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Genetic Diversity Analysis in Indian Mustard [*Brassica juncea* (L.) Czern and Coss.] Genotypes

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ABSTRACT: The production and productivity of Indian mustard is not as sufficient as it can fulfil the current demand of edible oils of the country. This regard, there is an urgent need of high productive varieties of Indian mustard. Availability of sufficient genetic diversity is the basic necessity of any breeding programme for the improvement in desirable traits. The present investigation was carried out at Students Instructional Farm of Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya consisting of sixty Indian mustard genotypes including three checks sown in Augmented Block Design during *rabi* 2021-2022 to study the diversity present among Indian mustard genotypes for seed yield and its component traits. The sixty genotypes of Indian mustard were grouped into six clusters. Cluster I and IV highest genotypes *i.e.*, 13 each while lowest genotypes were noted in cluster III having 6 genotypes. The average inter cluster D^2 values indicated that the most diverse groups were III & II and cluster III & I. The genotypes from the most diverse clusters can be used as donors for rewarding the trait improvement.

Keywords: *Brassica juncea*, genetic diversity, inter cluster distance, Euclidean cluster analysis.

INTRODUCTION

Indian mustard [*Brassica juncea* (L.) Czern and Coss.] belongs to the genus Brassica of the family *Brassiacaceae* (former Crucifereae), is mainly a self-pollinating crop, although on an average 7.5-30% out-crossing occurs under open or natural field conditions (Abraham, 1994; Rakow and Woods 1987). Cytologically it is an amphidiploid (2n=36), derived from interspecific cross of *Brassica campestris* (2n=20) and *Brassica nigra* (2n=16) followed by natural chromosome doubling (Tomar *et al*., 2017).

Brassica are economically of prime important genus comprising of oilseeds, vegetables and forage crops. Indian mustard is the second most important oilseed crop of the country next to groundnut, sharing 27.8% in the Indian oilseed economy. *Brassica napus*, *B. campestris* and *B. juncea* are the three chief species of mustard which produce edible oil. The major mustard producing regions are China, Indian subcontinent, Canada and Northern Europe (Ram and Hari 1998). According to an estimate, the area, production and yield of rapeseed-mustard in the world was 36.59 million hectares (mha), 72.37 million tonnes (mt) and 1980 kg/ha, respectively, during 2018-19. The area under rapeseed-mustard increased from 5.98 mha (2017-18) to 6.12 mha (2018-19), production increased from 8.43 mt (2017-18) to 9.26 mt (2018-19), and productivity got increased from 1840 kg/ha in 2010-11 to 1980 kg/ha in 2018-19 in India (DRMR, annual report 2019-20). However, the production and productivity of Indian mustard is still low as compared to current demand of edible oils of the country (Jat *et al*., 2019). Therefore, productivity of Indian mustard must be boost up in order to fulfil the increasing demand of edible oils in country.

The hereness of genetic variability is the basic need for genetic improvement through systematic breeding programmes for developing high yielding and stress resistant varieties in any crop. The genetic divergence analysis is an important tool to estimate genetic diversity present among selected genotypes of any plant which determine family relationships and genetic affinity or distance of genotypes from each other studying cluster analysis (Mellingers, 1972).

Keeping this in view, the present study of genetic diversity identification between selected genotypes and local cultivars of Indian mustard done by cluster distance analysis.

MATERIALS AND METHODS

The present investigation was carried out at Students Instructional Farm of Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya consisting of 60 Indian mustard genotypes including three checks taken from the Department of Genetics and Plant Breeding. Geographically, this place is located at an altitude of 113 meters above from mean sea level in between 26.47°N latitude, 82.12°E longitude. This area falls in sub-tropical zone (Indo-gangatic plain) and the soil texture is characterized by silty loam in nature having 0.40% organic carbon 2.21dSm^{-1} EC, and 45 ESP, 9.2 pH. The climate of district Ayodhya is semi-arid with hot summer and cold winter. The genotypes long with checks were sown in Augmented Block Design during *rabi* 2021-2022 to estimate the variability and heritability for various traits. Each genotype was planted in two rows of 5m long and 45cm apart; plant to plant distance was maintained 15cm by thinning. All the recommended cultural practices were followed to raise a healthy crop.

Five plants in each genotype were taken randomly for each treatment in each replication and tagged for recording observations for twelve metric characters *viz*., 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 on main raceme, number of seeds per siliqua, biological yield per plant (g), harvest index (%), 1000-seed weight (g) and seed yield per plant (g).

Genetic divergence among sixty genotypes planted in augmented design was studied through Non-hierarchical Euclidean cluster analysis (Beale, 1969; Spark, 1973).

