**	0.251
PL	rg							1	0.690***	0.333
	rp							1	0.684***	0.329
TSW	rg								1	0.237
	rp								1	0.236
SY(Kg/ha)	rg									1
	rp									1

*ns, *, ** not significant, significant at P≤0.05 or significant at P≤0.01, respectively*

DTF = days to 50% flowering; PH = plant height; DTM = days to 95% maturity; PB= primary branches; SB=secondary branches; NPP = number of pods per plant; PL = pod length; TSW = thousand seed weight and SY = grain yield per hectare

Table 5. Direct and indirect effects for different characters on seed yield per plant in 25 germplasm lines of Indian mustard

Characters	DTF	PH	DTM	PB	SB	NPP	PL	TSW
DTF	**0.131**	0.014	0.051	0.025	0.039	0.038	0	-0.03
PH	-0.017	**-0.16**	0.049	-0.034	-0.016	-0.032	0.01	0.045
DTM	-0.162	0.127	**-0.416**	-0.144	-0.054	0.007	0.023	0.077
PB	0.041	0.045	0.073	**0.211**	0.12	0.181	-0.075	-0.101
SB	0.062	0.021	0.027	0.119	**0.21**	0.151	-0.15	-0.165
NPP	0.119	0.082	-0.007	0.349	0.292	**0.407**	-0.165	-0.256
PL	-0.001	-0.027	-0.024	-0.155	-0.312	-0.177	**0.438**	0.302
TSW	-0.083	-0.103	-0.067	-0.174	-0.287	-0.229	0.251	**0.364**
SY Kg/ha	**0.091**	**-0.003**	**-0.314**	**0.197**	**-0.009**	**0.346**	**0.333**	**0.237**

Residual effect = 0.6671; Direct effect on main diagonal (Bold Figure)
DTF = days to 50% flowering; PH = plant height; DTM = days to 95% maturity; PB= primary branches;
SB=secondary branches; NPP = number of pods per plant; PL = pod length;   TSW = thousand seed weight and
SY = grain yield per hectare

(-0.103) *via* PH; had a negative indirect effect on SY. The most negligible indirect effect was recorded for PL *via* DTF. The high estimate of residual effect (0.667) indicates the involvement of some other characters besides studied ones that contribute to yield. NPP and TSW were only two traits that showed a significant and positive correlation (0.346 and 0.237) with SY and the highest positive direct effect (0.407 and 0.364) on SY in the traits studied.

3.6 Yield Performance

Based on yield performance, the top five lines are Maya (2729 kg/ha) followed by RH 119 (2678 kg/ha), IC 571649 (2568 kg/ha), Durgamini (2442 kg/ha), and IC 447111 (2427 kg/ha) whereas IC 355856, IC 589690, IC 571678, Basanti and IC 405235 were the lowest yielder (Table 1). It is also depicted in Tukey's mean compression Maya (2728.5a) grouped into "a" while, RH 119 (2678.5ab) shares the same letter and is grouped as "ab" ranking. Therefore, the identification of high-yielding donor parents with desirable yield component traits for mustard improvement is of paramount importance.

4. CONCLUSION

From the results of the present study, it is inferred that the indirect selection via contributing traits could be an effective strategy for the selection of higher-yielding lines. Attention should be given to these yield contributing traits during the selection programme to obtain high-yielding lines of mustard which could, in turn, be used to develop hybrid varieties with desirable agronomical characters. A considerable genetic variation has been observed among the breeding lines for studied traits. Most of the studies traits like TSW, SY, PL, SB, and PB had high heritability coupled with high genetic advances. The number of siliquae plant⁻¹, PB and SB, and PL are the most contributing traits to SY, and selection of genotypes based on these traits would be effective. Similarly, the traits such as siliquae length, number of NPP, TSW, PB, SB, and DTF showed a highly direct effect on seed yield and these traits could be used for the direct selection of high yielding genotypes. The high-yielding lines Maya, RH 119, IC 571649, Durgamini, and IC 447111 have been identified, may be used in the hybridization program for mustard improvement.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Meena ML and Singh D. Dissemination of salt-tolerant mustard varieties through frontline demonstrations approach for sustainable mustard production in Pali district of Rajasthan. Journal of Oilseed Brassica. 2019;10(2):122-129.
2. Yadav S and Pandey A. Genetic variability and trait association studies in Indian mustard (*Brassica juncea* L.). International Journal of Chemical Studies. 2018;6(5): 1726-1731.

3. Singh S, Dwivedi AK, Ashutosh OM and Kumar K. Genotypic variability, heritability and genetic advance in Indian mustard [*Brassica juncea*(L.) Czern & Coss.] Genotypes. International Journal of Pharmacognosy and Phytochemistry. 2018;7(3):350-352.

