Original Research Article

Genetic Diversity in Indian mustard (*Brassica juncea* L.) genotypes for Yield & its attributing traits under TeraiAgro-Climatic Zone of West Bengal, India

ABSTRACT

A comprehensive investigation was undertaken to evaluate the genetic variability among seventy-one genotypes of Indian Mustard (*Brassica juncea* L.) during the rabi season (winter season)of 2019-2020, employing a randomized complete block design with three replications.The primary objective of crop improvement programmes is to identify and use diverse lines, as genetic diversity is essential for agricultural phenomena such as heterosis and transgressive segregation.The analysis encompassed seven agronomic traits: plant height (cm), number of siliquae on the main shoot, siliquae on branches, seeds per siliqua, 1000-seed weight (g), oil content (%), and seed yield per plant (g). Genetic divergence was quantified using Mahalanobis D^2 statistics, classifying the genotypes into six distinct clusters. Cluster III, comprising 32 genotypes, was the largest, followed by Cluster I (17 genotypes), Cluster VI (10 genotypes), Cluster V (8 genotypes), and Clusters II and IV, each containing two genotypes. The greatest mean intracluster divergence was observed in Cluster VI, whereas Cluster II displayed the least. The maximum intercluster distancebetween Clusters I and VI, while the minimum was noted between Clusters II and IV. Among the traits assessed, seed yield per plant emerged as the most substantial contributor to genetic divergence, followed sequentially by siliquae on branches, oil content, 1000-seed weight, seeds per siliqua, siliquae on the main shoot, and plant height.

1. INTRODUCTION

Indian mustard [*Brassica juncea* (L.) Czern&Coss.], also known as "rai," "raya," "laha," or "banga sarson," is a significant oilseed crop belonging to the family *Brassicaceae*. Mustard is the primary oilseed Brassica, accounting for approximately 85–90% of the total area under cultivation of all oilseed crops (Rao et al., 2017).Indian mustard is an essential part in diet of Indians because it is the source of oils and fats which are important dietary components. The oil content of mustard is estimated to be in between 28.6 and 45.7% **(Turi*et al.*, 2006).** It is a multipurpose crop as its products could serve as vegetables, condiments, both industrial and cooking oil, fodder etc. **(Rahman *et al.*, 2018).** Mustard oil is used for human consumption throughout northern and north-

eastern India for cooking and frying. The sole production of Rapeseed mustard from Canada, European, China, India contributes to around 78.6% of total cultivated area and account for 50-80% of total production. In terms of cultivated area India ranks second and fourth in production **(Nanjundan*et al.*, 2022).** The production volume of rapeseed and mustard in India during 2020-21 is around 11.46 million metric tons. In India, the current demand for edible oils exceeds the production and productivity of mustard **(Singh *et al.*, 2022).**In crop improvement programs, greater emphasis should be placed on increasing seed yield because it is a complex trait dependent on numerous other characteristics (Rout *et al*. 2018). Genetic diversity has become increasingly important in the context of climate change and associated unforeseen events, as it may serve as a reservoir for many novel traits that confer tolerance to various biotic and abiotic stresses (Limbalkar*et al*. 2024, Sandhu *et al*. 2019). Genetic diversity is the underlying cause of many agriculturally important phenomena, such as heterosis and transgressive segregation. Diverse lines are necessary for defect correction in commercial varieties and the development of novel varieties. Hence, the identification of diverse lines (if available), creation of diversity (if not available or limited), and their subsequent utilization are the primary objectives of any crop improvement program (Bhandari *et al*. 2017). Genetic diversity plays a crucial role in plant breeding, because hybrids between lines of diverse origin generally display greater heterosis and facilitate the attainment of desirable segregants in segregating populations (Govindaraj *et al*. 2015). The creation and assessment of divergence in Indian mustard are essential for the development of high-yielding genotypes with desirable traits (Meena *et al*., 2017). Therefore, the present study was conducted to assess the genetic divergence of 71 genotypes of Indian mustard estimated using the Mahalanobis D2 statistics method.

