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ASSESSMENT OF GENETIC DIVERSITY IN MUSTARD GENOTYPES

Ravi Nagda[1], Nidhi Dubey[2]*, Harshal Avinashe[3] and Dattesh Tamatam[4]

Department of Genetics and Plant Breeding, Lovely Professional University, Phagwara - 144 411, India.

Abstract

Mustard is a major oil seed crop having 32-44% oil content. A field experiment was conducted during *Rabi,* 2017-18 under Agriculture farm, Department of Plant Breeding and Genetics, School of Agriculture, Lovely Professional University, Phagwara (Punjab), India, to study the genetic divergence in 36 Mustard genotypes and observations on 13 traits of were recorded. The analysis of variance indicated that significant variation was present among the different genotypes of the Mustard for all the traits under study. Genetic divergence assessed using D^2 statistics for characters enabled grouping of all the genotypes in seven clusters. Among seven clusters, cluster I was the biggest with 13 genotypes followed by cluster II with 11 genotypes, cluster IV with 5 genotypes and cluster III with 4 genotypes. Cluster V, VI and VII were solitary. Maximum differences among the genotypes within the same cluster (intra-cluster) were shown by cluster IV (267.22) followed by cluster III (217.06), cluster II (133.07) and cluster I (92.53). Solitary clusters V, VI and VII showed zero intra-cluster distances. Diversity among the clusters varied from 171.51 to 1645.64 inter-cluster distances. Cluster VI and VII showed maximum inter cluster distance (1645.64).

Key words : Mustard, genetic divergence, analysis of variance, D^2 analysis, cluster analysis, inter and intra-cluster distance.

Introduction

Indian mustard [*Brassica juncea* (L.) Czen & Cross] is an important oilseed crop belong to family Brassicacae (Crucifereae) and Genus Brassica. It is a natural amphidiploid and it has indigenous species like, toria (*Brassica rapa* L. var. toria), brown sarson (*Brassica rapa* L.var. brown sarson), yellow sarson [*Brassica rapa* L. var. yellow sarson), Indian mustard (*Brassica juncea* (L.) Czern & Cross], black mustard (*Brassica nigra*) and taramira (*Erica sativa* Mill). It is mostly self-pollinated but (2-5%) cross pollination happen due to honeybees (Vaghela *et al*., 2011).

Mustard was originated in Chine and it was introduced to India (Vaughan, 1977). Oilseed crop have been recognized as a major source of fats and proteins in human diet, 85% or more than 85% of country's vegetable oil supply or depends on 7 edible oil like (groundnut, mustard, soybean, sesame, sunflower, safflower, etc.) Rapeseed-mustard is the third major oilseed crop of the world after soybean and palm (Yadav *et al.,* 2014).

Mustard is widely grown in majority of Continents with largest area of 8 million ha in Canada followed by China (7 million ha) and India (6 million ha) and World average of 2144 kg/ha, highest productivity of 3640 kg/ha of Europeon Union, the Indian average yield was only 1161 kg/ha during 2013-16. Longer crop duration and high carbon content in the soil are the major factors attributing to high productivity of rapeseed in Western part of the World. In India irrigated area under mustard has increased more rapidly from 10% (1955-56) to 76% (2012-13). In India the area coverage under mustard is largely depends on the late *Kharif* rains. Rajasthan, MP, Haryana, UP and West Bengal contributes >80% of area and >85% of production of mustard and Rajasthan play the major role in increase the production 32.69 lakh tone (2015-16) in mustard.

The assessment of genetic variability is almost importance in all the crop improvement programmes. This is important for several reasons: the ability to distinguish reliably different genotypes is important for designing the breeding programmes, population-genetic analysis, genetic engineering and an estimation of the amount of variation within genotypes and between genotypes is useful for predicting potential genetic gains in a breeding programme and in setting up appropriate cross-breeding strategies (Kumar *et al.,* 2017). Genetic variability is the basic

