

GENETIC DIVERGENCE FOR SEED YIELD AND COMPONENT TRAITS IN INDIAN MUSTARD [*Brassica juncea* (L.) CZERN & COSS.]

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ABSTRACT

*An experiment was conducted at the experimental farm at G.B. Pant University of Agriculture and Technology, Pantnagar in 2006. The broad objective was to quantify genetic divergence for 13 quantitative characters including seed yield and oil content in Indian mustard (*Brassica juncea* L. Czern&Coss). The wide genetic variability was elucidated in the materials for all the 13 characters, whereas genetic advance in per cent of mean was found high only for 1000-seed weight, number of secondary branches/plant, number of primary branches/plant, length of main raceme and siliquae on main raceme. The seed yield/plant had significant correlation in desirable direction with days to maturity, plant height, siliquae length and 1000-seed weight both at genotypic and phenotypic level. The divergence analysis grouped the 64 genotypes into seven non-overlapping clusters. The maximum number of genotypes were grouped in Cluster-III (17) followed by Cluster-I (14), Cluster-II (13), Cluster-V (6), Clusters-VI and VII (5 in each), and Cluster-IV (4). No regular geographical demarcation was discernible from clustering pattern of the genotypes. Clusters pair III and IV followed by VII and VI was found to be most divergent. Days to flowering followed by days to maturity and plant height contributed maximum towards genetic diversity.*

KEY WORDS: Genetic divergence, heritability, genetic advance

INTRODUCTION

Rapeseed-mustard are the major *radioilseed* crops of India. They occupy a prominent place being next in importance to groundnut, both in area and production, meeting the fat requirement of about 50 per cent population in the state of Rajasthan Uttar Pradesh, Punjab, Haryana, Madhya Pradesh, Bihar, Orissa, West Bengal and Assam. India's contribution in the world rapeseed-mustard production is the highest of any country.

Botanically oilseed *Brassicas* constitutes different crops comprising two distinct forms from their breeding

point of view. One is self compatible and self pollinated form, comprising yellow sarson, tora type brown sarson (*Brassica rapa* L.), Indian mustard (*B. juncea* L. Czern and Coss.) and Gobhisarson (*B. napus* L.) and Ethiopian mustard (*B. carinata*) while other group consists of self incompatible and highly cross pollinated crops viz. lotni type brown sarson and toria (*B. rapa* L.), black mustard (*Brassica nigra*) and taramira (*Eruca sativa* L.). All these crops are grown under diverse agro-climatic conditions. However, mustard occupies largest acreage and accounts for more

than 80% of the area under oilseed *Brassic*as.

The success of any crop improvement programme through hybridization followed by selection depends primarily on the choice of parents having high genetic variability for different characters. Mahalanobis D^2 statistic helps the breeder to estimate the genetic divergence. Heterosis studies indicate significant level of heterosis for seed yield (13 to 91%) in *B. juncea* (Mahaket *al.*, 2003 and Monalisa, 2005). It was also observed that hybrids between genetically distant groups showed greater heterosis than within the group combinations. Among the biometrical techniques, diallel analysis has been used extensively for deciphering nature of gene action and selection of large number of parents for hybridization. It seems that information on genetic architecture of parents, their combining ability, extent of heterosis, transmissibility of characters and expected genetic advance will be of immense value to ascertain the selection of desirable parents in the choice of suitable breeding methodology for the improvement of Indian mustard

MATERIALS AND METHODS

The present investigation was carried out at the Crop Research Centre, G. B. Pant University of Agriculture & Technology, Pantnagar (Uttarakhand). The set of 64 genotypes was evaluated in a Randomized Block Design with three replications. Each treatment was raised in a single row of 3 meter length and 30 cm spaced between rows. The approximate distance of 10 cm between plants was maintained by thinning. All the recommended agronomic practices were adopted for raising a good crop. Five random competitive plants were selected from each row and tagged for

recording observations for days to 50% flowering, days to maturity, plant height (cm), length of main raceme (cm), siliquae on main raceme, number of primary branches per plant, number of secondary branches per plant, siliqua length, number of seeds per siliqua, number of siliquae/plant, 1000-seed weight (g), seed yield per plant (g) and oil content (%).

