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Variability, Genetic Diversity and Principal Component Analysis in Indian Mustard (*Brassica juncea* (L.) Czern. & Coss.) for Seed Yield and Attributing Traits

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A B S T R A C T

Fifty genotypes of Indian mustard [*Brassica juncea* (L.) Czern.& Coss.] were evaluated for fourteen quantitative traits. The experiment was conducted at research of farm, ICAR-Directorate of Rapeseed-Mustard Research, Sewar, Bharatpur, (Rajasthan) during rabi 2019-20. Both genotypic and phenotypic coefficients of variation were higher for important traits including main shoot length, days to maturity, seed yield per plant, thousand seed weight. High heritability in conjunction with high genetic advance were observed for seed yield per plant, thousand seed weight, fruiting zone length, days to initial flowering, first basal branch, siliqua length, seeds per siliqua, primary branches, main shoot length, days to maturity, secondary branch, plant height, siliqua on main shoot, days to 50% flowering. The fifty germplasm were grouped in seven clusters. Cluster 1 was the largest group (12 germplasm) followed by cluster 2 (11 germplasm), cluster 5 (9 germplasm), cluster 4 (8 germplasm) and cluster 3 (7 germplasm), cluster 7 (2 germplasm) and cluster 6 is the smallest having only one germplasm (Table 3 and Fig 1). The Principal component analysis **(**PCA) was conducted using quantitative traits. First PC had 262.479 variance (eigen value) which is 67.08 % of total variation explained (Table 3), followed by PC-II (10.48%) and PC-III (8.35%), PC-IV (4.78%), PC-V (4.55%). Cumulatively first five components explained 95.25% of the total variation in the data.

Introduction

Indian Mustard (*Brassica juncea* L. czern.& coss.2n=36, AABB genome), is an allopolyploid brassica species. It contributes more than 80% to the total rapeseed-mustard production in the country and is an important component in the oilseed sector. It is known to be more drought tolerant and shattering resistant than *B. napus* and *B. rapa*, therefore, has an enormous cultivation potential in semi-arid areas. It is mainly self-pollinating species,

despite that an average of 7.5 to 30 percent out-crossing does occur under natural field conditions. Mustard is a cool season crop, which requires temperature range from 6 to 27°C, mustard follows C3 pathway for carbon assimilation. Mustard is generally grown under rainfed conditions. It requires well drained soil having pH near to neutral. It has a low water requirement (240–400 mm) which fits well in the rainfed cropping system. Nearly 20% area of mustard is under rainfed condition.

Rapeseed-mustard accounts for nearly one-third of the oil produced in India, making it the country's key edible oilseed crop. Rapseed and mustard sown in 5.96 million hectare and production was 8.32 million tonnes in 2017-18. Rajasthan is one of the major mustard producing states in the country, contributing 40.87 % of total production of India. National and state yield of mustard in 2017-18 are 1397 kg/ha and 1558 kg/ha, respectively (Agricultural statistics at a glance 2018) Although, yield of mustard in Rajasthan is more than its national average yield.

Among the various constraints attributing to low productivity of mustard in arid and semi-arid region, the erratic nature of climate, inefficient irrigation water, biotic stresses (white rust, stem rot, aphids, painted but) and abiotic stresses (high temperature at sowing time), fertilizer management and poor soil physical conditions are the most important factors which lead to the low crop yield.

Evaluation of genetic divergence and relatedness among breeding materials has significant implications for the improvement of crop plants. Furthermore, genetic diversity could help breeders and geneticists to understand the structure of germplasm, predict which combinations would produce the best offsprings (Hu *et al.,* 2007), and facilitate to widen the genetic basis of breeding material for selection (Qi *et al.,* 2008). Genetic diversity among individuals or populations can be determined using morphological, biochemical and molecular approaches (Mohammadi and Prasanna 2003). Assessment of genetic diversity in *B. juncea* using phenotypic characters has previously been done by many researchers (Vaishnava *et al.,* 2006, Alie *et al.,* 2009, Singh *et al.,* 2010).

Materials and Methods

The materials for the present investigation consisted of 50 genotypes of Indian mustard obtained from germplasm unit of ICAR-Directorate of Rapeseed-Mustard Research, Sewar, Bharatpur. 50 genotypes of Indian mustard including 5 check varieties (NPJ-112, Pusa bold, PM-26, CS-56, Kranti) were evaluated in RCBD with two replications under irrigated timely sown condition. Sowing was done on 15-10-2019.

