International Journal of Bio-resource and Stress Management https://ojs.pphouse.org/index.php/IJBSM

Crossref

IJBSM December 2023, 14(12):1625-1630 Print ISSN 0976-3988 Online ISSN 0976-4038 **Article** AR4902

Research Article *Natural Resource Management*

DOI: HTTPS://DOI.ORG/10.23910/1.2023.4902

Analysis of the Genetic Diversity in Indian Mustard (*Brassica juncea* L. Czern&Coss) Genotypes

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ABSTRACT

A study was undertaken during the *rabi* season (October, 2021 to March, 2022) at the crop research center Sardar Vallabhbhai Patel University of Agriculture and Technology Meerut, Uttar Pradesh, India to find out the genetic divergence in 40 genotypes of Indian mustard using the D^2 statistical approach. Forty (40) diverse genotypes of Indian mustard were examined for genetic divergence using a randomized complete block design (RCBD) with three replications. Observations were recorded on various 14 characters viz; days to 50% flowering, days to maturity, plant height (cm), number of primary branches plant^{-1}, number of secondary branches plant^{-1}, siliquae on main axis, length of main axis (cm), siliqua length (cm), number of seeds siliqua^{-1}, 1000 seed weight (g), biological yield plant^{-1} (g), harvest index (%), oil content (%) and seed yield plant^{-1} (g). Mahalanobis D^2 statistics were applied to the analysis of genetic divergence. Based on D^2 values 40 genotypes were grouped into 5 clusters, maximum genotypes eleven obtained in cluster IV after that cluster I with nine genotypes, cluster V with eight genotypes, cluster III with seven genotypes and cluster II with five genotypes. The maximum intra-cluster was in cluster IV. The maximum inter-cluster distance was revealed between cluster II and V. It is clearly indicated that the genotypes included in this cluster are having a wide spectrum of genetic diversity. According to the role of many traits under examination in the manifestation of genetic divergence, plant height had the biggest contribution to divergence.

KEYWORDS: Cluster, d^2 statistics, genetic divergence, Indian mustard, RCBD

***Citation* (VANCOUVER):** Chauhan et al., Analysis of the Genetic Diversity in Indian Mustard (*Brassica juncea* L. Czern&Coss) Genotypes. *International Journal of Bio-resource and Stress Management,* 2023; 14(12), 1625-1630. HTTPS://DOI.ORG/10.23910/1.2023.4902.

Data Availability Statement: Legal restrictions are imposed on the public sharing of raw data. However, authors have full right to transfer or share the data in raw form upon request subject to either meeting the conditions of the original consents and the original research study. Further, access of data needs to meet whether the user complies with the ethical and legal obligations as data controllers to allow for secondary use of the data outside of the original study.

Conflict of interests: The authors have declared that no conflict of interest exists.

RECEIVED on 09th September 2023 RECEIVED in revised form on 16th November 2023 ACCEPTED in final form on 30th November 2023 PUBLISHED on 24th December 2023

