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Genetic diversity analysis for qualitative and quantitative traits in Indian mustard (*Brassica juncea* L. Czern & Coss)

Anurag Tripathi, Mahak Singh and Amit Tomar

Abstract

All the 25 genotypes were grouped into 6 clusters based on D² analysis. The cluster-I with 9 strains had maximum genotypes among all the clusters followed by cluster-III, II, IV, V and VI. The inter cluster distance was recorded highest between cluster-III and cluster-IV (90.88). The minimum inter cluster distance was observed between cluster-I and IV (15.38) indicating their close relationship.

Keywords: Genetic diversity, *Brassica juncea* L.

Introduction

Rapeseed and mustard oil is used primarily for edible purposes and is the principle cooking oil in the mustard growing area of the country. Known for its great taste and subtle flavor, this vegetable oil is the world's second leading source of protein meal. Besides seeds, it is used as condiments. The meal cake left after oil extraction forms important cattle feed and may also be used as organic manure. The availability of genetic variation is advantageous for crop improvement. Such type of variability brought about by a group of genes which have a small individual effect, can be studied through quantitative measurements. The genetic facts are inferred from observations on phenotypes. Since phenotype is determined by the joint effect of genotype and environment, non-genetic parts exerts large influence on genetic variability. The exploitable variability is, therefore, required to be judged through various genetic parameters like heritability, genetic advance and others. Such a study appears to be extremely necessary for planning genetic improvement in Indian mustard. It is generally assumed by the plant breeders that cultivars originating from widely separated parts of the world are more likely to be genetically different.

Materials & Methods

The present experiment was conducted using 25 diverse origin genotypes/ varieties/ lines/ hybrids of Indian mustard (*Brassica campestris* L. Czern & Coss). Materials were tested in randomized block design with two replications at Nawabganj, Research farm of the Chandra Shekhar Azad University of Agriculture and Technology, Kanpur during rabi 2016-18. The materials used in the study comprised of 25 germplasm namely; DRMRIJ-31, Basanti, LAHAR, Pusa Bahar, NRH-101, NRC-DR-2, Mutant Varuna, Selection 2016/10, Selection ns/4, Pusa Bold, B-85, Vardan, KR-5610, Ashirvadh, Nav Gold, Pusa Barani, Pusa Jai Kisan, Kranti, Vaibhav, RH-30, Urvashi, Maya, Agarani, NDR-8501 and RLM-198 of Indian mustard. The experiment was laid out in Randomized Block Design with three replications. These lines were grown in single row plot of 5 meter length. The spacing between row to row and plant to plant was 45 cm and 15 cm, respectively maintained by thinning. Recommended agronomic practices were adopted to raise a good crop. Five competitive plants from each plot were randomly selected for recording observations for all the quantitative characters except days to flowering and days to maturity which were recorded on the plot basis. Observations were recorded on thirteen character namely, days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, length of main raceme, number of siliquae per plant, number of seeds per siliqua, 1000-seed weight (g), biological yield per plant (g), harvest index (%), oil content (%) and seed yield per plant (g). The genetic divergence among fifty genotypes was analysed by using Mahalanobis D² statistic suggested by (Rao, 1952). Oil content was estimated by using Near Infra-Red Analyzer (NIR) at Directorate of rapeseed-mustard, Bharatpur (Rajasthan).

Results & Discussion

Tocher's method-cluster analysis: The D² values were computed in each possible combination of 25 mustard genotypes. All genotypes were grouped into six different clusters according to closeness of the genotype in respect of their D² values. The distribution of 25 genotypes of mustard in different clusters were presented in Table-1. The Intra and inter cluster distance were calculated and presented in Table-3 and Intra cluster distance showed divergence among the genotypes within a cluster while inter cluster distances expressed relative divergence between the clusters. The cluster mean for 13 characters among the 6 cluster is also presented in Table-2. The minimum and maximum mean values of different clusters for 13 characters were presented in Table-3. The detailed description of different clusters are given below:

Cluster-I: This cluster had 9 genotypes of mustard viz; NRC-DR-2, Nav Gold, Kranti, Vaibhav, RH-30, Selection 2016/10, Selection ns/4, Pusa Jai Kisan and DRMRIJ-31. The intra cluster distance was 11.89. This cluster had maximum distance 52.70 from cluster III and minimum 11.89 distance from cluster-I. In this cluster minimum mean value for 1000-seed weight (3.39) and maximum mean value for number of siliquae per plant (325.56).

Cluster-II: This cluster had 6 genotypes of mustard viz; Pusa Bold, Ashirvadh, Pusa Bahar, Vardan, Mutant Varuna and Basanti. The intra-cluster distance was 18.37. This cluster has maximum distance from cluster III (48.63) and minimum distances from cluster II(18.37). The genotypes in this cluster had maximum mean value for number of siliquae per plant (311.72) and minimum mean value for 1000-seed weight (3.60).

Cluster-III: This cluster had 7 genotypes of mustard viz.; Urvashi, NDR-8501, Agarni, Maya, Pusa Barani, RLM-198 and KR-5610. The intra cluster distance was 35.05. This cluster had maximum inter cluster distance from cluster VI (90.88) and minimum from cluster III (35.05). In this cluster genotypes had minimum cluster mean value for 1000-seed weight (313.14), while maximum cluster mean value for number of siliquae per plant (3.70).

Cluster-IV: This cluster had 1 genotype of mustard viz; B-85. The intra cluster distance was 0.00. This cluster had maximum inter cluster distance from cluster-VI (58.42) and minimum from cluster IV (0.00). In this cluster maximum mean value for 1000-seed weight (307.67) and minimum for number of siliqua per plant (2.96).

