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Quantitative analysis for yield and its components in IC lines of Indian mustard [*Brassica juncea* (L.) Czern and Coss.]

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Abstract
Genetic divergence assessed in 41 IC lines of Indian mustard [*Brassica juncea* (L.) Czern & Coss.] using D^2 statistics for nine characters enabled grouping of all the genotypes into seven clusters *viz* plant height, number of primary branches/ plant, number secondary branches/ plant, number of siliquae/ plant, siliqua length, number of seeds/ siliqua, total number of seeds/ plant, total seed yield/ plant and test weight. Out of 7 clusters, cluster I was the largest comprising 10 lines followed by cluster II consisting of 7 lines, cluster IV and VI with 6 lines, whereas, clusters III, V and VI contained 4, 5 and 3 lines, respectively. VII exhibited highest cluster mean value for siliqua length, number of seeds/ siliqua, total seed yield/plant and test weight whereas cluster II number of primary branches/ plant, number secondary branches/ Plant, number of siliquae/ plant. Cluster means for different clusters and inter cluster distances were used to judge the importance of different clusters in the improvement programme.

Keywords: mustard, genetic divergence, D^2 analysis, cluster analysis

Introduction

Indian mustard [*Brassica juncea* (L.) Czern & Coss.] is one of the most important oilseed crops of the country occupying considerably larger acreage among the Brassica crops (Lodhi *et al*., 2013) [3]. Mustard is the premier oilseed *Brassica* which covers about 85-90% of the total area under cultivation of all these crops (Rao *et al.,* 2017) [8]. It is second most important edible oilseed crop of the India after groundnut. Mustard seed contains about 38 to 43 percent oil which is yellow fragrant and is considered to be the healthiest and nutritious cooking medium (Patel *et at.,* 2012) [7]. It is cultivated in Rabi season mainly in Northwest India and contributes nearly 27 per cent to edible oil pool of the country (Singh *et al*., 2010) [12]. Assemblage and assessment of divergence is essential to know the spectrum of diversity in any crop. Genetic divergence study is essential to develop cultivars with increased yields, wider adaptation, desirable qualities and pest and disease resistance (Lodhi *et al*., 2013) [3].

These promising genotypes were needed to be further tested vigorously under protected and unprotected conditions respectively with a view to observe formation of groups before going for hybridization programme to improve these genotypes (Doddabhimappa *et al.* 2010) [1]. Inclusion of more diverse parents in hybridization programme increases the chances of obtaining maximum heterosis and gives a broad spectrum of variability in segregating generations.

Material and Methods

The experiment consisting of 41 Indigenous mustard lines received from NBPGR, New Delhi was laid out in a randomized block design with three replications and the lines were sown in two rows each of 5.0 m length with a spacing of 45 cm between rows and 15 cm between the plants. Observations were recorded on five randomly selected plants for nine different characters *viz.* plant height (cm.), number of primary branches/ plant, number secondary branches/ plant, number of siliquae/ plant, siliqua length (cm), number of seeds/ siliqua, total number of seeds/ plant, total seed yield per plant (g), test weight (g) in each genotype and replication.

Mahalanobis (1936) [5] D² statistic analysis was used for assessing genetic divergence among the test entries. The clustering of D² values was formed by using Tocher's method as described by Rao (1952) [9] while the intra and inter cluster distance was calculated using formula given by Singh and Choudhary (1977) [11].

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Results and Discussion

Genetic Divergence (D² Analysis): Variability differs from diversity in the sense that the former has observable phenotypic differences, whereas the latter may or may not have such an expression. One of the powerful techniques for assessing genetic divergence is the D^2– statistic proposed by Mahalanobis in 1928 [4]. This technique measures the forces of differentiation at two levels, namely, intra-cluster and inter-cluster levels, and thus helps in the selection of genetically divergent parents to be ordered in hybridization programme.

