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Delineation of inbred lines of Indian mustard into diverse gene pools based on agro-morphological traits

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Abstract: The present study was conducted to explore the variability generated through recombination breeding for nine economically important traits in Indian mustard (*Brassica juncea* L. Czern & Coss.). Delineation of the inbred lines to different gene pools, based on genetic diversity, enables their utilisation in hybrid breeding. The unweighted pair group method with arithmetic mean (UPGMA) and a Euclidean distance matrix was used to delineate the inbred lines to clusters. The variability was studied using the range and coefficients of variation of the traits. Significant variability was observed for all studied traits except for oil content and days to maturity. 128 Indian mustard genotypes were grouped into four distinct gene pools based on genetic diversity. A set of 20 most diverse genotype combinations was produced. Promising inbred lines were identified and recommended as donors for the respective trait. The pedigree analysis of the inbred line groups revealed, that recombination breeding caused a large diversity as confirmed by the assignment of inbred lines with the same parentage to specific clusters.

Keywords: *Brassica juncea*; characterization; genetic diversity

*Brassica*s, collectively known as rapeseed-mustard, are important oilseed crops in India and stand second after soybeans in production among the eight annual edible oilseeds cultivated in India. Among the four oleiferous *Brassica* species grown in India, a major area is under Indian mustard (*Brassica juncea)*, which contributes about 80% of the total rapeseed-mustard production in the country (Thakur et al. 2020). All four oleiferous *Brassicas* are cultivated over about 6.12 million ha with 9.26 million tonnes of oilseed production with yield levels of 1 511 kg/ha, contributing about 24.7% and 29.4%, respectively, to the total area and production of oilseeds during 2018–2019 (Anonymous 2019). The current productivity level of 1 511 kg/ha in India is far below than that of the world's average of about 1 979 kg/ha. Though India has the varieties with a high yield potential ranging between 2 000–2 500 kg/ha, there is a wide fluctuation in the area, production and productivity of this crop due to the diverse agroclimatic conditions of the growing regions and vulnerability of these crops to diseases and insect pests.

Estimation of the genetic diversity is essential for genetic improvement. It is generally acknowledged that information about germplasm diversity and genetic relatedness in elite breeding materials is a central component in plant breeding (Mukhtar et al. 2002). Genetic diversity is a very significant factor for any hybridisation programme focusing on genetic improvement of the yield, particularly in self-pollinating crops. Genetic diversity among the population can be resolved utilising morphological,

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biochemical and molecular approaches (Mohammadi & Prasanna 2003). Evaluation of the genetic diversity in *B. juncea* using phenotypic characteristics has been carried out by many researchers (Singh et al. 2010, 2018; Sharma et al. 2022). Heterosis breeding can play an important role in bringing self-reliance in the edible oil sector of India through increasing the productivity of mustard plants. The success of heterosis breeding necessitates the creation of variability, the characterisation of genotypes generated through recombination breeding, the delineation of recombined genotypes into diverse gene pools, identification of parents from diverse gene pools on the basis of combining ability, and conversion of the identified inbred lines into the respective male sterile/restorer lines for hybrid seed production. In the present investigation, our objectives were to quantify the extent of the variability for the economically important traits in Indian mustard inbred lines, the delineation of inbred lines into diverse gene pools, identification of promising inbred lines for each trait and diverse combinations based on the distance for further studying their combining ability and establishing the relationship among the economically important traits and their direct effects on the seed yield.

MATERIAL AND METHODS

The plant material of the present study comprised 124 inbred lines of Indian mustard developed under a hybrid development programme and four released varieties used as checks; Pusa Mustard (PM) 25, NRCHB 101, Kranti and RGN 73 (Table 1). The inbred lines were developed over the years through hybridisation, followed by selection and these inbred lines are maintained through selfing. All 128 genotypes of Indian mustard were evaluated in an augmented block design for two consecutive years, 2018–2019 and 2019–2020. Each genotype was seeded in 2 rows 3 m in length spaced 45 cm apart, with a plant-to-plant distance of 15 cm maintained by proper thinning. A standard package of practices was followed to raise a good crop. The data were recorded on 9 traits, *viz*, the days to flower initiation, days to flower senescence, days to maturity, plant height (cm), main raceme length (cm), 1 000-seed weight (g), seeds per siliqua, seed yield (g) and oil content. Observations on the days to flower initiation, days to flower senescence and days to maturity were recorded on a plot basis. Five competitive plants from each genotype were used for recording the observations on the plant height (cm), main raceme length (cm) and seeds per siliqua. The seed yield was recorded on a plot basis and the seed weight (g) was recorded on randomly drawn 1 000 seeds from the bulk yield of a plot. The oil content (%) was recorded on a randomly drawn seed sample from the bulk yield.

