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

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.

1. INTRODUCTION

Indian mustard [*Brassica juncea* (L.) Czern&Coss.], also known as "rai," "raya," "laha," or "bangasarson," 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). Genetic divergence was estimated using D2 statistics (Mahalanobis, 1936) following Rao (1952).

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, 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)], ten genotypes in cluster VI [Kranti-NC, GIRIRAJ, RH-406, DRMR-IJ-31, NRCHB-101, DRMR-150-35, CS 54, PHR 2, RL 1359 & KRANTI], eight genotypes in cluster V [DRMR-15-9, KMR-L-15-6, PRD-2013-9, DRMRIJ-15-66, RH-1368, RH-1325, RNWR-09-3 & PRD-2013-2], two genotypes in cluster II [RGIN-73, Pusa mustard-26(NPJ 113)], as well as cluster IV(RGN-386, BPR-540-6). There was no parallelism between genetic and geographic diversity, as all clusters were heterogeneous and included genotypes from different geographical regions. 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. 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. 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. 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.

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