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Genetic divergences for seed quality parameters in Indian mustard [*Brassica juncea* (L.) Czern & Coss.]

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Abstract

Genetic divergence analysis in 65 genotypes of Indian mustard [*Brassica juncea* (L.) Czern & Coss.] by applying Mahalanobis's D2 statistics indicated the presence of wider genetic diversity among the materials for 8 characters. The genotypes were grouped into nine clusters by Tocher's method. Cluster IV was the largest group comparing with 15 genotypes, whereas cluster III and V was the second largest group consisting 10 genotypes followed in order by cluster VI and VII (8 genotypes), cluster II and VIII (5 genotypes), cluster IX (4 genotypes) and cluster I (2 genotypes). The highest intra-cluster distance was observed for cluster III (0.22). The highest inter-cluster distance was observed between cluster VI and IV (2.22). The maximum contribution to divergence was from seedling dry weight (44.71%) followed by speed of germination (30.1%), germination (8.85%), shoot length (5.67%), vigour index-I (3.66%), vigour index-II (3.08), root length (2.02%) and seedling length (1.92). These findings could be utilized in breeding high quality seed parameters in Indian mustard.

Keywords: genetic divergence, Mahalanobis's D2 statistics, *Brassica juncea*

1. Introduction

Indian mustard [*Brassica juncea* (L.) Czern & Coss] is an important *Rabi* oilseed crop, belongs to family Cruciferae and genus *Brassica*. It is a natural amphidiploid ($2n=36$), a cross between *Brassica rapa* ($2n=20$) and *Brassica nigra* ($2n=16$). Mustard is largely self-pollinated but certain amount (2-14%) of cross pollination may take place and is mainly grown in northern part of India. Rajasthan contributes 44.60% in area and 52.05% in production of total rapeseed-mustard of India. Mustard crop required lower water requirement (240–400 mm) for completing life cycle, therefore it fits well for rain fed cropping system. Four oleiferous *Brassica* species viz. *Brassica juncea*, *Brassica napus*, *Brassica rapa* and *Brassica carinata* are cultivated in about 6.2 million hectares area producing 9.3 million tons with a productivity of 1499 kg/ hectare. Rajasthan has 2.38 million hectares cultivated area with the production of 3.95 million tons and productivity is 1656 kg/ hectares. (Anonymous, 2018-19) [1-3]. Rapeseed mustard are the third most important oilseed crops of the world and also the first most important oilseed crop of India. The availability of genetic variability engraved in the breeding material plays major role in planning breeding programme to develop superior cultivars or hybrids. In general, the genetically divergent parents are utilized to obtain the desirable recombinants in segregating generations. Therefore, the present study was undertaken to study the nature of magnitude of genetic divergence 65 diverse and geographic origin in 65 genotypes of Indian mustard Mahalanobis D2 technique in order to explore genetic potential in creating valuable breeding variation.

Materials and Methods

The present study was administered at the Seed Science and Technology Section, Achayra Narendra Dev University Agriculture and Technology Kumarganj, Ayodhya (U.P.), during *Rabi* 2018-19 and 2019-20. Sixty five genotypes of Indian mustard [*Brassica juncea* (L.) Czern & Coss.] were planted in completely randomized design with four replications. The data were recorded on 9 quantitative characters viz., germination (%), speed of germination, root length (cm), shoot length (cm), seedling length (cm), seedling dry weight (mg), vigour index-i, vigour index-ii. Simultaneous variations in all characters of 65 Indian mustard genotypes were tested for assessment of the nature of genetic divergence among them following Mahalanobis D2 statistics. The D2 values between the genotypes were obtained as the sum of squares of differences of the values of the corresponding transformed variables. For each pair of combination, the mean deviation *ie.* $d_i = \frac{1}{n} \sum_{j=1}^n (Y_i - Y_j)^2$, where Y_i denotes the transformed variables