In each replication each genotype was sown in a plot of one row of 3-meter length. Plant to plant spacing was maintained at 10 cm by thinning after 15-20 days of sowing. Observation Recorded five competitive plants were randomly selected at the time of maturity (except the days to 50 per cent flowering and days to maturity which were recorded on plot basis) Plant height (cm), Primary branches per plant, Secondary branches per plant, Main shoot length (cm), Siliqua on main shoot, Fruiting zone length (cm), First basal branching (cm), Initial flowering, Days to 50 per cent flowering, Days to maturity, Siliqua length (cm), Seeds per siliqua, Seed yield per plant (g), Thousand seed weight (g). The phenotypic and genotypic coefficients of variation (GCV and PCV), heritability in broad sense, genetic advance as % of mean, correlation coefficients at genotypic and phenotypic level and principal component analysis computed using standard statistical methods.

Results and Discussion

The analysis of variance was carried out for twelve characters and showing the significant difference amongst all the parents except biological yield, among the F1's except number of secondary branches per plant, no. of seed per siliqua and biological yield per plant, parents vs F1's for all the characters revealed significant difference (Patel *et al.*, 2012; Arifullah, 2013). Highly significant differences were recorded among the treatments for all the characters namely fruiting zone length, first basal branch, initial flowering, siliqua length, and significant differences were observed for the characters plant height, primary branches per plant, secondary branches per plant, main shoot length, siliqua on main shoot, days to 50 % flowering, days to maturity, seeds per siliqua, thousand seed weight (Table 1 and 2).

Estimates of PCV and GCV were observed that phenotypic variance were higher than the corresponding genotypic variance for all the traits studies. Data presented in (Table 2) showed maximum GCV and PCV was recorded for First basal branch, Seed yield/ plant (g), Thousand seed weight, Fruiting zone length, Seeds/ siliqua. High heritability in conjunction with high genetic advance were observed for seed yield per plant, thousand seed weight, fruiting zone length, days to initial flowering, first basal branch, siliqua length, seeds per siliqua, primary branch, main shoot length, days to maturity, secondary branch, plant height, siliqua on main shoot, days to 50% flowering,

Multivariate analysis

Principal component analysis

The PCA was conducted using 14 quantitative traits in Indian mustard and presented in table 3. First PC had 262.479 variance (eigen value) which is 67.08 % of total variation explained (Table 3), followed by PC-II (10.48%) and PC-III (8.35%), PC-IV (4.78%), PC-V (4.55%). Cumulatively five six components explained 95.25% of the total variation in the data.

PC-I had significantly positive correlation ($P < 0.30$) with five variables (plant height, fruiting zone length, first basal branching, days to initial flowering, days to 50% flowering). PC-II had positive correlation ($P < 0.05$) with two variables (secondary branches, seed yield/plant) whereas, PC-III had positive correlation ($P<0.05$) with three variables (plant height, silique on main shoot, seed yield/plant). Similar results have also been reported earlier by Zada *et al.,* (2013) in Ethiopian mustard; Avtar *et al.,* (2014) in toria and Neeru *et al.,* (2015) in Indian mustard.

Genetic diversity based on Hierarchical cluster analysis

The random clustering pattern of genotypes i.e. grouping of genotypes from different regions in the same cluster (three local genotypes CAULC-2, CAULC-3, CAULC-4 from Manipur were grouped together with Kranti from Pantnagar and PM-28 from New Delhi) indicated that the genetic diversity of the genotypes is not necessarily related with the distribution of genotypes in different parts of the country, as supported by earlier findings of Jeena and Sheikh (2003), Pandey *et al.,* (2013), Dar *et al.,* (2010) and Gupta *et al.,* (2015).

The genetic diversity, among the genotypes in the present study may be resulted from genetic drift and selection that cause greater diversity than geographical distribution as suggested by Murty and Arunachalam (1966). Based on usual Euclidean distance, fifty genotypes of Indian mustard were grouped into seven major clusters. Dendrogram was constructed based on 14 quantitative traits using DARwin 6 software (Fig. 1).