RESULTS AND DISCUSSION

In *Brassica* oil crops, major emphasis of breeding programme has been on improving productivity. The success of any crop improvement programme is dependent upon the extent of variability present in the crop. The *Brassica* crops have a vast reservoir of potential genetic variability at both intra and inter-specific level. For selection of desired genotypes information about *per se* performance of genotypes, selection parameters, inter-character correlations and genetic basis of a character plays a crucial role in success of any breeding programme. The present investigation aims to study extent of genetic variability, heritability, genetic advance, inter-character association and genetic divergence in Indian mustard (*Brassica juncea* L. Czern and Coss.).

Higher value of phenotypic and genotypic coefficients of variation for seed number of secondary branches/plant and 1000-seed weight was observed (Kumar *et al.* (2002). Moderate genotypic and phenotypic coefficient of variation for number of primary branches/plant, length of main raceme, siliquae on main raceme, total siliquae/plant, siliqua length and days to flowering was observed (Mahlaet *al.*, 2003).

The lowest phenotypic and genotypic coefficient of variance for oil content followed by days to maturity was observed. The close

correspondence and higher magnitude of phenotypic as well as genotypic coefficients of variation showed that the genotypes evaluated had sufficient variability to generate transgressive segregants for seed yield and other key components. The highest heritability was observed for seed yield per plant (97%) followed by total siliquae/plant (95%), number of primary branches/plant (95%), length of main raceme (94%), days to flowering (93%), number of secondary branches/plant (93%), siliquae on main raceme (89%), plant height (91%), siliqua length (89%), number of seeds/siliqua (87%) and 1000-seed weight (63%). Days to maturity showed moderate heritability (45%) and minimum for oil content (29%).

High heritability estimates were also reported for seed yield/plant, number of secondary branches/plant, length of main shoot and siliqua length by Kumar *et al.*, (2004). High value of genetic advance was observed for total siliquae/plant (53.00) followed by plant height (26.75) and length of main raceme (21.09). moderate genetic advance was observed for siliquae on main raceme (11.77) and days to flowering (11.36) while 1000-seeds weight (9.99), number of secondary branches/plant (4.29), days to maturity (2.41), number of seeds/siliqua (2.30), number of primary branches/plant (1.96), siliqua length (1.22), oil content (0.56) and seed yield/plant (0.41) exhibited low genetic advance (Table 1).

Seed yield/plant showed significant and positive association with days to maturity (0.272*, 0.382**), plant height (0.281*, 0.406**), siliqua length (0.266*, 0.347**) and 1000-seed weight (0.359*, 0.463**) both at genotypic and phenotypic level. Oil content was negatively associated with siliqua

length and number of seed/siliqua, while 1000-seed weight manifested positive association with siliqua length (Table 2). Selection of diverse parents belonging to distant groups leads to a wide spectrum of gene combinations for the quantitative and qualitative traits. Several measures of distance have been proposed in the past to suit various objectives, of which Mahalanobis generalized distance (Mahalanobis, 1936 and Rao, 1952) has taken an important and unique place in plant breeding. Multivariate analysis with D^2 technique measures the amount of genetic diversity in the given population in respect of several characters considered together.

In clustering pattern, 64 genotypes fell into seven clusters. Among the seven clusters, 14 genotypes fell in cluster-I, 13 genotypes in cluster-II, 17 genotypes in cluster-III, four genotypes in cluster-IV, six genotypes in cluster-V, five genotypes each in cluster-VI and cluster-VII (Table.4.1.1). Random distribution of genotypes was evident from clustering pattern. Cluster -III was the largest, comprising 17 genotypes from nine different breeding centers of the country viz., IARI New Delhi (4), Hisar (3), Morena (3), S.K. Nagar (2), Pantnagar (1), Kanpur (1), Ludhiana (1) and Bharatpur (1). Cluster-I, the second largest cluster had 14 genotypes developed at eight different breeding centers namely Pantnagar (5), Faizabad (2), Hisar (2), Kanpur (1), Kota (1), Jodhpur (1), Karnal (1) and Sriganganagar (1) (Table 3). On the contrary some genotypes belonging to same geographical area but they fell into different clusters because they have more genetic distance. The grouping pattern, thus indicated that no regular relationship between geographical

demarcations and genetic divergence (Verma and Sachan, 2000). The intra-cluster average D^2 values ranged from 2.43 (cluster- II) to 2.79 (cluster-VII). The higher intra-cluster distance in Cluster-VII comprising five genotypes followed by in Cluster-V (6 genotypes) indicated the existence of substantial variability within these clusters revealing thereby the possibility of selection of desired genotype within these clusters.

