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Genetic diversity analysis for qualitative and quantitative traits in Indian mustard (*Brassica junceaL.* Czern & Coss) under normal sowing condition in Bundelkhand region

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ABSTRACT
All the 25 genotypes were grouped into 6 clusters based on D^2 analysis. The cluster-I with 9 strains had maximum genotypes among all the clusters followed by cluster-III, II, IV, V and VI. The inter cluster distance was recorded highest between cluster-III and cluster-IV (90.88). The minimum inter cluster distance was observed between cluster-I and IV (15.38) indicating their close relationship.
Key words: *Clusters, Genetics divergence (D^2) and Indian mustard.*

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INTRODUCTION

Botanically, the genus *Brassica* comprises six species (*B. nigra, B.oleracea, B. campestirs, B. carinata, B. juncea, and B.napus*). Among them first three species are elementary and diploid with 2n=16, 18 and 20chromosomes and other three are tetraploids with chromosomes numbers 2n=34, 36 and 38. All these crops are grown under wide range of agro-climatic conditions. Indian mustard [*Brassica juncea* (L.)Czern&Coss], which is cultivated under the genus *Brassica* is cultivated all over India and it is throughout the world belongs to family Cruciferae(Brassicaceae). It has 38 to 42 % oil and 24% protein. The availability of genetic variation is advantageous for crop improvement. Such type of variability brought about by a group of genes which have a small individual effect, can be studied through quantitative measurements. The genetic facts are inferred from observations on phenotypes. Since phenotype is determined by the joint effect of genotype and environment, non-genetic parts exerts large influence on genetic variability.

The literature available on these aspects in Indian mustard is relevant to the materials and environments of respective studies and cannot be generalized. Therefore, study on the above aspects on the available germplasm under the prevailing environment, where it is to be exploited is essential for successful utilization of germplasm resources for the development of superior varieties. In eastern Uttar Pradesh, a large acreage of mustard is under saline-alkaline soil condition. However, for such situation, screening of genotypes will help in identification of suitable genotypes.The exploitable variability is, therefore, required to be judged through various genetic parameters like heritability, genetic advance and others. Such a study appears to be extremely necessary for planning genetic improvement in Indian mustard. It is generally assumed by the plant breeders that cultivars originating from widely separated parts of the world are more likely to be genetically different. Therefore, the more diverse the parents, the more chance of increased spectrum of

variability. On the basis such cultivars are included in hybridization programme in the hope that their presumed genetic diversity would provide a greater likelihood of promising genetic rearrangements.

MATERIAL AND METHODS

The present experiment was carried out during rabi, 2018-19 using 25 germplasma namely; DRMRIJ-31, Basanti, LAHAR, PusaBahar, NRH-101, NRC-DR-2, Mutant Varuna, RH-749, NRCHB-101, Pusa Bold, RH-406, Vardan, PusaKrishma, Ashirvadh, Nav Gold, PusaBarani, Pusa Jai Kisan, Kranti, Vaibhav, PM-26,Urvashi, Maya, Agarani, NDR-8501 and RLM-198 of Indian mustard made available collected from the Section of Oilseed, Department of Genetics and Plant Breeding of Chandra Shekhar Azad University of Agriculture and Technology Nawabganj, Kanpur. The experiment was laid out in Randomized Block Design with three replications. These lines were grown in single row plot of 5 meter length. The spacing between row to row and plant to plant was 45 cm and 15 cm, respectively maintained by thinning. Recommended agronomic practices were adopted to raise a good crop. Five competitive plants from each plot were randomly selected for recording observations for all the quantitative characters except days to flowering and days to maturity which were recorded on the plot basis. The data were recorded for thirteen characters namely; days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, length of main raceme (cm), number of siliquae per plant, number of seeds per siliqua, 1000-seed weight (g), harvest index (%), biological yield per plant (g), oil content (%) and seed yield per plant (g). Oil content was estimated using NMR method. D^2 analysis is done as per P.C. Mahalanobis (1928).

RESULTS AND DISCUSSION

25 strains/varieties of Indian mustard were grouped into 6 clusters under normal sown condition. The genotypes from one source of origin clustered with the genotypes of other source of origin. This indicated that there was no parallelism between geographical distribution and genetic diversity. Anand and Rawat [1], Singh *et al.* [2] and Verma and Sachan [3], Chaubey and Katiyar [4] also found the similar trend. The grouping of genotypes from same geographical origin into different clusters may be due to the different genetic backgrounds and wide divergence in features. Different genetic background is perhaps due to the free exchange of materials among different regions of country for breeding purpose; genetic drift and selection in different environments could be the other important factors contributing to the divergence. Murty and Anand [5], Singh and Gupta [6], Singh *et al.* [2] also reported similar reasons for genetic diversity.

