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Research Article

Genetic diversity analysis in Indian mustard (*Brassica juncea* L. Czern and Coss) genotypes using agro-morphological parameters

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Abstract
An experiment was conducted using 45 genotypes including local cultivars, advanced lines and notified varieties of Indian mustard for genetic diversity analysis through Mahalanobis's D^2 method. The study was conducted in RBD design with 3 replications having plot size of 1.5 x 5 m^2 and row spacing of 30 x 10 cm. Data were recorded on 14 different agro-morphological characters *viz.* days to 50% flowering, days to maturity, plant height (cm), number of primary and secondary branches per plant, main shoot length (cm), leaf area index, root width and length ratio, number of siliqua per plant, siliqua length (cm), number of seeds per siliqua, seed yield per plant (g), 1000 seed weight (g) and oil content (%). The analysis of variance revealed significant differences among the genotypes for all characters under study. The genotypes were grouped into 7 clusters using Tocher's method, with cluster I containing maximum genotypes (18 genotypes) followed by cluster III (9 genotypes), cluster IV (8 genotypes), cluster II (6 genotypes), cluster VI (2 genotypes) while cluster V and VII with single genotype each. Root width and length ratio, siliqua per plant, main shoot length and 1000 seed weight were the major contributors for genetic diversity among the genotypes with 23%, 21.80%, 21.32% and 20.51% respectively. The cluster IV exhibited maximum intra-cluster distance followed by cluster VI (844.272) while maximum inter-cluster distance was found between cluster V and VII (7273.532). Selection of diverse genotype containing desirable characters from the cluster and utilizing in hybridization programme will likely produce trangressive segregants and heterotic F_1s.

Key words
Brassica juncea L., genetic divergence, Mahalanobis's D^2 analysis, cluster analysis.

Introduction

Rapeseed-mustard is one of the most important oilseed crops of India. Out of the total rapeseed-mustard production of India, Indian mustard accounts for 75-80% and contributes 24.2% of the total edible oil pool of the country (DRMR, 2013). The major mustard growing states of India are Rajasthan, Uttar Pradesh, Gujarat, Madhya Pradesh, Assam, Bihar, Odissa, Haryana, Punjab and West Bengal. Genetic diversity in general is the total variability present among different genotypes of a species. In plant breeding, genetic diversity plays an important role because hybrids between lines of diverse origin, generally, display greater heterosis than those between closely related parents and may generate broad spectrum of genetic variability in segregating population (Arunachalam, 1981). The availability of genetic variability present in the breeding material plays major role in planning breeding programme to develop superior cultivars or hybrids. In general, the genetically divergent parents are utilized to obtain the desirable recombinants in segregating generations. Thus, knowledge of genetic diversity in *Brassica juncea* could help breeders and geneticists to understand the organisation of genetic variability in the germplasm, predict combinations that would produce the best genotypes and facilitate to widen the genetic basis of breeding material for selection. Under these premises, the present study was carried out to measure the genetic divergence present among the available genotypes of Indian mustard and to find out the possible parents for use in hybridization programme for development of commercial hybrids or varieties.

Materials and Methods

Forty five Indian mustard genotypes were grown in Randomized Block Design (RBD) with three replications at the experimental field of Department of Plant Breeding and Genetics, College of Agriculture, Central Agricultural University, Imphal. Each genotype was sown in a plot size of 1.5 x 5 m^2 consisting of 5 rows of 5m in each replication with a spacing of 30 cm x 10 cm. The recommended package of practices was followed to raise a good crop of mustard. Data were recorded on 10 randomly selected plants from each genotype for 14 different agro-morphological parameters *viz.* days to 50% flowering, days to maturity, plant height (cm), number of primary and secondary branches per plant, main shoot length (cm), leaf area index, root width and length ratio, number of siliqua per plant, siliqua length (cm), number of seeds per siliqua, seed yield per plant (g), 1000 seed weight (g) and oil content (%). The data were subjected to analysis of variance for single factor experiments according to Gomez and Gomez (1984) and genetic distance was measured using Mahalanobis's D^2 statistic. The genotypes were grouped into different clusters by Tocher's method (Rao, 1952).

