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Variability and genetic diversity study based on agro-morphological traits in a diverse set of Indian mustard [*Brassica juncea* (L.) Czern. & Coss.] germplasm

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Abstract

Aim: The present investigation was designed to evaluate 150 diverse germplasm of Indian mustard along with five checks for seed yield and attributing traits.

Methodology: A total of 150 genotypes of Indian mustard were evaluated in Augmented Block Design along with five check cultivars (Kranti, Maya, Pusa Bold, NPJ-112, RGN 73) in five blocks. Data were collected for 16 different quantitative traits on each genotype.

Results: ANOVA revealed significant differences between genotypes for all traits studied. Seed yield/plant¹ had significant and positive correlation with most of the yield contributing traits. For seed yield/plant, 15 accessions (DRMR-1722, BDJ-I-538, DRMR-4, JMG-113, DRMR-681, DRMR-1849, DRMR-1697, DRMR-1610, DRMR-1996, DRMR-107, DRMR-1588, DRMR-1379, DRMR-1995, IB-26, DRMR-2116) were significantly superior over best check.

Interpretation: The present study was found useful for identification of diverse genotypes of Indian mustard for different yield attributing traits. The promising lines will be utilized in Indian mustard breeding for improving seed yield and oil content.

Key words: *Brassica juncea*, Correlation, Genetic diversity, Indian mustard, Variability

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Introduction

The family *Brassicaceae* comprises 338 genera and 3709 species (Warwick *et al.*, 2006) including economically important crops, weeds and ornamental plants with aesthetic values (Love *et al.*, 2005). The genus *Brassica* include crop Brassicas which are major source of edible oil, vegetables and condiments. Diploid and allotetraploid species of U triangle are termed as crop Brassicas. Among crop Brassicas, *Brassica napus* L. and *Brassica rapa* L. are categorized as rapeseed and these are cultivated mainly for the production of canola oil, while *Brassica juncea* (L.) Czern. & Coss., *B. carinata* Braun and *B. nigra* (L.) Koch are placed in the mustard group and play a major role in the production of mustard oil and commercial spices (Labana and Gupta, 1993; Singh *et al.*, 2012; Singh *et al.*, 2018). *B. oleracea* L., is used as vegetable and fodder crops, under the common names of cabbage, cauliflower, broccoli, Brussels-sprout and others (Balkaya *et al.*, 2005). Indian mustard (*Brassica juncea*; 2n=36, AABB) is a self-compatible and largely a self-pollinated crop (85-90%). It contributes more than 80% to the total rapeseed-mustard production in the country and is an important component in the oilseed sector (Rambhajan *et al.*, 1991; Shekhawat *et al.*, 2014). Rapeseed-mustard is traditionally grown as a pure crop as well as an intercrop (mixed crop) in marginal and sub-marginal soils in the eastern, northern and north-western states of India. Among these states Rajasthan, Uttar Pradesh, Madhya Pradesh, Haryana, Gujarat are major producer of mustard crop. It requires cool and moist climate during winter season for better growth and productivity (Rathi *et al.*, 2015; Priyanka *et al.*, 2020).

Rapeseed-mustard accounts for nearly one-third of the oil produced in India, making it country's key edible oilseed crop. Among the seven major oilseeds grown in India, rapeseed-mustard shares 28.6% in the total production of oilseeds (Priyanka *et al.*, 2020). During 2019-20, Rapeseed-mustard was sown across 5.52 million hectare area (Second advance estimates, Agricultural Situation in India, 2020) and production was 9.116 million tones (Fourth advance estimates; https://eands.dacnet.nic.in/Advance_Estimates.htm). Rajasthan is one of the major mustard producing states in the country, contributing 40.87 % of total production of India (Agricultural Statistics at a glance, 2018). Despite being the third largest producer (11.3%) of oilseed brassica after Canada and China in the world, India meets 57% of the domestic edible oil requirement through imports (Jat *et al.*, 2019). Hence, there is a need to enhance the edible oil production of the country to meet the domestic demand to reduce our spent on oil import.