Adjusted mean values for each trait were obtained through a statistical analysis in the augmented block design for each year, separately. The mean of the two year adjusted mean estimates for each trait were subjected for further statistical analysis. The variability was studied through a range as well as coefficients of variation. The genetic divergence was estimated based on the Euclidean distance using DARwin 6.0 software (Perrier & Jacquemoud-Collet 2006). The delineation of the different genotypes into different clusters was performed through the unweighted pair group method with arithmetic mean (UPGMA) using a Euclidean distance matrix. The correlation coefficients at the phenotypic level were estimated according to Johnson et al. (1955). The path coefficient investigation was accomplished by using the correlation coefficients as recommended by Dewey and Lu (1959). The path coefficient analysis was conducted by taking the seed yield/plant as the dependent variable and the other observed characteristics as the independent variable.

RESULTS AND DISCUSSION

In the present study, the highest variability was recorded for the seed yield (coefficient of variation, *CV* 19.2%) followed by the 1 000-seed weight, seeds per siliqua, main raceme length and days to flower initiation (Table 2). While the least variability was recorded for the oil content (*CV* 2.5%). The days to maturity and days to flower senescence also reflected the low variability in the present material. It inferred that all the Indian mustard genotypes evaluated in the present study require almost a similar time duration for maturity. However, nine inbred lines flowered earlier than the check, PM 25 for earliness. Sharma et al. (2022) also reported low variability for the maturity duration in Indian mustard germplasm accessions. The flowering duration was estimated by subtracting the days to flower initiation from the days to flower senescence. Among the check cultivars, PM 25 had longest (46 days) flowering duration, however, 61 inbred lines had a flowering duration more than PM 25, being the longest in DRMRIJ18-9

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Table 1. Inbred lines of the Indian mustard used in the present study and their parentage