***Author for correspondence :** E-mail: drnidhi355@gmail.com

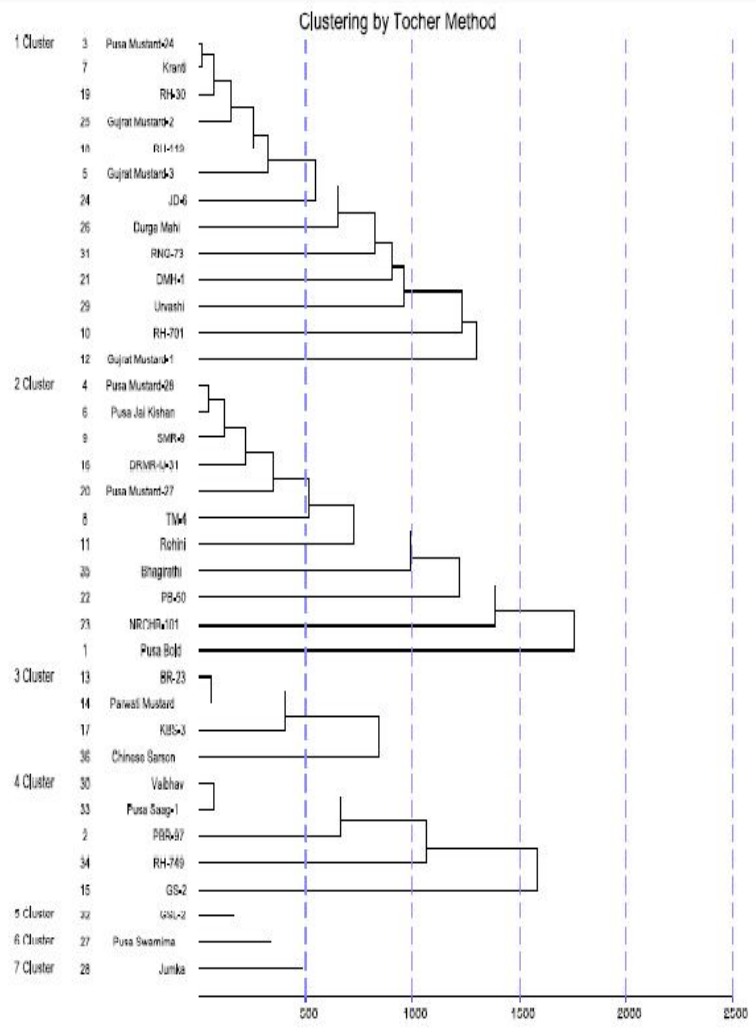

Fig. 1 : Clustering by Tocher Method.

requirement for crop improvement as this provides wider scope for selection. Knowledge of diversity patterns will allow breeders to better understand the evolutionary relationships among accessions, to sample germplasm in a more systematic fashion and to develop strategies to incorporate useful diversity in their breeding programs (Rout *et al*., 2018).

The D^2 analysis exhibit diversity on the basis of phenotypic expression of the different traits which restricts the resolving power mainly because of small number of variables available and some of them are developmental traits.

Materials and Methods

The present study was conducted under Agriculture farm, Department of Plant Breeding and Genetics, School of Agriculture, Lovely Professional University, Phagwara (Punjab), to analyze the genetic among Mustard genotypes diversity during *Rabi*, 2017-18. Source and pedigree of the material are given in table 1.

The field experiment was laid out in randomized block design (RBD) with three replications. Thirty-Six genotypes were planted with a spacing of 15 cm row to row and 50 cm plant to plant distance. All the recommended agronomical practices and plant protection measures were adopted to raise the healthy crop. The data was recorded on plant height at harvest (cm), number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, biological yield per plant (g), siliqua length (cm), number of seeds per siliqua, 1000 seed weight (g), harvest index (%), oil content (%), seed yield per plant (g) on a sample of 5plants/replication in each genotypes whereas for days to flowering and days to maturity data were taken on whole plot basis.

The data on morphological traits was subjected to analysis of variance on the basis of model described by Panse and Sukhatme (1985) for individual characters. The replicated data were subjected to genetic divergence analysis using Mahalanobis's D^2 - statistic (Mahalanobis 1936).

Results and Discussion

In the present investigation, 13 important yield and yield contributing traits have been studied to evaluate the pattern and extent of genetic variability and relation among 36 genotypes of mustard. The ANOVA for different characters revealed that mean sum of squares due to genotypes were highly significant for all the characters indicating the presence of significant genetic variability among genotypes, which provides scope for selection and further use of these genotypes in crop improvement (table 2). Similar findings were reported by Rout and Kerkhi (2018).