Cluster-V: This cluster had 1 genotypes of mustard viz.; LAHAR. The intra cluster distance was 0.00. This cluster had maximum inter cluster distance from cluster-VI (66.71) and minimum from cluster-V (0.00). This cluster had higher mean value for the number of siliquae per plant (329.00) and lowest mean value for 1000-seed weight (2.33).

Cluster-VI: This cluster had 1 genotypes of mustard viz; NRH-101. The intra cluster distance was (0.00). This cluster had minimum and maximum inter cluster distance (0.00) from cluster-VI and cluster-VI, respectively. This cluster had lower cluster mean value for 1000-seed weight (4.45) and higher for number of siliquae per plant (300.33).

These findings were also similar to Shalini *et al.* (2000)^[9], Srivastava *et al.* (2000)^[10], Verma *et al.* (2000)^[11], Singh *et al.* (2005), Goswami *et al.* (2006)^[6], Singh *et al.* (2007), Goyal *et al.* (2012)^[3], Lodhi *et al.* (2013)^[2] and Yong *et al.* (2014)^[5].

Table 1: Distribution of 25 genotypes of Indian mustard in different clusters.

Clusters	Strains/variety	No.
1.	NRC-DR-2, Nav Gold, Kranti, Vaibhav, RH-30, Selection 2016/10, Selection ns/4, Pusa Jai Kisan, DRMRIJ-31	9
2.	Pusa Bold, Ashirvadh, Pusa Bahar, Vardan, Mutant Varuna, Basanti	6
3.	Urvashi, NDR-8501, Agarni, Maya, Pusa Barani, RLM-198, KR-5610	7
4.	B-85	1
5.	LAHAR	1
6.	NRH-101	1

Table 2: The average intra and inter cluster value of different clusters in Indian mustard (*Brassica juncea*).

Clusters	1 cluster	2 cluster	3 cluster	4 cluster	5 cluster	6 cluster
1cluster	11.887	26.954	52.704	15.383	31.070	34.592
2 cluster		18.368	48.633	39.952	27.233	30.768
3 cluster			35.054	57.755	58.158	90.883
4 cluster				0.000	29.720	58.423
5 cluster					0.000	66.710
6 cluster						0.000

Table 3: Cluster mean for 13 characters in Indian mustard.

Clusters	Days 50% flowering	Days to maturity	Plant height (cm)	No. of primary branch / plant	No. of secondary branch / plant	Length of main raceme (cm)	No. of siliquae / plant	No. of seeds / siliqua	1000-seed Weight (g)	Biological Yield / plant (g)	Harvest index (%)	Oil Content (%)	Seed yield / plant (g)
Cluster1	80.444	131.148	174.424	7.963	18.667	56.843	325.556	13.148	3.388	51.630	23.228	39.287	12.000
Cluster2	75.500	128.778	170.838	7.667	18.556	45.871	311.722	12.889	3.600	51.833	22.097	38.678	11.444
Cluster3	67.048	122.190	155.975	7.476	15.429	57.668	313.143	13.048	3.703	51.905	22.785	38.971	11.857
Cluster4	78.000	133.333	166.477	9.333	21.333	60.700	307.667	15.000	2.960	52.333	21.055	40.840	11.000
Cluster5	75.333	127.333	175.143	9.333	20.000	44.973	329.000	13.333	2.327	52.333	22.953	37.950	12.000
Cluster6	84.667	132.667	182.163	8.000	20.000	47.173	300.333	14.333	4.453	52.333	23.510	38.753	12.333

Table 4: Range among cluster mean for different characters in mustard

Range	Days 50% flowering	Days to maturity	Plant height (cm)	No. of primary branch / plant	No. of secondary branch / plant	Length of main raceme (cm)	No. of siliquae / plant	No. of seeds / siliqua	1000-seed Weight (g)	Biological Yield / plant (g)	Harvest index (%)	Oil Content (%)	Seed yield / plant (g)
Lower	65.25	117.41	145.51	7.41	10.00	44.97	295.33	12.66	3.13	51.33	22.31	38.07	11.57
Upper	83.50	133.50	176.88	8.50	19.09	59.50	329.41	14.16	3.96	53.33	23.50	40.26	12.33

Table 5: Contribution of each character to words divergence for 13 characters in Indian mustard.

Characters	Days 50% flowering	Days to maturity	Plant height (cm)	No. of primary branch / plant	No. of secondary branch / plant	Length of main raceme (cm)	No. of siliquae / plant	No. of seeds / siliqua	1000-seed Weight (g)	Biological yield / plant (g)	Harvest index (%)	Oil Content (%)	Seed yield / plant (g)
Number of time appearing 1 st time	89	3	3	1	6	84	2	25	40	3	5	13	26
Per-cent (%) contribution	29.67	1.00	1.00	0.33	2.00	28.00	0.67	8.33	13.34	1.00	1.67	4.33	8.66

Contribution of individual character towards total divergence: The result pertaining to the contribution of each character towards the genetic divergence is depicted in Table-4. Each character are ranked on the basis of per cent contribution of that character. The perusal of Table-4 showed that maximum contribution towards divergence, days to 50% flowering (29.66%) followed by length of main raceme (28.00%), 1000-seed weight (13.34%), seed yield per plant (8.66%), number of seeds per siliqua (8.33%), oil content (4.33%), number of secondary branches per plant (2.00%), harvest index (1.67%), days to maturity (1.00%), plant height (1.00%), biological yield per plant (1.00%), number of siliquae per plant (0.67%) and number of primary branches per plant (0.33%). Similar finding were also observed by Singh *et al.* (2005), Doddabhinappa *et al.* (2010)^[4], Goyal *et al.* (2012)^[3], Lodhi *et al.* (2013)^[2], Yong *et al.* (2014)^[5] and Shalini *et al.* (2000)^[9].

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