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Genetic variability and Genetic diversity study in Indian mustard (*Brassica juncea* L.)

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Abstract

Present study was carried out with twenty genotypes of Indian mustard. Anova indicated significant differences for all the observed characters. PCV is higher than GCV for all the traits under study. High heritability coupled with high genetic advance recorded for secondary branches per plant, test weight and plant height. Twenty genotypes were grouped into five clusters based on mahalanobis D^2 analysis. The cluster I (14) with maximum number of genotypes followed by cluster V (3) while, cluster II, III & IV were solitary with single genotype each. Maximum inter cluster D2 value (70.90) recorded between cluster IV and cluster V. Minimum inter cluster distance (11.68) recorded between cluster III and Cluster II. The intra cluster divergence found to range between 20.93 for cluster I and 24.93 for cluster V.

Keywords: Indian mustard, variability, heritability, genetic advance, genetic diversity

Introduction

Oilseed occupies an important place in the agricultural and industrial economy of our country, constituting an important group of crops next to cereals. Mustard is the second most important oilseed crop in the world and in India. During the 2018-19 crop seasons, Indian mustard accounts for around 75-80 percent of the 6.23 million ha. During the Rabi season, in India about 7.40 million hectares of rapeseed-mustard are planted, yielding 9.77 million tones of seeds with an average productivity of 1.04 million tons per hectare (USDA, 2020). The seed is used as a condiment in the preparation of pickles, in curries and vegetables. Salad dressings, salads, and other dishes prepared from mustard paste. The protein-rich oil cake is more often used as livestock feed. It may also be used as processed organic compost. Mustard oil is used to smooth leather in the tanning industry. Present study was carried out with twenty genotypes of Indian mustard to estimate genetic variability, heritability, Genetic advance and Genetic diversity. The presence of genetic variability encoded in breeding material plays a significant role in developing superior hybrids. Genetic diversity study helps to estimate the divergent parents for the hybridization program.

Materials and Methods

The present investigation was carried out with twenty diverse genotypes of Indian mustard for 12 characters in Rabi 2020-21 in a randomized block design with three replications at Agriculture farm, Department of Genetics and Plant breeding, School of Agriculture, Lovely Professional University, Phagwara, Punjab. Geographically this place is located at latitude longitude range of 31.2554º and 75.7058º E and at an altitude of 234m above from mean sea level. Twenty genotypes of Indian mustard with a spacing of row to row 45cm and plant to plant distance of 15 cm were maintained. The observations recorded were Days to 50% flowering, Days to maturity, Plant height (cm), No. of primary branches/plant, No. of secondary branches/plant, No. of siliqua/plant, Siliqua length (cm), No. of seeds/siliqua, Biological yield (g), Harvest Index (%), Test weight (g), Seed yield/plant (g) on five randomly selected healthy plants in each line and in each replication whereas, Days to 50% flowering and Days to maturity were recorded on plot basis. The data of recorded characters subjected to analysis of variance on the basis of model described by Panse and Sukhame (1985), genetic divergence analysis by Mahalanobis D^2 statistic given by Rao (1952).

Result and Discussion

Anova indicated that the mean sum of squares due to genotypes were significant, for all the studied characters. Highly significant association indicates that considerable amount of genetic variability is present for the studied characters in the genotypes. Phenotypic coefficient of variation is higher than genotypic coefficient of variation for all the traits under analysis. Highest GCV recorded by Number of secondary branches per plant (26.738) and followed by siliqua per plant (18.167), test weight (14.157), seed yield (12.236), harvest index (8.568), plant height (8.375), biological yield (6.381), seeds per siliqua (5.81), siliqua length (5.737), primary branches per plant (5.444), days to maturity (3.578), days to flowering (3.551). Highest PCV recorded by secondary branches per plant (28.91), siliqua per plant (24.583), seed yield (20.8), biological yield (16.912), harvest index (16.632), primary branches per plant (14.729), test weight (14.728), plant height (9.265), seeds per siliqua (9.135), siliqua length (7.184), days to flowering (5.744), days to maturity (4.787). Similar findings had obtained by Sudheer Singh *et al.*, (2018) [8], Taslima Aktar *et al.*, (2019) [2], Jagadish Prasad Chaurasiya *et al.*, (2019) [5], Shailendra sagar Prajapati *et al.*, (2020).

