

Variability studies and multivariate analysis in Indian mustard [*Brassica juncea* (L.) Czern & Coss]

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ABSTRACT

A study on genetic variability and genetic divergence was done with 50 genotypes for 13 quantitative characters in Indian mustard (*Brassica juncea* (L.) Czern and Coss). The analysis of variance indicated the prevalence of sufficient genetic variation among the genotypes for all the 13 traits. The wider phenotypic range, high heritability coupled with high genotypic coefficient of variation (GCV) and high genetic advance as per cent of mean (GA %) were observed for seed yield per plant, biological yield per plant, number of secondary branches per plant, number of siliquae per plant and 1000-seed weight which, indicated that response to selection would be very high for these yield components ultimately leading to seed yield improvement in mustard crop. The genotypes grouped in 9 clusters when grouped using the Tocher's method. Cluster I topped with maximum (33) genotypes followed by cluster II (6) and cluster III and IV (each of 3). While, cluster VII to IX were solitary clusters. Maximum genetic distance (D) was found between cluster II and VI followed by between cluster III and IV. Four clusters viz., II, III, IV and VI were important with respect to construct plant ideotype including seed yield per plant, which could be utilized for breeding programme. Three traits viz., days to 50% flowering, days to maturity and 1000-seed weight also contributed more than 55% towards total genetic divergence.

Key words : Variability, heritability, genetic divergence, multivariate analysis.

Indian mustard [*Brassica juncea* (L.) Czern and Coss, $2n = 36$, *Brassicaceae*] popularly known as rai, raya or laha, is one of the most important edible oilseed crops of the country and it occupies considerably large acreage among the *Brassica* group of oilseed crops. India stands first both in acreage and production of rapeseed and mustard in Asia. Globally, India account for 19.29 % and 11.127% of the total acreage and production. In India area, production and productivity of rapeseed-mustard are 6.5 million hectares, 8.79 million tonnes and 1850 kg/ha, respectively during 1912-13 (Anonymous, 2010). Mustard and rapeseed are being grown largely in states like Rajasthan, Uttar Pradesh, Haryana, Gujarat, Punjab, Assam, West Bengal and Madhya Pradesh.

The morphological characterization of germplasm is used to understand the genetic variation since, a wide

range of genetic variation among parents is essential for hybridization programmes. Nature and magnitude of genetic variability and heritability in a population as genetic and non-genetic factors are pre-requisites in any successful hybridization programme to get desirable segregants. Arunachalam (1981) stated that multivariate analysis using Mahalanobis' D^2 statistic is a powerful tool to know the clustering pattern to establish the relationship between genetic and geographical divergence and to determine the role of different quantitative characters towards total genetic divergence. Hence, the present experiment was planned on variability analysis along with genetic divergence using 50 genotypes of mustard.

MATERIALS AND METHODS

Fifty genotypes of Indian mustard procured from the Research Scientist (Castor-Mustard), Castor-Mustard Research Station, Sardarkrushinagar Dativada

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Agricultural University, Sardarkrushinagar were grown in R.B.D. with three replications during *rabi* 2011-12 at Instructional Farm, Junagadh Agricultural University, Junagadh, (Gujarat). Each replication consisted of a single row of 3m length for each entry with row to row and plant to plant spacing being 60 cm and 10 cm, respectively. Recommended agronomic practices and plant protection measures were followed to raise a healthy crop.

Five competitive plants were randomly selected in each entry for recording the observations on plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, number of seeds per siliquae, length of siliquae (cm), 1000-seed weight (g), biological yield per plant, harvest index (%) and oil content (%), while, days to 50% flowering and days to maturity were recorded on plot basis. The genotypic and phenotypic coefficient of variations were estimated as per Burton (1952), while heritability in broad sense and expected genetic advance were estimated as per Allard (1960). Genetic diversity was calculated using Mahalanobis (1936) D^2 statistic and genotypes were grouped into clusters by Tocher's method as described by Rao (1952).

RESULTS AND DISCUSSION

Analysis of variance (Table 1) revealed that variance due to genotypes was highly significant for all the 13 characters indicated the presence of sufficient variability in the genotypes under the study. The experimental materials showed wide range of phenotypic variation for seed yield per plant, number of secondary branches per plant, number of siliquae per plant, biological yield per plant, number of primary branches per plant, harvest index and 1000-seed weight as revealed high values of coefficient of range.