In modern plant breeding practice, use of limited germplasm as parents coupled with intensive unidirectional selection for yield over an extended period have critically reduced the genetic diversity in many cultivated crop plants that has led to enhanced susceptibility against diseases, insect pests and climatic vagaries. Chauhan *et al.* (2011) reviewed the Indian mustard cultivars based on their pedigree and reported that 46 of modern Indian mustard cultivars having Varuna variety as one of

the parents directly or indirectly. Chatterjee *et al.* (2016) reported that only limited amount of genetic diversity was transferred in to *B. napus* from its diploid progenitors and further intensive breeding eroded the variations for many traits. Hence, there is a need to incorporate fresh set of diverse lines in mustard breeding programme. Study of variability and genetic diversity can help to understand the structure of germplasm, predict which combinations would produce the best offsprings (Hu *et al.*, 2007), and facilitate to widen the genetic base of breeding material for selection (Qi *et al.*, 2008). Genetic diversity among germplasm lines or populations can be determined using morphological, biochemical and molecular approaches (Mohammadi and Prasanna, 2003). Variability and genetic diversity study in *B. juncea* using agro-morphological traits has previously been done by some researchers but with limited and less diverse genotypes (mostly using either limited varieties and germplasm of indigenous origin (Shekhawat *et al.*, 2014; Gupta *et al.*, 2018; Kumari *et al.*, 2019; Gadi *et al.*, 2020). Therefore, the present investigation was designed to study variability and genetic diversity in a diverse set of 150 germplasm (including indigenous landrace, advance breeding lines, varieties and exotic lines) of Indian mustard for seed yield and attributing traits and to identify promising accessions.

Materials and Methods

The experiment was conducted at research farm of ICAR-Directorate of Rapeseed-Mustard Research during Rabi, 2017-18. ICAR-DRMR is located at 77°3' E longitude, 27°15' N latitude and at an altitude of 178.37 meter above mean sea level. The region falls under Agro climatic Zone III (semi-arid Eastern plain) with sub-tropical and semi-arid climate. A total of 150 genotypes of diverse origin including Indigenous accessions (112), exotic accessions (08) and advanced breeding lines (30) of Indian mustard were evaluated in Augmented Block Design along with 5 checks [Kranti, Maya, Pusa Bold, Pusa Mustard 25 (NPJ-112), RGN 73]. Genotypes were grown in five blocks. Single row of 3m length was planted for each genotype. Five checks were replicated in five blocks. Single row of each genotype was considered as a plot. Row to row spacing was 45 cm and plant to plant spacing within a row was maintained at 10-15 cm by thinning of plants at 15-20 DAS. All recommended agronomic and plant protection measures were followed to grow a healthy, disease and pest free crop. List of genotypes and their origin are presented in Table 1 and features of check varieties is presented in Table 2.

Data were collected on five randomly selected plants for 16 different quantitative traits [IF: Days to initial flowering; F50: Days to 50% flowering; PB: No. of primary branches/plant; SB: No. of secondary branches/plant; FBB: First basal branching (cm); PH: Plant height (cm); FZL: Fruiting zone length (cm); SMS: Silique on main shoot (No.); MSL: Main shoot length (cm); SPY: Seed yield/plant (g); SPW: Dry weight/plant (g); DM: Days to physiological maturity; SL: Silique length (cm); SPS: No. of seeds/silique; TSW: 1000-seed weight (g); OC: Oil content (%)] on individual genotypes. All morphological data were collected in standard units as per DUS guidelines of Indian mustard as developed by

PPV & FRA (PPVFRA, 2009). Oil content in seeds was estimated by Fourier transform near-infrared (FT-NIR) Spectroscopy. Mean data of five plants were used for statistical analysis. Analysis of variance (ANOVA) for different agro-morphological traits was carried out in Augmented Block Design by using online software at SSCNARS website of ICAR (<https://sscnars.icar.gov.in/>). Descriptive statistics estimation and Principal component analysis was done using PAST 3.0 software (Hammer *et al.*, 2001), character association between different traits was estimated based on Pearson's correlation coefficient using SPSS 16.0 software (SPSS, 2007). Euclidean genetic distance between different genotypes were calculated using mean data of different

agro-morphological traits which was further used to construct Neighbor-joining (NJ) dendrogram using DAR win 6.0 software (Perrier *et al.*, 2006).

