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Research Article

Agro-morphological variability and diversity in Indian Mustard (*Brassica juncea* L.)

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Abstract The twenty eight genotypes of Indian mustard were collected from different locations to estimate genetic variability and genetic divergence for thirteen quantitative traits. Genetic divergence determine in twenty eight genotypes of Indian mustard (*Brassica juncea* L.) by applying D^2 statistics for thirteen traits facilitate grouping of all the genotypes into five clusters. Days to first flowering, days to 50% flowering, number of primary branches, number of secondary branches ,plant height, number of siliqua per plant, siliqua length, number of seed per siliqua, days to maturity, biological yield per plant, seed yield per plant, harvest index and test weight were the main contributors for genetic diversity among the genotypes. Out of 5 clusters, cluster V contained the highest 8 genotypes followed by cluster III consisting of seven genotypes, cluster II comprising 6 genotypes, cluster 4 comprising 4 genotypes and cluster I has 3genotypes. The cluster II presented maximum intra-cluster distance (2.829), while maximum inter-cluster distance was detected between cluster IV and I (5.338). The cluster IV had highest mean value for days to first flowering, days to 50% flowering, number of primary branches, siliqua length and seed yield per plant. Therefore the result suggested that these, genotype would be utilized as donor parent for accumulation of favorable genes in future breeding program.

Keywords: D^2, genetic divergence, mustard, Oilseed, quantitative traits

Introduction

Indian mustard [*Brassica juncea* (L.), 2n=36] is one of the significant oilseed crops of the country and having considerable contribution in area and production among the Brassica crops. India holds the premier position in mustard seed production accounting 11% of total planet production .Indian mustard commonly called Rai (Raya or Laha) cultivated under a very diverse situation. In India the main rapeseed-mustard growing states are Rajasthan, Uttar Pradesh, Madhya Pradesh, Gujarat, Haryana, Odisha, West Bengal, Assam and Punjab. The concept of D^2 analysis was originally developed by Mahalanobis (1928) to study the Anthropometry and Psychometry. Rao (1952) suggested the application of this technique for the assessment of genetic diversity in plant breeding. Now this system is highly utilized in plant breeding and genetics for the study of genetic divergence. To understand the spectrum of diversity in any crop, collection and assessment of divergence is foremost important. Genetic divergence study helps in the selection of genetically divergent parents for their exploitation in hybridization program. The forces of differentiation are measured at two levels, i.e., intra-cluster and inter-cluster levels. Thus keeping this information in sight, this study was undertaken to analyze genetic diversity among 28 recognized genotypes of Indian mustard.

Materials and Methods

A field experiment was conducted at Experimental Farm of CCR (PG) College Muzaffarnagar, Uttar Pradesh during winter season 2018-19. The experimental material included of twenty-eight diverse genotypes of Indian mustard. The spacing between row and plant was 30 cm and 15 cm respectively, maintained by thinning. On the basis of randomly selected plants, data were recorded on days to first flowering, days to 50% flowering, number of primary branches, number of secondary branches ,plant height, number of siliqua per plant, siliqua length, number of seed per siliqua, days to maturity, biological yield per plant, seed yield per plant, harvest index and test weight . All recommended package of practices was applied to boost the crop yield.

Estimation of genetic divergence using D^2 statistic

Mahalanobis's D^2 statistics (Rao, 1952) was applied for assessment of genetic divergence among twenty eight genotypes with reference to 10 selected traits. Genetic

divergence (D2) between two genotypes is given by the formula:

$$D^2 x = \Sigma^{p}_{i=`1} \Sigma^{p}_{j=1}(\lambda_{ij})d_i d_j$$

Where, x is that the number of metric trait during a point, λ_{ij} is that the inverse of the common dispersion matrix λij, p is that the number of populations / genotypes while di and dj are the difference within the means of two populations for i^{th} and jth traits. The computation of D2 using this formula gets complicated and laborious when more number of mutually correlated characters is involved in divergence analysis. Therefore the character means were altered into sets of uncorrelated variables with the help of pivotal condensation of common dispersion matrix following (Rao, 1952). After this transformation the formula for genetic divergence is:

$$D^2 = \Sigma di^2$$

$$I=1$$

Where, di is the difference between the transformed values of any two-population means for the ith character. The relative contribution of individual character towards genetic divergence was assessed from rank average.