Table.1 Analysis of variance (ANOVA) for seed yield and yield attributing characters in Indian mustard

Source of variation	Degree of freedom	Mean Square													
		Plant height	Primary branch	Secondary branch	Main shoot length	Siliqua on main shoot	Fruiting zone length	First basal branch	Days to initial flowering	Days to 50 % flowering	Days to maturing maturity	Seed yield per plant	Siliqua Length	Seeds per siliqua	Thousand seed weight
Replication	1	210.25	2.49	27.25	19.15	0.66	136	30.25	16	42.26	15.22	14.82	0.98	1.44	**0.89**
Treatment	49	10321.75 *	0.760 *	4.79 *	20.76 *	9.52 *	350.69 **	97.77**	29.58 **	14.44 *	6.55 *	30.05 **	0.16 **	3.39 *	**0.84***
Error	99	5709.25	.403	2.58	11.05	5.28	98.07	14.98	10.77	8.90	3.51	3.68	0.80	1.78	**0.21**
SEM (±)		7.632	0.449	1.137	2.35	1.625	7.002	2.73	2.321	2.109	1.325	1.35	0.2	0.945	**0.33**
CV (%)		5.854	8.673	9.714	5.328	5.004	10.193	14.14	6.893	5.296	1.366	11.78	7.354	11.871	**11.85**
CD (1 %)		28.929	1.702	4.31	8.909	6.162	26.541	10.37	8.797	7.996	5.025	5.14	0.761	3.582	**1.25**
CD (5 %)		**21.692**	**1.276**	**3.231**	**6.68**	**4.62**	**19.901**	**7.77**	**6.596**	**5.996**	**3.768**	**3.85**	**0.57**	**2.686**	**0.93**

. * and ** Significance at 5% and 1% level of significance, respectively.

Table.2 Estimates of genotypic (GCV) and phenotypic (PCV) co-efficient of variation, heritability (bs) and genetic advance (% of mean) for seed yield and component traits in Indian mustard.

Characters	Mean	Range		GCV	PCV	Heritability %	Genetic advance (% of means)
		min.	max.				
Plant height	184.37	166	210	3.721	6.937	28.773	4.112
Primary branch	7.32	6.2	8.9	5.769	10.417	30.673	6.582
Secondary branch	16.55	12.9	20.8	6.349	11.605	29.924	7.154
Main shoot length	62.38	57.5	73	3.534	6.394	30.543	4.023
Siliqua on main shoot	45.94	41.5	50	3.169	5.924	28.622	3.493
Fruiting zone length	97.15	67.5	146	11.569	15.419	56.292	17.88
First basal branch	27.37	16.5	47.5	18.325	31.135	34.641	22.218
Days Initial flowering	47.62	42	57	6.44	9.433	46.601	9.056
Days to 50 % flowering	56.33	52	61	2.954	6.065	23.723	2.964
Days to maturity	137.21	132	140	0.898	1.635	30.159	1.016
Seed yield/ plant (g)	16.27	8.8	24.7	22.31	25.233	78.172	40.634
Siliqua length	3.86	3.3	4.5	5.272	9.049	33.941	6.327
Seeds/ siliqua	11.26	8	13	7.958	14.292	31.001	9.127
Thousand seed weight	3.93	2.38	5.05	14.212	18.507	58.967	22.481

Table.3 Eigen vectors, eigen values and proportion of variation explained by different components for different quantitative traits of Indian mustard

Trait	PC 1	PC 2	PC 3	PC 4	PC 5
Plant height	0.561	0.439	0.637	-0.283	-0.001
Primary branch	0.001	0.028	0.012	0.021	0.051
Secondary branch	-0.006	0.112	0.004	0.085	0.106
Main shoot length	0.028	0.076	0.053	0.489	0.081
Siliqua on main shoot	0.003	0.093	0.084	0.291	-0.030
Fruiting zone length	0.789	-0.098	-0.576	0.100	-0.143
First basal branch	0.216	-0.849	0.454	0.123	0.041
Days Initial flowering	0.105	0.044	-0.056	0.129	0.779
Days to 50 % flowering	0.048	0.020	-0.043	0.009	0.558
Days to maturity	-0.009	0.032	0.064	0.052	-0.068
Seed yield/ plant (g)	0.034	0.207	0.190	0.730	-0.174
Siliqua length	0.003	-0.005	0.002	-0.003	0.007
Seeds/ siliqua	0.007	0.051	-0.030	0.100	-0.054
Thousand seed weight	0.007	0.002	0.007	0.026	-0.026
Eigenvalue	262.479	41.011	32.678	18.708	17.828
% variance	67.085	10.482	8.352	4.782	4.556
Cummulative variance	67.085	77.567	85.919	90.701	95.257