In present investigation, on the basis of magnitude of D^2 values, 25 genotypes of Indian mustard were grouped into 6 clusters. The distribution ofgenotypes in both the environments was different. Maximum genotypes (8) were present in cluster-I. The perusal of Table-7 revealed that the maximum inter cluster distance was observed between cluster-III and cluster-IV (90.88) indicated wide diversity between these groups. Hybridization among the genotypes separated by high inter cluster distance will result in most heterotic crosses. The estimates of genetic divergence for most of the characters under study are in accordance with earlier reports [8, 9, 10].

The maximum intra cluster distance was observed for cluster-III (35.05) followed by cluster-II and cluster-I. The maximum intra cluster value indicated maximum divergence among various genotypes within the cluster. A comparison of cluster mean for thirteen characters under study revealed considerable genetic differences between the clusters regarding one or more characters. The maximum character contribution towards divergence was observed for days to 50% flowering (29.66%). Similar findings were also reported [11, 8, 12, 7, 14, 9].

CONCLUSION

The present investigations on the basis of studies made on genetic divergence it was suggested that cross between the genotypes of clusters-III and IV may give better results during hybridization programme. The maximum contribution towards divergence for days to 50% flowering (29.66%). It indicate that the germplasms are contributed to cluster-III namely; Urvashi, NDR-8501, Agarni, Maya, PusaBarani, RLM-198, PusaKrishma and for

clusters-IV namely; RH-406 can be utilized for future breeding programme.

Table- 1: Distribution of 25 genotypes of Indian Mustard in different clusters.

Clusters	Strains/variety	No.
1.	NRC-DR-2, Nav Gold, Kranti, Vaibhav, RH-30, Selection 2016/10, Selection ns/4, Pusa Jai Kisan, DRMRIJ-31	9
2.	Pusa Bold, Ashirvadh, PusaBahar, Vardan, Mutant Varuna, Basanti	6
3.	Urvashi, NDR-8501, Agarni, Maya, PusaBarani, RLM-198, KR-5610	7
4.	B-85	1
5.	LAHAR	1
6.	NRH-101	1

Table-2: The average intra and inter cluster value of different clusters in Indian mustard (*Brassica juncea*).

Clusters	1 cluster	2 cluster	3 cluster	4 cluster	5 cluster	6 cluster
Cluster 1	11.887	26.954	52.704	15.383	31.070	34.592
Cluster 2		18.368	48.633	39.952	27.233	30.768
Cluster 3			35.054	57.755	58.158	90.883
Cluster 4				0.000	29.720	58.423
Cluster 5					0.000	66.710
Cluster 6						0.000

Table-3: Cluster mean for 13 characters in Indian mustard.

Clusters	Days 50% flowering	Days to maturity	Plant height (cm)	No. of primary branch / plant	No. of secondary branch / plant	Length of main raceme (cm)	No. of siliquae / plant	No. of seeds / siliqua	1000-seed Weight (g)	Biological Yield / plant (g)	Harvest index (%)	Oil Content (%)	Seed yield / plant (g)
Cluster1	80.444	131.148	174.424	7.963	18.667	56.843	325.556	13.148	3.388	51.630	23.228	39.287	12.000
Cluster2	75.500	128.778	170.838	7.667	18.556	45.871	311.722	12.889	3.600	51.833	22.097	38.678	11.444
Cluster 3	67.048	122.190	155.975	7.476	15.429	57.668	313.143	13.048	3.703	51.905	22.785	38.971	11.857
Cluster4	78.000	133.333	166.477	9.333	21.333	60.700	307.667	15.000	2.960	52.333	21.055	40.840	11.000
Cluster5	75.333	127.333	175.143	9.333	20.000	44.973	329.000	13.333	2.327	52.333	22.953	37.950	12.000
Cluster6	84.667	132.667	182.163	8.000	20.000	47.173	300.333	14.333	4.453	52.333	23.510	38.753	12.333

Table- 4: Range among cluster mean for different characters in mustard.

Range	Days 50% flowering	Days to maturity	Plant height (cm)	No. of primary branch / plant	No. of secondary branch / plant	Length of main raceme (cm)	No. of siliquae / plant	No. of seeds / siliqua	1000-seed Weight (g)	Biological Yield / plant (g)	Harvest index (%)	Oil Content (%)	Seed yield / plant (g)
Lower	65.25	117.41	145.51	7.41	10.00	44.97	295.33	12.66	3.13	51.33	22.31	38.07	11.57
Upper	83.50	133.50	176.88	8.50	19.09	59.50	329.41	14.16	3.96	53.33	23.50	40.26	12.33

Table-5: Contribution of each character to words divergence for 13 characters in Indian mustard.

Characters	Number of time appearing 1st time	Per-cent (%) contribution
Days 50% flowering	89	29.67
Days to maturity	3	1.00
Plant height (cm)	3	1.00
No. of primary branch / plant	1	0.33
No. of secondary branch / plant	6	2.00
Length of main raceme (cm)	84	28.00
No. of siliquae / plant	2	0.67
No. of seeds / siliqua	25	8.33
1000-seed Weight (g)	40	13.34
Biological yield / plant (g)	3	1.00
Harvest index (%)	5	1.67
Oil Content (%)	13	4.33
Seed yield / plant (g)	26	8.66

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