Plant Archives Vol. 26, Supplement 1, 2026 pp. 3313-3316 e-ISSN:2581-6063 (online), ISSN:0972-5210

Plant Archives

Journal homepage: http://www.plantarchives.org
DOI Url : https://doi.org/10.51470/PLANTARCHIVES.2026.v26.supplement-1.441

GENETIC DIVERGENCE AND CLUSTER FOR YIELD CONTRIBUTING CHARACTER IN INDIAN MUSTARD (*BRASSICA JUNCEA* L.) USING D² ANALYSIS

Satyam Sanjay Ingle[1], Vishwanath Kumar[1*], Sanjeev Kumar[2], Kshitij Sanjay Shahare[1], Amrita Sharma[1], BhushanUmesh Jadhao[1], Arpita Atul Chaudhari[1], R.K. Patel[3] and Lokesh Pratap Narayan Chandel[1]

[1]Lakshmi Narain College of Technology University, Bhopal, (M.P.), India
[2]Department of Extension, Govt. of Uttar Pradesh, Lucknow, (U.P.), India
[3]SAM Global University, Bhopal, (M.P.), India
*Corresponding author E-mail: vishwa8159@gmail.com
(Date of Receiving : 29-11-2025; Date of Acceptance : 30-01-2026)

ABSTRACT

The present investigation was under at Research Farm of Genetics & Plant Breeding, LNCTU, Bhopal during *Rabi*, 2024-25. Thirty genotypes were grouped into six different clusters. This indicated the presence of substantial genetic diversity in the evaluated germplasms. The highest intra-cluster distance was observed in case of cluster III (112.66) followed by cluster V (109.49), cluster I (69.27) and cluster II (68.24) while the cluster IV displayed lowest degree of divergence (58.14) suggesting close relationship amongst them. The maximum inter cluster distance was found between cluster IV and VI (1336.32) followed by cluster I and VI (981.92), cluster II and VI (906.67) and cluster V and VI (698.798). The minimum inter-cluster distance was observed between cluster I and II (97.02) followed by that between clusters I and IV (132.02). This indicated that the genotypes of cluster I and II and I and IV are very close to each other. The different clusters showed considerable differences in intra cluster group means of ten characters and genotypes having distinctly different mean performance for various characters were separated into different clusters. Genotypes of cluster IV exhibited highest mean for seed yield, days to maturity, plant height, siliquae per plant and 1000-seed weight. However, cluster VI registered lowest mean for days to 50 (%) flowering, days to maturity, plant height, 1000-seed weight, oil content and seed yield per plant but exhibited higher mean for secondary branches per plant. Exploited heterosis the hybridization programme postulated on the basis of D^2 may be successful between the genotypes of cluster IV and VI.

Keywords **:** Genetic divergence, D^2 analysis, cluster analysis, Intra and Inter cluster divergence.

Introduction

Diploids like *B. campestris* and tetraploids like *B. juncea* allow breeders to experiment with cross-species variability. With states like Uttar Pradesh showing productivity exceeding national averages, studying regional practices could uncover transferable success strategies. Despite being a top producer, India imports 40% of its edible oil-highlighting the need for better productivity and post-harvest technology. Mustard is not just about oil, its cake feeds cattle and fertilizes fields, while Brassica crops help with soil health and erosion control. *Brassica juncea* thrives in marginal soils and withstands drought and salinity, making it a sustainable choice for climate-stressed regions (Chauhan *et al*., 2007). Indian mustard, scientifically D² analysis for seed yield and component traits. The clustering pattern suggested that geographical diversity was not necessarily an index of genetic diversity. The selection of parents based on diversity estimates, coupled with combining ability analysis would be effective.

Sandhu and Gupta (1996) reported that inter specific variation was more than intra specific and the range of variation was the highest in *B. juncea*

followed by *B. napus*and *B. carinata*. Shalini (1998) reported that considerable amount of genetic diversity was prevalent among genotypes representing diverse eco-geographical region of the country, which were randomly distributed into clusters. The characters ranking indicated that the major contributors towards genetic divergence. The investigation also revealed that possessed the potential genotypes which had the superiority in economic traits which needs to be considered in the genetic improvement of mustard.