Cluster Pattern: The 41 lines of Indian mustard were grouped in 7 clusters following Tocher's method Table– 1 and Figure 1. Cluster I constituted of 10 genotypes and was the largest one followed by Cluster II consisting 7, cluster IV and cluster VI consisting of 6 genotypes. Cluster V was consisted of 5 genotypes, whereas cluster III and VII consisted of 4 and 3 genotypes, respectively. 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 by Singh *et al*. (2005) [10], Goyal *et al.* (2012) [2], Mohan *et al*., (2017) [6]. The discrimination of genotypes in to discrete clusters suggested presence of high degree of genetic diversity in the material evaluated. Presence of substantial genetic diversity among the parental material screened in the present study indicated that this material may serve as good source for selecting the diverse parents for hybridization programme.

The average inter and intra cluster distances were calculated and presented in Table 2 and figure 2. The average inter and intra cluster D- values are presented with the help of a cluster diagram, which represent the average distances among the different clusters. The maximum intra-cluster distance was found in cluster IV (12.024) followed by cluster VII (9.629) and cluster VI (7.974). The most divergent clusters indicated highest inter-cluster distance which was found between clusters VI and VII (228.271) followed by clusters V and VII (188.223), whereas lowest distance was between cluster III and I (7.203) suggested a closer relationship between these two clusters and low degree of diversity among the genotypes. Similar findings were also reported by Goyal *et al*. (2012) [2], Mohan *et al*., (2017) [6]. Since, high or optimum genetic divergence is desired between the parents of hybridization plan for obtaining higher frequency of desirable recombinants, the chances of obtaining good segregants by crossing the little diverse genotypes belonging same cluster are very low. In order to increase the possibility of isolating good segregants in the segregating generations it would be logical to attempt crosses between the diverse genotypes belonging to clusters separated by large inter-cluster distances. In order to increase the possibility of isolating good segregants in the segregating generations it would be logical to attempt crosses between the diverse genotypes belonging to clusters separated by large inter-cluster distances.

Table 1: Distribution of 41 lines of mustard into different clusters Tocher Method

Cluster	No. of genotypes in cluster	Lines
I	10	IC589669, IC589681, IC597879, IC571648, IC571655, IC571678, IC571683, IC447111, IC317528, IC339953
II	7	IC589670, IC589680, IC598692, IC599679, IC571630, IC311734, IC335152
III	4	IC589662, IC589690, IC597919, IC338586
IV	6	IC589686, IC571649, IC424414, IC538699, IC538737, IC335856
V	5	IC571661, IC571663, IC342777, IC393232, IC589662
VI	6	IC571635, IC571697, IC571699, IC405235, IC538719, IC571627
VII	3	IC558816, IC571625, IC335858

Table 2: Intra- and inter-cluster distance (D-value) of clusters formed with 41 lines of mustard

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	3.883	44.002	7.203	32.363	11.174	24.643	123.439
Cluster II		5.256	44.621	12.635	82.683	110.505	27.862
Cluster III			6.768	35.420	13.151	25.407	125.082
Cluster IV				12.024	64.372	90.200	47.284
Cluster V					0.000	8.922	188.223
Cluster VI						7.974	228.271
Cluster VII							9.629