1. INTRODUCTION

After groundnut, Indian mustard is the second most significant oilseed crop in both the globe and India. It is popularly known as raya, laha and rai. It is a member of the genus Brassica and the family Cruciferae (Brassicaceae) (Gupta et al., 2022). The genomic constitutions of the *Brassica juncea* (AABB), 2n=36 is the amphidiploids and originated by combinations of the diploid species (Nagaharu U, 1935). 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). The plants are tall, erect, heavily branched and the flower has four sepals, four petals with deep yellow to pale yellow in color. It is a natively autogamous plant, but due to environmental factors and the sporadic visits of pollinating insects, there is frequent out crossing, which can range from 12 to 20% (Nandi et al., 2021). Rapeseed and mustard are crops of tropical as well as temperate zone and require 20–35°C optimum temperature for growing the crop and it requires cool and dry weather for satisfactory growth. They require a fair supply of soil moisture during the growth period and dry clear weather at the time of maturity. In India, it is grown in the *rabi* season from September-October to February-March. The rapeseed and mustard take 140–150 days to maturity, with some early varieties maturing in 105–110 days after sowing. Rapeseed and mustard are long-day plants or crops and these crops are not drought and water-logging tolerant. The seeds of mustard are used for different purposes such as medicine, spices, and as components in the preparation of salad, juices, curries, and pickles. The mustard crop is mainly grown for oil and cake obtained after oil extraction which is widely used for cattle feeding (Priyanka and Pandey, 2021). In India area, production and productivity of rapeseed-mustard are 8.06 mha, 11.75 mt, and 1458 kg ha^{-1} respectively. In Uttar Pradesh area, production and productivity of rapeseed and mustard are 0.76 mha, 1.03 mt, and 1370 kg ha^{-1} respectively (Anonymous, 2022). The fundamental requirement for genetic improvement through systematic breeding programs to create high yielding, stress-resistance cultivars in any crops is the heredity of genetic diversity. In order to quantify the genetic diversity among specific genotypes of any plant and ascertain genetic affinity or the genetic separation between genotypes using cluster analysis, genetic divergence analysis is a crucial technique (Lodhi et al., 2013, Kaur and Banga, 2015, Nagda et al., 2018, Rout et al., 2019, Tarkeshwar et al., 2022, Margam et al., 2022, Gupta et al., 2023). Quantification of genetic diversity existing within and between groups of germplasm is important and particularly useful in the proper choice of parents for realizing higher heterosis and obtaining useful recombinants. 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, Kumari et al., 2018, Saikrishna et al., 2021, Reddy et al., 2022, Sur et al., 2023). Several methods have been advocated by various workers to estimate the genetic divergence in crop plants (Murthy and Arunachalam, 1966). Mahalanobis generalized distance estimated by D^2 statistic (Rao, 1952) is a unique tool for discriminating populations considering a set of parameters together rather than inferring from indices based upon morphological similarities, eco-geographical diversity, and phylogenetic relationships. Determining the genetic divergence in 40 genotypes of Indian mustard using the D^2 statistical approach was the purpose of the current study.

2. MATERIALS AND METHODS

2.1. Study site

The research trial was carried out at the crop research center SardarVallabhbhai Patel University of Agriculture and Technology Meerut, Uttar Pradesh during the *rabi* season (8 October 2021-March 2022). Geographically, Meerut is located at 28°57' to 29°01' North latitude 77°40' to 77°45' East longitude and an altitude of 277 meters above MSL represents the Northwest Plain. The soil of the experimental field was fertile and sandy loam. The experimental material consists of 40 genotypes and the experiment was sown in a randomized complete block design with three replications. Each genotype was sown in four rows and the row length was 5.0 m. Row-to-row spacing was 45 cm and the plant to plant spacing of 10 cm was maintained through proper thinning. All The recommended package of practices was followed during planting to improve the honest crop.

2.2. Method of data collection

Five competitive plants were randomly selected from each plot to record the observation of all quantitative characters except days to 50% flowering and days to maturity recorded based on the plot. Data were recordedfrom14 characters such as days to 50% flowering, days to maturity, plant height (cm), number of primary branches $plant^{-1}$, number of secondary branches $plant^{-1}$, siliquae on main axis, length of main axis (cm), siliqua length (cm), number of seeds $siliqua^{-1}$, 1000 seed weight (g), biological yield $plant^{-1}$ (g), harvest index (%), oil content (%) and seed $yield^{-1}$ plant. The oil content was estimated by using Fourier Transform Near-Infrared Reflectance Spectroscopy (FT-NIRS) at the Central Soil Salinity Research Institute, Karnal. The genetic divergence among 40 genotypes of Indian mustard was estimated by using Mahalanobis D^2 (1963) described by Rao (1952) (Figure 1 and Table 1).