(i = 1, 2, 3, 4, 5.....p) were calculated and the D2 was then calculated as sum of the squares of those deviations, *ie.* $D^2 = \sum (x_i - \bar{x})^2 / p$ Where, p = Number of characters. The significance of D2 values was tested by treating them as Chi-square (χ^2) at p degrees of freedom where p is the number of characters considered. Grouping of genotypes by Tocher's method after arranging the D2 values of all combinations of one genotype with the others in ascending order of magnitudes. The genotypes were grouped into a number of clusters by Tocher's method described by Rao (1952) [9]. The criterion used in this method was that any two varieties belonging to the same cluster, at least on an average, show a smaller D 2 - value than those belonging to two different clusters. Then inter-cluster and intra cluster distances were calculated and their relationships were also diagrammatically represented.

Results and Discussion

Sixty five genotypes of Indian mustard, included in the present study were grouped into nine different clusters on the basis of genetic divergence or genetic closeness by D2 following Tocher's method of clustering. The clustering pattern of the genotypes has been shown in Table 1. Cluster IV was the largest group of 15 genotypes, whereas clusters III and V were the second largest group consisting 10 genotypes grouped together. Cluster VI and VII were the third largest cluster based on the genotypes (8 genotypes) followed by cluster II and VIII (5 genotypes), cluster IX (4 genotypes) and cluster I (2 genotypes). Two clusters, VI and VII comprised of three genotypes each cluster. It was concluded that, in general, there was parallelism between genetic and geographic diversity.

The findings are in support to the works of Shathi *et al.*, (2012) [11], Khan *et al.*, (2013) [5], Kumar and Pandey (2013) [6], Singh *et al.*, (2014), Yong *et al.*, (2014) [4] and Tripathi *et al.*, (2019), maximum intra-cluster D2 value (0.22) was recorded in cluster III among the nine intra cluster distances, which revealed maximum genetic diversity among the genotypes of this group. Second highest average intra-cluster distance was observed by cluster II (0.19) followed in order by cluster I (0.11), cluster IV (0.06), cluster V, VI, VII, VIII and IX (0.00) to presented in Table 2. The inter-cluster distances ranged from 0.06 (between VI and V) to 2.22 (between VI and IV). The other clusters with high inter

cluster distances were VI and IV (2.22) followed by cluster VIII and IV (1.91), IX and VI (1.89), IX and IV (1.88), VII and IV (1.79) and IX and V (1.78). The minimum average inter-cluster distance (D2 value) was observed between VI and V (0.06) followed by cluster V and I (0.18), cluster VII and I (0.23) and cluster VII and VI (0.25). The lowest inter cluster distances indicate that the genotype of these clusters had close relationship and hence, may not be emphasized upon to be used in hybridization programme. These results are somewhat in accordance with the findings of Yadav *et al.*, (1990) [16], Singh *et al.*, (2010) [13], Singh *et al.*, (2011) [14], Kumar and Pandey (2013) [6], Tudu *et al.*, (2018), Tripathi *et al.*, (2019) and Yadav *et al.*, (2020) [15]. Cluster IV had higher mean values for most of the desirable characters like vigour index-i (1367.70) followed by vigour index-ii (1367.70), germination (90.75%), speed of germination (19.38), seedling length (15.09 cm), shoot length (7.56 cm), root length (7.26 cm) and seedling dry weight (2.93 mg). The genotypes accommodate under cluster III were found desirable for vigour index-ii (219.64). Similarly, other traits like germination per cent (90.50), speed of germination (18.68), root length (6.38)cm, shoot length (6.81)cm, seedling length (13.46)cm, seedling dry weight (2.44)mg and vigour index-ii (1262.08) were also found quite desirable as presented in Table 3. Percent contribution parameter-wise in genetic divergence is presented in Table 4 and Fig 2. The highest per cent contribution in genetic divergence is obtained by seedling dry weight (44.71%) followed by speed of germination (30.1%), and germination (8.85%). The contribution of rest five are (5.67) shoot length, (3.65) vigour index-I, (3.08) vigour index-II, (2.02%) root length and (0.68%) seedling length.