S. No.	Name of inbred	Parentage	S. No.	Name of inbred	Parentage
1	DRMRIJ18-3	QM-16	27	DRMRIJ18-39	YM 6 × EC 399307
2	DRMRIJ18-5	EC 399288 × PCR 11) × (B 33 × Sanjucta Asech)	28	DRMRIJ18-40	EC 597313/MJR 9
3	DRMRIJ18-6	EC 552577/EC 597309	29	DRMRIJ18-41	MJR 1-3
4	DRMRIJ18-7	MJR 9	30	DRMRIJ18-44	KLM 227/EC597313
5	DRMRIJ18-9	QM-16	31	DRMRIJ18-46	MJA 11/SSR1-9
6	DRMRIJ18-10	PM 28	32	DRMRIJ18-47	HB9908/HB9916
7	DRMRIJ18-12	MJA 40/MJR 9	33	DRMRIJ18-49	MJA 39/MJR 14
8	DRMRIJ18-13	DR7/HB101	34	DRMRIJ18-51	EC597309/NUDHYJ3/RL1359
9	DRMRIJ18-15	ZEM2/HB9916	35	DRMRIJ18-53	MJA 11/SSR1-9
10	DRMRIJ18-16	IJ- 31/LET- 36	36	DRMRIJ18-54	39-3-2-2/EC597313
11	DRMRIJ18-17	PM 28	37	DRMRIJ18-55	(HB9908/HB9916) × (RH30/RH8812)
12	DRMRIJ18-19	EC 597340/EC552577	38	DRMRIJ18-56	MJA 40/MJR 9
13	DRMRIJ18-20	ZEM 2/BPR 6-166	39	DRMRIJ18-57	EC 597313/MJR 13
14	DRMRIJ18-21	39-3-2-3/EC597313	40	DRMRIJ18-59	MJA 15/MJR 13 (early)
15	DRMRIJ18-22	PM 28	41	DRMRIJ18-60	MJA 36/MJR 8
16	DRMRIJ18-23	78-1-1-2/EC 597313	42	DRMRIJ18-62	IJ 31 × LET 36
17	DRMRIJ18-25	JGM1-11/HB101/HB101/ HB101 × HB 101	43	DRMRIJ18-64	HB 9918/HB 9914
18	DRMRIJ18-26	MJA 40/MJR 9	44	DRMRIJ18-65	YS juncea
19	DRMRIJ18-27	MJA 36/MJR 8	45	DRMRIJ18-67	MJA 34/SSR1-8
20	DRMRIJ18-30	NRCDRM 62	46	DRMRIJ18-68	HB 9912/HB 9924-1
21	DRMRIJ18-31	EC 597313	47	DRMRIJ18-70	MJA 27 × MJR 9 × 39-3-2-2
22	DRMRIJ18-33	MJA 2 × MJR 4 × EC 552577	48	DRMRIJ18-71	78-1-1-2/EC 597313
23	DRMRIJ18-34	ZEM2 × HB101	49	DRMRIJ18-72	EC 597311
24	DRMRIJ18-35	78-1-1-2/EC 597313	50	DRMRIJ18-75	MJA 34 × MJR 4 × 39-3-2-2
25	DRMRIJ18-36	NRCDRM 34	51	DRMRIJ18-77	HB 9909 × EC 597309
26	DRMRIJ18-37	MJR 13	52	DRMRIJ18-78	KLM 227/EC597313
53	DRMRIJ18-80	DR7/HB101	82	DRMRIJ18-122	MJR- 3/MCB 1-3
54	DRMRIJ18-81	Zem 2/Varuna	83	DRMRIJ18-123	MJR3/MCB 1-3
55	DRMRIJ18-83	HB 9914/HB9918	84	DRMRIJ18-125	MCB 1
56	DRMRIJ18-84	MJA34/SSR1-8	85	DRMRIJ18-126	MCB 1
57	DRMRIJ18-85	MJA 2 × MJR 2 × DRMRIJ 20	86	DRMRIJ18-127	MCB 1
58	DRMRIJ18-87	MJA 39/MJR 14	87	DRMRIJ18-128	MCB 1
59	DRMRIJ18-88	MJA 39/MJR 14	88	DRMRIJ18-129	MJR3/Pusa Swarnim
60	DRMRIJ18-90	MJA 25/MCR 1-11	89	DRMRIJ18-131	MJR3/Pusa Swarnim
61	DRMRIJ18-91	EC 597320/EC 597313	90	DRMRIJ18-132	MJR3/Pusa Swarnim
62	DRMRIJ18-93	MJA34/SSR1-8	91	DRMRIJ18-133	MJR3/Pusa Swarnim
63	DRMRIJ18-94	MJA25/HB 101	92	DRMRIJ18-135	MJR3/Pusa Swarnim
64	DRMRIJ18-95	Mori R/Zem 2	93	DRMRIJ18-136	MJR3/Pusa Swarnim
65	DRMRIJ18-96	EC597309/NUDHYJ3/RL1359	94	DRMRIJ18-137	MJR3/Pusa Swarnim
66	DRMRIJ18-99	39-3-2-3/EC597313	95	DRMRIJ18-138	MJR3/Pusa Swarnim
67	DRMRIJ18-100	IJ 31 × LET 36	96	DRMRIJ18-139	MJR3/Pusa Swarnim
68	DRMRIJ18-102	SSR2/WF2	97	DRMRIJ18-140	MCB 1