High heritability coupled with high or moderate genetic advance is exhibited by secondary branches per plant, test weight and plant height. High heritability accompanied with high or moderate genetic advance indicates that heritability is due to additive gene effects and selection may be effective. High heritability in broad sense recorded by Test weight followed by secondary branches per plant, plant height, siliqua length Maximum genetic advance as percent of mean (> 20) at 5% intensity recorded for secondary branches per plant followed by test weight, siliqua per plant. Similar findings by Sanghamitra Rout *et al.* (2019), Anil Kumar *et al.*, (2018), Asheesh kumar Tiwari (2016), Jagendra singh (2020).

Table 1: Genotypic and Phenotypic coefficients of variation, heritability in broad sense and genetic advance as percent of mean for different characters in Indian Mustard

S. No.	Characters	Range			GCV	PCV	Heritability (Broad sense) %	Genetic advance	Genetic advance as % of mean
		Min.	Max.	Mean					
1.	Days to flowering	66.00	76.33	70.57	3.551	5.744	38.2	3.191	4.521
2.	Days to maturity	131.33	152.00	143.88	3.578	4.787	55.9	7.926	5.508
3.	Plant height (cm)	145.80	196.40	168.15	8.375	9.265	81.7	26.223	15.595
4.	No. of primary branches/plant	3.67	5.13	4.63	5.444	14.729	13.7	0.192	4.144
5.	No. of secondary branches/plant	4.10	12.13	8.72	26.378	28.91	85.5	4.440	50.942
6.	No. of siliqua/plant	163.87	319.47	237.13	18.167	24.583	54.6	65.586	27.658
7.	Siliqua length (cm)	4.53	5.81	5.08	5.737	7.184	63.8	0.480	9.439
8.	No. of seeds/ siliqua	13.29	17.77	14.94	5.81	9.135	40.5	1.137	7.613
9.	Biological yield (g)	49.00	74.20	62.25	6.381	16.912	14.2	3.087	4.959
10.	Harvest Index (%)	12.67	20.07	16.16	8.568	16.632	26.5	1.470	9.092
11.	Test weight (g)	4.13	6.27	4.69	14.157	14.728	92.4	1.313	28.035
12.	Seed yield/plant (g)	7.87	12.93	9.99	12.236	20.8	34.6	1.481	14.828

Genetic Divergence

The 20 genotypes of Indian mustard were grouped into 5 clusters were presented in table 2. The intra and inter cluster distances were presented in table 3. The mean values of different clusters for the recorded characters were presented in table 4.

Mahalanobis D^2 static is a powerful tool used for measuring the degree of genetic divergence between the genotypes and related clustering patterns with the geographic origin. Distance between the clusters measures the degree of diversification, the greater the distance between two clusters the greater the divergence and vice versa. The genotypes in the same cluster are more closely related than those of the other clusters. The little diversity with maximum cluster mean values is also useful for the hybridization program.

A total of 5 clusters were formed from 20 genotypes. The cluster I was the largest had 14 genotypes. In cluster 1 the genotypes (14) BR-40, Geeta, Basanti, Bhagirathi, Jagannath, Aravali, Gujarat mustard-1, Ashirwad, DR BRIJ-31, Kranti, Krishna, Navgold, Laxmi, CS-52 were included. In cluster 2 (1) Jawahar mustard 1 is included. In cluster 3 (1) Kanti is included. In cluster 4 (1) Jawahar mustard-2 is included. In cluster 5 (3) Gujarat mustard-2, Maya and Durgamani are included.