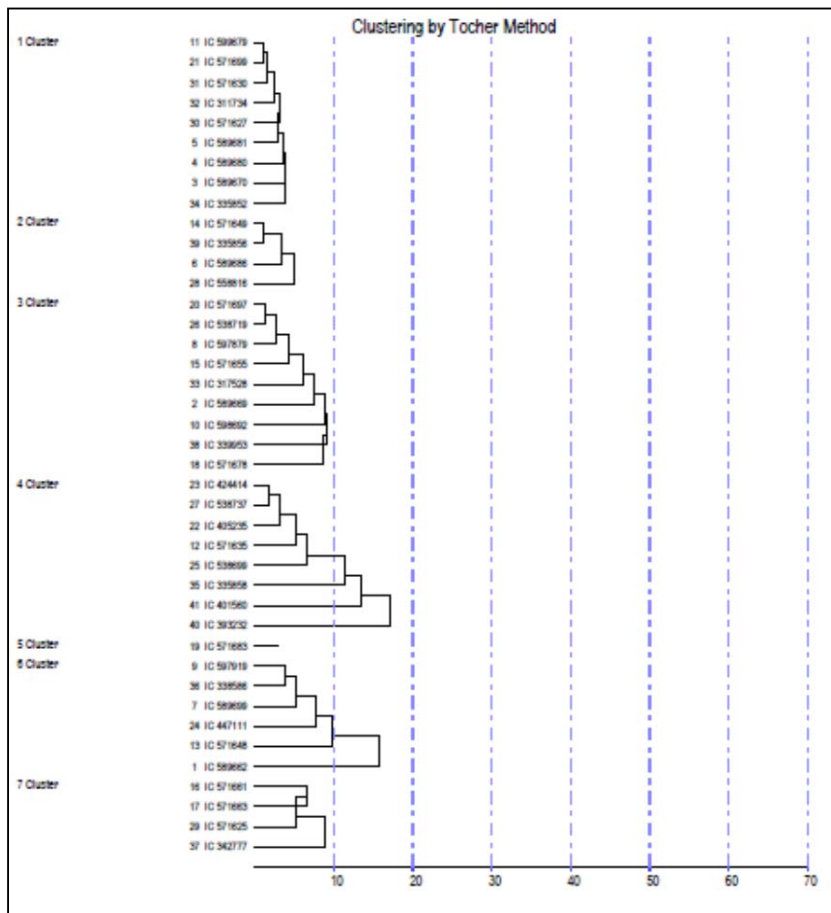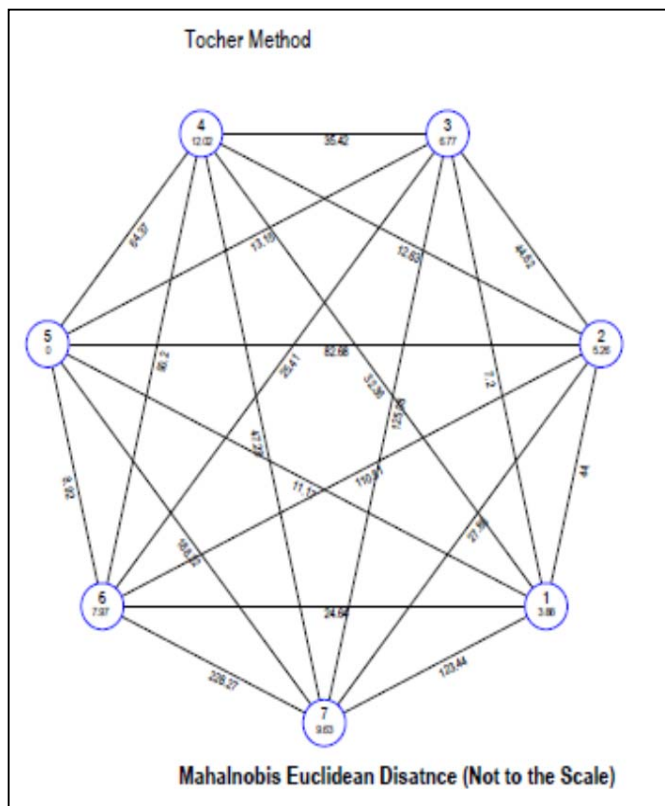**Fig 1:** Grouping of lines into different Clusters by Tocher Method

Fig 2: Average inter and intra cluster distance among different groups of mustard lines

Cluster means: A comparison of the mean values for fifteen characters of different clusters has been presented in Table-3. Cluster means showed considerable differences among the clusters. Cluster I containing ten lines were characterized by lines/cultivars having lowest mean value for siliqua length (3.62). Cluster II having seven genotypes and having moderate mean number of primary branches/ plant (7.00), number secondary branches/ plant (22.33), number of siliquae/ plant (443.33) and lowest mean value for number of total number of seeds/plant (4097.66) and total seed weight/plant (6.42). Cluster IV having six genotypes which can be characterized by highest mean value for plant height (171.31), total number of seeds/plant (4846.83) and lowest mean value for number of seeds/ siliqua (13.00), test weight (1.94). Cluster VI contains lowest mean value for plant height (161.84), number of primary branches/ plant (5.40). Lowest mean value for number secondary branches/ plant (13.50), number of siliqua/ plant (304.58) and high cluster mean value for siliqua length (4.02), number of seeds/ siliqua (14.34), total Seed yield/plant (17.09) and test weight (4.46) was the characteristic of the cluster VI which consisted of three genotypes.

