Research Article

GENETIC VARIABILITY AND DIVERSITY ANALYSIS IN INDIAN MUSTARD (*Brassica juncea* (L.) Czern and Coss.)

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Abstract: Background: Indian mustard (*Brassica juncea* (L.) Czern & Coss.) is an important oil seed crop grown in *rabi* season, extensively grown in Rajasthan, Haryana, Madhya Pradesh, Uttar Pradesh and Gujarat. The present research is carried out on 40 Indian mustard genotypes to identify the genetically diverse genotypes and using them in further breeding programme that aimed to improve yield and yield attributing characters.
Methods: These genotypes are evaluated under randomized block design with three replications and observations were recorded from five randomly selected plants for 14 quantitative traits from each replication that are effective to identify yield potential from the forty genotypes and the experiment is conducted at field experimentation center, Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj during *rabi* 2019-20. A detailed analysis of the results on Indian mustard varieties are studied using different statistical tools in this project.
Results: Analysis of variance revealed that all the traits have significant variability and thus have adequate scope for the selection of superior genotypes that can be used in further research. Higher estimates of GCV and PCV were recorded for number of secondary branches and number of siliquae per plant; indicating that these characters could be selection tools for yield improvement. High heritability coupled with high genetic advance as percent mean is observed in number of secondary branches and test weight (g) indicating the scope for their improvement through selection. The 40 genotypes are grouped into V clusters using Torcher's method of clustering. Among the 5 clusters, cluster III has maximum genotypes (13), followed by cluster II (11), cluster I has 7 genotypes and cluster IV has 5 genotypes followed by cluster V (3) with least number of genotypes. The maximum intra-cluster distance is observed for cluster V (4.43) followed by cluster I (3.87) and cluster IV (3.77). From the cluster mean values, using of genotypes from cluster I and cluster IV in crossing programme will give desirable recombinants for early maturity along with seed yield per plant. Diversity analysis also revealed that cluster I and cluster V has the highest inter-cluster distance (7.92) followed by cluster IV and V (7.66) indicating that the genotypes of these clusters have maximum diversity and crossing programme between these clusters will yield better segregants. Euclidean distance matrix also suggests that the crosses of Jagannath × RGN 236, BR 40 × RB 50 and Jagannath × Pusa Bold are expected to give better yield segregants.

Keywords: *Analysis of Variance, Cluster mean, Diversity Analysis, Euclidean distance, Genetic advance as percent of mean, Heritability and Indian mustard*

Introduction

Indian mustard (*Brassica juncea* (L.) Czern & Coss.) is an important oil seed crop grown during *rabi* season as a rainfed or as a under irrigated crop. It belongs to the family Cruciferae having 2n=36 chromosomes. It is mainly self-pollinated crop. Indian mustard is locally known as rai/ raya or sarson and it is especially grown in Northern-eastern part of India. It is extensively grown in Rajasthan, Haryana, Madhya Pradesh, Uttar Pradesh and Gujarat which contributes about 80 percent in area and production. India is the fourth largest producer of Rapeseed and Mustard after Canada, China and European Union that accounts 8.54% of world's total production. In India it is the second largest oilseed crop produced after soyabean with total of 26.24% (2018-19) production.

Brassica juncea (AABB) (n=18) is a natural amphidiploid species which is the result of inter-specific cross between *Brassica nigra* (BB) (n=8) and *Brassica rapa* (AA) (n=10). A rich source of vitamins and minerals, *Brassica* contains many medicinal properties. As the success of any breeding programme depends mainly upon the genetic variability present in the breeding material, the assessment of parameters including phenotypic and genotypic coefficients of variation, heritability in broad sense and genetic advance as percent of mean is a pre-requisite for making effective selection. Mahalanobis's D^2 statistics is adopted to identify the diverse group of genotypes for selection in hybridization programme.

Material and Methods

The present study was conducted to identify the extent of genetic variability and genetic divergence among the 40 Indian mustard genotypes and is conducted at field experimentation center, Department of Genetics & Plant breeding farm, Sam Higginbottom University of Agriculture, Technology and Sciences (Naini), Prayagraj (U.P) during the *rabi* 2019-20. The material used in the study, forty indigenous germplasm lines of *Brassica juncea* (L.) Czern & Coss that are listed below, were received from Dr Hariom Sharma, Scientist, Directorate of Rapeseed-Mustard Research, Sewar, Bharatpur. The experiment comprising 40 germplasm accessions was laid out in Randomized Block Design (RBD) with three replications. These lines were grown in two rows of 1 meter length in three plots. The spacing between row to row and plant to plant is 30cm and 15cm respectively.