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Result and Discussion

The analysis of variance indicated highly significant differences among the genotypes for all the 14 characters under study, which revealed the presence of considerable genetic variability among the genotypes. The genotypes under study were grouped into 7 clusters using Tocher's method, with cluster I containing maximum genotypes (18 genotypes) followed by cluster III (9 genotypes), cluster IV (8 genotypes), cluster II (6 genotypes), cluster VI (2 genotypes) while cluster V and VII with single genotype each (Table 1).

The random clustering pattern of genotypes i.e. grouping of genotypes from different regions in the same cluster (three local genotypes CAULC-2, CAULC-3, CAULC-4 from Manipur were grouped together with Kranti from Pantnagar and PM-28 from New Delhi) indicated that the genetic diversity of the genotypes is not necessarily related with the distribution of genotypes in different parts of the country, as supported by earlier findings of Jeena and Sheikh (2003), Pandey *et al*. (2013), Dar *et al*. (2010) and Gupta *et al*. (2015). The genetic diversity, among the genotypes in the present study may be resulted from genetic drift and selection that cause greater diversity than geographical distribution as suggested by Murty and Arunachalam (1966).

On the other hand, the presence of genetic diversity within the genotypes of same region could be distributed into different clusters. It was also observed that genotypes of quite different pedigree may fall into the same cluster, due to unidirectional selection pressure that could yield the genotypes which were genetically closer than their parents. Likewise, it is also true that selection produce genetically diverse genotypes of same pedigree. This indicates that the pedigree record may not necessarily be an indicator of genetic divergence as suggested by Singh *et al*. (2010). The characters contributing maximum to the divergence in order of descending magnitude (Table 2) were root width and length ratio (23%), number of siliqua per plant (21.80%), main shoot length (21.32%), 1000 seed weight (g) (20.51%), leaf area index (7.07), number of primary branches per plant (4.00%), oil content (1.62%), siliqua length (1.10%), days to 50% flowering (0.70%), number seeds per siliqua (0.20%), seed yield per plant (0.10%) and number of secondary branches per plant (0.10%) while days to maturity and plant height contributed 0.00% towards divergence.

The low contribution of the character seed yield per plant in the total divergence of the genotypes under study may be due to the high contribution of correlated characters like number of siliqua per plant, 1000 seed weight, leaf area index etc.

The data on cluster mean for 14 agro-morphological characters are presented in Table 3. The highest mean value for days to maturity (135.66), seed yield/plant(8.48), siliqua length 4.47), seeds/ siliqua (15.38), 1000 seed weight(5.55), leaf area index(4.63), plant height (140.78), main shoot length (112.12) were observed in cluster VI; for days to 50% flowering (64.33), primary branches/plant(8.33), secondary branches/plant (13.20), siliqua/plant (391.07) and root width/length ratio (1.09) were observed in cluster VII and for oil content it was observed in cluster III (39.21). Minimum days to 50% flowering and days to maturity was observed in cluster II (57.27) and cluster VII (118.66) respectively.

The intra-cluster D^2 values ranged from 0.000 to 863.638 and inter-cluster D^2 values ranged from 605.139 to 7273.532, suggesting the presence of diversity among clusters (Table 4). The maximum inter-cluster distance was found between cluster V and VII (7273.532) followed by cluster II and VII (6818.108), cluster III and VI (5725.832) and cluster I and VII (5679.354). The highest intra-cluster distance was observed in cluster IV (863.638) and the lowest in cluster V (0.00) and VII (0.00) (Table 4). The genotypes grouped into same cluster displayed the lowest degree of divergence from one another. The hybridization programmes should always be formulated in such a way that the parents belonging to different clusters with maximum divergence could be utilized to get desirable transgressive segregants. Varied cluster means and *per se* performance for all the characters under study indicated the responsiveness of these characters for the cause of genetic divergence. Such results were also supported by earlier findings of Goswami and Behl (2006) and Kumar *et al*. (2007).