Results and Discussion

Variability and correlation: 150 genotypes of Indian mustard were evaluated in Augmented Block Design along with 5 checks (Kranti, Maya, Pusa Bold, NPJ-112, RGN 73). ANOVA revealed significant differences between genotypes for all traits studied. Descriptive statistics of the Indian mustard genotypes is presented in Table 3. A good range for different traits was

Table 1: List of genotypes used in the present study

Groups	Origin/Source	Genotypes	No.
Indigenous accessions	Assam, Nagaland, Bihar, Jharkhand, Delhi, Punjab, Himachal Pradesh, Uttar Pradesh, Madhya Pradesh, Andhra Pradesh, Karnataka	DRMR-425, DRMR-473, DRMR-2044, DRMR-1620, DRMR-2065, DRMR-2006, DRMR-390, DRMR-2058, DRMR-2052, DRMR-2055, DRMR-2063, DRMR-1995, DRMR-995, DRMR-1996, DRMR-107, DRMR-1245, DRMR-1327, DRMR-1374, DRMR-1322, DRMR-1311, DRMR-2084, DRMR-1343, DRMR-1346, DRMR-1571, DRMR-2089, DRMR-1635, DRMR-1509, DRMR-1581, DRMR-1242, DRMR-1372, DRMR-1379, DRMR-1993, DRMR-1505, DRMR-1599, DRMR-64, DRMR-1145, DRMR-1215, DRMR-1412, DRMR-1429, DRMR-1458, DRMR-1596, DRMR-1389, DRMR-2024, DRMR-1109, DRMR-1427, DRMR-1105, DRMR-1829, DRMR-2119, DRMR-1644, DRMR-2093, DRMR-2099, DRMR-1631, DRMR-1697, DRMR-2097, DRMR-2102, DRMR-2122, DRMR-2116, DRMR-2152, DRMR-325, DRMR-981, DRMR-1002, DRMR-1489, DRMR-212, DRMR-1615, DRMR-1978, DRMR-1982, DRMR-293, DRMR-929, DRMR-972, DRMR-1073, DRMR-1619, DRMR-1674, DRMR-1684, DRMR-1690, DRMR-1428, DRMR-44, DRMR-1610, DRMR-304, DRMR-901, DRMR-1487, DRMR-1618, DRMR-1688, DRMR-1987, DRMR-966, DRMR-967, DRMR-1067, DRMR-1617, DRMR-1675, DRMR-1845, DRMR-1847, DRMR-1980, DRMR-1986, IB-452, IB-299, B-154, NC-57688, JMG-55 (388), JMG-12, NC-58311, B-56, BDJ-I-164, BDJ-I-778, B-634, BDJ-I-538, IB-714, NC-58396, IB-26, JMG-113, JMG-29, JMG-27, JMG-51, BDJ-I-509	112
Exotic accessions	Canada, Sweden, UK	DRMR-20, DRMR-4, DRMR-36, DRMR-733, DRMR-742, DRMR-743, DRMR-266, DRMR-681	08
Advanced breeding lines	Developed through breeding methods	DRMR-1033, DRMR-1787, DRMR-1722, DRMR-1039, DRMR-1071, DRMR-1072, DRMR-1082, DRMR-1252, DRMR-1309, DRMR-1549, DRMR-1553, DRMR-1634, DRMR-1749, DRMR-1750, DRMR-1753, DRMR-1820, DRMR-1866, DRMR-360, DRMR-1234, DRMR-1554, DRMR-1034, DRMR-1783, DRMR-1849, DRMR-1905, DRMR-138, DRMR-1588, DRMR-1758, DRMR-364, DRMR-974, DRMR-918	30