Variability Analysis

The values of phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV), in most of the cases, indicated more influence of environmental factors (Table 2). However, low differences were also observed between PCV and GCV for days to 50% flowering, days to maturity, plant height, number of seeds per siliquae and length of siliquae which revealed that these five traits were comparatively less influenced by the environments. High PCV and GCV were observed for seed yield per plant followed by number of secondary branches per plant, biological yield per plant, number of siliquae

Table 1 Analysis of variance for 13 characters in 50 genotypes of mustard

Mean squares														
Source	d.f.	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches per plant	No. of secondary branches per plant	No. of siliquae per plant	No. of seeds per siliqua	Length of siliqua (cm)	1000 seed weight (g)	Seed yield per plant (g)	Biological yield per plant (g)	Harvest index (%)	Oil content (%)
Replications	2	13.547**	1.040	146.060*	0.097	13.313	6512.903*	0.090	0.308**	0.091	36.806*	2133.142**	139.249**	0.334
Genotypes	49	37.500**	45.641**	254.691**	1.477**	35.065**	12790.855**	3.914**	0.327**	0.940**	59.866**	273.511**	49.077**	16.303**
Error	98	2.492	1.809	35.647	0.257	4.632	1621.463	0.562	0.044	0.092	10.130	128.356	17.144	5.665

* ** Significant at 5 and 1 % levels, respectively

Table 2 Phenotypic range, coefficient of range, phenotypic and genotypic coefficient of variation, heritability, genetic advance and genetic advance (as per cent of mean) for various characters in mustard

Characters	Phenotypic range	Coefficient of range (%)	Mean $\pm$ S.E.m	Phenotypic coefficient of variation (%)	Genotypic coefficient of variation (%)	Heritability in broad sense (%)	Genetic advance	Genetic advance (percent of mean)
Seed yield/plant	14.24 - 33.01	39.73	20.73 $\pm$ 1.838	24.94	19.65	62.1	6.61	31.89
Days to 50% flowering	37.33 - 57.33	21.13	48.23 $\pm$ 0.912	7.80	7.08	82.4	6.39	13.24
Days to maturity	95.33 - 109.67	6.99	101.22 $\pm$ 0.777	4.05	3.82	89.3	7.53	7.34
Plant height (cm)	134.40 - 187.33	16.45	167.30 $\pm$ 3.447	6.23	5.11	67.2	14.43	8.62
No. of primary branches/plant	4.33 - 7.87	28.96	5.98 $\pm$ 0.293	13.63	10.67	61.2	1.03	17.20
No. of secondary branches/plant	11.40 - 25.53	38.27	16.80 $\pm$ 1.243	22.88	18.96	68.7	5.44	32.36
No. of siliques/plant	262.80 - 581.27	37.73	410.94 $\pm$ 23.245	17.79	14.85	69.7	104.91	25.53
No. of seeds/silique	10.80 - 16.67	21.36	13.21 $\pm$ 0.433	9.81	8.00	66.5	1.78	13.45
Length of silique (cm)	4.40 - 5.90	14.56	5.07 $\pm$ 0.122	7.33	6.04	68.0	0.52	10.26
1000 seed weight (g)	3.13 - 5.32	26.02	4.15 $\pm$ 0.175	14.74	12.80	75.5	0.95	22.91
Biological yield/plant	48.30 - 97.79	33.88	68.32 $\pm$ 6.541	19.46	10.18	27.4	7.50	10.97
Harvest index (%)	21.15 - 37.62	28.04	30.55 $\pm$ 2.391	17.25	10.68	38.3	4.16	13.62
Oil content (%)	29.88 - 41.30	16.03	36.92 $\pm$ 1.374	8.22	5.10	38.5	2.41	6.52

per plant, harvest index, 1000-seed weight and primary branches per plant indicated the presence of wide variation for these traits to allow selection for individual traits. Similar findings pertaining to presence of high genetic variability were reported by Kumar *et al.*, (2000) and Choudhary *et al.*, (2003). Moderate estimates of GCV and PCV were observed for number of seeds per silique, oil content, days to 50% flowering and length of siliques, while low estimates of GCV and PCV were observed for days to maturity and plant height indicated narrow genetic variability for both characters.