A method suggested by Tocher (Rao, 1952) was used to group the genotypes into different clusters based on the D^2 values. 36 genotypes were grouped into seven clusters. Among thirteen clusters, cluster I was the biggest with 13 genotypes followed by cluster II with 11 genotypes and cluster IV with 5 genotypes and cluster III with 4 genotypes. Cluster V, VI and VII were solitary. The clustering pattern and the distribution of genotypes into different clusters are presented in table 3 (fig. 1).

The average D^2 value of intra and inter cluster distances are given in table 4 (fig. 2). Maximum differences among the genotypes within the same cluster (intra-cluster) were shown by cluster IV (267.22) followed by cluster III (217.06), cluster II (133.07) and cluster I (92.53). Solitary clusters V, VI and VII showed

Table 1 : Pedigree and source of 36 genotypes of mustard.

S. no.	Entries	Pedigree/source
1	PUSA BOLD	VARUNAXBIC1780
2	PBR-97	(DIR202XPR-34XV3) X (RLM619XVARUNA)
3	PUSA MUSTARD-24	PUSA BOLDXLEB) XLES-29
4	PUSA MUSTARD-28	SEJ8XPUSA JAGANNATH
5	GUJRAT MUSTARD-3	RSK-78XVARUNA
6	PUSA JAI KISHAN	SOMACLONE OF VARUNA
7	KRANTI	SELECTION FOR VARUNA
8	TM-4	VARUNAXTM-1
9	SMR-9	DRMR
10	RH-701	DRMR
11	ROHINI	SELECTION FROM NATURAL POPULATION OF VARUNA
12	GUJRAT MUSTARD-1	MR 71-3-2XTM-4
13	BR-23	SELECTION FROM LOCAL GERMPLASM OF PURNEA, BHIHAR
14	PARWATI MUSTARD	DRMR
15	GS-2	PS-66XYS-31
16	DRMR-IJ-31(GIRIRAJ)	HB 9908XHB9916
17	KBS-3	PUSA KALYANIXYUKINA
18	RH-119	PUSA BOLDXRAJAT(PCR-7)
19	RH-30	SELECTION FROM P26/3-1
20	PUSA MUSTARD-27	DIVYA/ PUSA BOLD// PR666EPS///PR704EPS2
21	DMH-1	DEVLOPED BY CMS
22	RB-50	LAXMIXRH-9617
23	NRCHB-101	BL-4XPUSA BOLD
24	JD-6	PUSA BOLDXGLOSSY
25	GUJRAT MUSTARD-2	SELECTION FROM MATERIAL COLLECTED FROM VENDACHU, GUJRAT
26	DURGA MAHI	SELECTION FROM MATERIAL COLLECTED FROM SRIGANGANAGR, RAJASTHAN
27	PUSA SWARNIMA	HC-4XEARLY MUTANT
28	JUMKA	SINGLE PLANT SELECTION FROM THE MATERNAL COLLECTED FROM RANAGHAT NADIA, WEST BENGAL
29	URVASHI	VARUNAXKRANTI
30	VAIBHAV	DRIVED THOUGHT BIPARENTAL MATTING INVOLVING VARUNA, KESHARI, CSU10 AND B1775, B1786, B1866
31	RGN-73	RNG8XPUSA BOLD
32	GSL-2	TRITONXGSL8851
33	PUSA SAAG-1	WONG BOK(SUTTON) XTURNIP
34	RH-0749	RH-781XRH-9617
35	BHAGIRATHI	SELECTION FROM PUSA JAI KISHAN
36	CHINES SARSON	DRMR

Table 2 : ANOVA and percent contribution of characters toward divergence in 36 Mustard genotypes.