Table 2: Features of check varieties

Varieties	Pedigree	Ecology	Suitable regions
Kranti	Selection from Varuna	Wider adaptability, Timely sown irrigated conditions	Zone-II, III, V (Delhi, Haryana, Punjab, JK, Rajasthan, Uttar Pradesh, Madhya Pradesh, Bihar, Odisha, West Bengal)
Maya	Varuna x KRV 11	Suitable for timely sown irrigated conditions	Zone-III (Uttar Pradesh, Uttarakhand, Madhya Pradesh and parts of Rajasthan)
Pusa Bold	Varuna x BIC 1780	Suitable for rainfed areas, early as well as late sown, bold seeded	Zone-V (Delhi, Uttar Pradesh, east India)
NPJ-112	SEJ8 x Pusa Jagannath	Suitable for early sown irrigated conditions	Zone-II (Delhi, Haryana, Punjab, J&K, Rajasthan, Western Uttar Pradesh)
RGN 73	RGN 8 x Pusa Bold	Suitable for timely sown irrigated conditions	Zone-III (Uttar Pradesh, Uttarakhand, Madhya Pradesh and parts of Rajasthan)

Table 3: Descriptive statistics of different traits studied in Indian mustard

Traits	IF	F50	PB	SB	FBB	PH	FZL	SMS	MSL	SPY	SPW	DM	SL	SPS	TSW	OC
Min.	42.24	42.88	4.2	8.38	5.94	105.32	56.74	29.2	53.64	4.14	34.16	138.36	2.39	5.02	2.05	36.79
Max.	63.24	70.68	12.48	20.52	65.24	254.32	159.84	63.32	106.44	40.15	415.7	145.56	5.45	25.02	7.14	42.57
Mean	49.47	53.72	7.21	17.45	38.67	202.07	119.90	48.16	77.23	25.19	122.43	142.41	4.03	15.75	4.92	39.94
SEM ($\pm$)	0.28	0.38	0.11	0.39	1.59	1.82	1.48	0.51	0.78	0.69	4.47	0.13	0.05	0.36	0.08	0.09
SD ($\pm$)	3.47	4.77	1.33	4.83	19.82	22.65	18.47	6.31	9.77	8.60	55.62	1.67	0.60	4.43	1.00	1.09
PCV (%)	7.02	8.88	18.44	27.68	51.26	11.21	15.41	13.10	12.65	34.15	45.43	1.18	14.88	28.12	20.30	2.72

IF: Days to initial flowering; F50: Days to 50% flowering; PB: No. of primary branches; SB: No. of secondary branches; FBB: First basal branching (cm); PH: Plant height (cm); FZL: Fruiting zone length (cm); SMS: No. of Siliqua on main shoot; MSL: Main shoot length (cm); SPY: Seed yield per plant (g); SPW: Dry weight per plant (g); DM: Days to physiological maturity; SL: Siliqua length (cm); SPS: Seeds per siliqua; TSW: 1000-seed weight (g); OC: Oil content (%)

Table 4: Correlation coefficient (r) between different quantitative traits in Indian mustard

Trait	F50	FBB	FZL	MSL	PB	PH	SB	SL	SMS	SPS	SPW	SPY
FBB	0.418**											
FZL	0.372**	0.624**										
IF	0.920**	0.358**	0.318**									
MSL	0.206**	0.047	0.361**									
PB	0.078	-0.312**	0.201*	0.199*								
PH	0.376**	0.458**	0.843**	0.532**	0.359**							
SB	-0.029	-0.508**	0.054	0.252**	0.813**	0.169*						
SMS	0.227**	0.162*	0.331**	0.548**	0.180*	0.429**	0.174*	0.016				
SPS	0.045	0.170*	-0.004	-0.061	-0.349**	-0.084	-0.398**	0.145	-0.029			
SPW	-0.072	-0.419**	0.100	0.400**	0.675**	0.315**	0.748**	0.041	0.261**	-0.311**		
SPY	0.115	-0.088	0.192*	0.351**	0.376**	0.326**	0.451**	0.191*	0.269**	-0.010	0.543**	
TSW	-0.260**	-0.078	0.048	0.218**	-0.007	0.046	0.019	0.349**	0.004	0.075	0.211**	0.330**

** $p < 0.01$; * $p < 0.05$; Only significant correlations are presented; Trait coding is as per Table 3

Table 5: Eigen vectors and variance of first five Principal Components (PC) in Indian mustard