Grouping of genotypes into different clusters

Grouping of genotypes into different clusters was done following Tocher's method. Usually a cluster is defined as a gaggle of populations per clusters such any two populations belonging to an equivalent cluster should on the average, show a smaller D^2 than those belonging to 2 different clusters. an easy device suggested by Tocher (Rao, 1952) for construction of clusters is to start out with two most closely related populations (having the littlest D^2) then find a 3rd one which has small average D^2 from the primary two and so on. At certain stage when it's felt that after adding a specific population there's an abrupt increase within the average D^2, then that population isn't added to the cluster. Similarly construction of 2nd, 3rd and other clusters are formed till all the populations are included in one or the opposite cluster.

Average intra- and inter-cluster distance

For the measure of intra-cluster distances the formula Σ Di^2 / n was used, where Σ Di^2 is that the sum of distances between all possible combinations (n) of populations (genotypes) included during a cluster. For calculating inter-cluster distance the formula Di^2 / ninj was used; where Di^2 is that the sum of all possible pair wise D^2 values between the individuals of 1 cluster there upon of others, ni is that the number of population in cluster 'i' and nj is that the number of population in cluster 'j'. The information were analyzed within the computer using the Windostat, Hyderabad.

Result and Discussion

The analysis of variance revealed highly significant difference among all the genotypes for all traits indicating a large amount of variability was present in the studied material for effective selection. All the twenty eight genotype with their allotted number are presented in table-1. Based on Mahalanobis D^2 statistic, all the 28 genotype were grouped into five clusters (Table 3). The critical examination of clusters indicated the presence of high level of morphological diversity in the genotypes. The cluster V contained the highest 8 genotypes followed by cluster III comprised 7 genotypes, cluster II have 6 genotypes while cluster IV and I have 4 and 3 genotypes respectively. Genotypes included in particular cluster indicated their close relationship among themselves as compared to other clusters. Therefore, it could be expected that genotypes within a cluster were less genetically different with each other and were diverse from the genotypes belonging to other clusters. This view point has been supported by the work of Monalisa *et al*. (2005), Goswami and Behl (2006), Doddabhimappa *et al.* (2010) and Goyat *et al*. (2012) . The clustering pattern shows that there was a substantial diversity among the genotypes, and no relationship between the genetic and geographical diversity of the genotypes, but the distribution of the genotypes was quite random and mostly independent. Similar results have also been reported earlier by Singh *et al.* (2010) in Indian mustard. The cluster means for various characters are presented in (Table 2). The cluster IV had highest mean value for days to first flowering (48.50), days to 50% flowering (60.08), number of primary branches (6.67), siliqua length (5.45), test weight (7.67) and seed yield per plant (30.80) while cluster III for number of seed per siliqua (15.86) along with number of secondary branches per plant (29.05) and cluster II for harvest-index (34.47) along with number of siliqua per plant (291.39).

The intra cluster distance among various clusters exhibited maximum intra cluster distance for cluster II (2.829) and lowest intra cluster distance was recorded for cluster IV (1.598) Similarly, Verma *et al*. (2000) got 5 clusters. Aunwinithul *et al*. (2004) obtained 8 clusters.. In present study, the highest inter cluster distance was revealed between cluster IV and cluster I (5.338) followed by cluster II and cluster I (4.926), cluster IV and cluster II (4.855), cluster III and cluster I (4.807), cluster III and cluster II (4.791), cluster V and cluster IV (4.153), cluster V and cluster II (4.105),

cluster V and cluster I (3.984) , cluster IV and cluster III (3.558) and cluster V and III (2.467) (Table. 3). The genotypes included in higher intercluster distances have broad spectrum of genetic diversity and will proficiently be utilized in hybridization programme of Indian mustard for improving seed yield and genotypes having smallest inter cluster distances indicated that clusters were homogenous within themselves and heterogeneous between themselves.