RESULTS AND DISCUSSION

The non-hierarchical Euclidean cluster analysis was studied to survey the genetic divergence among sixty Indian mustard germplasms on the basis of twelve quantitative characters. The outcome is being described as follows:

Distributions of genotypes in different clusters: The 60 genotypes of Indian mustard were grouped into six clusters **(**Table 1) (Fig. 1). Cluster I and IV highest genotypes *i.e.*, 13 each followed by cluster VI with 10 genotypes and cluster I and V with 9 genotypes each. The lowest genotypes were noted in cluster III having 6 genotypes. Verma (2021) earlier also noted six clusters among ninety Indian mustard genotypes.

Average intra and inter cluster distance: The average intra and inter - cluster distance between different clusters is given in Table 2. The intra - cluster D^2 values ranged from 2.084 (cluster II) to 2.529 (cluster III). The average inter cluster D^2 values indicated that the most diverse groups were III and II (6.347) followed by cluster III and I (5.869), IV and I (4.739). The lowest inter cluster value was found among II and I (2.346) indicate that this group is less diverse. Earlier workers Verma (2021) also noted highest cluster distances among Cluster III&II and Cluster II&V respectively.

Cluster group mean for 12 quantitative traits: The mean performance of all the 12 quantitative characters in various clusters is presented in Table 3. Cluster I showed highest mean for length of main raceme (81.24), number of siliques on main raceme (62.80), number of seeds per siliqua (16.81), biological yield per plant (62.27) and seed yield per plant (18.23); and lowest mean for days to 50% flowering (51.62). Cluster II showed highest mean for number of secondary branches per plant (21.92) while lowest mean performance for 1000-seeds weight (3.61). Cluster III exhibited highest mean for days to maturity (137.33), plant height (cm) (194.14), 1000-seeds weight (5.74) and harvest index (36.78) whereas it had lowest mean for number of primary branches per plant (5.75), number of secondary branches (12.92), length of main raceme (57.45) and number of seeds per siliqua (13.37). Cluster VI showed highest mean for days to 50% flowering (58.54) and it also showed lowest mean for number of siliques on main raceme (46.32) and biological yield per plant (46.93). Cluster V showed highest mean for number of primary branches per plant (7.63), and it did not show lowest mean for any trait. Cluster VI did not show highest mean for any trait under investigation while it showed lowest mean for harvest index (16.16). Devi (2017); Verma (2021) also noted similar results for most of the traits mentioned above.

Table 1: Clustering pattern of 60 Indian mustard genotypes based on Euclidean cluster analysis.

Clusters	No. of genotypes	Genotypes
I	13	RH-30-12-17-18, KMR-18-4, KMR-14-1, KMR-18-5 KMR-16-5, KMR-14-2, KMR-17-3, Rohini, PusaBahar, Jagannath, Varuna, Pusa Mustard 22, Kranti
II	9	NRCDR 2, KMR-19-5, KMR-18-3, Urvashi, KMR-15-1, KMR-18-1, UJM 14, GM-02, NDR-8501
III	6	SIVT-17-26, SIVT-17-92, SIVT-17-94, SIVT-17-82, SIVT-17-15, SIVT-17-10
IV	13	SIVT-17-60, SIVT-17-6, SIVT-17-29, SIVT-17-38, SIVT-17-46, SIVT-17-4, SIVT-17-2, SIVT-17-130, SIVT-17-49, SIVT-17-18, SIVT-17-24, SIVT-17-91
V	9	SIVT-17-22,SIVT-17-14, SIVT-17-57, SIVT-17-29, SIVT-17-17, SIVT-17-7, SIVT-17-79, SIVT-17-88, Pusa Gaurav
VI	10	SIVT-17-52, SIVT-17-127, SIVT-17-9, SIVT-17-39, SIVT-17-93, SIVT-17-53, SIVT-17-25, SIVT-17-85, SIVT-17-14, SIVT-17-100

Table 2: Estimate of average Inter and Intra-cluster distances for six clusters in Indian mustard germplasms.

Clusters	I	II	III	IV	V	VI
I	**2.161**					
II	2.346	**2.084**				
III	5.869	6.347	**2.529**			
IV	4.739	4.532	3.04	**2.502**		
V	3.372	4.157	3.834	3.314	**2.245**	
VI	4.197	3.879	4.236	3.222	2.425	**2.141**

Table 3: Cluster group means for 12 traits among Indian mustard genotypes.