Material and Method

The experimental material consisted of 30 genotypes *viz.* NPJ 141, RHO 735, KMR 10-2, PRB 2008-13, PARASMANI 33, RGN 73, RH 58, DIVYA 44, KMR 10-1, DRMR 868-3, RHO 555 B, RRN 722, ACN 83, NDRS 2017-1, DRMR 1331, KM 9201, NARENDRA RAI, URVASHI, KANTI, VARDAN, KARGIL SELECTION, KRANTI, BASANTI, SWARNA RAI, CS 54CS 52, PRB 2004-3, NDRE 4, RHO 830, RMMO 9-3 of *Brassica juncea*. L. var. Indian mustard. Each entry was sown in single row of 3 m length spaced at 45 cm apart. The distance between plant to plant (15 cm) was maintained by thinning after 15 days of sowing. The Fertilizers were applied @ 50 kg N, 30 kg P_2O_5, 30 kg K_2O per hectare. Half of Nitrogen fertilizer and full dose of P_2O_5 and K_2O as basal was applied as basal. Remaining half of nitrogen was applied after first irrigation. The experimental material was sown in Randomized Block Design with three replications. The data were recorded on plots basis for days to 50% flowering and days to maturity and on five randomly selected plants basis for plant height (cm), primary branches per plant, secondary branches per plant, siliquae per plant, seeds per siliqua, 1000-seed weight (g), oil content (%) and seed yield per plant (g). Non-hierarchical Euclidean cluster analysis (Beale, 1969 and Spark, 1973), numerical method is the following data are provided as input to the algorithm like matrix of observations, number of clusters, initial cluster centres. Initially each observation is allocated to its closest cluster centre. The means of the clusters are then calculated and are taken to be the new cluster centres. At the same time, the sum of squared deviations of the observations from their respective cluster centres is computed. The observations are then checked in turn to see if a move to a different cluster centre results in a decrease in the total sum of squares.

Result and Discussion

Intra and Inter cluster divergence, all the 30 genotypes were grouped into 6 clusters (Table 1). Cluster I comprised the highest (11) number of genotypes *viz*., RH O555B, RH O735, SWARNA RAI, DIVYA 44, CS 54, RH 58, KMR 10-1, RMMO 9-3, DRMR 868-3, PRB 2008-13, RGN-73 followed by Cluster II (7) number of genotypes *viz*., NDRS 2017-1, KARGIL SELECTION, KMR 10-2, URVASHI, RRN-722, KANTI, NARENDRA RAI. Cluster III number of genotypes *viz*., BASANTI, RH 0830, CS 52, VARDAN and Cluster IV number of genotypes *viz*., PARASMANI, KRANTI, PRB 2004-3, KM 9201 comprised the same number of genotypes (4) in both the clusters. Cluster V contained 3 number of genotypes *viz*., DRMR 1331, NPJ 141, ACN-83 and remaining cluster VI contained single genotype is NDRE-4.

Intra and inter cluster D^2 values are given in Table 2. Intra cluster D^2 values ranged from 0.00 to 112.66, it was maximum in cluster III (112.66) with 4 genotypes *viz*., BASANTI, RH 0830, CS 52, VARDAN. Next to this, cluster V (109.49) with 3 genotypes viz. DRMR 1331, NPJ 141, ACN-83, cluster I (69.28) 11 genotypes viz. RH O555B, RH O735, SWARNA RAI, DIVYA 44, CS 54, RH 58, KMR 10-1, RMMO 9-3, DRMR 868-3, PRB 2008-13, RGN-73 and cluster II (68.24) with 7 genotypes viz. NDRS 2017-1, KARGIL SELECTION, KMR 10-2, URVASHI, RRN-722, KANTI, NARENDRA RAI, respectively. Cluster IV displayed lowest degree of divergence (58.14) viz. PARASMANI, KRANTI, PRB 2004-3, KM 9201 genotypes suggesting close relationship amongst them.

In table 2 inter cluster D^2 analysis was maximum (1336.32) between cluster IV and VI followed by cluster I and VI (981.92), cluster II and VI (906.67), cluster V and VI (698.80) and cluster III and VI (596.77). The minimum inter cluster D^2 value was found between cluster I and II (97.3) followed by that between clusters I and IV (132.03. This indicated that the genotypes of cluster I and II and I and IV are much closed to each other.