For yield improvement cluster VII exhibited highest cluster mean value for siliqua length, number of seeds/ siliqua, total seed weight/plant and test weight whereas cluster II number of primary branches/ plant, number of secondary branches/ plant, number of siliquae/ plant and lowest mean value for number of total number of seeds/plant and total seed yield/plant. The lines present in cluster IV may be used as parents in hybridization programmes for developing high yielding mustard varieties.

Table 3: Cluster means for nine yield attributes in 41 IC lines of Indian mustard

Characters / Clusters	Plant Height (cm.)	Number of primary branches/ plant	Number secondary branches/ Plant	Number of Siliquae/ plant	Siliqua Length (cm)	Number of seeds/ siliqua	Total number of Seeds/plant	Total Seed yield/plant (g)	Test Weight (g)
Cluster 1	164.42	5.63	14.59	321.63	3.62	13.59	4371.59	10.51	2.46
Cluster 2	167.13	7.00	22.33	443.33	3.93	14.33	4097.66	6.42	2.22
Cluster 3	167.47	6.27	14.69	333.06	3.70	13.36	4369.42	11.52	2.80
Cluster 4	171.31	6.00	15.41	366.25	3.63	13.00	4846.83	10.06	1.94
Cluster 5	166.33	5.19	14.38	306.38	4.01	13.66	4196.61	15.51	3.78
Cluster 6	161.84	5.40	13.86	326.33	3.70	12.86	4465.46	14.88	3.29
Cluster 7	163.48	5.41	13.50	304.58	4.02	14.34	4450.41	17.09	4.46
Mean	165.90	5.74	14.65	328.325	3.77	13.48	4399.95	12.66	3.02

Contribution of Traits in Divergence: The contribution of different characters towards the expression of genetic divergence was calculated Table- 4. On the basis of number of first rank earned by every character out of 1 to 9 in each combination of genotypes (total no. of combination in present study were 820) during the calculation of D^2 values. Each character was ranked on the basis of $d_i = Y_i^j - Y_i^k$ values, where d_i represents the mean difference between the same character for two different genotypes and Y_i^j and Y_i^k represents the mean value of ith character for genotype j and k. Rank 1st was given to the highest mean difference and rank last to the lowest mean difference. Percent contribution was calculated by taking total number of combination as 100 per cent, *i.e.*820 = 100%. By the above stated method it was found that test weight (81.22), number of secondary branches/ plant (4.39), number of seeds/ siliqua (4.02), plant height (2.68), siliqua length (2.32), total seed yield /plant (2.07), primary branches/ plant (1.46), number of seeds/plant (1.22) and number of siliquae/ plant (0.61).

This finding was strongly supported with identification of similar cluster combinations from interpretation of inter-cluster distance made in the present study. Hence, apart from selecting genotypes from the clusters which have an increased inter-cluster distance for hybridization, one can also think of selecting parents based on the extent of divergence with respect to a character of interest within a cluster.

Table 4: Percent contribution of each character toward the total divergence in 41 lines of mustard

S. No.	Character	Number of times appearing first in the ranking	Per cent contribution
1.	Plant Height (cm.)	22	2.68
2.	Number of primary branches/ plant	12	1.46
3.	Number secondary branches/ Plant	36	4.39
4.	Number of Siliqua/ plant	5	0.61
5.	Siliqua Length (cm)	19	2.32
6.	Number of seeds/ siliqua	33	4.02
7.	Total number of Seeds/ plant	10	1.22
8.	Total Seed Weight (g)	17	2.07
9.	Test Weight (g)	666	81.22

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