Observations were recorded on five randomly selected plants from each replication for 14 quantitative traits Viz.,
Days to 50% flowering
Days to maturity
Plant height (cm),
Number of primary branches,
Number of secondary branches,
Main raceme length,

Table-2 *Estimation of variability parameters for 14 quantitative traits in Indian mustard*

Character	V_g	v_p	PCV	GCV	h^2 (bs)	Genetic advance	GA%
Days for 50%flowering (DF50)	22.46	23.05	5.3	5.2	97.4	9.6	10.6
Days for maturity(DM)	52.39	53.47	5.4	5.3	98	14.8	10.9
Plant height (PH)	272.29	298.6	9.8	9.3	91	32.5	18.4
Number of primary branches (NPB)	0.37	0.46	17.1	15.2	79.3	1.1	28
Number of secondary branches (NSB)	1.36	1.51	46.1	43.7	89.8	2.3	85.4
Main raceme length (MRL)	36.27	50.8	14.5	12.2	71.4	10.5	21.4
Silique on main raceme (SMR)	12.99	18.91	11.3	6.3	68.7	6.2	16
Number of silique per plant (NSP)	937.59	1041.83	36.4	34.5	90	59.8	67.5
Siliqua length (SL)	0.06	0.08	5.6	4.9	76.7	0.4	8.9
Number of seeds per Silique (NS_silique)	0.33	0.42	6	5.3	78	1	9.9
Biological yield (BY)	2.26	2.95	7.5	6.6	76.5	2.7	11.9
Harvest index (HI)	9.83	12.16	7.9	7.1	80.9	5.8	13.2
Test weight (TSW)	0.55	0.58	22	21	93.9	1.5	42.6
Seed yield per plant (SYPP)	1.51	1.95	14	12.3	77.2	2.2	22.3

vg = genotypic variance and vp = phenotypic variance, GCV = Genotypic Coefficient of Variation, PCV = Phenotypic Coefficient of Variation, h^2 = Heritability (broad sense) and GA% = Genetic advance as percent of mean.

Siliquae on main raceme,
Number of siliquae per plant,
Siliqua length (cm),
Number of seeds per siliqua,
Biological yield (g),
Harvest index (%),
Test weight (g) and
Seed yield per plant (g).

The experimental data thus recorded on these characters were subjected to statistical and biometrical analysis to obtain results for Analysis of variance (Randomized block design) [1], Genetic variability [2], Heritability [3], Genetic advance [4] and Johnson *et al.* (1955) [5] and Mahalanobis / D² statistics [6]. The 40 genotypes under study are grouped in five clusters using Ward's method of clustering. Statistical analysis was performed using Genstat 17th edition.

Results and Discussion
Analysis of variance
Analysis of variance presented in [Table-1], revealed that all the characters viz., days to 50% flowering, days to maturity, plant height, number of primary branches, number of secondary branches, siliquae on main raceme, number of siliquae per plant, seeds per siliqua, seed yield per plant, biomass, test weight and harvest index shows high significant for the treatments, which indicates that considerable amount of genetic variability is present for these traits in the experimental material. High magnitude of variability has been earlier reported in Indian mustard germplasm by Sohan and Verma (2010) [7], Verma *et al.* (2016) [8] and Tantuway *et al.* (2018) [9] in which analysis of variance showed significant differences for all the characters under their study.

Table-1 *Mean sum of squares for 14 characters in 40 Indian mustard varieties*

Character	Replication	Treatments	Error
Days for 50%flowering (DF50)	6.95	2696.46**	137.72
Days for maturity (DM)	56.12	6255.97**	251.88
Plant height (PH)	3081.77	34963.03**	6156.84
Number of primary branches (NPB)	7.06	53.91**	22.28
Number of secondary branches (NSB)	0.14	176.51**	35.85
Main raceme length (MRL)	142.62	5944.10**	3400.36
Silique on main raceme (SMR)	98.49	2212.97**	1385.96
Number of siliques per plant (NSP)	1201.33	121894.32**	24391.5
Siliqua length (SL)	0.03	8.95**	4.17
Number of seeds per Silique (NS_silique)	0.49	48.69**	20.89
Biological yield (BY)	4.14	345.29**	161.96
Harvest index (HI)	62.24	1422.26**	543.65
Test weight (TSW)	0.37	68.8**	8.3
Seed yield per plant (SYPP)	6.48	228.61**	104.41

Note: *, **significant at 5% and 1% probability level, respectively.