2. MATERIALS AND METHODS

The field experiment was conducted at the Instructional Farm of Uttar Banga Krishi Viswavidyalaya, Pundibari, West Bengal, India, during the rabi(winter)season of 2020-21. The farm is situated at 26º23’59” North latitude and 89º23’22” East longitude and an altitude of 47 meters above mean sea level. The soil at the experimental site is sandy loam in texture, and the agroclimatic zone is lower Gangetic plain region (III); New Alluvial Zone (WB-4)-NARP.The two primary seasons of the year are the long winter, which is also known as the dry Rabi and the wet Kharif. The average annual rainfall in this area ranges from 2100 to 3300 mm. At the lowest position, the temperature ranges from 7.1 to 8 °C, while at the highest, it reaches 34.8 °C. It's hot and slippery from May to September and cool from November to March. The

experimental material comprised seventy-one genotypes of Indian mustard(*Brassica juncea*) that were collected from four differentsources *i.e.*Pulses and Oilseed Research Station, Berhampur, West Bengal;Banaras Hindu University, Varanasi, Uttar Pradesh; Directorate of Rapeseed and Mustard Research (ICAR-DRMR), Bharatpur, Rajasthan and Bidhan Chandra Krishi Viswavidyalaya, Mohanpur, West Bengal.The study employed a Randomized Complete Block Design (RCBD) with three replications, as described by Rajput et al. (2023). The crop was sown on 10th November, 2020-21 for experimental trials. During the period when the experiment was in the field, the weather condition remained suitable for the normal healthy growth of the crop. Each genotype was cultivated in two rows, each measuring 5 meters in length, with inter-row spacing of 30 cm and intra-row spacing of 10 cm, achieved through meticulous thinning. All requisite agronomic practices were meticulously followed to ensure optimal crop establishment and growth under competitive conditions. Observations were recorded for seven morphological and agronomic traits from five randomly selected, vigorous plants per genotype in eachreplication. The traits evaluated included plant height (cm), siliquae count on the main shoot, siliquae count on branches, seeds per siliqua, 1000-seed weight (g), oil content (%), and seed yield per plant (g). Genetic divergence was estimated using D2 statistics (Mahalanobis, 1936) following Rao (1952).The clustering pattern was followed as suggested by Ward (1963). The statistical analysis was carried out using the software GENRES.

$$D^2 = \lambda^{IJ}\delta_I\delta_J$$

Where,

λ^{IJ} = reciprocal matrix to the common dispersion matrix.

δ_I = Difference between the mean values of the two populations for I^{th} character.

δ_J= Difference between the mean values of the two populations for J^{th} character.

The parameter D^2can be estimated as D^2statistics Rao (1952)

$$D^2 = \Sigma\Sigma\ \delta_{IJ},\ d_i\, d_J = \text{Sample estimate of } X_{IJ}$$

Where,

δ_{IJ} = Sample estimates of X^{ij}

d_i = Sample estimates of δ_I

d_J = Sample estimates of δJ

3. RESULTS AND DISCUSSION

The genetic divergence analysis classified all seventy-one genotypes of Indian mustard into six distinct clusters. Cluster I comprised 17 genotypes, including B-85 (Seeta), RW-351 (Bhagarathi), RW-85-59 (Sarna), RW-4C-6-3 (Sanjukta Asech), NPJ-194, TM-276, Rohini (SC), KMR-15-4, PR-2012-9, Divya-88, RL-JEB-52, DRMRIJ-15-85, RH-1202, NPJ-196, KM-126, RB-77, and Pusa Mustard-27 (EJ 17). Cluster III, the largest, contained 32 genotypes, including RMM-09-10, JMM-927-RC, RRN-871, SKM-1313, DRMR-15-5, KMR-53-3, RL-JEB-84, Ganga, RGN-73-JC, RH-1209, PR-2012-12, RGN-385, NPJ-195, Maya-C, SKJM-05, SVJ-64, Sitara-Sreenagar, RH-0923, DRMR-15-16, NPJ-19, DRMR-15-47, RGN-389, RAURD-214, DRMR-15-14, DRMR-4001, RGN-384, NPJ-197, RB-81, NPJ-200, RH-749, and Pusa Mustard-25 (NPJ 112). Cluster VI included 10 genotypes: Kranti-NC, Giriraj, RH-406, DRMR-IJ-31, NRCHB-101, DRMR-150-35, CS 54, PHR 2, RL 1359, and Kranti. Cluster V consisted of 8 genotypes: DRMR-15-9, KMR-L-15-6, PRD-2013-9, DRMRIJ-15-66, RH-1368, RH-1325, RNWR-09-3, and PRD-2013-2. Clusters II and IV were the smallest, each containing 2 genotypes. Cluster II included RGIN-73 and Pusa Mustard-26 (NPJ 113), while Cluster IV comprised RGN-386 and BPR-540-6.