Cluster mean for 10 characters are given in Table 3. A close perusal of these cluster means for different characters indicated considerable difference between the clusters for all the characters studied. The performance of cluster means was as under:

Cluster I with 11 genotypes had highest cluster means only for plant height (182.71 cm). Cluster III (49.83) for days to 50% flowering and primary branches/plant (4.42). Cluster IV exhibited highest cluster means for days to maturity (141.52), plant height (181.52), siliquae/plant (226.75), 1000-seed weight (6.37) and seed yield/plant (7.73 g) but exhibited maximum cluster means for secondary branches/plant (9.00). Cluster II and III showed more

or less equal means for seed yield/plant, secondary branches/plant and plant height. The lowest cluster mean for primary branches (3.56) and secondary branches (3.89) was recorded by cluster V.

Conclusion

The genetic divergence study grouped 30 genotypes into six distinct clusters, revealing substantial variability among them. Cluster I contained the largest number of genotypes (11), while Cluster VI was represented by a single genotype. Cluster IV showed the lowest intra-cluster divergence, indicating close genetic similarity among its members. Cluster III and V exhibited the highest intra-cluster divergence, suggesting greater variability within these groups. Maximum divergence was observed between Cluster IV and VI, followed by Cluster I and VI, indicating wide genetic distance and potential for hybridization to exploit heterosis. Minimum divergence was recorded between Cluster I and II and Cluster I and IV, reflecting close genetic relationships. Cluster I recorded the highest mean for plant height. Cluster III excelled in early flowering and number of primary branches per plant. Cluster IV showed superiority for days to maturity, siliquae per plant, 1000-seed weight, seed yield per plant and secondary branches, making it highly promising for yield improvement. Cluster V exhibited the lowest mean values for primary and secondary branches, indicating limited potential for these traits.

Table 1: Clustering pattern of 30 genotypes of Indian mustard on the basis of D^2 analysis

Clusters	No. of genotypes	Genotypes
I	11	RH O555B, RH O735, SWARNA RAI, DIVYA 44, CS 54, RH 58, KMR 10-1, RMMO 9-3, DRMR 868-3, PRB 2008-13, RGN-73
II	7	NDRS 2017-1, KARGIL SELECTION, KMR 10-2, URVASHI, RRN-722, KANTI, NARENDRA RAI.
III	4	BASANTI, RH 0830, CS 52, VARDAN
IV	4	PARASMANI, KRANTI, PRB 2004-3, KM 9201
V	3	DRMR 1331, NPJ 141, ACN-83
VI	1	NDRE-4

Table 2: Estimates of average intra and inter-cluster distances for the six clusters in Indian mustard

Sr. No	Clusters	I	II	III	IV	V	VI
1.	**I**	**69.277**	97.028	194.890	132.028	173.926	981.923
2.	**II**		**68.244**	156.303	214.514	198.495	906.674
3.	**III**			**112.664**	423.082	245.914	596.769
4.	**IV**				**58.141**	206.421	1336.320
5.	**V**					**109.494**	698.798
6.	**VI**						**0.000**

Bold figures represent inter-cluster distance.

Table 3: Cluster means for ten different characters of Indian mustard

Sr. No	Clusters	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches/ Plant	Secondary branches/ Plant	siliquae / plant	Seeds / siliqua	1000-seed weight (g)	Oil content (%)	Seed yield/ plant (g)
1.	**I**	45.909	136.909	182.715	4.303	7.455	226.333	13.485	5.045	41.494	13.153
2.	**II**	46.283	137.733	176.733	4.143	6.333	157.571	12.333	4.852	41.105	8.154
3.	**III**	49.833	135.350	176.350	4.417	6.500	186.250	13.833	3.933	42.050	9.017
4.	**IV**	48.250	141.517	181.517	4.417	7.833	226.750	14.250	6.367	41.492	13.958
5.	**V**	43.222	127.356	163.356	3.556	3.889	156.556	15.000	5.944	42.111	10.067
6.	**VI**	37.000	98.533	112.533	4.333	9.000	158.000	14.667	3.700	40.600	7.733

References

Beale, E. M. L. (1969). Euclidean cluster analysis. Paper presented at the 37th Session of the International Statistical Institute.