Thus, present study revealed that there was considerable genetic diversity for seed quality parameters namely, germination (%), speed of germination (%), root length (cm), shoot length (cm), seedling length (cm), seedling dry weight (mg), vigour index-I and vigour index-ii of Indian mustard. There finding could further be utilized for production of high quality seed of promising genotype(s) being related directly from their 65 genotypes on one hand and on other hand the genotypes possessing high values of seed quality parameters could further be utilized for breeding superior genotypes having high quality parameters in Indian mustard.

Table 1: Cluster classification of 65 genotypes of mustard

Clusters	Genotypes
I (2)	URVASHI, MAYA
II (5)	NDRE-4,NDRE-7,UDN16-8,SIVT17-66, SIVT17-33
III (10)	SIVT17-15,SIVT17-29,SIVT17-47,SIVT17-34,NDN16-9,SIVT17-61,SIVT17-38,UDN16-38,SIVT17-37,SIVT17-93
IV (15)	NDN16-8,SIVT17-23,NDN16-2,SIVT17-24,SIVT17-28,SIVT17-46,SIVT17-73,SIVT17-51,SBG16-27,SIVT17-71,SIVT17-95,SIVT17-36,UDN16-35,SIVT17-90,SIVT17-41
V (10)	ROHINI,NDRS2017,ASHIRVAD,SBG16-17,SIVT17-22,SIVT17-55,SIVT17-12,SIVT17-57,SIVT17-129,SIVT17-94
VI (8)	SIVT16-90,SIVT17-83,SIVT17-46,SIVT17-11,SIVT17-30,ROHINI,SIVT17-15,SIVT17-63
VII (8)	UDN16-6,SIVT17-30,SIVT17-11,UDN16-41,SIVT17-63,SIVT17-59,SIVT17-62,SIVT16-91
VIII (5)	SIVT16-90,SIVT17-17,SIVT17-60,SIVT17-40,SIVT17-103
IX (4)	VARUNA,NDR8501,KANTI,VARDAN

Table 2: Intra and Inter Cluster Distances of 65 genotypes of mustard

Clusters	I	II	III	IV	V	VI	VII	VIII	IX
I	0.11	0.32	0.33	1.14	0.18	0.29	0.23	0.52	1.38
II	0.32	0.19	0.51	1.34	0.59	0.62	0.33	0.49	1.22
III	0.33	0.51	0.22	0.58	0.59	0.83	0.72	0.79	1.30
IV	1.14	1.34	0.58	0.06	1.74	2.22	1.79	1.91	1.88
V	0.18	0.59	0.59	1.74	0.00	0.06	0.27	0.60	1.78
VI	0.29	0.62	0.83	2.22	0.06	0.00	0.25	0.67	1.89

VII	0.23	0.33	0.72	1.79	0.27	0.25	0.00	0.54	1.58
VIII	0.52	0.49	0.79	1.91	0.60	0.67	0.54	0.00	1.60
IX	1.38	1.22	1.30	1.88	1.78	1.89	1.58	1.60	0.00

Table 3: Cluster Means of 65 genotypes of mustard by Tochers' Method

Cluster	Germination (%)	Speed of Germination	Root length(cm)	Shoot length(cm)	Seedling length(cm)	Seedling dry weight(mg)	Vigour index-1	Vigour index-2
Cluster I	90.23	18.01	6.38	6.16	12.81	2.09	1157.65	188.97
Cluster II	88.72	16.41	6.34	5.98	12.59	2.19	1118.88	194.67
Cluster III	90.17	18.57	6.28	5.93	12.49	2.44	1121.63	219.64
Cluster IV	90.75	19.38	7.26	7.56	15.09	2.93	1367.70	265.62
Cluster V	90.50	18.68	5.71	5.77	11.75	1.84	1081.89	167.00
Cluster VI	90.00	18.10	6.09	5.08	11.45	1.71	1072.07	153.71
Cluster VII	90.75	16.61	6.38	6.81	13.46	1.90	1262.08	172.50
Cluster VIII	89.25	16.53	4.38	5.77	10.77	2.09	949.42	186.72
Cluster IX	89.25	16.72	6.35	5.97	12.59	2.41	1113.65	181.48