4. Yadava DK, Giri SC, Vignesh M, Vasudev S, Yadav AK, Dass B, Singh R, Singh N, Mohapatra T and Prabhu KV. Genetic variability and trait association studies in Indian mustard (*Brassica juncea L.).* Indian Journal of Agriculture Science. 2011;81: 712-716.

5. Meena HS, Kumar A, Singh VV, Meena PD, Ram B and Kulshrestha S. Genetic variability and interrelation of seed yield with contributing traits in Indian mustard (*B. juncea* L.). Journal of Oilseed Brassica. 2017;8:131-137.

6. Tripathi N, Kumar K and Verma OP. Genetic variability, heritability and genetic advance in Indian mustard [*Brassica juncea* (L.) Czern and Coss] for seed yield and its contributing attributes under normal and saline/alkaline conditions. International Journal of Scientific Research. 2013;6(4): 190-290.

7. Singh BP and Chowdhury RK. Correlation and path coefficient analysis of seed yield and oil content in mustard (*B. juncea L.*). Canadian Journal of Genetics and Cytology. 1983;25:312-317.

8. Gulles AA, Bartolome VI, Morantte RIZA, Nora LA, Relente CE, Tala DT and Ye G. Randomization and analysis of data using STAR [Statistical Tool for Agricultural Research]. Philippine Journal of Crop Science. 2014;39:137.

9. Ahuja S, Malhotra PK, Bhatia VK and Parsad R. Statistical package for agricultural research (SPAR 2.0). J. Ind. Soc. Agril. Statist, 2008;62(1):65-74.

10. Rauf MA and Rahim MA. Genetic Variability Studies among Yield and Its Contributing Traits in Mustard (*Brassica napus* L.). Adv. Zoo. Bot. Res. 2018;6(4): 101-108.

11. Mondal SK and Khajuria MR. Genetic analysis for yield attributes in mustard. Environment and Ecology. 2000;18(1):15.

12. Ram S and Verma N. Genetic variability for yield and yield components in Indian mustard (*Brassica juncea L.*). Journal of Oilseeds Research. 2011;27(2):170-171.

13. Shekhawat K, Rathore SS, Premi OP, Kandpaland BK and Chauhan JS. Advances in Agronomic Management of Indian Mustard (*Brassica juncea* (L.) Czern and Coss: An Overview Journal of Agronomy. 2012:1-14.

14. Rathod VB, Mehta DR and Solanki HV. Genetic variability and divergence for oil content and yield attributes in Indian mustard [(*B. juncea* L.) Czern&Coss]. Journal of Pharmacognosy and Phytochemistry.2017; 6: 1507-1509.

15. Meena HS, Kumar A, Ram B, Singh VV, Singh BK, Meena PD and Singh D. Combining ability and heterosis for seed yield and its components in Indian mustard (*Brassica juncea L.*). Journal of Agriculture, Science and Technology. 2015;17:1861-1871.

16. Chaudhary SK and Sharma SK. Notes on the inheritance of some quantitative characters in a cross of Indian mustard. Indian Journal of Agricultural Sciences. 1982; 5(2):23-25.

17. Bind D, Singh D and Dwivedi VK. Genetic variability and character association in Indian mustard [*Brassica juncea* L. czerns & coss]. Agricultural Science Digest. 2014;34(3):183–188.

18. Iqbal MS, Haque MS, Nathand UK and Hamfim I. Genetic diversity analysis of mustard germplasm based on phenotypic traits for selection of short duration genotypes. International Journal of Agriculture Science. 2014;3(8):141-156.

19. Semahegn Y and Tesfaye M. Variability, Heritability and Genetic Advance Analysis for Some Morphological Characters in Oilseed Brassica Breeding Lines. Molecular Plant Breeding. 2016;7(20):1-8.

20. Johnson HW, Robinson HF and Comstoc R. Estimates of genetic and environmental variability in soybeans. Agronomy Journal. 1955;47:314-318.

21. Kumar R, Kaur S, Bala K, Kaur S and Sharma L. Assessment of genetic variability, correlation and path analysis for yield traits in F1 hybrids of Indian mustard (*Brassica juncea* L.). Agriways. 2019;7(1): 1-7.

22. Afrin S, Mahmud K, Rahid F, Bhuiyan M and Rahim M. Assessment of genetic variation among advanced lines of *Brassica napus* L. Agronomski Glasnik. 2011;4(5):201-225.

23. Synrem GJ, Rangare NR, Myrthong I and Bahadur DM. Variability studies in Intra-specific crosses of Indian mustard [*Brassica juncea* (L.) Czern and Coss.] genotypes. IOSR Journal of Agriculture and Veterinary Science.2014;7:29-32.