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Table 1 to be continued

S. No.	Name of inbred	Parentage	S. No.	Name of inbred	Parentage
69	DRMRIJ18-106	MJA 11/SSR1-9	98	DRMRIJ18-141	MCB 1
70	DRMRIJ18-107	DR7/HB 101	99	DRMRIJ18-142	DRMRIC 16-58
71	DRMRIJ18-108	78-1-1-2/EC 597313	100	DRMRIJ18-143	MJA 39-3-2-2/MJR 8
72	DRMRIJ18-109	78-1-1-2/EC 597313	101	DRMRIJ18-144	MJA 39-3-2-2/MJR 8
73	DRMRIJ18-111	OJR-1	102	DRMRIJ18-145	MJA 25/MCR 1-11
74	DRMRIJ18-112	EC 552577	103	DRMRIJ18-146	MJA 36/MJR 8
75	DRMRIJ18-113	EC 399286 (OP)	104	DRMRIJ18-147	MJA 36/MJR 8
76	DRMRIJ18-114	EC 597309	105	DRMRIJ18-149	MJA 14/MJR 3
77	DRMRIJ18-115	EC 597316	106	DRMRIJ18-150	IJ 31 × LET 36
78	DRMRIJ18-116	EC 552574	107	DRMRIJ18-152	IJ 31 × LET 36
79	DRMRIJ18-117	IJ 31 × YSH 401	108	DRMRIJ18-153	IJ 31 × LET 36
80	DRMRIJ18-118	MJA11/MJR4//IJ31	109	DRMRIJ18-154	IJ 31 × LET 36
81	DRMRIJ18-119	EC 399288/EC 597309	110	DRMRIJ18-155	IJ 31 × LET 36
111	DRMRIJ18-156	EC 597340/EC552577	121	DRMRIJ18-168	MCR1-1 juncea
112	DRMRIJ18-157	MH 7-9 A (OJA1)/OJR4	122	DRMRIJ18-169	MCR1-1 juncea
113	DRMRIJ18-158	JN 018/EC597313	123	DRMRIJ18-170	MCR1-1 juncea
114	DRMRIJ18-159	MJA 27/MCR1-10	124	DRMRIJ18-171	MCR1-1 juncea
115	DRMRIJ18-160	EC 552577/EC 597313	125	PM 25	Pusa Mustard 25 (check)
116	DRMRIJ18-162	IJ 31/Kranti	126	NRCHB 101	NRCHB 101 (check)
117	DRMRIJ18-163	IJ 31/Kranti	127	Kranti	Kranti (check)
118	DRMRIJ18-164	EC 552577/EC 597309	128	RGN 73	RGN 73 (check)
119	DRMRIJ18-165	MCR1-1 juncea			
120	DRMRIJ18-167	MCR1-1 juncea			

S. No. – serial number

(64 days). PM 25 was the earliest maturing among the check cultivars, but five inbred lines matured earlier than PM 25. Similarly, 14 inbred lines were shorter in height than PM 25. Likewise, 27 inbred lines had a longer main raceme than PM 25; 32 lines had bolder seeds than the best check NRCHB 101. Twenty-three lines produced a higher seed yield than the best check NRCHB 101; 47 inbred lines possessed a higher oil content than PM 25; though the range was very low. A total of 39 lines had more seeds per siliqua than the best check NRCHB 101 (Table 3). These genotypes may be used as donors for trait-specific breeding in Indian mustard improvement.

All 128 genotypes were grouped into four clusters based on the agro-morphological traits (Figure 1).

Table 2. Mean, range and coefficients of variation for nine agronomic traits of *B. juncea* inbred lines

Traits	Mean	Range	Minimum	Maximum	*CV* (%)
Days to flower initiation	51.2	25.0	39.5	64.5	11.5
Days to flower senescence	97.4	31.5	82.0	113.5	5.6
Days to maturity	133.6	30.0	114.5	144.5	3.7
Plant height (cm)	184.0	78.0	139.0	217.0	8.2
Main raceme length (cm)	72.2	52.5	49.5	102.0	12.5
1 000-seed weight (g)	4.7	3.9	2.8	6.7	18.6
Seeds per siliqua	14.9	15.2	9.9	25.1	16.0
Oil content (%)	39.9	5.1	37.5	42.7	2.5
Seed yield (g/plot)	643.2	599.5	352.5	952.0	19.2

CV – coefficient of variation

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Cluster 1 was the largest cluster comprising 62 genotypes, which was further subdivided into two subclusters 1A and 1B – each comprising 31 genotypes. Clusters 2, 3 and 4 were comprised of 18, 43 and 5 genotypes, respectively. Cluster 3 was also subdivided into two subclusters 3A and 3B, comprising 24 and 19 genotypes, respectively. There was no much difference among the cluster's mean for the days to flower initiation, days to flower senescence, days to maturity, plant height, main raceme length and oil content, however, the clusters differed for the seed weight, seed yield and seeds per siliqua, indicating their contribution to the diversity among the present set of inbred lines (data not shown). Cluster 4 possessed five inbred lines which displayed the highest cluster mean for the seed weight, seed yield, oil content and seeds per siliqua. In the present set of inbred lines, we analysed the grouping pattern of the inbred lines sharing a common parentage. Nine inbred lines; DRMRIJ18-129, DRMRIJ18-131, DRMRIJ18-132, DRMRIJ18-133, DRMRIJ18-135, DRMRIJ18-136, DRMRIJ18-137, DRMRIJ18-138 and DRMRIJ18-139 (serial No. 88–96, respectively), derived from the cross MJR3 X Pusa Swarnim, were grouped into three different clusters 1, 2 and 3. Similarly, eight inbred lines; DRMRIJ18-16, DRMRIJ18-62, DRMRIJ18-100, DRMRIJ18-150, DRMRIJ18-152, DRMRIJ18-153, DRMRIJ18-154, and DRMRIJ18-155 at S. No. 10, 42, 67, 106, 107, 108, 109 and 110, respectively, derived from the cross IJ 31 ×

