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Research Article

Assessment of genetic diversity based on agro-morphological traits in Indian mustard [*Brassica juncea* (L.) Czern. & Coss.] germplasm

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Abstract
In the present study, a set of 36 Indian mustard genotypes were evaluated in three replications for twelve agro-morphological traits. D^2 analysis was done to study the diversity pattern which enabled the grouping of genotypes into 11 clusters. Cluster I was the largest (D^2=7.53) comprising of 20 genotypes followed by cluster II (D^2=7.20) of 7 genotypes, while other 9 clusters contained one genotype each. Estimates of average inter cluster distance revealed that clusters IX and XI were most divergent (D^2=118.49) followed by clusters V and XI (D^2=88.48). Hence, crossing between genotypes Pusa Agrani × Rohini (cluster IX × cluster XI); PM-28 × Rohini (cluster V × cluster XI) may yields a considerable amount of heterosis in F_1 generation. Days to maturity (31.9 %) had the highest contribution, followed by seed yield per plant (25.4 %), days to 50% flowering (13.33 %), beak length (7.30 %) and 1000 seed weight (6.67 %) towards the observed genetic diversity. Selection for divergent parents based on concerned traits could enhance the development of transgressive segregants with increased vigor in Indian mustard.

Keywords: Indian mustard, Genetic divergence, D^2 analysis.

INTRODUCTION

Indian mustard [*Brassica juncea* L. (Czern & coss)] is the second most important oil seed crop in the World and in India after Groundnut (*Arachis hypogea* L.) which accounts for 28.6 % of the total production among the seven major oilseeds making it a key edible oilseed crop (Priyanka *et al*., 2020). India is the third largest producer (11.3 %) of oilseed Brassica after Canada and China in the world, still 57 % of the edible oil is imported to meet the domestic demand (Jat *et al*., 2019). During 2021-22, Rapeseed-mustard production was only 11.4 million tonnes (Anonymous, 2022). Hence, there is a need to enhance the present production by developing superior varieties, which could be possible by reshuffling of genes through hybridization from suitable compatible parents. Genetic divergence analyses help in the selection of suitable compatible cross combinations to produce the desired offspring (Hu *et al*., 2007) and to broaden the genetic base of breeding material for selection (Qi *et al*., 2008). To develop cultivars with higher yields, broader adaptation, desirable qualities, and pest and disease resistance, genetic divergence research is required. Incorporating more diverse parents into the hybridization programme increases the likelihood of achieving maximum heterosis, while also providing a wide range of variability in segregating generations. Keeping this in view, the present investigation was designed to study genetic diversity in a set of 36 germplasm of Indian mustard for agro-morphological traits to identify promising accessions.

MATERIALS AND METHODS

The field experiment was conducted with a diverse set of 36 mustard germplasm (received from Pulses and Oilseeds Research Station, Berhampur, West Bengal) during the *Rabi* season (November-March) 2019-2020 at the Agriculture Farm of Palli Siksha Bhavana (Institute of Agriculture), Visva-Bharati University, Sriniketan, West Bengal ($23^0$19' N, $87^0$42' E)**.** They were sown in Randomized complete block design (RBD) with three replications in four rows of each plot size 2.5 x 2.0 m^2 with a spacing of 40 cm between rows and 20 cm between the plants. All cultural practices essential for the good crop of mustard were applied for obtaining a healthy and competitive crop stands (Shekhawat *et al*., 2012). Five competitive plants were randomly selected from each germplasm in each replication and tagged for recording the observations for twelve different characters plant height (cm), the number of primary branches and secondary branches per plant, the number of siliqua on main shoot, the total number of siliqua per plant, siliqua length (cm), beak length (cm), the number of seeds per siliqua, seed yield per plant (g) and 1000 seed weight (g), while days to 50% flowering and days to maturity were taken on a plot basis. Mahalanobis (1936) D^2-statistics was used for the estimation of genetic divergence among 36 genotypes. D^2 values were clustered using Tocher's approach, as reported by Rao (1952), and intra and inter cluster distances were computed using the standard procedure given by Singh and Choudhary (1985).