3. RESULTS AND DISCUSSION

Based on D^2 values 40 genotypes of Indian mustard were grouped into five clusters i.e. cluster I, II, III, IV, and

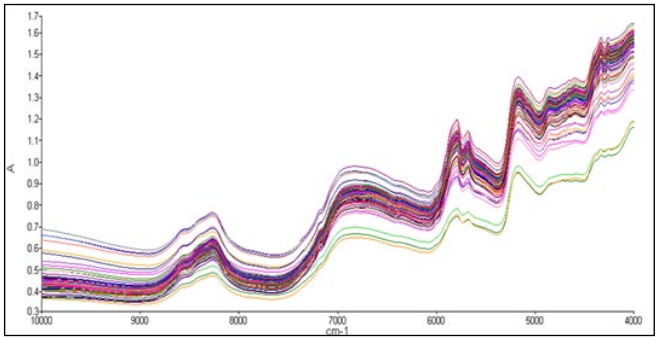

Figure 1: Near infrared spectra of intact seed samples of mustard in the whole NIR range

Table 1: List of Genotypes

Sl. No.	Genotype	Sl. No.	Genotype
1.	DRMRCI- 127	21.	ACNMM- 23
2.	DRMR 2018-17	22.	ORM 2019-02
3.	DRMRHT- 1318	23.	AKMS- 20-1
4.	SKM- 1728	24.	BAUM 08-17
5.	SKM- 1620	25.	Kranti (NC)
6.	RGN- 491	26.	RH- 749
7.	RGN- 483	27.	Giriraj
8.	PBR- 507	28.	Pusa Mustard- 26
9.	RH- 1974	29.	RH-749-12-18
10.	RH- 1975	30.	Laxmi- 2
11.	KMR- 20-3	31.	GM- 2
12.	KMR- 20-4	32.	KMR- 19-3
13.	NPJ- 241	33.	Vaibhav
14.	NPJ- 242	34.	Rohini
15.	JM- 14-8	35.	PusaTarak
16.	PR- 2017-5	36.	Azad
17.	PRB- 2012-3	37.	KMR- 15-1
18.	TM- 274	38.	UJM- 28
19.	HUJM- 19-11	39.	BR- 40
20.	RMM- 19-18	40.	UJM- 22

V. The clustering pattern of the genotypes is presenting in Table 2**.** Cluster IV was the largest and comprising of eleven genotypes (PBR 507, KMR- 20-4, NPJ- 241, NPJ- 242, HUJM- 19-11, ACNMM- 23, BAUM 08-17, RH749, Laxmi- 2, BR- 40 and UJM- 22) followed by cluster I with nine genotypes (DRMR 2018-17, SKM 1620, RGN- 483, PR- 2017-5, RMM- 19-18, ORM 2019-02, PusaTarak, Azad and KMR- 15-1), cluster V with eight genotypes (DRMRHT 1318, SKM 1728, RH 1974, TM 274, AKMS-20-1, BAUM 08-17, Pusa Mustard- 26 and UJM- 28), cluster III with seven genotypes (RGN- 491, RH 1975, JM-

Table 2: Grouping of forty genotypes of Indian mustard (*Brassica juncea* L.) in five clusters

Clus-ters	No. of genotypes	Genotypes
I	9	DRMR 2018-17, SKM 1620, RGN-483, PR- 2017-5, RMM- 19-18, ORM 2019-02, PusaTarak, Azad, KMR- 15-1
II	5	DRMRCI- 127, KMR- 20-3, PRB-2012-3, Giriraj, Vaibhav
III	7	RGN- 491, RH 1975, JM- 14-8, RH-749-12-18, GM- 2, KMR- 19-3, Rohini
IV	11	PBR 507, KMR- 20-4, NPJ- 241, NPJ-242, HUJM- 19-11, ACNMM- 23, BAUM 08-17, RH- 749, Laxmi- 2, BR- 40, UJM- 22
V	8	DRMRHT 1318, SKM 1728, RH 1974, TM 274, AKMS- 20-1, BAUM 08-17, Pusa Mustard- 26, UJM- 28