Bell, L., Oruna-Concha, M. J., & Wagstaff, C. (2015). Identification and quantification of glucosinolate and flavonol compounds in rocket salad (*Eruca sativa*, *Eruca vesicaria* and *Diplotaxis tenuifolia*) by LC–MS: Highlighting the potential for improving nutritional value of rocket crops. *Food Chemistry, **172***, 852–861.

Beniwal, V., Aggarwal, H., Kumar, A., & Chhokar, V. (2015). Lipid content and fatty acid change in the developing

silique wall of mustard (*Brassica juncea* L.). *Biocatalysis and Agricultural Biotechnology,* ***4***, 122–125.

Chauhan, J. S., Tyagi, M. K., Kumar, A., Nashaat, N. I., Singh, M., Singh, N. B., Jakhar, M. L., & Welham, S. J. (2007). Drought effects on yield and its components in Indian mustard (*Brassica juncea* L.). *Plant Breeding,* ***126***, 399–402.

Goyal, B., Singh, D., Avtar, R., & Singh, A. (2012). Genetic divergence in elite gene pool of Indian mustard (*Brassica juncea* L. Czern & Coss.). *Research on Crops,* ***13***(3), 1102–1104.

Khan, M. H., Ali, M. M., Vhuiyan, S. R., & Mahmud, F. (2013). Genetic divergence in rapeseed-mustard (*Brassica rapa* L.). *Bangladesh Journal of Agricultural Research,* ***38***(3), 417–423.

Kumar, B., & Pandey, A. (2013). Diversity analysis in Indian mustard (*Brassica juncea* L.). *Madras Agricultural Journal,* ***100***(3), 62–66.

Rout, S., Das, A., Sur, B., Umamaheswar, N., Sadhu, S., Ghimiray, T. S., Mondal, H. A., Hijam, L., Chakraborty, M., & Roy, S. K. (2019). Genetic divergence in Indian mustard (*Brassica juncea* L.) under sub-Himalayan region. *Journal of Crop and Weed,* ***15***(2), 18–24.

Sandhu, S. K., & Gupta, N. P. (1996). Genetic divergence and correlation studies in *Brassica* species. *Crop Improvement,* ***23***(2), 253–256.

Shalini, T. S. (1998). *Genetic divergence in Indian mustard [Brassica juncea L. (Czern and Coss)]* (Master's thesis, University of Agricultural Sciences, Bangalore, India).

Singh, A. K., Meena, R. N., Kumar, A. K. S., Meena, R., & Singh, A. P. (2017). Effect of land configuration methods and sulphur levels on growth, yield and economics of Indian mustard (*Brassica juncea* L.) under irrigated condition. *Journal of Oilseed Brassica,* ***8***(1), 151–157.

Shathi, D. A., Arifuzzaman, M., Biswas, B. K., Hasanuzzaman, M., & Azad, A. K. (2012). Genetic divergence in mustard (*Brassica* spp. L.). *African Journal of Plant Science,* ***6***(8), 239–243.

Shekhawat, N., Jadeja, G. C., Singh, J., & Ramesh. (2014). Genetic diversity analysis in relation to seed yield and its component traits in Indian mustard (*Brassica juncea* L.). *The Bioscan,* ***9***(2), 713–714.

Singh, D., Arya, R. K., Chandra, N., Niwas, R., & Salisbury, P. (2010). Genetic diversity studies in relation to seed yield and its component traits in Indian mustard (*Brassica juncea* L.). *Journal of Oilseed Brassica,* ***1***(1), 19–22.

Singh, M., Tomar, A., Mishra, C. N., & Srivastava, S. B. L. (2011). Genetic parameters and character association studies in Indian mustard (*Brassica juncea* L.). *Journal of Oilseed Brassica,* ***2***(1), 35–38.

Singh, S. K., Singh, A. K., & Kumar, K. (2016). Genetic variability for yield and its components in Indian mustard (*Brassica juncea* L. Czern & Coss.). *New Botanist,* ***34***(1–4), 147–150.

Spark, D. N. (1973). Euclidean cluster analysis: Algorithm AS 58. *Applied Statistics,* ***22***(1), 126–130.

Sirohi, S. P. S., Malik, S., & Kumar, A. (2015). Correlation and path analysis of Indian mustard (*Brassica juncea* L. Czern & Coss.). *Annals of Agricultural Research,* ***25***(4), 491–494.