RESULTS AND DISCUSSION

Analysis of variance showed significant differences for all the twelve characters studied among the genotypes. Following Tocher's method, all the 36 mustard genotypes were grouped into eleven different clusters (**Table 1**). Cluster I was the largest comprising 20 genotypes followed by cluster II with 7 genotypes. The other 9 clusters contained one genotype each. Gadi *et al*. (2020) grouped 36 mustard genotypes into 11 clusters. Clustering of genotypes was irrespective of their geographical origin and no definite correlation was observed between genetic and geographical diversity. The present findings are in agreement with Saroj *et al*. (2021), Sharma *et al*. (2021), Devi *et al*. (2017), Gupta *et al*. (2015), Pandey *et al*. (2013), Singh *et al*. (2013), Dar *et al*. (2010) and Doddabhimappa *et al*. (2010). Further diverse origin may not always be used as an index for genetic diversity because divergence may also be due to genetic drift and selection pressure as concluded by Kole and Chakraborty (2012) and Murty and Arunachalam (1966).

Estimates of average intra and inter cluster distances among the 11clusters (**Table 2**) showed that inter cluster distance was higher than intra cluster distance representing wider genetic diversity among the genotypes. Clusters *viz*., III, IV, V, VI, VII, VIII, IX and X being solitary clusters, had the lowest intra cluster distance of '0', while cluster I had the highest intra cluster distance D^2=7.53 followed by cluster II had D^2=7.20. Hence, selection for improvement of a particular trait based on a higher intra cluster value would be rewarding for intervarietal hybridization. Estimates of average inter cluster distance revealed that clusters IX and XI were most divergent (D^2=118.49), followed by clusters V and XI (D^2=88.48), cluster VII and IX (D^2=87.94), cluster IV and XI (D^2=83.46) and cluster VI and XI (D^2=77.07) indicating wider genetic diversity among the genotypes between these groups resulting in transgressive segregants when used in hybridization programmes. The smallest average inter cluster distance was found between clusters IV and V (D^2 = 6.60), followed by clusters V and IX (D^2 = 8.34), cluster III and X (D^2 = 8.68), cluster III and VI (D^2 = 8.84) and cluster VII and XI (D^2 = 9.18) indicating narrow divergence as they are genetically similar within and between these

Table 1. Clustering of mustard genotypes into different clusters

Cluster	Number of genotypes	Name of genotypes
I	20	Gujarath Mustard- 2, Jagannath, Gujarath Mustard- 3, PM- 27, Shivani, Pusa Bold, TPM, Pusa Mahak, Swarna Jyothi, Jawahar Mustard, Gujarath Mustard- 1, NRCDR-02, Jawahar Mustard- 1, NRCHB-101, Vasundhara, Pusa jaikisan, Geetha, Saurabh (RH-8113), PM-25, T1TPM
II	7	PM-30, Kanti, RH- 30, PM- 21, PM-26, PM-29, Vaibhav
III	1	Laxmi
IV	1	PV
V	1	PM-28
VI	1	PM-22
VII	1	Varuna-T59
VIII	1	Pathan Mustard
IX	1	Pusa Agrani
X	1	Durgamani
XI	1	Rohini

Table 2. Average intra-and inter-cluster D^2values

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	7.53	15.45	9.57	11.02	10.83	14.80	37.82	13.25	19.54	19.61	55.86
II		7.20	22.08	27.62	31.63	29.71	15.61	15.47	48.82	32.13	26.02
III			0.00	16.60	11.85	8.84	51.16	11.96	20.62	8.68	66.38
IV				0.00	6.60	11.97	55.27	23.42	14.39	24.87	83.46
V					0.00	10.94	64.74	26.36	8.34	22.93	88.48
VI						0.00	60.13	16.01	28.26	13.76	77.07
VII							0.00	27.69	87.94	65.67	9.18
VIII								0.00	37.84	16.07	36.32
IX									0.00	34.00	118.49
X										0.00	74.53