The efficacy of selection not only depends on magnitude of variability present in a trait, but also on the extent of heritability of desirable character. To obtain heritable portion of variability, it was essential to know the heritability estimates for different traits (Burton, 1952). Johnson *et al.*, (1955) suggested that the heritability estimate along with genetic advance is more useful than the heritability alone in predicting the resultant effect of selection. In the present study, estimates of high heritability coupled with high genetic advance as per cent of mean was observed for days to 50% flowering, number of primary branches per plant, number of secondary branches per plant, number of siliques per plant, 1000-seed weight and seed yield per plant indicated preponderance of additive gene action and selection pressure could profitably be applied on these characters for improving the seed yield (Panse, 1957). On the other hand, moderate to high heritability along with low GCV and low genetic gain were observed for days to maturity, plant height and length of silique could be due to preponderance of non-additive (dominant and epistatic) gene actions and/or less genetic variability for these three traits in the materials. For the remaining traits viz., number of seeds per siliques, biological yield per plant, harvest index and oil content, major variation was environmental, leading to low heritability and low expected genetic advance. Hence, little gain is expected through straight selection.

Multivariate Analysis

Multivariate analysis using Wilk's ' Λ ' criterion was carried out to test the differences among 50 genotypes for aggregate of 13 characters. The value of V-statistic (3796.890) which follows χ^2 distribution for 637 degrees of freedom showed highly significant differences among the genotypes for aggregate of 13 characters. Thus, one can proceed for further diversity analysis. The D^2 -values computed for 1125 pairs ranged from 4.89 (between GDM 4 and PAB 9337) to 309.94

Table 3 Groups of 50 genotypes of mustard in various clusters on the basis of D² statistic

Cluster	No. of genotypes	Name of genotypes	Place of origin
I	33	GDM-4, 614-4-4, SKM-9825, GM-3, SKM-9824, SKM-9813, RSK-86, AA-66, 508-4, 5422-2, GM-2, Bharkawada-2	SDAU, Sardarkrushinagar (Gujarat)
		PSR-48, BIO-902, PBN-9501, DIR-437, PusaJaganath, BIO-341-92, PAB-9337, NM-919	IARI (New Delhi)
		UP-11-90, NRCM-8-1, NRCM-421, NRCM-141, JMG-416	NRCRM (Rajasthan)
		R.K.-9501, PRKS-28	CSAUA&T (UP)
		HUM-9901, HUJM-9720	JNKVV (MP)
		TM-1	BARC (Maharashtra)
		DHR-9405	HAU (Haryana)
		B-1328	PORS (West Bengal)
		SAL-6	CSSRI (Haryana)
II	6	B-351, RW-B-94	PORS (West Bengal)
		C-111, SAL-3	CSSRI (Haryana)
		NUDH-YJ-1	Dhara Vegetable Oil and Foods Co. Ltd. (Gujarat)
		PCR-7	NRCRM (Rajasthan)
III	3	DLM-52	PAU (Punjab)
		Aravali (RN 893)	RAU (Rajasthan)
		Ranasan-2	SDAU (Gujarat)
IV	3	NPJ-91, NPJ-95	IARI (New Delhi)
		SKM-9916	SDAU (Gujarat)
V	1	SKM-0287	SDAU (Gujarat)
VI	1	PYM-7	GBPUA & T (Uttarakhand)
VII	1	SKM-9142	SDAU (Gujarat)
VIII	1	SKM-0110	SDAU (Gujarat)
IX	1	IC-355327	NBPGR (New Delhi)

Table 4 Average inter and intra-cluster distance ($D = \sqrt{D^2}$) values in mustard

Characters	I	II	III	IV	V	VI	VII	VIII	IX
I	7.27	8.99	9.72	10.9	9.22	9.42	8.56	9.11	9.57
II		8.58	11.66	12.74	12.53	33.15	10.92	11.74	11.77
III			7.18	15.35	9.86	10.10	11.40	9.95	9.98
IV				7.52	12.35	13.70	8.08	13.25	12.64
V					0.00	9.03	8.96	6.11	9.49
VI						0.00	9.64	10.94	12.27
VII							0.00	9.97	9.08
VIII								0.00	8.31
IX									0.00

(between NPJ 91 and Ranasan 2) indicated the presence of high genetic diversity among genotypes for all the traits.

