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Trait-based genetic diversity assessment for strategic breeding in Indian Mustard (*Brassica juncea* L. Czern & Coss)

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Abstract

An investigation was conducted to assess the extent and nature of genetic diversity among 36 genotypes of Indian mustard (*Brassica juncea*), comprising eight parental lines and 28 F_1 hybrids using Mahalanobis D^2 statistics. The presence of genetic diversity among genotypes offers significant potential for their utilization in breeding programs aimed at improving yield and related agronomic traits. Cluster analysis grouped the 36 genotypes into eight distinct clusters. Cluster II was the largest, containing nine genotypes followed by Clusters I, III and VII, each comprising five genotypes. The distribution of genotypes across clusters appeared to be random and did not correspond to their geographical origin or region of adaptation. The maximum inter-cluster distance was recorded between Clusters I and VII (5.79) followed by Clusters IV and V (5.73) indicating a high degree of genetic divergence between these groups. Among the intra-cluster distances, Cluster VIII showed the highest value (5.21) followed by Cluster II (4.79) suggesting that genotypes within these clusters also possess considerable variability. Therefore, hybridization among genotypes within or between these divergent clusters may result in promising cross combinations. Based on cluster mean values, genotypes grouped in Clusters VIII, II and VI are particularly noteworthy and may be considered as potential parents in future hybridization programs aimed at developing high-yielding varieties of Indian mustard.

Keywords*: *Cluster analysis, D^2 statistics, inter and intra cluster distance, genetic divergence

Introduction

Brassica juncea L., commonly known in India as rai, raya, or laha is a widely recognized species belongs to the Cruciferae (*Brassicaceae*) family. It is a naturally occurring amphidiploid, resulting from hybridization between two species *Brassica campestris* and *Brassica nigra*, resulting in a chromosome count of 2n = 36 (Nagaharu, 1935). Indian mustard alone contributes around 75-80% of the country's total rapeseed-mustard output. It also plays a significant role in edible oil sector, making up approximately 24.2% of India's total edible oil production.The primary mustard-producing states in India include Rajasthan, Uttar Pradesh, Gujarat, Madhya Pradesh, Assam, Bihar, Odisha, Haryana, Punjab and West Bengal. India emerged as the world's third-largest producer of *Brassica* oilseeds, cultivating over 9.12 million hectares and yielding 13.16 million tonnes.

The country achieved an average productivity of 1499 kg per hectare, contributing 16.05% to global production, following Canada and China (Anonymous, 2023-24). Rajasthan is the top producer of rapeseed-mustard in India, followed by Uttar Pradesh, Haryana, Madhya Pradesh, West Bengal, Gujarat, and Assam. Rajasthan cultivated mustard over approximately 3.37 million hectares, yielding 5.48 million metric tons with average productivity of 1627 kg per hectare (Anonymous, 2023-24). In Rajasthan, Alwar district leads in both the cultivation area and production of mustard, followed by Bharatpur, Sriganganagar, Tonk, Jodhpur, Hanumangarh, and Sawai Madhopur. Genetic diversity refers to the overall range of genetic differences found among various genotypes within a species.

In the context of plant breeding, this diversity is highly valuable. Selection of suitable divergent parents for hybridization is required because the cross involving diverse parents offers a great possibility of obtaining desirable segregants in segregating generations (Moll and Robinson, 1962). Therefore, this study on genetic divergence was taken up to assess the genetic variability present in 36 Indian mustard genotypes. Crosses made between genetically distinct lines tend to exhibit higher levels of heterosis compared to those between closely related parents. Such crosses can also lead to a wide range of genetic variation in the resulting segregating populations, which is crucial for selecting superior traits.

Materials and Methods

The experiment was conducted during the *Rabi* season of 2022–23 at the Agronomy Farm of S.K.N. College of Agriculture, Jobner, Jaipur, Rajasthan. A total of thirty-six advanced lines/genotypes of Indian mustard were evaluated using a randomized block design (RBD) with three replications. The spacing between rows and plants were maintained at 30 cm and 10 cm, respectively. Observations were recorded for fourteen agronomic and quality traits, including days to 50% flowering, days to maturity, plant height, number of primary and secondary branches per plant, siliquae per plant, siliqua length, seeds per siliquae, 1000-seed weight, seed yield and biological yield per plant, harvest index, oil content, and protein content. Data on days to 50% flowering, days to maturity, protein content, and oil content were collected on a plot basis, while the remaining traits were recorded on per-plant basis. Data for the remaining morphological traits were recorded from ten randomly selected, healthy, and competitive plants per plot across all three replications. Genetic diversity among the 36 genotypes was assessed using Mahalanobis's generalized distance (D^2) method (Mahalanobis's, 1936) and clustering was performed following Tocher's method as described by Rao (1952), which resulted in the classification of genotypes into eight distinct clusters.

