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Assessment of genetic diversity in Indian mustard [*Brassica juncea* (L.) Czern & Coss.] genotypes for yield and its component traits.

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Abstract

Genetic diversity analysis in 40 genotypes of Indian mustard [*Brassica juncea* (L.) Czern & Coss.] using Mahalanobis D^2 statistics for 13 characters enabled grouping these 40 genotypes into 6 clusters. Cluster V was the largest comprised 11 genotypes followed by cluster IV consisting of 10 genotypes, cluster III with 7 genotypes whereas cluster I, II & VI with 4 genotypes each. It was observed that number of secondary branches/ plant, length of siliqua, number of primary branches, plant height, number of siliqua per plant and seeds per siliqua were the major contributors towards genetic divergence. The cluster IV had maximum intra cluster distance (2.815) while maximum inter cluster distance observed between cluster IV and I (6.346), suggesting that the genotypes constituted in these clusters may be used as parents for future hybridization programme in mustard.

***Keywords*:** *Genetics diversity, D^2 statistics, Indian mustard, cluster analysis*

Introduction

Indian mustard [*Brassica juncea* (L.) Czern & Coss.] popularly known as rai, raya or laha is one of the most important oil seed crop of the country and it occupies considerably large acreage among the brassica group of oil seed crops. It is a member of the genus Brassica and the family Cruciferae (Brassicaceae) (Gupta *et al*., 2022), It is cultivated in *rabi* season mainly in northwest India, contributes nearly 33 percent to edible oil pool of the country. India is a major producer of mustard oil and now become rank 1 in oilseeds production of rapeseed-mustard with total production of 13.16 million tonnes (ICAR-DRMR, 2023-24). Rapeseed-mustard production contributes to 33.24% of total oilseeds production. These crops are cultivated on an area 9.18 million hectares with a total net production of 13.26 million tonnes and with an average yield of 1444 kg/ha (Anonymous 2023). It is mostly produced in the rain-fed ecosystem of the Indian states of Rajasthan, Uttar Pradesh, Madhya Pradesh, Haryana, Bihar, Gujarat, Punjab, West Bengal and Assam (Shyam *et al*., 2021). Since ancient times, many spices of mustard plants have been widely formed and used as food, medicine and spices. Numerous studies have already assessed the genetic diversity of *B. juncea* using phenotypic traits (Bind *et al*., 2015; Devi *et al*., 2017; Rout et al., 2018; Saikrishna *et al*., 2021; Reddy *et al*., 2022; Sur *et al*., 2023). Analysis and assessment of genetic divergence is very essential to know the spectrum of divergence in any crop. The D^2 analysis is a powerful statistics technique to assess the genetic diversity among the number of genotypes. The extent of genetic divergence present in any crop decides the success of any crop improvement programme. Forty genotypes of Indian mustard were taken in present investigation to assess the genetic diversity.

Materials and Methods

The present investigation was conducted at research farm, Department of Genetics and Plant Breeding, Kisan P.G. College, Hapur (U.P.) during *rabi* season 2022-23 under early sown condition. The 40 genotypes of Indian mustard were taken and planted under Randomized Block Design (RBD) with three replications and each plot was consisted of single row of 3 meter length. The inter row and intra row spacing were 30 cm and 15 cm respectively. The sowing was carried out by hand drilling. All agricultural practices were adopted to raise a good crop. Three plants from each row were randomly selected for recording of data. The data were recorded for the following 13 characters namely days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, biological yield (g), number of siliqua per plant, length of siliqua (cm), seeds per siliqua, thousand seed weight (g), harvest index (%), oil content (%) and seeds yield per plant (g). The oil content was recorded by using Fourier Transform Near-Infrared Reflectance Spectroscopy (FT-NIRS) at ICAR-Directorate of Rapeseed-Mustard Research, Bharatpur, Rajasthan. Mahalanobis D^2 statistics analysis was used for assessing genetic diversity among 40 genotypes of Indian mustard [*Brassica juncea* (L.) Czern & Coss.]. The clustering of D^2 values was formed by using Tocher's

method as described by Rao (1952) while the intra and inter cluster distances were calculated using formula given by Singh and Chaudhary (1985).

Results and Discussion

All 40 genotypes of Indian mustard were grouped into 6 clusters using the Tocher's method (Table 1). Out of 6 clusters, cluster V being the largest one with 11 genotypes (PM 28, Kranti, JaganNath, DRMR-IJ-31, TKM-19-1,RH-30R- 17-18,Pusa Jai Kisan, KMR-19-4, PM-29, Pusa Agrani, Gujrat Mustard) followed by cluster IV with 10 genotypes (KMR-850, Pusa Bahar, Jawahar Mustard, CS-54,Vaibhav, Varun, KMR-18-3, KMR-15-2, KMR-16-2, RH-40-6) cluster III with 7 genotypes (Aravali, KMR 17-4, RH-819, RLM619, Pusa Bold, KMR-15-1, KMR-40-60), cluster I with 4 genotypes (PusaTarak, KMR-17-2, KMR-18-4, KMR-17-5), cluster II with 4 genotypes (PusaMahak, Azad Chetna, KMR-19-5, KMR-16-3) and cluster VI with 4 genotype (KMR-14-1, BR-40, KMR-17-3, KMR-18-1).