Component	PC 1	PC 2	PC 3	PC 4	PC 5
Eigenvalue	3281.28	978.043	123.499	76.602	48.967
% Variance	70.797	21.10	2.66	1.65	1.06
Cummulative variance	70.79	91.89	94.56	96.21	97.27

Table 6: Promising genotypes of Indian mustard identified as significantly superior over best check

Traits	Best check and performance	LSD (5%)	Significantly Superior lines (N=total lines)
PH (<155 cm)	NPJ-112 (171.2 cm)	15.7	DRMR-2089, DRMR-390, DRMR-1322, DRMR-1489, DRMR-1787, DRMR-1644 (N=06)
MSL (>89 cm)	Kranti (77.6 cm)	11.05	DRMR-967, DRMR-2055, DRMR-1073, DRMR-742, DRMR-64, DRMR-974, JMG-113, DRMR-1428, DRMR-1374, DRMR-1505, DRMR-20, DRMR-1588, DRMR-2052, DRMR-1487 (N=14)
SMS (>55 no.)	Kranti (47.68 no.)	06.86	DRMR-1599, DRMR-1631, DRMR-901, DRMR-733, DRMR-4, DRMR-1245, DRMR-36, DRMR-360, BDJ-I-538, DRMR-929, DRMR-1987, DRMR-1234, JMG-113, DRMR-2063, DRMR-1783, DRMR-1610, DRMR-1615, DRMR-1675, DRMR-2065, DRMR-743, DRMR-1722 (N=21)
SL (>5 cm)	Maya (4.1 cm)	0.99	DRMR-1072, DRMR-1829, DRMR-974, DRMR-1596 (N=04)
SPS (>23no.)	RGN-73 (18.25 no.)	04.36	DRMR-1849, DRMR-1620, DRMR-2065, DRMR-473, DRMR-1039, DRMR-1619, DRMR-364, DRMR-1458, DRMR-304 (N=09)
TSW (>6.5g)	Pusa Bold (5.02 g)	01.36	DRMR-1458, DRMR-1995, DRMR-2024, JMG-27, DRMR-1610, IB-26, DRMR-2065, JMG-113, DRMR-1252, BDJ-I-164, DRMR-1427, DRMR-1588, DRMR-1596, DRMR-2055 (N=14)
FZL (>138 cm)	RGN-73 (112.6 cm)	25.52	DRMR-733, BDJ-I-538, DRMR-36, DRMR-1581, DRMR-1234, DRMR-742, DRMR-1849, DRMR-360, DRMR-1674, DRMR-1505, B-634, DRMR-1571, DRMR-1847, DRMR-995, DRMR-1039, DRMR-1993, DRMR-1995, DRMR-2063, DRMR-1634, DRMR-1596 (N=20)
SPY (>37g)	Pusa Bold (30.88 g)	06.24	DRMR-1722, BDJ-I-538, DRMR-4, JMG-113, DRMR-681, DRMR-1849, DRMR-1697, DRMR-1610, DRMR-1996, DRMR-107, DRMR-1588, DRMR-1379, DRMR-1995, IB-26, DRMR-2116 (N=15)
OC (>42 %)	RGN-73 (41.07%)	01.29	DRMR-1684 (N=01)

Trait coding is as per Table 3

Fig.1: Neighbor joining dendrogram depicting clustering of 155 accessions of Indian mustard.

observed. Days to 50% flowering varied from 43 to 71 days with a general mean of 54 days. Not much difference was observed in genotypes for days to maturity (range: 138-146 days, mean: 142 days) which is evident from lowest PCV (1.18%). Seed yield per plant varied from 4.14 to 40.15 g with a general mean of 25.19 g. 1000-seed weight ranged from 2.05 to 7.14 g, with a mean of 4.92 g. Oil content varied from 36.79 to 42.57 %. Variability for different agro-morphological traits was estimated

in terms of phenotypic coefficient of variation (PCV). A good range of variation was noticed for almost all the traits, except days to maturity and oil content. High estimate of PCV was noticed for first basal branching (51.26%), followed by dry plant weight (45.43%), seed yield per plant (34.15%) and seeds/siliqua (28.11%) whereas low estimates of PCV was observed for days to maturity (1.18%), followed by oil content (2.72%), initial flowering (7.02%), Days to 50% flowering (8.88%). Yadava *et al.* (2012)