Results and Discussion

The thirty-six genotypes of Indian mustard evaluated through D^2 analysis based on fourteen yield-contributing traits were grouped into eight distinct clusters. The clustering pattern indicated the presence of substantial genetic divergence among the genotypes sufficient to justify the formation of separate and distinct clusters. Based on D^2 values thirty-six genotypes of mustard were grouped into eight clusters (Table 1). Cluster II had maximum number of genotypes (9), followed by cluster I, III and VII (5), Clusters V and VI (4) and Clusters IV and VIII (2). Similar findings were also observed by Malik *et al.* (2006), Devi *et al.* (2017) and Reddy and Shrivastav (2022). The distribution pattern of genotypes across different clusters indicated a significant level of genetic diversity among the genotypes analyzed. In the present investigation the inter cluster and intra cluster distance was estimated among eleven characters (Table 2). The maximum intra cluster distance was recorded in cluster VII (5.21) followed by cluster II (4.76), cluster VII (4.59) and cluster III (4.38). The maximum intra cluster distance in cluster VII was because of wide genetic diversity among its genotypes. Similar results were also reported by Bind *et al.* (2015) and Chandra *et al.* (2018). The maximum inter cluster distance was between clusters I and VII (5.79) followed by cluster IV and V (5.73), cluster II and IV (5.58) and cluster III and IV (5.56). The smallest inter-cluster distance (2.42) was observed between IV and VIII followed by VI and VII (2.78) and IV and VII (3.78). Similar findings were also observed by Khan *et al.* (2013) and Bind *et al.* (2015). The analysis of average intra- and inter-cluster distances among the seven clusters showed that genotypes within the same cluster exhibited lower genetic divergence compared to those from different clusters. This suggests that genotypes grouped together are more genetically similar to each other. As a result, crossing genotypes within the same cluster is unlikely to produce transgressive segregants. Hence, for an effective hybridization program, it is recommended to select parent genotypes from different clusters that show the highest genetic divergence, in order to enhance the chances of obtaining desirable transgressive segregants.

The cluster mean for different quantitative characters of different clusters are presented in Table 3. The days to 50% flowering was earliest in cluster VII (48.00) followed

Table 1: Grouping of genotypes into clusters

Cluster	Genotypes	Genotypes (no.)
I	DRMR-150-35, DRMR-1165-40, DRMR-150-35× DRMR-1165-40, DRMR-150-35 × BRIJRAJ, DRMR-150-35× BPR-540-6	5
II	DRMR-2059, BRIJRAJ, RH-725, KRANTI, BPR-540-6, DRMR-150-35 × RH-406, DRMR-150-35 × RH-725, DRMR-1165-40× BPR-540-6, BRIJRAJ × BPR-540-6	9
III	RH-406, DRMR-150-35 × KRANTI, DRMR-1165-40 × DRMR-2059, DRMR-2059 × BRIJRAJ, DRMR-2059 × RH-725	5
IV	DRMR-150-35 × DRMR-2059, KRANTI × BPR-540-6	2
V	DRMR-1165-40 × BRIJRAJ, DRMR-1165-40 × RH-725, DRMR-1165-40× KRANTI, DRMR-2059 × RH-406	4
VI	DRMR-2059 × KRANTI, BRIJRAJ× RH-406, BRIJRAJ× RH-725, BRIJRAJ × KRANTI	4
VII	RH-406 × RH-725, RH-406 × KRANTI, RH-406× BPR-540-6, RH-725 × KRANTI, RH-725 × BPR-540-6	5
VIII	DRMR-1165-40 × RH-406, DRMR-2059 × BPR-540-6	2

Table 2: Average Intra and inter cluster distances

Cluster	I	II	III	IV	V	VI	VII	VIII
I	3.67	5.17	5.16	5.33	5.24	4.23	5.79	4.19
II		4.76	5.37	5.58	5.50	4.12	5.38	5.42
III			4.38	5.56	5.45	4.02	4.77	4.32
IV				1.75	5.73	4.22	5.21	2.42
V					3.54	4.12	3.78	4.16
VI						2.52	2.78	4.17
VII							4.59	4.38
VIII								5.21