14-8, RH-749-12-18, GM- 2, KMR- 19-3 and Rohini) and five genotypes in cluster II i.e. DRMRCI- 127, KMR-20-3, PRB- 2012-3, Giriraj and Vaibhav. According to this prediction, the genotypes clustered inside a single cluster were genetically more or less similar to one another, and the other genotypes distributed throughout the remaining clusters were mostly responsible for the seemingly high level of variety. There was no parallelism between genetic diversity and the geographic origin of the genotypes. Similar results were observed by Bind et al. (2015), Saleem et al. (2017), Nagda et al. (2018), Nandi et al. (2021).

Cluster III (56.67) had the highest cluster mean value for days to 50% flowering; cluster IV (144.36) had the highest cluster mean value for days to maturity; cluster III (212.63) had the highest cluster mean value for plant height; number of primary branches plant^{-1} revealed highest mean in cluster V (6.62); highest cluster mean value for number of secondary branches^{-1} was observed in cluster I (14.59); Cluster V (60.37) had the highest cluster mean value for siliquae on main axis; Cluster V (87.83) had the highest cluster mean value for length of main axis; Cluster V (7.15) had the highest cluster mean value for siliqua length; mean value for number of seeds siliqua^{-1} had maximum in cluster V (7.15); 1000 seed weight showed highest mean value in cluster I (5.76); Cluster V had the highest mean value (27.74) for harvest index; maximum mean value for oil content was in cluster I (38.99); cluster V (21.58) had the highest cluster mean value for seed yield plant^{-1}. These results showed that the genotypes with high mean values for the corresponding characters clustered together inside the clusters with high cluster mean for the corresponding characters (Table 3).

Table 3: Cluster mean values for fourteen characters of forty genotypes in Indian mustard (*Brassica juncea* L.)

Clusters		DF	DM	PH	NPBP	NSBP	SMA	LMA	SL	NSS	SW	BYP	HI	OC	SYP
I	Mean	51.11	140.41	193.75	5.75	13.43	50.42	79.56	6.88	13.25	5.76	72.39	25.74	38.99	18.60
II	Mean	52.87	141.13	201.34	5.07	9.66	46.58	69.55	5.33	11.16	5.21	51.91	25.85	38.68	13.43
III	Mean	56.67	146.52	212.63	6.46	14.58	55.72	87.11	6.82	13.67	5.60	84.20	24.86	38.90	20.84
IV	Mean	55.09	144.36	210.30	5.71	11.12	49.76	74.16	6.26	12.58	4.67	63.47	23.56	37.85	14.89
V	Mean	55.17	140.21	210.39	6.62	14.59	60.37	87.83	7.15	13.40	4.71	78.05	27.74	38.82	21.58

DF: Days to 50% flowering; DM: Days to maturity; Plant height (cm); NPBP: No. of primary branches plant^{-1}; nsbp: No. of secondary branches plant^{-1}; SMA: Siliquae on Main Axis; LMA: Length of main axis (cm); SL: Siliqua length (cm); NSS: No. of seeds siliqua^{-1}; SW: 1000 seed weight (g); BYP: Biological yield plant^{-1} (g); HI: Harvest index (%); OC: Oil content (%); SYP: Seed yield plant^{-1} (g)

Cluster IV had a maximum intra-cluster distance (2.784), followed by cluster V (2.694), cluster I (2.609), and cluster II (2.568). Whereas cluster III had the minimum intra-cluster distance (2.558). This revealed the existence of divergent genotypes within different clusters. The opportunity of developing good segregates by crossing the genotypes of the similar cluster showing low value for intra-cluster distance are very low. Crosses between the genotypes from cluster IV (PBR 507, KMR- 20-4, NPJ- 241, NPJ- 242, HUJM-19-11, ACNMM- 23, BAUM 08-17, RH- 749, Laxmi- 2, BR- 40 and UJM- 22) might be made based on the greater intra- cluster distance value. The cluster genotypes may be chosen for crossing on the basis of their superior mean values and seed yield and yield components.