Table 3. Promising inbred lines for the economically important traits in *Brassica juncea*

Trait	Estimates of best check*	Estimates of promising inbreds	Promising inbreds
DFI	44 (PM 25)	< 43 days	DRMRIJ18-44, DRMRIJ18-41, DRMRIJ18-55, DRMRIJ18-54, DRMRIJ18-9, DRMRIJ18-10, DRMRIJ18-116, DRMRIJ18-77, DRMRIJ18-93
DM	126 (PM 25)	< 126 days	DRMRIJ18-84, DRMRIJ18-54, DRMRIJ18-34, DRMRIJ18-17, DRMRIJ18-93
DFS	102 (RGN 73)	> 105 days	DRMRIJ18-9, DRMRIJ18-164, DRMRIJ18-95, DRMRIJ18-25, DRMRIJ18-126, DRMRIJ18-72, DRMRIJ18-15, DRMRIJ18-170
FP	46 (PM 25)	> 54 days	DRMRIJ18-12, DRMRIJ18-13, DRMRIJ18-136, DRMRIJ18-46, DRMRIJ18-23, DRMRIJ18-25, DRMRIJ18-15, DRMRIJ18-20, DRMRIJ18-154, DRMRIJ18-3, DRMRIJ18-9
PH	165 (PM 25)	< 160 cm	DRMRIJ18-55, DRMRIJ18-56, DRMRIJ18-135, DRMRIJ18-133, DRMRIJ18-156, DRMRIJ18-44, DRMRIJ18-93, DRMRIJ18-160, DRMRIJ18-137, DRMRIJ18-70
MRL	79 (NRCHB 101)	> 85 cm	DRMRIJ18-119, DRMRIJ18-116, DRMRIJ18-108, DRMRIJ18-171, DRMRIJ18-91, DRMRIJ18-138, DRMRIJ18-158, DRMRIJ18-111, DRMRIJ18-41
SW	5.3 (NRCHB 101)	> 6.0 g	DRMRIJ18-131, DRMRIJ18-171, DRMRIJ18-159, DRMRIJ18-70, DRMRIJ18-57, DRMRIJ18-83, DRMRIJ18-123, DRMRIJ18-141, DRMRIJ18-85, DRMRIJ18-138
SY	764 (NRCHB 101)	> 835 g/plot	DRMRIJ18-35, DRMRIJ18-16, DRMRIJ18-5, DRMRIJ18-153, DRMRIJ18-123, DRMRIJ18-64, DRMRIJ18-62, DRMRIJ18-155, DRMRIJ18-159, DRMRIJ18-39
OC	40.1 (PM 25)	> 41.5%	DRMRIJ18-7, DRMRIJ18-81, DRMRIJ18-35, DRMRIJ18-143, DRMRIJ18-149, DRMRIJ18-96, DRMRIJ18-90, DRMRIJ18-118, DRMRIJ18-150
S/S	15.8 (NRCHB 101)	> 18.0	DRMRIJ18-109, DRMRIJ18-16, DRMRIJ18-96, DRMRIJ18-159, DRMRIJ18-118, DRMRIJ18-171, DRMRIJ18-39, DRMRIJ18-143, DRMRIJ18-150, DRMRIJ18-137, DRMRIJ18-21, DRMRIJ18-13, DRMRIJ18-170

DFI – days to flower initiation; DM – days to maturity; DFS – days to flower senescence; FP –flowering period; PH – plant height; MRL – main raceme length; SW – seed weight; SY – seed yield; OC – oil content; S/S – seeds per siliqua; *name of the best check for each trait is given in parentheses