Fig. 2: Cluster means for some important traits of Indian mustard.

reported high estimates of PCV for plant height, primary branches per plant, secondary branches per plant, silqua on main per shoot, seeds/silqua, 1000-seed weight and seed yield per plant. They reported low variability for days to flowering, maturity and oil content. The reported high variability for yield attributing traits will help in selection of desirable genotypes of trait of interest for their further utilization in mustard breeding programme (Singh *et al.*, 2016; Kumari *et al.*, 2019; Lakra *et al.*, 2020).

Improvement in seed yield can be achieved by selection using the correlated traits. Hence, Pearson's correlation coefficient was estimated to study character association between different agro-morphological traits studied and presented in Table 4. Seed yield/plant had significant and positive correlation with FZL (0.192*), MSL (0.351**), PB (0.376**), PH (0.326**), SB (0.451**), SL (0.191*), SMS (0.269**), DPW (0.543**), TSW (0.330**). Therefore, it is indicative that indirect selection for these associated traits will be effective in selecting Indian mustard genotypes for high seed yield (Hasan *et al.*, 2014; Ompal *et al.*, 2018; Tiwari, 2019).

Principal Component Analysis: Principal component analysis of 16 quantitative traits is presented in Table 5. First PC had 3281.28 variance (eigen value) which was 70.79 % of total variation explained indicating this axis represents majority of variations for the characters studied. It showed positive

correlation with plant dry weight, plant height, seed yield, main shoot length and secondary branches. PC-II contributed 21.10% followed by PC-III (2.66%), PC-IV (1.65%) and PC-V (1.06%). Cumulatively first five components explained 97.27% of the total variation in the data. Kumari and Kumari (2018) investigated principal component analyses in 31 *B. juncea* genotypes, using morphological traits and reported that the first six principal components accounted for 80.92 % of the diversity among the genotypes for all the traits investigated.

Identification of promising accessions: For important yield attributing traits promising accessions significantly superior over best check were identified and presented in Table 6. For plant height six accessions (DRMR-2089, DRMR-390, DRMR-1322, DRMR-1489, DRMR-1787, DRMR-1644) having significantly less (<155cm) height over best check (NPJ-112; 171.2cm) were identified. For main shoot length (>89cm) and silqua on main shoot (>55cm), 14 and 21 accessions, respectively were found significantly superior over best check (Kranti). For seeds/silqua 09 accessions (DRMR-1849, DRMR-1620, DRMR-2065, DRMR-473, DRMR-1039, DRMR-1619, DRMR-364, DRMR-1458, DRMR-304) superior over best check (RGN-73) were noticed. A total of 14 accessions (DRMR-1458, DRMR-1995, DRMR-2024, JMG-27, DRMR-1610, IB-26, DRMR-2065, JMG-113, DRMR-1252, BDJ-I-164, DRMR-1427, DRMR-1588, DRMR-1596, DRMR-2055) were superior over best check (Pusa Bold) in

terms of 1000-seed weight (>6.5g). Fifteen accessions (DRMR-1722, BDJ-I-538, DRMR-4, JMG-113, DRMR-681, DRMR-1849, DRMR-1697, DRMR-1610, DRMR-1996, DRMR-107, DRMR-1588, DRMR-1379, DRMR-1995, IB-26, DRMR-2116) recorded significantly higher seed yield per plant (>37.0 g). But for oil content one line DRMR 1684 was significantly superior over best check. The promising accessions identified for different traits could be used in mustard breeding programme as donors for development of transgressive segregants for important extent of economic traits (Saroj *et al.*, 2021).