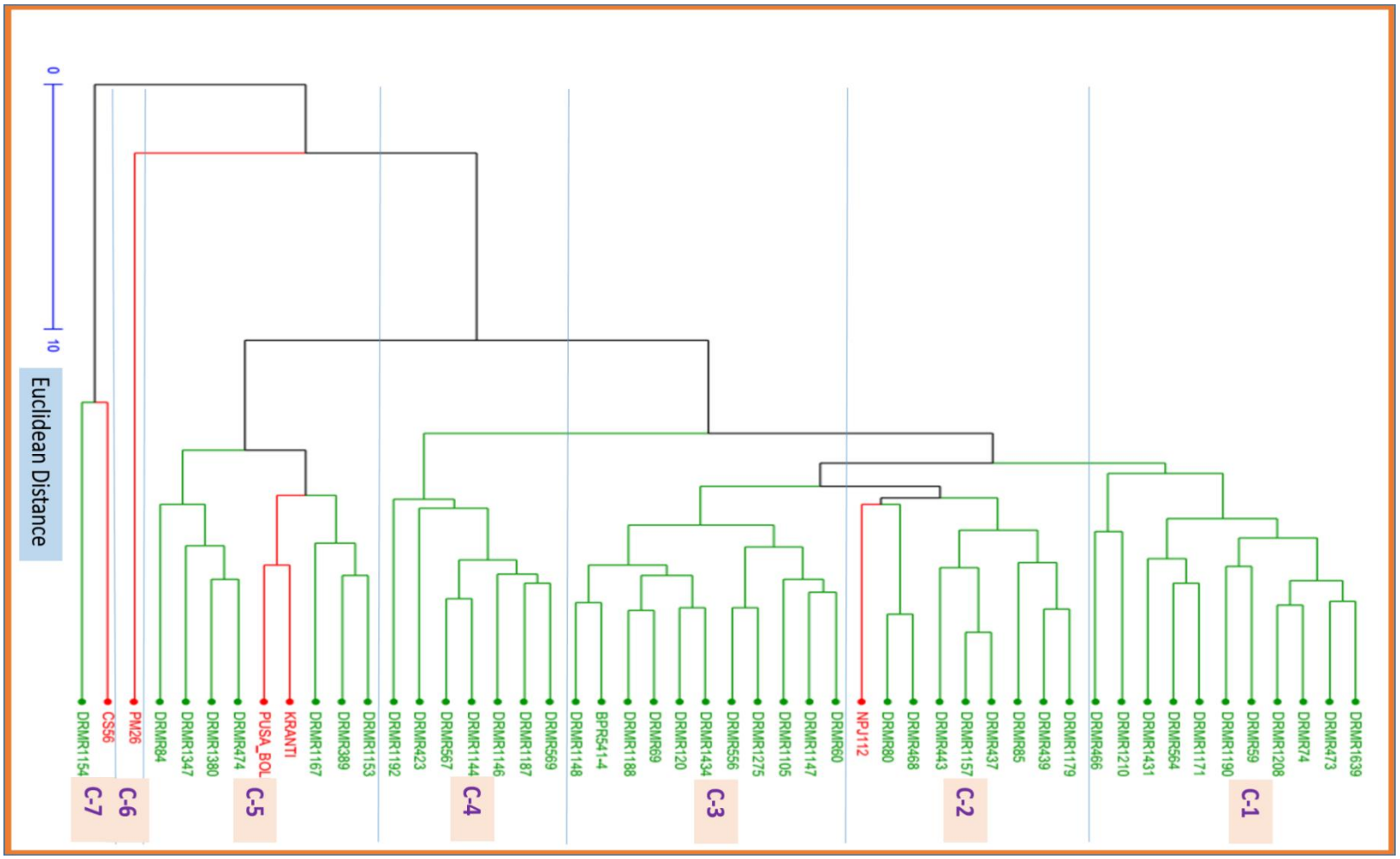
Table.4 Cluster mean for different quantitative traits of Indian mustard

Clusters	Plant height	Primary branch	Secondary branch	Main shoot length	Siliqua on main shoot	Fruiting zone length	First basal branch	Days to initial flowering	Days 50 % flowering	Days to maturity	Seed yield/ plant	Siliqua length	Seeds/ siliqua	Thousand Seed Weight
1	187.87	7.54	16.95	62.96	45.35	99.08	26.16	50.08	57.33	137.45	15.89	3.87	11.29	3.65
2	184.4	7.29	16.5	61.45	45.79	89	23.13	44.72	55.27	138.36	16.48	3.75	11.31	3.77
3	180	7.11	15.7	63.64	46.18	92.14	35.07	46.35	55.42	136.64	17.44	3.8	10.71	4
4	170.62	7.38	17.1	62.31	46.31	87	22.56	47.18	56	136.75	14.76	3.85	11.12	3.84
5	194.5	7.02	15.91	62.05	46.44	111.77	32.88	48.94	56.94	136.11	16.93	3.99	11.16	4
6	154	7.3	17.6	58.5	45.9	67.5	16.5	42.5	54.5	137.5	8.8	3.8	10	2.725
7	203	8	17.55	63.25	45.8	137.5	30.75	51.5	58.75	138	14.9	3.77	11.75	4.07