S. no.	Characters	Source of variation				Percent contribution	Rank
		Replication	Treatments	Error	CV		
	Degree of freedom	2	35	70			
1	Days to 50% Flowering	4.453	215.983**	4.167	2.561	0.16%	
2	Days to Maturity	6.027	59.837**	2.103	1.073	0.00%	
3	Plant Height (cm)	17.167	2089.58**	6.041	1.287	29.84%	II
4	Primary Branches/ Plant	1.641	20.982**	0.533	8.623	0.63%	
5	Secondary Branches/plant	6.981	312.423**	4.129	6.967	3.02%	
6	Siliqua/ Plant	83363.76	192814.70**	4771.84	7.603	3.33%	
7	Biological Yield/ Plant(g)	1019.18	16223.88**	329.96	7.536	0.48%	
8	Siliqua Length (cm)	0.0705	2.432**	0.024	2.854	8.41%	IV
9	Seeds/Siliqua	0.831	46.147**	0.324	3.239	7.94%	V
10	1000 grain Weight (g)	0.002	1.009**	0.005	1.840	14.13%	III
11	Seed Yield/Plant (g)	3.136	1100.87**	4.535	3.552	30.95%	I
12	Harvest Index %	13.821	247.349**	9.665	11.99	0.48%	
13	Oil Content %	1.113	7.986**	0.575	1.994	0.63%	

Table 3 : Cluster profile of 36 genotypes of mustard.

S. no.	Cluster	No. ofgenotypes	Name of genotypes
1	I	13	PM-24, kranti, RH-30, GM-2, RH-119, GM-3, JD-6, Durga Mahi, RNG-73, DMH-1, Urvashi, RH-701, GM-1
2	II	11	PM-28, Pusa jai kishan, SMR-9, DRMR-IJ-31, PM-27, TM-4, Rohini, Bhagirathi, PB-50, NRCHB-101, Pusa bold,
3	III	4	BR-23, Parwati mustard, KBS-3, Chinese sarson
4	IV	5	Vaibhav, Pusa saag-1, PBR-97, RH-749, GS-2
5	V	1	GSL-2
6	VI	1	Pusa swarnima
7	VII	1	Jumka

Table 4 : Estimation of intra (diagonal) and inter- cluster distances in 36 genotypes of mustard.

Cluster	I	II	III	IV	V	VI	VII
I	92.53	171.51	645.05	283.42	473.13	472.17	1364.46
II		133.07	373.73	310.79	391.98	483.33	993.48
III			217.06	654.78	599.30	895.24	668.16
IV				267.22	451.98	544.25	1211.43
V					0.000	698.773	481.43
VI						0.000	1645.64
VII							0.000

*Diagonal value Intra-cluster distance.

zero intra-cluster distances.

Diversity among the clusters varied from 171.51 to 1645.64 inter-cluster distances. Cluster VI and VII showed maximum inter cluster distance (1645.64) followed by that between cluster I and VII (1364.46), cluster IV and VII (1211.43). The lower inter-cluster distance was noticed between cluster I and II (171.51) followed by that between cluster II and IV (310.79), cluster II and III (373.73). The perusal of mean in table 4 revealed that inter-cluster distances were greater than intra-cluster distances revealing considerable amount of genetic diversity among the genotypes studied. Genotypes

Table 5 : Mean of thirteen characters in seven clusters in Mustard genotypes.

S. no.	Clusters	No. of genotypes	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13
1	I	13	**82.23**	**136.23**	**205.13**	8.34	**30.95**	**95.31**	**278.98**	5.14	16.43	**4.54**	**69.65**	**25.07**	**38.56**
2	II	11	**80.09**	134.06	**182.12**	7.65	**30.23**	**991.29**	225.19	5.19	16.81	**4.03**	**63.03**	**27.9**	**38.25**
3	III	4	62.83	128	141.32	6.91	22.45	790.75	177.55	5.68	17.3	3.33	40.78	24.06	37.06
4	IV	5	**87.47**	**137.47**	**213.85**	8.65	25.71	814.32	216.13	5.8	17.09	**3.78**	45.5	**26.94**	**38.06**
5	V	1	**88**	**141.33**	**195.07**	**13.07**	23	**890.2**	224.8	**8.61**	**27.37**	**3.83**	**61.57**	**27.6**	**39.7**
6	VI	1	73	**149.67**	**226.93**	**20**	**67.4**	**1005**	**407.07**	4.51	16.66	3.24	**71.24**	17.53	34.15
7	VII	1	70	129	149.13	8.27	6.33	281.4	150.13	**7.91**	**35.97**	3.04	36.19	24.28	35.25
		Mean	**77.66**	**136.53**	**187.65**	**10.41**	**29.43**	**818.03**	**239.97**	**6.12**	**21.09**	**3.68**	**55.42**	**24.76**	**37.29**