Cluster II and V (6.14) had the maximum inter-cluster distance, followed by clusters II and III (6.072), cluster IV and V (4.443), cluster I and II (4.169), cluster III and IV (3.935), cluster I and III (3.789), cluster I and V (3.691), cluster I and IV (3.629) and cluster II and IV (3.037) cluster II and IV (3.037), while, cluster III and V (2.635) had the minimum inter-cluster distance. The maximum inter-cluster distance shows that cluster II and V genotypes are not closely related, however, the minimum inter-cluster distance showed that the genotypes of these clusters are closely related. Cluster III and V genotypes had the lowest inter-cluster distance, showing that they are closely linked. The genotypes contained in this cluster have a wide range of genetic variation, which is readily evident. A hybridization program should be carried out between the genotypes of cluster II (DRMRCI-127, KMR-20-3, PRB-2012-3, Giriraj, and Vaibhav) and V (DRMRHT 1318, SKM 1728, RH 1974, TM 274, AKMS-20-1, BAUM 08-17, Pusa Mustard-26, UJM-28) to expect transgressive segregants, which provides the opportunity to select genotype in the case of mustard, heterotic cross combinations may even be used to generate hybrids. Similar results were suggested by Rout et al. (2017), Bind et al. (2015), Nagda et al. (2018), Rout et al. (2019) (Table 4).

Table 4: Average intra and inter cluster distance (D^2 value) among five clusters of forty genotypes in Indian mustard (*Brassica juncea* L.)

Clusters	I	II	III	IV	V
I	2.609				
II	4.169	2.568			
III	3.789	6.072	2.558		
IV	3.629	3.037	3.935	2.748	
V	3.691	6.14	2.635	4.443	2.694

The involvement of different characteristics under investigation in the expression of genetic divergence reveals that plant height (9.54) had the highest contribution to divergence, followed by days to maturity (8.89), number of primary branches plant^{-1} (8.20), number of seeds siliqua^{-1} (8.07), days to 50% flowering (7.78), seed yield plant^{-1} (7.61), siliqua length (7.24), number of secondary branches plant^{-1} (7.04), length of main axis (6.99) and 1000 seed weight (4.34). Among the 14 characters Plant height, days to maturity, number of primary branches plant^{-1} and number of seeds siliqua^{-1} were identified as high contributors towards genetic diversity and may be used as parameters while selecting diverse parents in hybridization programs for further improvement in yield. Similar findings were reported by Lodhi et al. (2013), Singh et al. (2014), Tahira et al. (2017), Rout et al. (2018), Nagda et al. (2018) and Nandi et al. (2021).

Table 5: Contribution (%) of fourteen characters towards genetic divergence in Indian mustard (*Brassica juncea* L.)

Sl. No.	Characters	Contribution (%)
1.	Plant height	9.54
2.	Days to maturity	8.89
3.	No. of primary branches plant^{-1}	8.20

Table 5: Continue...

Sl. No.	Characters	Contribution (%)
4.	Number of seeds siliqua^{-1}	8.07
5.	Days to 50% flowering	7.78
6.	Seed yield plant^{-1}	7.61
7.	Siliqua length	7.24
8.	No. of secondary branches plant^{-1}	7.04
9.	Length of main axis	6.99
10.	1000 seed weight	6.85
11.	oil content	6.70
12.	siliquae on main axis	5.75
13.	Harvest index	5.01
14.	Biological yield plant^{-1}	4.34

4. CONCLUSION

Cluster IV (PBR 507, KMR-20-4, NPJ-241, NPJ-242, HUJM-19-11, ACNMM-23, BAUM 08-17and RH-749) demonstrated the highest levels of genetic diversity. Based on the high inter-cluster distance, a hybridization programme could be started between the varieties of cluster II and cluster V to anticipate transgressive segregants and choose genetically.

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