Table 2: Distribution of 20 genotypes into different clusters

S. No.	Cluster	No. Of Genotypes	Name Of Genotypes
1.	I	14	Geeta, BR-40, Gujarat mustard-1, Navgold, Basanti, Bhagirathi, Jagannath, Aravali, Ashirwad, DRMR IJ-31, kranti, Krishna, CS-52, Laxmi
2.	II	1	Jawahar mustard-1
3.	III	1	Kanti
4.	IV	1	Jawahar mustard 2
5.	V	3	Gujarat mustard-2, Maya, Durgamani

Table 3: Average inter and intra cluster distances values

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
Cluster 1	20.93	27.85	31.54	31.73	62.11
Cluster2		0.00	11.68	21.63	46.15
Cluster 3			0.00	28.18	54.53
Cluster 4				0.00	70.90
Cluster 5					24.93

The bold values shows Intra cluster distances

Table 4: Cluster means for twelve traits of 20 genotypes

Traits clusters	DF	DM	PH	PB	SB	NSP	SL	NSS	BY	HI	TW	SY
cluster 1	70.81	143.1	166.4	4.73	8.5	242.4	4.97	14.88	62.93	15.74	4.41	9.86
cluster 2	71	148.6	176.2	5.13	11.57	319.4	5.52	14.77	49.4	18.14	4.63	9
cluster 3	69	149.3	162.4	4.93	8.2	211.6	5.59	17.14	64.07	16.51	4.43	10.4
cluster 4	68.33	140.6	191.5	4.2	11.6	194.8	5.81	15.99	68.87	18.4	4.37	12.4
cluster 5	70.56	144.7	167.4	4.07	7.98	207.4	5.04	14.17	60.58	16.63	6.19	9.97

DF: Days to flowering DM: Days to maturity PH: Plant height (cm) PB: No. of primary branches/plant SB: No. of secondary branches/plant NSP: No. of siliqua/plant SL: Siliqua length (cm) NSP: No. of seeds/siliqua BY: Biological yield (g) HI: Harvest Index (%) TW: Test weight (g) SY: Seed yield/plant (g)

Maximum inter cluster D2 value (70.90) recorded between cluster IV and cluster V. Minimum inter cluster distance (11.68) recorded between cluster III and Cluster II. The inter cluster distance between cluster IV & V (70.90), cluster I&V (62.11), cluster III & V (54.53), cluster II & IV (46.15), cluster I & IV (31.73), cluster I&III (31.54), cluster III & IV (28.18), cluster I & II (27.85), cluster II & IV (21.63), cluster II&III (11.68). The intra cluster divergence found to range between 20.93 for cluster I and 24.93 for cluster V. The three clusters (II, III, IV) contained a single genotype and therefore, their intra-cluster distances were zero.

The cluster means calculated for 12 characters under study are presented in table. Days to 50% flowering showed highest mean for cluster II (71.00) and lowest mean for cluster IV (68.33). Days to maturity showed the highest mean for cluster III (149.33) and lowest mean for cluster IV (140.67). Plant height exhibited highest mean for cluster IV (191.53) and lowest mean for cluster III (162.40). Number of primary branches per plant recorded the highest mean for cluster II (5.13) and lowest mean for cluster V (4.07). Number of secondary branches per plant showed the highest mean for cluster IV (11.60) and lowest mean for cluster V (7.98). Number of siliquas per plant exhibited the highest mean for cluster II (319.47) and lowest mean for cluster IV (194.87). Siliqua length showed the highest mean for cluster IV (5.81) and lowest mean for cluster I (4.97). Number of seeds per siliqua exhibited the highest mean for cluster III (17.14) and lowest mean for cluster V (14.17). Biological yield recorded the highest mean for cluster IV (68.87) and lowest mean for cluster II (49.40). Harvest index showed the highest mean for cluster IV (18.40) and lowest mean for cluster I (15.74). Test weight showed highest mean for cluster V (6.19) and lowest mean for cluster II (4.63). Seed yield per plant showed highest mean for cluster IV (12.40) and lowest mean for cluster II (9.00). So, from the present study it is observed that genotypes in clusters IV & V can be utilized for the hybridization program to obtain the maximum heterosis in indian mustard.