Table 4: Per cent Contribution of parameters towards divergence in Indian mustard

Characters	Contribution%
Germination (%)	8.85
Speed of Germination	30.1
Root length(cm)	2.02
Shoot length(cm)	5.67
Seedling length(cm)	1.92
Seedling dry weight(mg)	44.71
Vigour index-1	3.65
Vigour index-2	3.08

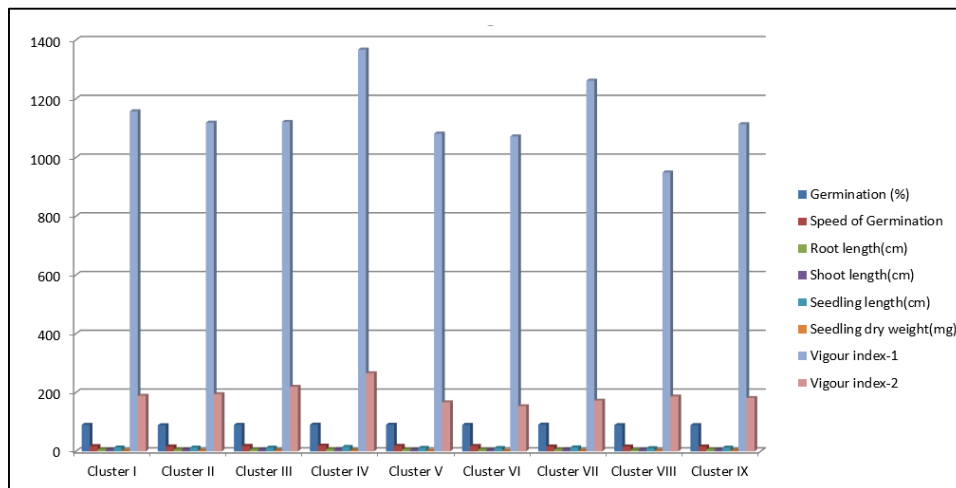


Fig 1: Cluster means of 65 genotypes of mustard by tochers' method

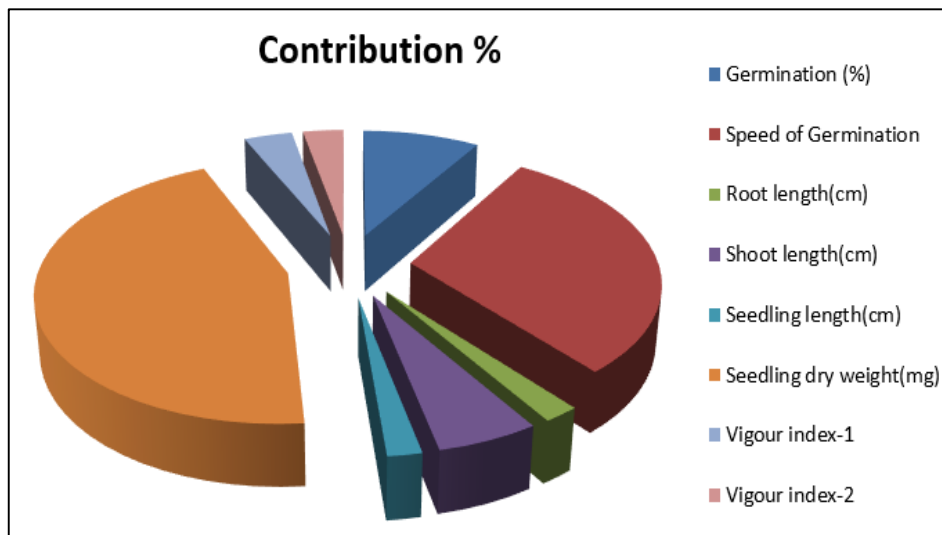


Fig 2: Percent contribution of parameters towards divergence in Indian Mustard

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