Variability, heritability and genetic advance
Estimates of variability among the 40 genotypes are presented in [Table-2]. It is identified from the table that phenotypic coefficient of variation showed very close value to the genotypic coefficients of variation in respect of almost all the characters except for siliquae on main raceme in the present investigation. Thus, suggesting the least influence of environment in the expression of a character and can be used in selection for improving the mustard yield. The high estimates of coefficient of variation were registered for number of secondary branches, number of siliquae per plant and test weight. These results are in agreement with the findings of Singh *et al.* (2014) [10], Akabaari *et al.* (2015) [10] and Kumari *et al.* (2018) [11]. Moderate estimates of coefficient of variation were observed for number of primary branches, main raceme length, seed yield per plant and siliquae on main raceme. The high heritability (broad sense) coupled with high genetic advance as per cent of mean is found for number of secondary branches, number of siliquae on main raceme, test weight, seed yield per plant and number of primary branches. This is due to the major effect of additive genes and therefore selection of genotypes based on these traits will give more effective results. These results are in agreement with the findings of Lodhi *et al.* (2013) [12] and Lyngdoh *et al.* (2017) [13].

Table-3 *Grouping of Indian mustard genotypes into different clusters*

Group	I	II	III	IV	V
I	3.87				
II	4.71	3.64			
III	6.32	4.58	3.42		
IV	4.76	4.87	5.34	3.77	
V	7.92	6.67	7.10	7.66	4.43

Table-4 *Intra and Inter cluster distance of 5 clusters*

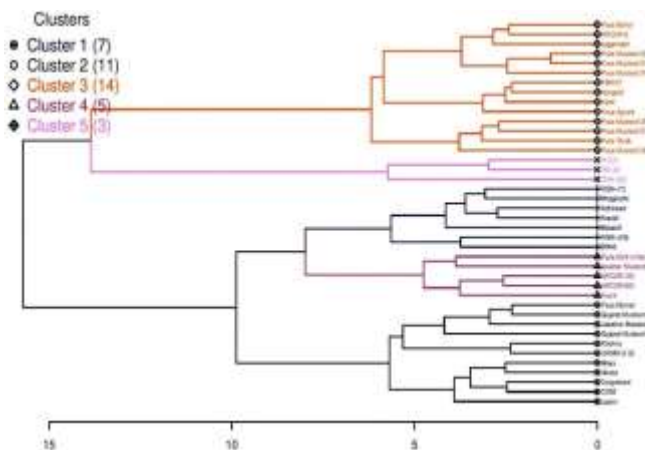| Clusters	Genotypes
I	Aravali, Ashirwad, Basanti, Bhagirathi, BR40, RGN-236, RGN-73
II	CS52, DRMR IJ 32, Durgamani, Geeta,Gujarat Mustard 1, Gujarat Mustard 2, Jawahar Mustard 1, Krishna, Laxmi, Maya, Pusa Mahak
III	Jagannath, Kanti, Navgold, NRCDR 2, PBR 97, Pusa Agrani, Pusa Bahar, Pusa Mustard 21, Pusa Mustard 22, Pusa Mustard 24, Pusa Mustard 26, Pusa Mustard 27, Pusa Mustard 28, Pusa Tarak
IV	Jawahar Mustard 2, Kranti, NRCDR 101, NRCDR 601, Pusa Bold (check)
V	RB-50, RCC4, RGN 229

D² analysis
The 40 genotypes were grouped into 5 clusters resulting of D² analysis. Cluster III has maximum number of genotypes among all the clusters with 14 genotypes, followed by cluster II (11 genotypes), cluster I (7 genotypes) and cluster IV have 5 genotypes. The grouping of genotypes into different clusters are shown in [Table-3] and [Fig-1]. Cluster V constitutes only 3 genotypes and stands as cluster with minimum number of genotypes. Bansal *et al.* (1990) [14] reported that the clustering pattern basically represents the pedigree of breeding lines. The cluster distances among the 5 clusters are presented in [Table-4]. Cluster V shows the maximum intra-cluster distance followed by cluster I. The maximum inter-cluster distance is observed between cluster I and cluster V, followed by cluster IV and cluster V. Similar results were observed by Pandey *et al.* (2013) [15], Singh *et al.* (2014) [16] and Shekhawat *et al.* (2014) [17].

Table-5 *Cluster mean values for 14 quantitative traits in Indian mustard*

Traits	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
DF50	89.86	90.79	88.93	90.27	107
DM	130.38	133.27	135.5	135.47	155.89
PH	178.83	189.83	162.36	167.04	199.51
NPB	4.76	4.15	3.49	3.65	4.11
NSB	3.93	2.14	2	3.36	3.54
MRL	57	50.18	44.31	48.75	48.74
SMR	43.19	41.31	34.6	35.84	39.71
NSP	118.3	97.23	55.37	114.27	100.78
SL	5.29	4.85	4.8	4.97	4.83
NS_Siliqua	10.94	10.67	10.52	10.79	9.73
BY	24.38	22.29	21.63	24.64	22.16
HI	45.87	44.33	41.3	49.27	41.08
TSW	3	3.31	3.54	3.25	5.16
SYPP	11.12	9.79	8.93	12.09	9.04

Table-6 *Top ten most diverse lines, most similar and diverse lines in relation to the popular mustard variety Pusa Bold (Check)*