References

1. Akbari VR, Niranjana M. Genetic variability and trait association studies in Indian mustard (*Brassica juncea*). International Journal of Agricultural Sciences 2015;11(1):35-39.
2. Aktar T, Nuruzzaman Md, Rana S Md, Huda M Md, Hossain A Md, Hassan L. Genetic parameters and diversity studies of yield and yield contributing characters in Brassica genotypes. J Bangladesh Agril Univ 2019;17(3):295-300.
3. Awasthi D, Tiwari VK, Kandalkar VS. Evaluation of Heritability and Genetic Advance for Morphological Traits of Indian Mustard Germplasms. Current Journal of Applied Science and Technology 2020;39(21):39-47
4. Belete YS, Yohannes MTW, Wami TD. Analysis of Genetic parameters for some agronomic traits of introduced Ethiopian mustard (*Brassica carinata A. Brun*) genotypes. International Journal of Agricultural Research 2012;7(3):160-165.
5. Chaurasiya JP, Singh M, Tomar P. Genetic variability, heritability, genetic advance and character association of Indian mustard (*Brassica juncea* L). Journal of Oilseed Brassica 2019;10(2):80-86.
6. Pandey SK, Srivastava KK, Neigi S, Khan NA, Singh RK. Variability, trait relationship and path analysis for seed yield and seed quality parameters in Indian mustard (*Brassica juncea* L.). Journal of Oilseed Brassica 2020;11(1):69-76.
7. Rout S, Kerkhi SA, Gupta A. Estimation of genetic variability, heritability and genetic advance in relation to seed yield and its attributing traits in Indian mustard [*Brassica juncea* (L.) Czern and Coss.]. Journal of Pharmacognosy and Phytochemistry 2019;8(3):4119-4123
8. Singh S, Dwivedi AK, Ashutosh, Meena O, Kumar K. Genotypic variability, Heritability and genetic advance in Indian mustard [*Brassica juncea* (L.) Czern & Coss.] Genoypes. Journal of Pharmacognosy and Phytochemistry 2018;7(3):350-352.
9. Singh V, Bhajan R, Kumar K, Genetic diversity in Indian mustard (*Brassica juncea* L. Czern and coss.). Prog. Agric. 2007;7(1, 2):105-109.
10. Synrem GJ, Rangare NR, Myrthong I, Bahadure DM. Variability studies in Intra specific crosses of Indian mustard [*Brassica juncea* (L.) Czern and Coss.] genotypes. IOSR Journal of Agriculture and Veterinary Science 2014;7(9):29-32.
11. Tahira, Mahmood T, Tahir MS, Saleem U, Hussain M, Saqib M. The estimation of heritability, association and selection criteria for yield components in mustard (*Brassica juncea*). Pak. J Agri. Sci 2011;48(4):251-254.
12. Tripathi AM, Devi B, Gosh PB, Bishat A. Estimation of genetic variability parameters for different traits in Indian mustard [*Brassics juncea* (L.)] in Bundelkhand zone (Jhansi). International Journal of Chemical Studies 2020;8(4):2434-2436.
13. Uzair M, Shahzadi I, Jatoi GH, Bibi T, Rauf S, Mahmood T *et al*. Genetic variability and heritability studies in relation to seed yield and its components traits in mustard (*Brassica juncea* L.). Sci. Int. (Lahore) 2016;28(4):4267-4270.
14. Rathod VB, Mehta DR, Solanki HV. Genetic variability and divergence for oil content and yield attributes in Indian mustard [*Brassica juncea* (L.) Czern & Coss]. Journal of Pharmacognosy and Phytochemistry 2017;6(5):1507-1509.
15. Yadava DK, Giri SC, Vignesh M, Vasudev M, Yadav AK, Dass B *et al*. Genetic variability and trait association studies in Indian mustard (*Brassica juncea*). Indian Journal of Agricultural Sciences 2011;81(8):712-716.