There was no correlation between genetic and geographic diversity, as each cluster displayed heterogeneity, incorporating genotypes from diverse geographic origins.

Similar results have been reported by, Kumar *et al (2024)*, Lodhi *et al.* (2013), Shekhawat *et al.* (2014), Dilip *et al.* (2016), Rout *et al.* (2018) and Chaturvedi *et al.* (2021).

The highest mean intra-cluster divergence was observed in Cluster VI (32.763), followed by Cluster III (29.255), Cluster I (29.064), Cluster V (24.189), Cluster IV (5.857), and Cluster II (1.494). Given the elevated intra-cluster divergence values, potential hybridization efforts may prioritize genotypes from Cluster VI (Kranti-NC, GIRIRAJ, RH-406, DRMR-IJ-31, NRCHB-101, DRMR-150-35, CS 54, PHR 2, RL 1359, and KRANTI) and Cluster III (RMM-09-10, JMM-927-RC, RRN-871, SKM-1313, DRMR-15-5, KMR-53-3, RL-JEB-84, Ganga, RGN-73-JC, RH-1209, PR-2012-12, RGN-385, NPJ-195, Maya-C, SKJM-05, SVJ-64, Sitara-Sreenagar, RH-0923, DRMR-15-16, NPJ-19, DRMR-15-47, RGN-389, RAURD-214, DRMR-15-14, DRMR-4001, RGN-384, NPJ-197,

RB-81, NPJ-200, RH-749, and Pusa Mustard-25 [NPJ 112]) to generate superior segregants.

Genotypes from these clusters should be prioritized for crossing, especially those exhibiting higher mean values for seed yield and yield-related traits. Conversely, the likelihood of obtaining promising segregants is minimal when crossing genotypes within clusters characterized by low intra-cluster divergence. This type of result regarding intracluster distance was also reported by Jahan *et al.* (2013), Lodhi *et al.* (2013), Bind *et al.* (2015) and Gupta *et al.* (2015).

The highest inter-cluster D^2 value was observed between Cluster I and Cluster VI (55.088), followed by Cluster V and Cluster VI (42.793), Cluster I and Cluster IV (39.006), Cluster I and Cluster III (37.374), Cluster I and Cluster II (35.525), Cluster III and Cluster VI (35.080), Cluster I and Cluster V (34.880), Cluster III and Cluster V (30.331), Cluster II and Cluster VI (29.654), Cluster IV and Cluster V (23.352), Cluster II and Cluster III (23.315), Cluster III and Cluster IV (22.162), Cluster IV and Cluster VI (21.325), Cluster II and Cluster V (19.307), and the lowest between Cluster II and Cluster IV (10.122).

These findings underscore the substantial genetic diversity among the genotypes across these clusters, making them valuable resources for mustard hybridization programs aimed at enhancing seed yield. Consequently, crosses between genotypes from clusters exhibiting the greatest inter-cluster distances—particularly between Cluster I and Cluster VI, as well as between Cluster V and Cluster VI—are recommended. Such crosses are likely to produce superior progenies in the segregating generations and contribute to the development of high-yielding mustard hybrids.Such inter-cluster distance results have also been reported by Lodhi *et al.* (2013) and Bind *et al.* (2015).

The highest cluster mean for plant height was observed in Cluster VI, while the number of siliquae on the main shoot reached its peak mean value in Cluster III. Cluster I exhibited the highest mean value for the number of siliquae on branches, whereas Cluster II recorded the maximum mean for the number of seeds per siliqua. For 1000-seed weight, the highest mean was noted in Cluster VI, while Cluster I demonstrated the highest cluster means for both oil content and seed yield per plant.