Table.5 Distribution pattern of 50 genotypes of Indian mustard into seven cluster based on Euclidean distance

Cluster	Genotype	No. of genotypes	Best performing genotype for seed yield/plant (g)	Best performing genotype for 1000-seed weight (g)
1	DRMR 1179, DRMR 439, DRMR 85, DRMR 437, DRMR 1157, DRMR 443, DRMR 1171, DRMR 564, DRMR 1431, DRMR 468, DRMR 80, NPJ 112	12	DRMR 468 (24.7)	DRMR 1431 (4.735)
2	DRMR 60, DRMR 1147, DRMR 1105,DRMR 1275, DRMR 556, DRMR 1434, DRMR 120, DRMR 69, DRMR 1188, BPR 541-4, DRMR 1148	11	DRMR 1148 (22.6)	DRMR 1188 (4.58)
3	DRMR 59, DRMR 1190, DRMR 466, DRMR 74, DRMR 1208, DRMR 1639, DRMR 473	7	DRMR 59 (24.4)	DRMR 466 (4.58)
4	DRMR 1146, DRMR 569, DRMR 1187, DRMR 1144, DRMR 567, DRMR 423, DRMR 1192, DRMR 1210	8	DRMR 1192 (24.3)	DRMR 1144 (4.84)
5	DRMR 1153, DRMR 389, DRMR 1167, Kranti, Pusa Bold, DRMR 474, DRMR 1380, DRMR 1347, DRMR 84	9	KRANTI (21.7)	PUSA BOLD (4.98)
6	PM 26	1	PM 26 (8.8)	PM 26 (2.72)
7	CS 56, DRMR 1154	2	CS 56 (17.2)	CS 56 (4.69)

Fig.1 UPGMA dendrogram based on Euclidean hierarchical clustering



Cluster 1 was the largest group (12 genotypes; DRMR 1179, DRMR 439, DRMR 85, DRMR 437, DRMR 1157, DRMR 443, DRMR 1171, DRMR 564, DRMR 1431, DRMR 468, DRMR 80, NPJ 112), followed by cluster 2 (11 genotypes; DRMR 60, DRMR 1147, DRMR 1105,DRMR 1275, DRMR 556, DRMR 1434, DRMR 120, DRMR 69, DRMR 1188, BPR 541-4, DRMR 1148), cluster 5 (9 genotypes; DRMR 1153, DRMR 389, DRMR 1167, Kranti, Pusa Bold, DRMR 474, DRMR 1380, DRMR 1347, DRMR 84), cluster 4 (8 genotypes; DRMR 1146, DRMR 569, DRMR 1187, DRMR 1144, DRMR 567, DRMR 423, DRMR 1192, DRMR 1210) and cluster 3 (7 genotypes; DRMR 59, DRMR 1190, DRMR 466, DRMR 74, DRMR 1208, DRMR 1639, DRMR 473), cluster 7 (2 genotypes; CS 56, DRMR 1154) and cluster 6 is the smallest having only one genotype (PM 26) (Table 4).

The cluster mean of fourteen different characters are being presented in Table 4. Cluster 3 showed high cluster mean for seed yield (17.4g), while cluster 3, 5, 7 showed high cluster mean for 1000-seed weight (>4.0g).

As far as best performing line is concern, for cluster 1 DRMR 468 showed high seed yield/plant (24.7g). In cluster 3, DRMR 59 is best performing genotype (24.4g) while in cluster 4, DRMR 1192 recorded highest yield (24.3g) (Table 4).

For 1000-seed weight 5.05g (DRMR473) exhibited highest in cluster 3. Genotypes in same cluster are genetically more similar as compared to genotypes in other clusters. Hence, to get more seed yield/plant genotypes of cluster 3 can be crossed with genotypes of cluster five. Best performing lines from each cluster can be used in hybridization programme to generate more variability for different traits of interest.

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