Characters		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 on main raceme	Number of seeds per siliqua	1000-seed weight (g)	Biological yield per plant (g)	Harvest index (%)	Seed yield per plant
I	**Mean**	51.62	127.46	164.53	7.22	20.06	81.24	62.80	16.81	4.71	62.27	29.34	18.23
	± SE	2.40	2.60	9.62	1.01	1.82	3.24	8.60	1.34	0.36	3.66	2.01	1.07
II	**Mean**	53.11	126.89	152.00	6.70	21.92	81.07	54.69	15.93	3.61	60.79	27.56	16.73
	± SE	2.20	3.26	11.76	1.11	1.65	7.12	5.57	0.84	0.62	1.99	2.02	0.96
III	**Mean**	58.33	137.33	194.14	5.75	12.92	57.45	52.18	13.37	5.74	47.50	36.78	17.38
	± SE	5.82	4.72	3.47	1.04	1.32	4.61	4.75	1.77	1.01	4.57	2.89	0.89
IV	**Mean**	58.54	134.69	187.11	7.01	19.10	66.28	46.32	13.79	4.39	46.93	35.92	16.79
	± SE	3.20	3.92	7.05	1.31	1.19	8.44	6.47	2.00	0.73	3.17	2.76	0.80
V	**Mean**	57.22	132.00	192.76	7.63	17.11	63.98	53.62	15.65	5.51	61.26	28.60	17.45
	± SE	3.99	2.83	6.85	0.60	2.37	5.82	8.85	1.53	0.76	4.20	2.08	0.67
VI	**Mean**	57.50	134.00	193.23	6.82	16.29	63.57	50.14	15.90	3.71	59.94	27.05	16.16
	± SE	3.14	3.71	7.55	0.83	1.78	5.42	6.32	1.37	0.48	4.44	1.98	1.05

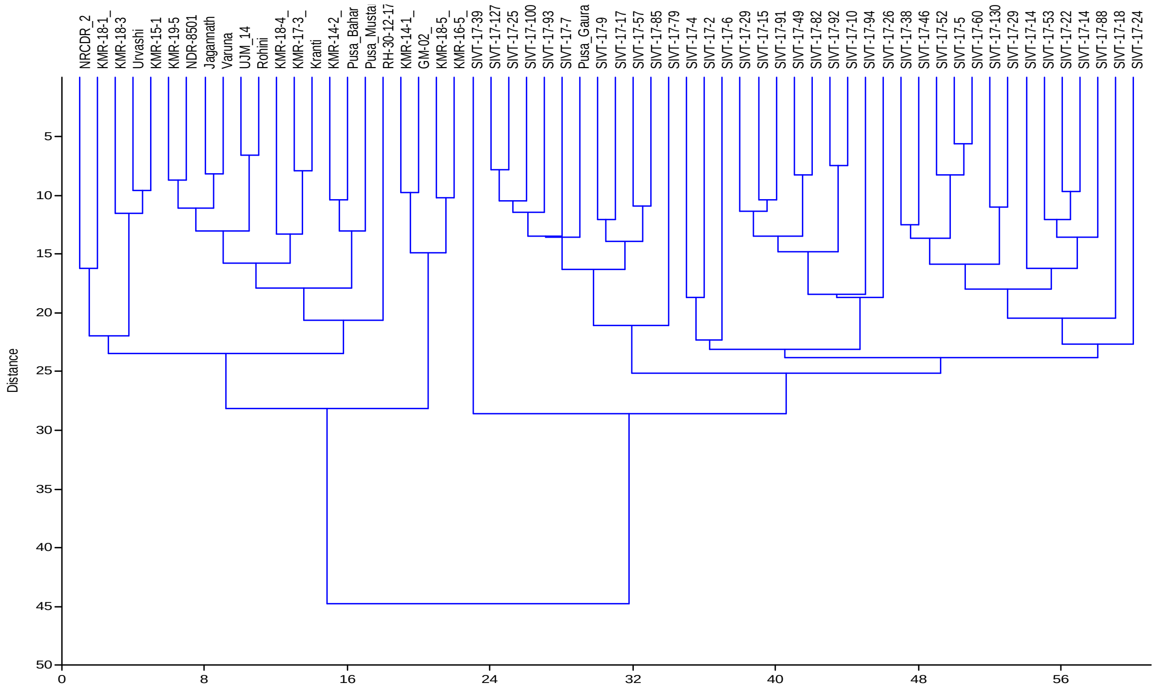

Fig. 1. Dendrogram of clustering pattern of 60 Indian mustard genotypes based on Non-hierarchical Euclidean cluster analysis.

CONCLUSION

The genotypes present in a single cluster show the relatedness in their genetic pattern, and the genotypes of various clusters show distinctness in their genetic pattern. In other words, the more the inter cluster value, the more will be diversity among the genotypes of that clusters. Hence, selection of genotypes from a single cluster while planning a breeding program, will not be of genetic worth. So, opting genotypes form distant clusters will be of eminent use in our breeding program. The average inter cluster D^2 values indicated that the most diverse groups were III & II and cluster III & I. Hence, while planning a breeding programme for higher test weight and a greater number of secondary branches per plant, the genotypes from these diverse clusters can be incorporated as donors.

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Conflict of Interest. None.

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