The present study revealed that the cluster VII (a monogenotype cluster having CAULC-1 genotype) possessed high mean values for almost all the characters and can be cross with the genotypes in cluster VI for higher heterotic effect of the characters seed yield per plant and 1000 seed weight.

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Table 1. Distribution of 45 genotypes of Indian mustard into different clusters

Sl. No.	Cluster	Number of genotypes	Name of genotypes
1.	I	18	CAUMC-17, CAU-27, CAU-25, JD-6, CAUMC-26, CAUMC-19, Kanti, CAUMC-12, PM-25, BPR-547-14, DRMR-IJ-31, CAUMC-23, CAUMC-10, CAUMC-18, PM-21, CAUMC-16, CAUMC-9, CAUMC-22
2.	II	6	CAUMC-28, NRCHB-101, Pusa Bold, Rajendra Suflam, RH-30, CAUMC-21
3.	III	9	CAUMC-6, CAUMC-11, CAUMC-14, GM-2, CAUMC-7, CAUMC-8, CAUMC-15, CAUMC-20, Urvashi
4.	IV	8	CAULC-2, CAULC-4, CAULC-3, Kranti, CAUMC-24, CAUMC-5, CAUMC-13, PM-28
5.	V	1	CAUMC-29
6.	VI	2	Laxmi, RH 749
7.	VII	1	CAULC-1

Table 2. Relative contribution of each character towards genetic divergence in Indian mustard

Sl. No.	Character	Contribution (%)
1.	Root width and length ratio	**23.00**
2.	Number of siliqua per plant	**21.80**
3.	Main shoot length (cm)	**21.32**
4.	1000 seed weight (g)	**20.51**
5.	Leaf area index	**7.07**
6.	Number of primary branches per plant	**4.00**
7.	Oil content (%)	**1.62**
8.	Siliqua length (cm)	**1.10**
9.	Days to 50% flowering	**0.70**
10.	Number seeds per siliqua	**0.20**
11.	Seed yield per plant	**0.10**
12.	Number of secondary branches per plant (0.10%).	**0.10**
13.	Days to maturity	**0.0**
14.	Plant height (cm)	**0.0**

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Table 3. Cluster means of different character in Indian mustard genotypes

Clusters	Days to 50% flowering	Days to maturity	Primary branches/ plant	Secondary branches/ plant	Siliqua/ plant	Seed yield/ plant(g)	Siliqua length (cm)	Seeds/ siliqua	1000 seed weight (g)	Oil content (%)	Leaf Area Index	Root width/ length ratio	Plant height (cm)	Main shoot length (cm)
I	57.81	122.11	3.96	6.83	137.73	4.75	4.02	14.56	3.56	37.68	2.44	0.58	120.99	99.11
II	57.27	125.44	3.90	6.73	117.72	4.72	4.01	13.93	4.68	36.71	2.35	0.55	119.26	98.39
III	63.48	125.62	4.25	7.46	144.84	5.89	4.19	15.09	4.20	39.21	2.45	0.81	129.75	107.79
IV	59.70	120.00	5.28	8.29	210.73	5.10	3.95	14.04	3.21	36.86	2.33	0.64	114.92	95.51
V	58.66	122.33	3.60	5.93	116.50	3.90	3.87	12.77	4.46	27.69	2.41	0.31	94.28	82.40
VI	63.16	135.66	5.84	8.48	246.33	8.82	4.47	15.38	5.55	36.39	4.63	0.75	140.78	112.12
VII	64.33	118.66	8.33	13.20	391.07	5.07	2.98	12.53	1.87	38.20	2.63	1.09	104.33	100.07

Table 4. Average inter-cluster (bold) and intra-cluster distances D^2 values

Clusters	I	II	III	IV	V	VI	VII
I	**435.61**						
II	605.14	**503.51**					
III	832.06	806.61	**606.82**				
IV	1004.19	1434.19	1485.42	**863.64**			
V	945.58	870.14	1951.37	1539.09	**0.00**		
VI	2258.90	2056.06	1681.52	2151.97	3325.72	**844.27**	
VII	5679.35	6818.11	5725.83	3388.96	7273.53	4581.10	**0.00**