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Assessment of genetic diversity in relation to seed yield and its component traits in Indian mustard (*Brassica juncea* L.)

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Abstract

The genetic divergence were tested of thirty eighty genotypes of Indian mustard (*Brassica juncea* L.) in randomized block design with three replications during *Rabi* 2015-16. Observations were recorded for twelve characters *viz.*, days to 50% flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, plant height (cm), number of seeds per siliqua, siliqua length (cm), biological yield per plant (g), harvest index (%), seed yield per plant (g) and 1000-seed weight (g). Genetic divergence was studied using Mahalanobis D^2 statistics. Genotypes were grouped into seven clusters. The I (eight genotype) and II (eight genotype) cluster having the maximum number of genotypes followed by cluster IV (seven genotype), V & VI have (five genotype) each, III (three genotype) and VII (two genotype). Maximum average intra cluster divergence value was found for cluster VII and minimum intra cluster divergence value was found for cluster V. Maximum inter cluster D^2 value was recorded between cluster VII and VI where as minimum inter cluster distance was observed between cluster II and cluster I. Based on the larger intra cluster distance value, the crosses could be made among the genotypes (PBR-210 & Sanjucta ASECH) with (RLM- 619, Pusa Tarak, Jawahar mustard, Swarnajyoti & RGN-73) for obtaining useful progenies in the segregating generation and also for development of hybrids in mustard. The characters biological yield per plant (g), number of siliquae per plant, number of seeds per siliqua, siliqua length (cm), days to 50% flowering and1000-seed weight (g) contributed more than 90.8 % of the total genetic diversity.

Key words: *D^2 statistics, genetic divergence, Indian mustard, seed yield*

Introduction

Indian mustard [*Brassica juncea* (L.) Czern & Coss.] belongs to the family cruciferae commonly known as Raya is an important oilseed crop, accounting more than 80% of the total area under rapeseed and mustard in India with a total area of 5762 thousand hectare, production of 6821 thousand tones and productivity is 1184 kg per hectare (Anonymous, 2011). The mustard oil is utilized for human consumption throughout north and north-east India in cooking and frying purposes. In crop improvement programme more emphasis should be given to increase the seed yield as it is a complex character which depends on number of other characters. Genetic diversity plays an important role in plant breeding because hybrids between lines of diverse origin generally display a great heterosis and also to get desirable segregants in segregating population. Creation and assessment of divergence in Indian mustard is highly needed to develop high yielding genotypes with desirable traits (Meena *et al.*, 2017). Therefore, the present study was conducted to assess the genetic divergence in 38 genotypes of Indian mustard estimated through D2 statistics method.

Materials and Methods

The field trail was carried out at APEDA centre, Sardar Vallabhbhai Patel University of Agriculture and Technology, Modipuram, Meerut campus, UP, India during *Rabi* season 2015-16. The experimental material consisted of thirty eight diverse genotypes of Indian mustard. The experiment was conducted in Randomized Complete Block Design with three replications. Each genotype was grown in a plot of 4.0 m^2 area. Each genotype was seeded in 2 rows of 5 m length spaced 40cm apart with plant to plant distance of 15 cm by proper thinning. All cultural practices essential for the good crop of mustard were applied for obtaining healthy and competitive crop stand.

Five randomly selected competitive plants from each genotype in each replication were used for recording the observations on twelve characters. However, observations on days to 50% flowering and days to maturity were recorded on plot basis. The data was recorded on 12 characters *viz.*, days to 50% flowering, days to maturity, number of primary branches per plant (cm), number of secondary branches per plant (cm), number of siliquae per plant (cm), plant height (cm), number of seeds per siliquae, length of the siliqua (cm), biological yield per plant, harvest index (%) and seed yield per plant (g) and 1000 seed weight (g). The genetic divergence was estimated using D^2 statistics (Mahalanobis, 1936) followed by Rao (1952).

Results and Discussion

Based upon the genetic divergence analysis, all 38 genotypes of Indian mustard were grouped into seven clusters. A total of eight genotypes fell into cluster I (NRCHB101, NRCDR-2, PBR-97, local selection, Pusa Bold, Shatabdi, Pusa Jay Kisan & Krishna) as well as in cluster II (Gujarat mustard 3, Gujarat mustard1, Rohini, RB-50, Aashirwad, Durgamani, RH 749 & Pusa Mahak), seven genotypes in cluster IV (Maya, Pusa Jagannath, RH 406, NRCDR 601, RCC-4, PBR 91 & RH 819), five genotypes in cluster V (DRMRIJ-31, Pusa Vijay, Pusa Mustard 25, BPR-540-6 & Pusa Mustard 24) as well as in cluster VI (RLM 619, Pusa Tarak, Jawahar Mustard, Swarnajyoti & RGN 73), three genotypes in cluster III (Pusa Mustard 26, Pusa Mustard 28 & Pusa Basant) and two genotype in cluster VII (PBR 210 & Sanjucta ASECH). It was observed that except the case of cluster III in general, there was no parallelism between genetic and geographic diversity as all other clusters revealed to be heterogeneous that included the genotypes from different geographical regions. Similar types of results were also reported by Singh *et al.* (2010), Chaurasia *et al.* (2015) and Singh *et al.* (2016).