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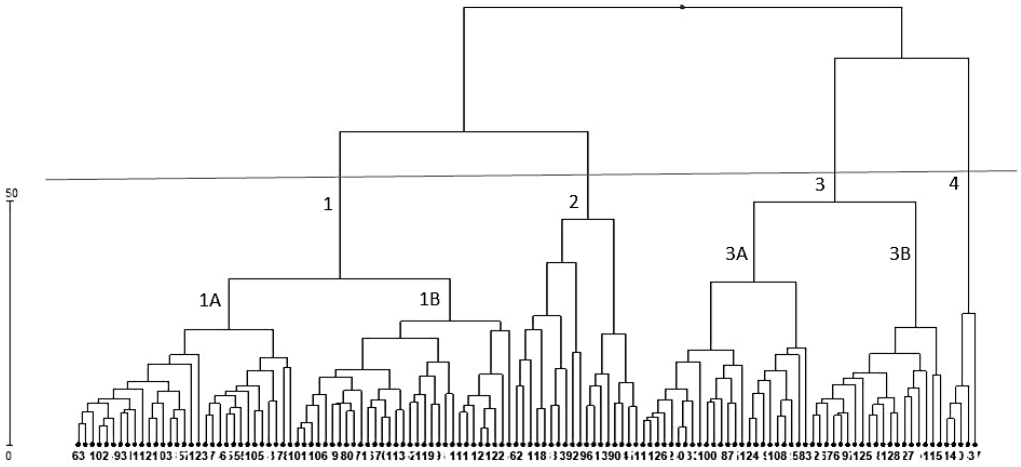

Figure 1. UPGMA-based dendrogram depicting the genetic relationships among the 128 genotypes of Indian mustard

LET 36, were grouped into three different clusters; 1, 3 and 4. Out of five inbred lines; DRMRIJ18-23, DRMRIJ18-35, DRMRIJ18-71, DRMRIJ18-108 and DRMRIJ18-109 at S. No. 16, 24, 48,71 and 72, respectively, derived from the cross 78-1-1-2 × EC 597313, four were grouped into cluster 3, while one inbred line, DRMRIJ18-108, of the same parentage moved to cluster 1. The grouping of the inbred lines derived from the common parentage into different clusters clearly indicates the large extent of the diversity created by the recombination and subsequent selection. Based on the Euclidean distance, the most diverse genotype combinations were derived through the multivariate analysis (Figure 2). These genotypes are most likely to result in high heterosis in the F_1 generation and are also recommended for the hybridisation programme as diverse genotypes are likely to throw a wide spectrum of transgressive segregates in the early generations.

The relationship between the physiological and yield contributing characteristics was studied through the correlation analysis between the characteristics (Table 4). The seed yield had a positive and significant correlation with the 1 000-seed weight (0.326**), seeds per siliqua (0.251**) and oil content (0.194**); while it showed positive, but a non-significant correlation with the days to flower initiation (0.059), days to flower senescence (0.003), days to maturity (0.019), plant height (0.138) and main shoot length (0.056). For the most part, the positive relationship

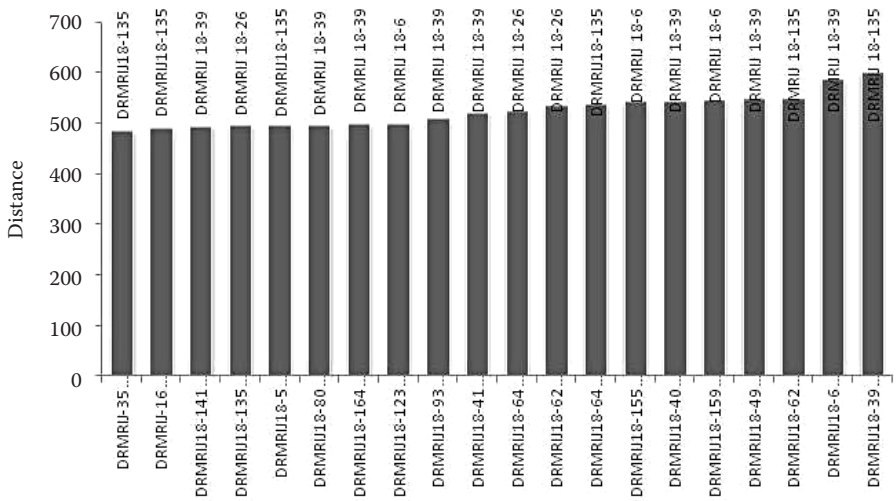

Figure 2. The twenty most genetically diverse combinations of inbred lines in the Indian mustard genotypes under the present investigation

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Table 4. Correlation coefficient among the different traits of the Indian mustard genotypes