Conclusions

To achieve a wide spectrum of variation among the segregates, genotypes having distant cluster, cluster IV could be hybridized with cluster I and cluster II. The separation and selection of varieties based on high heritability of traits make it easy for breeders to exploit their knowledge and skill in transgressive segregation breeding programme. The result based on cluster mean, intra and inter cluster distances indicated that genotype collected from different places were grouped into same cluster, whereas genotypes originating from same place were found scattered in different clusters. This suggest that pattern of clustering of genotypes was independent of their collection sites. In general it was found that there is no association between the geographical region and clustering of genotypes. This may be due to free exchange of material from one place to another. Therefore selection of diverse genotypes with desirable traits would be more effective in hybridization programme for developing high yielding varieties in Indian mustard.

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Table 1: List of genotype of Indian mustard with their alloted number

Alloted number to genotype	Name of genotype	Alloted number to genotype	Name of genotype
1	IC447111	15	IC339953
2	IC589690	16	IC342777
3	RH119	17	IC355856
4	Ashriwad	18	IC335858
5	Kanti	19	IC-597919
6	Basanti	20	IC-598692
7	Geeta	21	IC-571649
8	Maya	22	IC-405235
9	Kranti	23	IC-571630
10	CS-54	24	Geeta
11	IC571649	25	Basanti
12	IC571668	26	BR-40
13	IC571678	27	Jawahar Mustard
14	IC338586	28	Narinder Rye

Table 2. Cluster mean of the different traits in *Brassica juncea* L.

Characters		Days to first flowering	Days to 50% flowering	No. of primary branches	No. of secondary branches	Plant height (cm)	No. of silique per plant	Silique length (cm)	No. of seeds per siliqua	Days to maturity	Biological yield per plant (g)	Seed yield per plant(g)	Harvest index	Test weight(g)
I	Mean	39.22	52.00	4.59	18.33	168.02	288.21	5.24	14.10	132.44	144.77	13.93	10.43	6.10
	± SE	3.98	1.00	0.51	6.49	19.15	53.39	0.66	0.92	5.18	45.98	0.93	3.44	0.81
II	Mean	42.17	55.00	5.74	18.10	153.39	291.39	4.45	14.12	149.56	57.06	19.38	34.47	6.94
	± SE	1.96	2.56	0.63	9.04	12.60	164.85	0.21	1.04	10.37	12.40	3.93	3.88	1.03
III	Mean	40.62	57.81	6.48	29.05	183.48	195.90	4.27	15.86	137.29	140.26	27.85	20.61	3.90
	± SE	3.62	1.83	0.81	8.65	18.16	16.63	0.36	1.49	8.65	29.46	3.61	3.68	0.97
IV	Mean	48.50	60.08	6.67	25.77	181.47	211.33	5.45	15.62	138.33	128.62	30.80	23.96	7.67
	± SE	2.83	2.57	0.90	4.59	2.50	26.43	0.20	0.80	5.10	9.87	3.06	2.06	0.49
V	Mean	37.96	51.54	6.21	23.67	175.88	201.92	4.89	14.90	135.04	111.23	26.84	24.35	3.43
	± SE	3.06	3.83	0.73	4.26	13.39	17.50	0.42	1.56	7.29	13.32	3.76	4.71	0.77

Table 3. Inter and intra cluster distances and number of genotypes in each clusters

Clusters	I	II	III	IV	V	No of genotypes per cluster	Genotypes
I	2.229					3	20,27,28
II	4.926	2.829				6	1,14,15,16,17,18
III	4.807	4.791	2.585			7	9,11,12,13,21,22,23
IV	5.338	4.855	3.558	1.598		4	2,3,4,5
	3.984	4.105	2.467	4.153	2.352	8	6,7,8,10,19,24,25,26