Maximum average intra cluster divergence value was found for cluster VII (509.72) followed by cluster VI (330.48), cluster III (266.94), cluster I (220.63), cluster IV (201.23), cluster II (188.62) and for cluster V (128.80). Based on the larger intra cluster distance value, the crosses could be made among the genotypes from cluster VII (PBR 210 & Sanjucta ASECH) followed by cluster VI (RLM 619, Pusa Tarak, Jawahar Mustard, Swarnajyoti & RGN 73) for expecting better segregants. The genotypes from these clusters may be selected for crossing on the basis of their better mean values for seed yield and yield components. The chances of obtaining good segregates by crossing the genotypes of the same cluster showing low value for intra cluster distance are very low. Such type of result regarding intra cluster 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 D^2 value was recorded between cluster VII and VI (3508.25) followed by cluster VII and V (2650.02), cluster VII and II (2265.08), cluster VII and I (2161.46), cluster VII and IV (1893.06), cluster VII and III (1204.77), cluster VI and III (1042.57), cluster V and III (790.30), cluster VI and IV(685.45), cluster VI and II (675.512), cluster VI and I (585.09), cluster VI and V (561.12),

Table 1: Distribution of thirty eight genotypes of Indian mustard in seven clusters

Clusters number	No. of genotypes	Genotypes
I	8	NRCHB101, NRCDR-2, PBR-97, Local selection, Pusa bold, Shatabdi, Pusa Jai Kisan & Krishna
II	8	Gujarat mustard 3, Gujarat mustard1, Rohini, RB-50, Aashirwad, Durgamani, RH-0749 & Pusa mahak
III	3	Pusa mustard 26, Pusa mustard 28 & Pusa Basant
IV	7	Maya, Pusa Jagannath, RH406, NRCDR-601,RCC-4, PBR-91 & RH-819
V	5	DRMR-IJ-31, Pusa Vijay, Pusa mustard 25, BPR-540-6 & Pusa mustard 24
VI	5	RLM 619, Pusa Tarak, Jawahar mustard, Swarnajyoti & RGN-73
VII	2	PBR-210 & Sanjucta ASECH

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

Cluster	I	II	III	IV	V	VI	VII
I	220.63	268.78	402.09	357.71	500.96	585.09	2161.46
II		188.62	528.32	328.38	528.49	675.512	2265.08
III			266.94	478.95	790.30	1042.57	1204.77
IV				201.23	323.32	685.45	1893.06
V					128.80	561.120	2650.02
VI						330.48	3508.25
VII							509.72

Table 3: Cluster mean for twelve characters in Indian mustard

Character Cluster	Days to 50 % Flowering	Days to maturity	No. of primary branches per plant	No. of secondary branches per plant	No. of siliquae per plant	Plant height (cm)	No. of seeds per siliqua	Siliqua length (cm)	Biological yield per plant (g)	Harvest index (%)	Seed yield per plant(g)	1000 seed weight (g)
I	69.7	124.7	4.7	16.1	302.7	133.8	12.8	4.7	60.1	30.6	18.3	4.5
II	77.1	125.1	6.0	13.6	295.8	146.4	12.7	4.5	57.7	31.1	17.9	4.9
III	67.3	120.0	4.9	17.2	359.9	137.8	14.1	4.5	59.3	36.5	21.6	4.5
IV	72.9	122.7	5.8	16.8	306.5	133.5	14.5	4.4	51.1	37.2	18.9	4.3
V	65.3	120.3	5.2	16.4	259.0	123.9	15.0	4.7	50.4	31.1	15.6	5.0
VI	71.5	122.8	5.9	17.9	269.1	143.4	16.2	4.7	65.5	25.7	16.7	4.8
VII	63.2	120.0	4.9	15.6	483.5	129.2	14.0	3.9	50.0	46.4	22.9	4.5

cluster V and II (528.49), cluster III and II (528.32), cluster V and I (500.96), cluster IV and III (478.95), cluster III and I (402.09), cluster IV and I (357.71), cluster IV and II (328.38), cluster V and IV (323.32) and between cluster II and I (268.78) . This clearly indicated that the genotypes included in these clusters had broad spectrum of genetic diversity and could be used in hybridization programme in mustard for improving seed yield. Therefore, it would be logical to attempt crosses between the genotypes of clusters separated by larger inter cluster distances (between cluster VII and cluster VI followed by between cluster VII and V) for obtaining useful progenies in the segregating generation and also for development of hybrids in mustard. Such type of result regarding inter cluster distance was also reported by Lodhi *et al.* (2013) and Bind *et al.* (2015).

Highest cluster mean value for days to 50% flowering was recorded in case of cluster II, for days to maturity highest cluster mean value was recorded in case of cluster II, number of secondary branches per plant in case of cluster VI, for number of siliquae per plant highest cluster mean value was recorded in case of cluster VII, for plant height in case of cluster number II, for number of seed per siliquae in case of cluster number VI, length of the siliqua in case of cluster number V, biological yield per plant in case of culture number VI, harvest index in case of cluster number VII, seed yield per plant in case of cluster number VII, 1000 seed weight highest cluster mean value was recorded in case of cluster number V. These findings indicated that the genotypes with high mean values gathered in the clusters which showed high mean for respective trait. Biological yield per plant exhibited maximum contribution towards divergence followed by number of siliquae per plant, number of seed per siliqua,

Table 4: Contribution of different characters towards genetics diversity in Indian mustard

Character	Contribution %
Days to 50 % flowering	5.7
Days to maturity	0.6
No. of primary branches per plant	2.3
No. of secondary branches per plant	2.7
No. of siliquae per plant	24.5
Plant height(cm)	1.0
No. of seeds per siliqua	20.5
Siliqua length (cm)	7.4
Biological yield per plant(g)	27.5
Harvest index (%)	0.01
Seed yield per plant (g)	2.7
1000- seed weight (g)	5.3

length of the siliqua, days to 50% flowering, 1000 seed weight, number of secondary branches per plant, seed yield per plant, number of primary branches per plant, length of the plant, days to maturity and harvest index. This indicated that diverse genotypes could be selected on the basis of the characters showing high contribution towards genetic diversity. These results were somewhat in accordance with the findings of Khan *et al.* (2013) and Shekhawat *et al.* (2014).

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