Characters	DFI	DFS	DM	PH	MRL	TW	S/S	OC	SY
DFI	1	0.605**	0.503**	0.575**	–0.136 NS	0.070 NS	0.085NS	–0.058NS	0.059 NS
DFS		1	0.517**	0.647**	–0.004 NS	–0.206*	–0.004 NS	–0.094 NS	0.003 NS
DM			1	0.390**	–0.036 NS	0.125 NS	–0.176*	–0.110 NS	0.019 NS
PH				1	0.246**	0.076 NS	–0.066 NS	0.038 NS	0.138 NS
MRL					1	0.129 NS	0.037 NS	0.088 NS	0.056 NS
TW						1	0.156 NS	0.168 NS	0.326**
S/S							1	0.435**	0.251**
OC								1	0.194*
SY									1

DFI – days to flower initiation; DFS – days to flower senescence; DM – days to maturity; PH – plant height; MRL – main raceme length; TW – 1 000-seed weight; S/S – seeds per siliqua; OC – oil content; SY – seed yield; *, ** indicate significance at 0.05 and 0.01 probability level, respectively; NS – non-significant

among these characteristics suggests the possibility of simultaneously improving these significant yield-contributing characteristics. A similar association in Indian mustard genotypes was also reported by Iqbal et al. (2014); Meena et al. (2015) and Singh et al. (2020). Among the other significant and positive correlations, the days to flower initiation with the days to flower senescence, days to maturity and plant height; the days to flower senescence with the days to maturity and plant height; the days to maturity with the plant height and the plant height with the main raceme length were noticeable. These positive relationships indicate that late maturing genotypes are most likely tall. Such results are in concurrence with the results of Banerjee et al. (2017) and Rout et al. (2018). Two significant, but negative, associations between the days to flower senescence with the 1 000-seed weight and between the days to maturity and the seeds per siliqua were observed indicating that as the longer flowering duration reduces the seed weight, which is most likely to happen due to an increase in the number of siliquae, similarly late maturing genotypes are likely to bear a smaller number of seeds per siliqua. Earlier researchers reported the positive and significant relationship of the number of siliquae per plant with the seed yield (Badsra & Chaudhary 2001; Rout et al. 2018; Pal et al. 2019). Consequently, it may be derived that by improving the seed weight, number of seeds per siliqua and number of siliquae per plant through selection either alone or in combination, it will bring improvement in the seed yield of mustard. A path coefficient analysis of nine yield contributing characteristics was also carried out to study the direct effects of these traits on the seed yield (Table 5), which clearly indicated that the 1 000-seed weight (0.28397) had the

Table 5. Path coefficient analysis showing a direct effect (bold) and an indirect effect of eight characteristics on the seed yield in Indian mustard

Characters	DFI	DFS	DM	PH	MRL	TW	S/S	OC
DFI	**–0.0928**	–0.001	–0.00347	0.11408	0.00731	0.0198	0.01775	–0.00272
DFS		–0.00165	–0.00356	0.12827	0.00019	–0.05847	–0.00089	–0.00444
DM			**–0.00689**	0.07722	0.00193	0.0356	–0.03654	–0.00518
PH				**0.19824**	–0.01322	0.02165	–0.01371	0.0018
MRL					**–0.05379**	0.03649	0.00763	0.00414
TW						**0.28397**	0.03246	0.00789
S/S							**0.2076**	0.02047
OC								0.04706

DFI – days to flower initiation; DFS – days to flower senescence; DM – days to maturity; PH – plant height; MRL – main raceme length; TW – 1 000-seed weight; S/S – seeds per siliqua; OC – oil content; bold and diagonal figures indicate the direct effect

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highest positive direct effect on the seed yield. The seeds per siliqua (0.2076) and plant height (0.19824) also displayed a positive direct effect on the seed yield. The days to flower initiation and main raceme length had negative direct effects on the seed yield thereby indicating that the early flowering and long main raceme bearing genotypes may be poor in the yield, hence these are undesirable traits and must be avoided during selection for a high yield. The seed weight and number of seeds per siliqua were the most dependable traits for the selection for the seed yield. The pedigree-wise analysis of the grouping of the inbred lines established the creation of a large extent of diversity through recombination breeding. This is one of the few reports where Indian mustard inbred lines have been thoroughly characterised using agro-morphological traits and are delineated into different diversity groups for further use in hybrid breeding programmes.

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