clusters. It would, therefore, be logical to effect crossing between genotypes separated by considerable statistical distance. The clustering pattern of these genotypes under the study suggested that geographic diversity may not be necessarily related with genetic diversity Chakraborty and Bhattachraya (2018). The cluster means for characters among all the clusters (**Table 3)** revealed considerable differences. Cluster X with one genotype showed the highest mean value for plant height (180.46 cm), primary branches (8.47), secondary branches (16.87), siliqua per plant (286.07) and seed yield per plant (14.04 g), while it is the lowest for 1000 seed weight (2.97 g). Cluster V and cluster IX had genotypes with a maximum number of siliqua on the main shoot (41.60) while cluster VI (30.40) recorded the least value. Cluster IV was characterized by maximum siliqua length (5.14 cm), beak length (1.19 cm) and 1000 seed weight (5.55 g). Cluster XI had maximum days to maturity (133.00 days) and late days to 50% flowering (63.67 days) but minimum siliqua length (4.11 cm). Cluster IX had the lowest mean value for plant height (180.46 cm), primary branches (4.47), minimum days to maturity (93.00 days) and earliest days to 50% flowering (39.67 days). Cluster III had a minimum number siliqua per plant (154.27) and beak length (0.68 cm). Minimum beak length (0.68 cm) was also observed in cluster VII which had a maximum number of seeds per siliqua (14.47), while a minimum number of seeds per siliqua (12.40) was observed in cluster VI and cluster XI. The mean value for secondary branches (6.93) and seed yield per plant (6.30 g) was lowest in cluster VIII and cluster II, respectively. The relative contribution of each of the 12 morphological characters (**Table 4**) revealed that days to maturity (31.9 %) had the highest contribution, followed by seed yield/plant (25.4 %), days to 50% flowering (13.33 %), beak length (7.3 %), 1000 seed weight (6.67 %) and the number of seeds per siliqua (5.71 %)

Table 3. Cluster mean value of twelve quantitative characters in mustard germplasm

Cluster	Plant height (cm)	Primary branches	Secondary branches	Days to 50% flowering	Number of siliqua on main shoot	Number of siliqua per plant	Siliqua length (cm)	Beak length	Number of seeds / siliqua	Days to maturity	Seed yield per plant (g)	1000 seed weight (g)
I	144.43	5.89	10.07	48.90	37.26	197.73	4.44	0.84	13.47	106.18	9.20	4.17
II	147.43	6.56	11.02	56.33	34.50	185.60	4.32	0.83	12.69	114.71	6.30	3.87
III	152.83	6.73	11.87	47.67	34.27	154.27	4.35	0.68	12.93	102.00	10.68	3.71
IV	136.89	5.70	8.00	46.67	33.20	170.67	5.14	1.19	14.20	102.00	9.65	5.55
V	127.07	5.80	13.67	42.00	41.60	225.80	4.75	0.83	12.93	103.00	11.63	4.89
VI	152.20	6.33	12.87	53.00	33.40	178.33	4.61	0.95	12.40	103.67	13.35	5.16
VII	141.60	5.87	9.47	61.33	30.73	172.67	4.51	0.68	14.47	124.00	7.15	4.56
VIII	158.07	5.07	6.93	59.00	36.93	201.07	4.55	0.89	14.27	109.00	12.43	3.41
IX	120.60	4.47	7.07	39.67	41.60	230.33	4.71	0.81	14.33	93.00	9.78	3.86
X	180.46	8.47	16.87	51.33	32.73	286.07	4.77	1.03	13.13	103.00	14.04	2.97
XI	162.55	5.93	7.13	63.67	36.87	198.80	4.11	0.73	12.40	133.00	8.51	3.29

Table 4. Relative contribution in percentage of each character towards total divergence

S. No.	Characters	Relative contribution (%)
1	Plant height	1.75
2	Primary branches	0.63
3	Secondary branches	0.48
4	Days to 50% flowering	13.33
5	Number of siliqua on main shoot	3.49
6	Number of siliqua per plant	1.43
7	Siliqua length	1.90
8	Beak length	7.30
9	Number.of seeds /siliqua	5.71
10	Days to maturity	31.90
11	Seed yield per plant	25.40
12	1000 seed weight	6.67

towards the observed genetic diversity. Contribution of primary branches per plant (0.63 %) and secondary branches per plant (0.48 %) was low. It is evident that none of the 12 morphological characters contributed very high or low compared to others to influence observed genetic diversity. Days to 50% flowering, seed yield per plant, days to maturity, the number of siliqua per plant, were the most important contributing towards seed yield. Similar findings were reported by Lien *et al*. (2021), Tudu *et al*. (2018) and Devi *et al*. (2017). Hence, the selection of divergent parents done on trait specific genotypes can be extensively used for recombination breeding in mustard.

Considering genetic divergence as well as the relative contribution of characters in determining the yield in a particular population, the crossing between the intra cluster genotypes i.e. Pusa Mahak × Jawahar Mustard, Pusa Mahak × Gujarat Mustard 03 (cluster I); Pusa Mustard 30 × Kanti, Pusa Mustard 30 × Vaibhav (cluster II); and inter cluster genotypes i.e. Pusa Agrani × Rohini (cluster IX × cluster XI); PM-28 × Rohini (cluster V × cluster XI) are most likely to yield a considerable amount of heterosis in F_1 generation. These combinations could provide a wide spectrum of recombinants in segregating generations.

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