All fifty genotypes were grouped into nine clusters, using the Tocher's method, in such a way that genotypes within the cluster had smaller D^2 values among themselves than those belonging to different clusters (Table 3). Cluster I was the largest having 33 genotypes from different geographical regions comprising 12 genotypes from SDAU, Sardarkrushinagar (Gujarat); 8 from IARI (New Delhi); 5 from NRCRM, Sear, Bharatpur (Rajasthan); 2 from CSAUA&T, Kanpur (Uttar Pradesh); 2 from JNKVV (Madhya Pradesh) and one each from BARC, Trombay (Maharashtra); CSSRI, Karnal (Haryana); PORS, Behrampur (West Bengal) and HAU, Hissar (Haryana). Likewise, cluster II comprised of 6 genotypes from different locations of India. While cluster III and VI both possessed three genotypes each. The clusters from V to IX had only single genotype in each cluster. The clustering pattern of genotypes showed that genetic origin was totally independent of their geographical origin. Murty and Arunachalam (1966) also stated that genetic drift and selection in varied environments could be caused for greater diversity than geographic distance. Further, free exchange of seed materials among the different regions consequently causes characters constellations because of the human interference and material may lose its individuality. Singh *et al.* (2007), Singh *et al.* (2009) and Sutariya *et al.*, (2011) also reported that there was no parallelism between geographic distribution and genetic diversity in mustard.

In general, intra-cluster distances were lower than the inter cluster distances (Table 4). Thus, the genotypes included within a cluster tended to diverse less from one another. Intra cluster distance (D) ranged from 7.18 in cluster III to 8.58 in cluster II. The analysis of data revealed that the maximum inter cluster distance ($D=33.15$) was observed between clusters II and VI followed by that between cluster III and IV ($D=15.35$) and minimum inter cluster distance ($D=6.11$) was observed between cluster V and VIII. The genotypes belonging to the clusters separated by high statistical distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregates. In this context, genotypes from cluster II (B 351, NUDH-YJ 1, C 111, SAL 3, PCR 7, RW-B 94), cluster III (DLM 52, Aravali (RN 893), Ranasan 2), cluster IV (NPJ 91, NPJ 95, SKM 9916) and cluster VI (PYM 7) could be selected as parents in hybridization programme.

Table 5 Cluster means for different characters in mustard

Clusters	Seed yield/plant (g)	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches/plant	No. of secondary branches/plant	No. of siliques/plant	No. of seeds/silique	Length of silique (cm)	1000 seed weight	Biological yield/plant	Harvest index (%)	Oil content (%)
I	19.71	48.40	101.01	168.07	5.95	17.07	400.46	12.97	5.09	4.28	67.02	29.65	36.69
II	24.34	48.44	99.33	172.03	6.33	20.11	493.02	12.61	4.76	3.63	77.70	31.84	39.42
III	18.43	53.33	108.00	179.40	6.58	13.36	466.60	13.62	5.58	3.70	66.43	27.70	35.39
IV	19.52	38.22	96.44	149.78	5.18	13.87	353.04	13.96	5.05	4.44	60.26	32.54	35.77
V	24.32	50.33	107.67	152.93	5.20	13.33	364.47	14.00	4.94	4.44	65.88	37.45	35.56
VI	14.58	53.33	103.33	163.27	5.53	16.53	398.93	15.07	4.40	3.13	59.80	24.98	38.86
VII	22.17	45.33	99.67	157.00	6.07	13.33	419.80	16.67	5.17	4.00	60.23	37.53	35.02
VIII	32.41	49.67	106.00	158.07	7.07	18.73	388.27	13.20	5.20	4.89	97.79	33.80	38.05
IX	32.35	50.33	101.67	167.53	5.53	12.27	343.67	14.87	5.86	3.68	74.72	43.63	37.65
Mean	20.73	48.23	101.22	167.30	5.98	16.80	410.94	13.21	5.07	4.15	68.32	30.55	36.92
S.E.m	1.838	0.912	0.777	3.447	0.293	1.243	23.245	0.433	0.122	0.175	6.541	2.391	1.374
Per cent Contribution towards total genetic divergence	6.61	12.16	32.73	2.69	2.94	4.98	6.69	7.59	7.18	10.29	0.16	0.08	5.88

The clustering pattern could be utilized in selection of parents for crossing and deciding the best cross combinations, which may generate the highest possible variability for various traits. In the present study, the cluster VIII differed from other clusters (Table 5) in respect of seed yield per plant, number of primary branches per plant, 1000-seed weight and biological yield per plant, while, cluster II was the best for number of secondary branches per plant, number of siliques per plant and oil content. The cluster IV had desirable rating for days to 50% flowering, days to maturity and plant height. The clusters VII, VI and IX were the best for number of seeds per silique, length of silique and harvest index, respectively.