SN	Pairs of Genotypes showing maximum diversity		Diversity	Accessions showing maximum diversity with 'Pusa Bold (check)'	Maximum Diversity	Accessions showing minimum diversity with 'Pusa Bold (check)'	Minimum diversity
1	Jagannath	RGN-236	9.84336	Jagannath	8.06823	NRCDR 601	3.6870
2	BR40	RB-50	9.2536	Pusa Bahar	7.73742	NRCDR 101	3.8042
3	RGN-236	Pusa Bahar	9.21828	NRCDR 2	6.89446	Jawahar Mustard 2	3.8685
4	BR40	Jagannath	9.19533	Basanti	6.65501	RGN-73	3.9836
5	BR40	Pusa Bahar	9.11864	Jawahar Mustard 1	6.41296	Kranti	4.1811
6	Kranti	RCC4	8.96252	BR40	6.35425	Durgamani	4.3630
7	RGN-236	RB-50	8.85517	DRMR IJ 32	6.33387	Maya	4.6254
8	RGN-236	RCC4	8.83263	Pusa Tarak	6.06191	Navgold	4.7212
9	BR40	RCC4	8.81525	Kanti	6.04303	CS52	4.9741
10	Pusa Tarak	RGN 229	8.56111	Pusa Agrani	5.94748	Gujarat Mustard 2	4.9813

Fig-1 D² cluster diagram following Wards method

The clustering of the genotypes is highly required in any breeding programme. Since the magnitude of heterosis largely depends on the degree of genetic diversity among the parents and the clusters having large inter-cluster distance will likely to produce more heterotic F1's. The genotypes that are grouped in a single cluster show low degree of divergence and the offsprings obtained from such crosses show very less segregations. Therefore, hybridization programme made from the genotypes of clusters having maximum divergence will report desirable transgressive segregants. Therefore, from the results it is revealed that hybridization between genotypes from these diverse clusters will yield desirable segregates with the accumulation of favorable genes in the segregating generations.

The variance for the cluster means were calculated for fourteen quantitative traits in Indian mustard. Maximum variance for cluster mean was observed for plant height, days to maturity, number of siliqua per plant, days to 50% flowering, main raceme length, siliqua on main raceme and harvest index, which suggests that the genetic divergence in the present material is due to these traits and the parents selected based on these traits in hybridization will show more genetic divergence. The present findings are in agreement with the reports of Iqbal (2014) [18], Bind *et al*. (2015) [19], Kumari *et al*. (2018) and Tantuway *et al*. (2018). The cluster mean values of 14 quantitative traits in 40 Indian mustard genotypes are presented in [Table-5].

Cluster mean value represents the genetic difference present between the clusters. Maximum mean value for number of primary branches, number of secondary branches, siliquae on main raceme, number of siliquae per plant, siliqua length and number of seeds per cluster were recorded in cluster I and the genotypes of this cluster shows early days to maturity. The mean values of Cluster III have earliness in days to 50% flowering, and shortest plant height. Cluster IV has high cluster mean values for biological yield, harvest index and seed yield per plant. The genotypes accommodated in Cluster V shows maximum cluster mean for test weight. Therefore, on the basis of the cluster mean values, using of genotypes from cluster I and cluster IV in crossing programme will give desirable recombinants for early maturity along with seed yield per plant and its most contributing components. Since, the inter-cluster distance with cluster V is high for other clusters, crossing of genotypes with this cluster would result in increased heterosis and more desirable segregants. Similar results were observed by Bind *et al*. (2015), Verma U *et al*. (2016), Devi *et al*. (2017) [20] and Kumari *et al*. (2018).

The genotypes Jawahar Mustard 2, RGN 229, RGN 236, NRCDR 601 and Basanti could be promising for most of the yield attributing characters. Crossing of these genotypes is suggested in further improvement of yield related traits in segregating generations. Pairs of genotypes are made from the Euclidean distance matrix that shows maximum diversity and genotypes showing maximum diversity with check variety (Pusa Bold) that are reported in [Table-6]. Pairs that have maximum diversity are Jaganath × RGN-236, BR-40 × RB-50 and RGN-236 × Pusa Bahar. Therefore, the pairs tabulated in the following table will help to get more diverse pairs of genotypes that would give more diverse and heterotic offsprings.

Conclusion

The results from the present experiment revealed that the variability exists among the selected genotypes and can be used in future breeding programme. High heritability coupled with genetic advance as percent mean shows the future scope of these genotypes in selection programme.

From diversity analysis it is concluded with the results, clustering of genotypes gives the diversity among the genotypes and crossing between the genotypes of cluster I and cluster V will result in more diverse offsprings. Cluster mean values suggests that crossing from genotypes of cluster I and cluster III will yield early mature along with high seed yield offsprings.

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