Table 1: Distribution of forty genotypes of Indian mustard in different clusters

Cluster no.	No. of genotypes	Name of genotypes
I	4	Pusa Tarak, KMR-17-2, KMR-18-4, KMR-17-5
II	4	Pusa Mahak, Azad Chetna, KMR-19-5, KMR-16-3
III	7	Aravali, KMR 17-4, RH-819, RLM619, Pusa Bold, KMR-15-1, KMR-40-60
IV	10	KMR-850, Pusa Bahar, Jawahar Mustard, CS-54, Vaibhav, Varun, KMR-18-3, KMR-15-2, KMR-16-2, RH-40-6
V	11	PM 28, Kranti, Jagan Nath, DRMR-IJ-31, TKM-19-1, RH-30R-17-18,Pusa Jai Kisan, KMR-19-4, PM-29, Pusa Agrani, Gujrat Mustard
VI	4	KMR-14-1, BR-40, KMR-17-3, KMR-18-1

This clustering pattern indicated that there was a considerable diversity among the genotypes. The grouping of genotypes from same geographical origin into different clusters may be due to the different genetic background and wide divergence in features. Similar results were observed by Nagda *et al*., (2028) and Nandi *et al*., (2021).

The character *viz.* number of secondary branches/plant (10.63), length of siliqua (10.29), number of primary branches (9.87), plant height (9.53), number of siliqua per plant (9.41) and harvest index (7.46) contributed more than 50% towards the total divergence (Table 2 & Fig. 1).

Table 2 : Contribution of different characters towards genetic divergence in Indian mustad

S.No.	Characters	% Contribution
1.	Days to 50% flowering	6.97
2.	Days to maturity	6.71
3.	Plant height	9.53
4.	No. of primary branches/ plant	9.87
5.	No. of secondary branches/ plant	10.63
6.	Biological yield	7.10
7.	No. of siliqua per plant	9.41
8.	Length of siliqua	10.29
9.	Seeds per siliqua	7.38
10.	Thousand seed weight	4.76
11.	Harvest index	7.46
12.	Oil content	2.75
13.	Seed yield	7.14

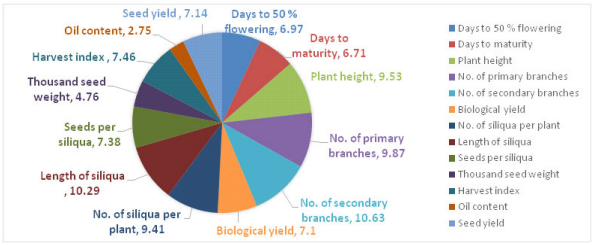

Fig. 1: Percent contribution of different character towards genetic divergence

Parallel to present results, maximum contribution towards the genetic diversity for number of secondary branches per plants was previously reported by Doddabhimappa *et al*., (2010).

The cluster means for different characters are present in Table 3. Cluster I possessed high mean values for number of primary branches/plant (7.16), length of siliqua (5.13), seeds per siliqua (19.67), and seed yield (20.31); cluster IV for days to 50% flowering (65.57), days to maturity (161.63); cluster VI for number of secondary branches/ plant (11.19), biological yield/plant (73.61), number of siliqua/plant (433.82); cluster V for plant height (181.86), oil content (41.01); cluster III for thousand seed weight (5.81) and harvest index (29.34). The cluster mean indicates good plants for hybridization programme could be selected on mean basis. These results are supported by Kumar *et al.*, (2007).

Table 3 : Cluster mean values for seed yield and its components in Indian mustard

Characters/Clusters	I	II	III	IV	V	VI
Days to 50% flowering	57.92	54.83	59.95	65.57	54.03	63.17
Days to maturity	150.42	148.33	156.52	161.63	155.30	154.00
Plant height (cm)	175.42	155.74	176.56	171.72	181.86	171.75
No. of primary branches/plant	7.16	5.11	5.85	5.50	5.94	6.19
No. of secondary branches/plant	11.05	9.36	9.90	9.59	10.29	11.19
Biological yield (g/plant)	69.69	57.85	48.94	52.46	56.28	73.61
No. of siliqua per plant	431.22	348.02	354.91	331.20	362.24	433.82
Length of siliqua (cm)	5.13	4.56	4.74	4.63	4.78	5.12
Seeds per siliqua (g)	19.67	16.61	16.58	14.88	15.66	17.91
Thousand seed weight (g)	5.28	4.11	5.81	3.99	3.96	4.41
Harvest index (%)	29.11	22.49	29.34	21.25	22.31	22.21
Oil content (%)	38.92	40.00	40.13	36.68	41.01	36.58
Seed yield (g/plant)	20.31	12.81	14.34	11.10	12.53	16.18

Table 4 : Average intra (bold values) and inter- cluster distances between different clusters

Cluster No.	I	II	III	IV	V	VI
I	**2.203**					
II	5.888	**2.482**				
III	4.535	3.686	**2.492**			
IV	6.346	3.479	3.356	**2.815**		
V	4.868	3.292	2.809	3.078	**2.468**	
VI	2.996	4.825	4.466	4.711	3.981	**2.097**

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