Contribution of different characters towards total genetic divergence (Table 5) revealed the highest contribution of days to maturity (32.73 %). Three traits contributed more than 55 % of diversity viz. days to maturity (32.73 %), days to 50% flowering (12.16 %) and 1000-seed weight (10.29 %). Hence, selection of divergent parents based on these 3 traits would be useful for hybridization programme followed by isolation of desirable transgressive segregants in mustard. Similar findings were also reported by Arha *et al.* (2006) and Budhanwar *et al.* (2010).

Overall, it can be concluded that high heritability along with high GCV and high genetic gain were observed for seed yield per plant, days to 50% flowering, number of primary branches per plant, number of secondary branches per plant, number of siliques per plant and 1000-seed weight which might be attributed to additive gene action in their inheritance and phenotypic selection could be effective. Maximum contribution of days to maturity, followed by days to 50% flowering and 1000-seed weight were observed on total genetic divergence. Hence due consideration should be given to these traits, while imposing selection for amenability in seed yield per plant in mustard.

REFERENCES

- Allard, R. W. 1960. *Principles of Plant Breeding*. John Wiley and Sons, New York.
- Anonymous, 2010. National Agricultural Statistics Service, Acreage Reports.
- Arha, M.D., Solanki, R.K. and Tomar, R.S. 2006. Genetic diversity in Indian mustard [*Brassica juncea* (L.) Czern and Coss]. *Journal of Oilseeds Research* 23(2): 156-158.

- Arunachalam, V. 1981. Genetic distance in plant breeding. *Indian Journal of Genetics* 41(2): 226-236.
- Budhanwar, P.D., Kalamkar, B.N.V. and Fulkar, P.I. 2010. Evaluation of recombinant lines for genetic potential and genetic diversity for yield contributing characters in mustard (*Brassica juncea* (L.) Czern and Coss). *Advances in Plant Science* 23(1): 227-229.
- Burton, G. W. 1952. *Quantitative Inheritance in Grasses*. Proc. 6th International Grassland Congress 1: 277-283.
- Choudhary, V.K., Kumar, R. and Shah, J.N. 2003. Variability studies in Indian mustard. *Journal of Applied Biology* 13(1/2): 9-12.
- Johnson, H. W., Robinson, H. F. and Comstock, R. E. 1955. Genotypic and phenotypic correlations in soybean and their implications in selection. *Agronomy Journal* 47: 477-483.
- Kumar, R., Haider, Z.A. and Kumar, A. 2000. Assessment of genetic variability in selected mutant lines of *Brassica juncea* L. *Journal of Research, BAU* 12(2): 175-178.
- Mahalanobis, P. C., 1936. On the generalized distance in statistics. *Proc. National Institute of Science (India)* 2: 49-55.
- Murty, B. R. and Arunachalam, V. 1966. The nature of genetic divergence in relation to breeding system in crop plants. *Indian Journal of Genetics* 26: 188-198.
- Panase, V. G. 1957. Genetics of quantitative traits in relation to plant breeding. *Indian Journal of Genetics* 17: 318-328.
- Rao, C. R. 1952. *Advanced Statistical Methods in Biometric Research*. John Wiley and Sons, New York, pp 357-363.
- Singh, U.K., Kumari, R. And Srivastava, S. 2009. Genetic divergence study in Indian mustard [*Brassica juncea* (L.) Czern and Coss] under abiotic stress. *Journal of Oilseed Research* 26: 151-152.
- Singh, V., Bhajan, R. and Kumar, K. 2007. Genetic diversity in Indian mustard [*Brassicajuncea* (L.) Czern and Coss]. *Progressive Agriculture*, 7(1/2): 105-109.
- Sutariya, D.A., Patel, K.M., Bhadauria, H.S., Vaghela, P.O., Prajapati, D.V. and Parmar, S.K. 2011. Genetic diversity for quality traits in Indian mustard [*Brassica juncea* (L.)] *Journal of Oilseed Brassica* 2(1): 44-47.