Genetic diversity analysis: Selection of parents based on the extent of genetic divergence has been successfully utilized in different crop species by different workers (Murty and Arunachalam, 1966; Sihag *et al.*, 2004). Based on 16 quantitative traits usual Euclidean genetic distances were estimated between different genotypes of Indian mustard. Maximum distance was found between DRMR 325 and DRMR 2024 whereas minimum distance was recorded between DRMR 2052 and DRMR 2099. Dissimilarity matrix was further used for construction of NJ dendrogram. The NJ dendrogram (Fig.1) grouped 155 accessions (including checks) of Indian mustard into five clusters. Cluster-I was the largest and diverse cluster harbouring 52 accessions and cluster-V was the smallest having 20 accessions. Cluster means for some important traits is presented in Fig.2.

Cluster-I had the highest mean for SPY (32.1g) and TSW (5.2), MSL (81.8) and SMS (50.4) whereas Cluster-IV had lowest mean for SPY (19.0g). Genotypes of cluster-I can be used for yield enhancement as it showed highest cluster mean for yield and important contributing traits. Clustering of genotypes was irrespective of their geographical origins. No definite correlation between genetic and geographical diversity has been found. The present findings are in agreement with Singh *et al.* (2013) and Saroj *et al.* (2021) who studied genetic diversity in Indian mustard including indigenous and exotic line and reported no relationship between place of origin and clustering of genotypes. Similarly other workers in different crops have reported similar inferences (Sharma *et al.*, 2016; Choudhary *et al.*, 2017). However, these results indicate that diverse origin is not sufficient as an index of genetic diversity and this kind of genetic diversity might be due to differential selection pressure, adaptation and acclimatization and environmental settings (Das and Gupta, 1984; Sharma *et al.*, 2013). Furthermore, Murty and Arunachalam (1966) concluded that genetic drift and selection could cause greater diversity than geographic diversity.

Advance breeding lines, indigenous and exotic accessions were distributed in all five clusters while four check cultivars namely NPJ-112, Maya, Pusa Bold and Kranti were grouped into cluster-II whereas, RGN-73 was in cluster-V. Among four checks grouped together in cluster-II, three checks (Maya, Pusa Bold, Kranti) are having one parent common (Varuna). However, grouping of four check cultivars into single cluster indicating their narrow genetic base, which is also

evident from their one common parent variety Varuna. Similarly, Tudu *et al.* (2018) reported that clustering pattern of the genotype is highly influenced by their pedigree as compared to geographical distribution in mustard. Genotypes of different groups tend to be more distant and diverse from each other. Therefore, trait specific genotypes of different origin from different clusters can be selected for their utilization in mustard breeding programme (Devi *et al.*, 2017; Tudu *et al.*, 2018). However, in our study genetic diversity analysis based on morphological traits helped in identification and selection of trait specific diverse genotypes from different groups.

Since the inception of modern plant breeding only limited number of parents has been used in breeding of mustard crop due to which present day cultivars share narrow genetic base. In earlier study, less variability between present day Indian mustard cultivars was reported due to common parentage (Chauhan *et al.*, 2011). Therefore, there is a need to infuse fresh set of diverse parents in Indian mustard breeding programme, which can be possible only through study of diverse set of germplasm for different ago-morphological traits. In this context, the present study was conducted with 155 genotypes of diverse origin in which we found broad spectrum of variability for important yield attributing traits, reported association of yield with important secondary traits and identified different trait specific diverse germplasm of Indian mustard for different yield attributing traits. Some lines were found promising for more than one traits [JMG 113 (for MSL, SMS, SPY, TSW); BDJ-I-538 (for FZL, SMS, SPY); DRMR 1849 (for FZL, SPS, SPY); DRMR-1610 (for SMS, SPY, TSW); DRMR-1995 (for FZL, SPY, TSW); DRMR-974 (for FZL, MSL, SL)]. The identified trait specific promising lines will be further revalidated in replicated trials before their further utilization in Indian mustard breeding programme.

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Add-on Information

Authors' contribution: H.K. Sharma: Design and conducting experiment, Data collection and analysis, Manuscript writing, editing, revisions; A. Kumar: Conducting experiment, data collection; V.V. Singh: Design of experiment, Manuscript proof reading and editing, guidance; H.S. Meena: Assistance in manuscript writing and editing; Priyamedha: Assisted in manuscript editing; P. Sharma: Assisted in manuscript editing; P.K. Rai: Manuscript editing, Overall guidance.

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