Study of Genetic Divergence in Indian Mustard(*Brassica juncea* L.)Genotypes for Yield and Yield-ContributingTraits

Genetic diversity in Indian mustard relation to yield attributes

Author name and institute affiliation   not mention ????

ABSTRACT

An investigation was conducted into the genetic diversity of seventy-one Indian Mustard (*Brassica juncea* L.) genotypes during the Rabi season of 2019-20, utilizing a randomized complete block design with three replications. The study assessed seven characteristics: plant height (cm), siliquae count on the main shoot, siliquae count on branches, seed count per siliqua, 1000 seed weight (g), oil content (%), and seed yield per plant (g). Genetic divergence analysis utilized Mahalanobis D2 statistics, resulting in the classification of genotypes into six clusters. Cluster III was the largest with 32 genotypes, followed by clusters I (17), VI (10), V (8), and both II and IV containing two genotypes each. The highest average intracluster divergence was found in Cluster VI, while Cluster II exhibited the lowest. Intercluster distances were most pronounced between clusters I and VI, and least between clusters II and IV. Among the traits studied, seed yield per plant contributed most significantly to divergence, followed by siliquae count on branches, oil content, 1000 seed weight, seed count per siliqua, siliquae count on the main shoot, and plant height.

A comprehensive investigation was undertaken to evaluate the genetic variability among seventy-one genotypes of Indian Mustard (*Brassica juncea* L.) during the Rabi season of 2019-2020, employing a randomized complete block design with three replications. 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 D² statistics, leading to the classification of 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 distance was recorded between 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). Mustard oil is used for human consumption throughout northern and north-eastern India for cooking and frying. 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. 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 trial was conducted at the Instructional farm, Uttar Banga Krishi Viswavidyalaya, Pundibari, West Bengal, India, during the Rabi season 2020-

21. The experimental material comprised of seventy one diverse genotypes of Indian mustard. The experiment used a Randomized Complete Block Design with three replications (Rajput *et al*. 2023). Each genotype was sown in two rows of 5 m length with 30 cm inter row spacing and 10 cm intra row spacing, which was achieved through appropriate thinning. All the necessary cultural practices for optimal mustard crop growth were implemented to ensure healthy and competitive crop stands. Observations of seven characters were recorded from five randomly selected competitive plants from each genotype in each replication. Data were collected for seven traits: plant height (cm), number of siliquae on the main shoot, number of siliquae on branches, number of seeds per siliqua, 1000-seed weight (g), oil content (%), and seed yield per plant (g).

The field experiment was conducted at the Instructional Farm of Uttar Banga Krishi Viswavidyalaya, Pundibari, West Bengal, India, during the Rabi season of 2020-21. The experimental material comprised seventy-one genetically diverse genotypes of Indian mustard. The study employed a Randomized Complete Block Design (RCBD) with three replications, as described by Rajput et al. (2023). 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 each replication. 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).

Mentioned the full formula

3. RESULTS AND DISCUSSION

Based on the genetic divergence analysis, all seventy one genotypes of Indian mustard were grouped into six clusters. A total of seventeen genotypes fell into cluster I [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)], thirty two genotypes in cluster III [RMM 09 10,

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 Lodhi *et al*. (2013), Shekhawat *et al*. (2014), Dilip *et al*. (2016), Rout *et al*. (2018) and Chaturvedi *et al.* (2021).

Maximum average intra cluster divergence value was found for cluster VI (32.763) followed by cluster III (29.255), cluster I (29.064), cluster V (24.189), cluster IV (5.857), and for cluster II (1.494). Based on the larger intra cluster distance value, the crosses could be made among the genotypes from cluster VI (Kranti NC, GIRIRAJ, RH 406, DRMR IJ 31, NRCHB 101, DRMR 150 35, CS 54, PHR 2, RL 1359, KRANTI) followed by 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, 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)) for expecting better segregants. The genotypes from these clusters may be selected for crossing based on their higher mean values for seed yield and yield components. The chance of obtaining good segregates by crossing the genotypes of the same cluster showing a low value for intra cluster distance is very low.

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).

Maximum inter cluster D2 value was recorded between cluster I and VI (55.088) followed by cluster V and VI (42.793), cluster I and IV (39.006), cluster I and III (37.374), cluster I and II (35.525), cluster III and VI (35.080),

cluster I and V (34.88), cluster III and V(30.331), cluster II and VI (29.654), cluster IV and V (23.352), cluster II and III (23.315), cluster III and IV (22.162), cluster IV and VI (21.325), cluster II and V (19.307) and between cluster II and IV (10.122). This clearly indicated that the genotypes included in these clusters had a broad spectrum of genetic diversity and could be used in mustard hybridization programs to improve seed yield. Therefore, it would be logical to attempt crosses between the genotypes of clusters separated by larger inter cluster distances (between cluster I and cluster VI followed by between clusters V and VI) to obtain useful progenies in the segregating generation and for the development of hybrids in mustard.