Note: X1-days to 50% flowering, X2-days to maturity, X3-plant height(cm), X4-primary branches, X5-secondary branches, X6-siliqua/ plant, X7-biological yield/plant(g), X8-siliqua length(cm), X9-seed/siliqua, X10-1000 grain seed weight(g), X11-seed yield/plant(g), X12-harvest index(%), X13-oil content (%)

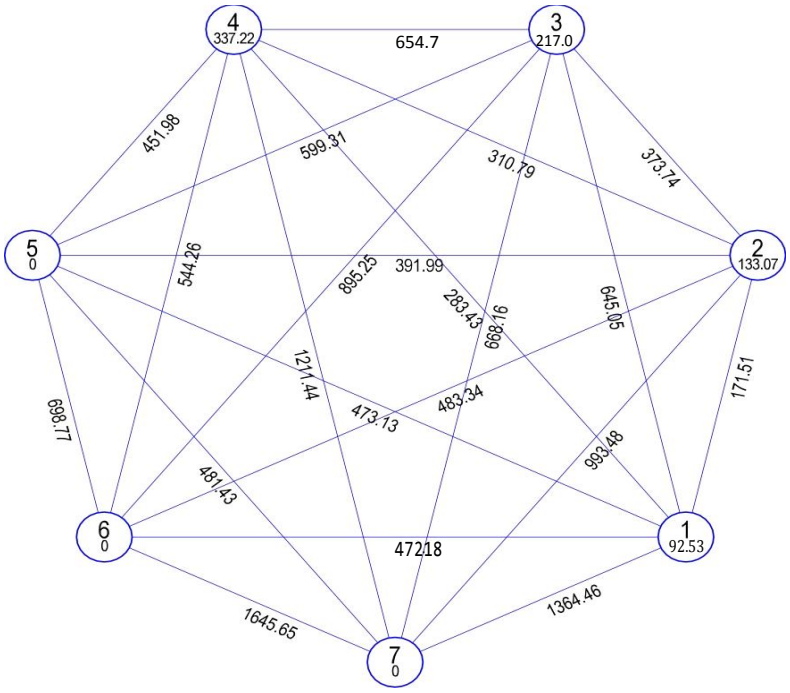

Fig. 2 : Intra and inter- cluster distance for 36 genotypes of Mustard.

belonging to clusters with maximum intra-cluster distance are genetically more divergent and hybridization between divergent clusters is likely to produce wide variability with desirable sergeants. The results are in close proximity with the findings of Kerkhi *et al*. (2018), Lodhi *et al*. (2013), Sutariya *et al*. (2011).

The cluster means and general mean values for 13 characters of 36 genotypes have been represented in table 5. The data revealed that differences in cluster means had existed. Cluster I comprised of 13 genotypes which were characterized as having above average values for days to 50% flowering, days to maturity, plant height, secondary branches, siliqua per plant, biological yield, 1000 seed weight, seed yield per plant, harvest index and oil content (%). Cluster II had 11 genotype that indicated above average values for days to 50% flowering, plant height, secondary branches, siliqua per plant, 1000 seed weight, seed yield per plant, harvest index and oil content (%). Cluster III comprised of 4 genotypes which was none of the characterized as having above average values. Cluster IV comprised of 5 genotypes which was characterized as having above average values for days to 50% flowering, days to maturity, plant height, 1000 seed weight, harvest index and oil content (%). Cluster V consisting of one genotype showed above average values for all the characters except secondary branches and biological yield. Cluster VI had one genotype showed above average values for days to maturity number, plant height, primary branches, secondary branches, siliqua per

plant, biological yield and seed yield per plant. Cluster VII comprising of one genotype showed above average values for siliqua length, seeds per siliqua. Similar findings were reported by Gangapur *et al*. (2010) and Sutariya *et al*. (2011).

Conclusion

The present study indicated that the distribution of genotypes into different clusters was at random and sufficient D^2 values among different cluster suggests that the genetic constitution of the promising lines in one cluster is in close proximity with the promising lines in other clusters of the pair may lead to desirable segregants having broad genetic base through hybridization between genotypes of two distant clusters. This finding will be helpful in planning future hybridization programme should involving diverse genotypes for crop improvement.

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