These results indicate that the genotypes within clusters exhibiting high mean values for specific traits contributed significantly to the overall trait performance. Among the evaluated traits, seed yield per plant made the greatest contribution to genetic divergence, followed by the number of siliquae on

branches, oil content, 1000-seed weight, number of seeds per siliqua, number of siliquae on the main shoot, and plant height. These findings underscore the potential for selecting genetically diverse genotypes based on traits with substantial contributions to genetic diversity, facilitating targeted improvement in mustard breeding programs.These results are somewhat in accordance with the findings of Khan *et al.* (2013) and Shekhawat *et al.* (2014), Chaturvedi *et al.* (2021).

Table 1: Distribution of seventy-onegenotypes of Indian mustard in six clusters

Cluster number	No. of genotypes	Genotypes
I	17	B-85(Seeta), RW-351(Bhagarathi), RW-85-59(Sarna), RW-4C-6-3(Sanjukta Asech), NPJ-194, TM-276, Rohini (SC), KMR-15-4, PR-2012-9, Divya-88, RL-JEB-52, DRMRIJ-15-85, RH-1202, NPJ-196, KM-126, RB-77, Pusa mustard-27(EJ 17).
II	2	RGIN-73, Pusa mustard-26(NPJ 113).
III	32	RMM-09-10, JMM-927-RC, RRN-871, SKM-1313, DRMR-15-5, KMR-53-3, RL-JEB-84, Ganga, RGN-73-JC, RH-1209, PR-2012-12, RGN-385, NPJ-195, Maya-C, SKJM-05, SVJ-64, Sitara-Sreenagar, RH-0923, DRMR-15-16, NPJ-19, JMM-927-RC, DRMR-15-47, RGN-389, RAURD-214, DRMR-15-14, DRMR-4001, RGN-384, NPJ-197, RB-81, NPJ-200, RH-749, Pusa mustard-25(NPJ 112).
IV	2	RGN-386, BPR-540-6.
V	8	DRMR-15-9, KMR-L-15-6, PRD-2013-9, DRMRIJ-15-66, RH-1368, RH-1325, RNWR-09-3, PRD-2013-2.
VI	10	Kranti-NC, GIRIRAJ, RH-406, DRMR-IJ-31, NRCHB-101, DRMR-150-35, CS 54, PHR 2, RL 1359, KRANTI.

Table 2: Average intra and inter cluster distance (D2 value) in Indian mustard

Cluster	I	II	III	IV	V	VI
I	**29.064**	35.525	37.374	39.006	34.88	55.088
II		**1.494**	23.315	10.122	19.307	29.654
III			**29.255**	22.162	30.331	35.080
IV				**5.857**	23.352	21.325
V					**24.189**	42.793
VI						**32.763**

Table 3: Cluster mean for seven characters in Indian mustard

Clusters	PH	SMS	SBR	SPS	TW	OC	SYP
1	131.939	23.918	141.865	11.706	3.825	33.645	6.975
2	108.067	17.823	57.788	13.333	3.705	33.487	2.658
3	132.235	26.088	91.127	12.203	3.954	32.102	4.123
4	121.217	18.333	81.352	13.167	4.240	31.012	3.625
5	134.096	20.545	84.308	13.125	3.593	30.487	3.883
6	136.553	24.876	67.829	11.967	4.334	31.954	3.227

Table 4:Contribution of different characters towards geneticdiversity in Indian mustard

Character	Contribution %
Plant height (cm)	3.1388
Number of siliquae on main shoot	3.6620
Number of siliquae on branches	19.2757
Number of seeds per siliquae	5.5533
1000-seed weight (g)	13.0785
Oil content(%)	19.1147
Seed yield per plant(g)	36.1771

4. CONCLUSION

Cluster VI exhibited the highest intra-cluster divergence, while Cluster II showed the lowest, highlighting the genetic variability within Cluster VI (Kranti-NC, GIRIRAJ, RH-406, DRMR-IJ-31, NRCHB-101, DRMR-150-35, CS 54, PHR 2, RL 1359, KRANTI). This makes it suitable for selecting diverse parental lines. The maximum inter-cluster divergence was noted between Clusters I and VI, offering potential for transgressive segregants. Hybridization between these clusters could yield heterotic combinations, enhancing seed yield and agronomic traits in mustard breeding programs.

Disclaimer (Artificial intelligence)

Option 1:

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

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