The highest inter-cluster D² 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 value for plant height was recorded in cluster VI; for the number of siliquae on the main shoot, the highest cluster mean value was recorded in cluster III; for the number of siliquae on branches, the highest cluster mean value was recorded in cluster I; for the number of seeds per siliquae, the highest cluster mean value was recorded in cluster II; for the 1000-seed weight, the highest cluster mean value was recorded in cluster VI, for Oil content, the highest cluster mean value was recorded in cluster I; and for seed yield per plant, the highest cluster mean value was recorded in cluster I. These findings indicate that the genotypes with high mean values gathered in the clusters showed a high mean for each trait. Seed yield per plant exhibited

maximum contribution towards divergence, followed by number of siliquae on branches, oil content, 1000-seed weight, number of seeds per siliquae, number of siliquae on main shoot, and plant height. This indicated that diverse genotypes could be selected based on the characteristics showing a high contribution to genetic diversity.

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-one genotypes 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:

Among all clusters, Cluster VI showed the greatest intra cluster distance, while Cluster II displayed the least. This suggests that exploring crosses between genotypes within Cluster VI (Kranti NC, GIRIRAJ, RH 406, DRMR IJ 31, NRCHB 101, DRMR 150 35, CS 54, PHR 2, RL 1359, KRANTI) could be advantageous, as they are separated by larger intra cluster distances compared to other clusters. Additionally, the restricted diversity and selection of parents within a cluster exhibiting a higher mean for a particular trait might prove valuable in developing high yield Indian mustard cultivars.

The largest inter cluster distance was noted between Clusters I and VI, indicating that genotypes in Cluster I (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)) and Cluster VI (Kranti NC, GIRIRAJ, RH 406, DRMR IJ 31, NRCHB 101, DRMR 150 35, CS 54, PHR 2, RL 1359 & KRANTI) possess a broad range of genetic diversity. Implementing a hybridization program between genotypes from these clusters may result in transgressive segregants, offering the potential to select genetically diverse genotypes. Furthermore, heterotic cross combinations could be investigated for mustard hybrid development. Genotypes from these clusters could be selected for hybridization programs based on their superior individual performance.

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.

REFERENCES

Bhandari, H. R., Bhanu, A. N., Srivastava, K., Singh, M. N., & Shreya, H. A. (2017). Assessment of genetic diversity in crop plants-an overview. *Adv. Plants Agric. Res*7: 279-286.

Bind D, Singh S and Dwivedi VK. 2015. Assessment of genetic diversity and other genetic parameters in Indian mustard [*B. Juncea* (L.) Czern& Coss]. *IndianJ Agric Res* 49: 334-338.

Chaturvedi, V. D., Maurya, K. N., Upadhyay, D. K., Singh, P. K., & Chaubey, S. (2021). Genetic diversity for yield and its contributing components in Indian mustard [Brassica juncea (L.) Czern& Coss.]. *J. Pharm. Innov*10: 748-754.

Dilip TS, Singh SK, Kumar R. (2016) Genetic divergence in Indian mustard. *Techno fame* 5:7-10.

Govindaraj, M., Vetriventhan, M., & Srinivasan, M. (2015). Importance of genetic diversity assessment in crop plants and its recent advances: an overview of its analytical perspectives. *Genetics research international*431487.

Gupta RK, Dwivedi VK and Meena B. 2015. Genetic divergence analysis for seed yield parameters and oil content in Indian mustard [*B. juncea* (L.) Czern& Coss]. *Indian Res J Genet Biotech* 7: 84 -86.

Jahan N, Bhuiyan SR, Talukder MZA, Alam MA and Parvin M. 2013. Genetic diversity analysis in *B. rapa* using morphological characters. *Bangladesh J AgrilRes* 38: 11-18.

Khan MH, Ali MM, Vhuiyan SR and Mahmud F. 2013.Genetic divergence in rapeseed-mustard (*B.rapa*L.). *Bangladesh J Agril Res* 38: 417-423.

Lodhi B, Thakral NK, Singh D, Avtar R and Bahadur R. 2013. Genetic diversity analysis in Indian mustard (*B. juncea*). *J Oilseed Brassica* 4: 57-60.

Mahalanobis PC. 1936. On the generalized distance in statistics, In: *Proc Natl Acad Sci India* 2: 49-55.

Meena HS, Kumar A, Singh VV, Meena PD, Ram B and Kulshrestha S. 2017. Genetic variability and interrelation of seed yield with contributing traits in Indian mustard (*B. juncea*). *J Oilseed Brassica* 8: 131-137.

Rajput, D., Patel, M. P., Kumar, S., Patel, R., &Katba, P. (2023). Screening of castor germplasm for wilt reaction and morpho-molecular characterization of resistant genotypes. *Heliyon9*.

Rao CR. 1952. Advance statistical methods in biometrical Research Edition I. John Willey and Sons, New York.

Rout, S., Kerkhi, S. A., Chand, P., & Singh, S. K. (2018). Assessment of genetic diversity in relation to seed yield and its component traits in Indian mustard (Brassica juncea L.). *J of Oilseed Brassica*, 9: 49-52.

Srivastava KK, Vimal SC, Giri SP and Verma AK. 2016. Studies on seed quality parameters in Indian mustard [*B. juncea* (L.) Czern and Coss]. *Int J Agri Sci* 12: 241-244.

Vermai U, Thakral NK and Neeru. 2016. Genetic diversity analysis in Indian mustard [*B. juncea* (L.) Czern& Coss]. *Int J Applied Math Stat Sci* 6: 2319-3980.