Table 3: Mean values of different characters for 36 Indian mustard genotypes grouped in different clusters

Cluster	DF	DM	PH	PBPP	SBPP	SPP	SL	SPS	SW	BY	HI	OC	PC	SY
I	49.58	135.27	184.47	5.67	20.28	294.23	5.66	12.60	5.33	80.28	16.15	40.06	20.56	12.90
II	49.20	133.33	185.02	6.86	22.79	353.20	5.89	12.25	4.97	97.62	17.98	40.31	22.80	17.48
III	51.78	135.50	186.06	5.77	18.58	258.98	5.64	12.41	4.94	53.58	23.75	39.51	21.53	12.69
IV	50.58	136.71	193.43	5.88	21.04	291.68	5.42	13.40	5.01	71.88	17.44	38.51	19.71	12.51
V	50.45	134.56	188.89	6.43	22.37	341.55	5.09	12.52	5.00	64.40	26.00	39.95	22.81	16.66
VI	52.67	135.33	173.90	5.93	22.77	352.70	5.33	12.37	4.85	72.67	21.00	40.72	22.71	17.07
VII	48.00	134.67	179.67	6.50	21.73	347.23	6.50	11.83	5.03	81.67	16.35	41.09	21.94	13.74
VIII	49.00	136.00	178.50	5.47	19.93	303.77	5.77	12.30	5.22	70.28	16.60	40.86	23.21	19.31

by cluster VIII (49.00) and cluster II (49.20) whereas, the highest value for days to 50% flowering was observed in cluster VII (52.67) followed by cluster III (51.78) and cluster IV (50.58). Early maturity was observed in cluster II (133.33 days) followed by cluster V (134.56 days) and cluster VII (134.67), whereas the late maturity was recorded in cluster IV (136.71 days) followed by cluster VIII (136.00 days) and cluster III (135.50 days). Cluster IV has the highest plant height (193.43 cm), followed by cluster V (188.89 cm). The lowest plant height (173.90 cm) was observed in cluster VI. The primary branch per plant was observed maximum in cluster II (6.86) followed by cluster VII (6.50) and cluster V (6.43). However, the minimum primary branch per plant was observed in cluster VII (5.47) followed by cluster I (5.67). Cluster II has the highest secondary branches per plant (22.79) followed by cluster VI (22.79) whereas, cluster III has the lowest secondary branches per plant (18.58) followed by cluster VIII (19.93). The maximum siliqua per plant was observed in cluster II (353.20) followed by cluster VI (352.70) and cluster VII (347.23), whereas the lowest siliqua per plant was reported in cluster IV (291.68). The highest siliqua length (cm) was recorded in cluster VI (6.50), followed by cluster II (5.89) and cluster VIII (5.77); whereas, the minimum siliqua length was reported in cluster V (5.09). The maximum seeds per siliqua were recorded in cluster I (12.60) followed by cluster V (12.52) and cluster III (12.41), whereas the minimum seeds per siliqua were recorded in cluster VII (11.83). The maximum 1000-seed weight was observed in cluster I (5.33 g) followed by cluster VIII (5.22) and minimum 1000-seed weight registered in cluster VI (4.85). Cluster II has maximum biological yield (97.62) followed by cluster VII (81.67) and cluster I (80.28). The maximum harvest index was recorded in cluster V (26.00) followed by IV (23.75) and cluster VI (21.00). Similarly, the maximum oil content was recorded in cluster VII (41.09%) and the minimum oil content found in cluster IV (38.51%). The protein content was recorded maximum in cluster VIII (23.21%) and the minimum protein content found in cluster IV (19.71%). The seed yield per plant was observed maximum in cluster VIII (19.31 g) followed by cluster II (71.48 g) and the minimum seed yield per plant registered in cluster IV (12.51 g). Similar findings were also observed by Shekhawat *et al*. (2014) and Singh *et al*. (2018).

Conclusion

A significant level of genetic divergence was observed among the 36 Indian mustard genotypes. Based on the analysis, it is recommended that parental lines for hybridization programs should be selected from the most genetically distant clusters that also demonstrate superior mean performance. This approach is more likely to produce transgressive segregants, which can contribute to increased seed yield. Relying solely on geographic diversity for selecting parents may not be as effective in identifying genetically diverse and useful lines.

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