The inter-cluster D^2 was maximum between cluster III and IV (5.62) followed by between cluster-VII and cluster- VI (5.55) and between cluster-V and cluster-IV (4.96). This indicates existence of considerable divergence between these clusters. The minimum genetic distance between cluster-I and III (2.36) suggests a fairly close relationship of genotypes belonging to these cluster pairs. Genotypes belonging to clusters separated by high genetic distance should be used in hybridization to obtain wide spectrum of variation.

The cluster IV had the maximum expression of total siliquae/plant (232.63), siliquae on main raceme (50.53), number of primary branches/plant (6.44) and number of secondary branches/plant (11.17). Cluster VI had the maximum expression of seed yield/plant (17.68g), number of seeds/silique (14.99) and silique length (6.05cm). Cluster VII showed the minimum desired expression for days to maturity (130.53) and plant height (156.61 cm) as well as maximum oil content (40.34%). Cluster V had desired minimum expression for days to flowering (40.89) and cluster II had maximum expression of length of main raceme (67.86 cm) and 1000-seed weight (4.00 g) (Malik and Sirohi (2006) (Table 4). Days to flowering (19.94%) followed by days to maturity

(13.89%) and plant height (13.68 %) showed highest contribution towards genetic divergence. Similar results were also reported Mahto *et al.* (1996) (Table 5).

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Table 1: Range, Mean, and Coefficient of Variation, Heritability and Expected Genetic Advance for Quantitative Characters of 64 genotypes of Indian mustard

S. N o.	Characters	Range	Mean	SEM $\pm$	PCV	GCV	Heritability (%)	Expected Genetic Advance	Genetic Advance as % of Mean
1.	Days to flowering	41.00 – 68.33	53.92	0.85	10.93	10.57	0.93	11.36	21.06
2.	Days to maturity	129.00-138.33	134.23	1.11	1.93	1.30	0.45	2.41	1.79
3.	Plant height (cm)	140.87-214.33	183.01	2.43	7.78	7.43	0.91	26.75	14.61
4.	Length of main raceme(cm)	39.53-78.52	59.03	1.39	18.26	17.79	0.94	21.09	35.72
5.	Silique on main raceme	24.76-57.43	36.26	1.23	17.71	16.70	0.89	11.77	32.46
6.	No. of primary branches/ pl.	3.20-7.82	4.92	0.12	20.24	19.77	0.95	1.96	39.82
7.	No. of secondary branches/ pl.	3.10-12.06	8.26	0.33	27.04	26.12	0.93	4.29	51.93
8.	Silique length(cm)	4.14-6.33	5.02	0.12	13.31	12.56	0.89	1.22	24.30
9.	No. of seeds/silique	11.35-17.70	13.65	0.27	9.41	8.77	0.87	2.30	16.84
10	Total silique/plant	267.66-123.26	189.51	3.21	14.18	13.87	0.95	53.00	27.96
11	1000-seed weight (gm)	3.16-4.20	3.70	0.11	8.58	6.81	0.63	0.41	11.08
12	Seed yield/plant (g)	36.14-11.22	10.23	0.41	17.17	16.88	0.97	9.99	54.79
13	Oil content (%)	37.83-41.03	39.76	0.45	2.34	1.26	0.29	0.56	0.01

Table 2: Genotypic correlation coefficient among various quantitative character pairs

S. No.	Characters	1	2	3	4	5	6	7	8	9	10	11	12	13
		Days to flowering	Days to maturity	Plant height (cm)	Length of main raceme (cm)	Silique on main raceme	No. of primary branches	No. of Secondary branches	Silique length (cm)	No. of Seeds/ siliqua	Total Siliquae/ plant	1000– seed weight (gm)	Seed yield /plant (g)	Oil Content (%)
1.	Days to flowering		0.442**	0.3323**	-0.0753	0.2037	.0327	0.0023	.02134	-0.2651*	0.0471	0.1999	0.3055*	0.025
2.	Days to maturity			0.3081*	-2.92	-1.080	0.008	-0.107	0.1834	0.0133	0.0542	0.1989	0.3822**	-0.0123
3.	Plant height (cm)				0.1875	0.4009	0.154	-0.064	0.165	0.120	0.3381**	.0522	0.4060**	.0035
4.	Length of main raceme (cm)					0.5017**	.0030	-0.1327	.0767	0.112	0.0175	0.220	0.026	0.2566*
5.	Silique on main raceme						0.151	0.067	0.097	0.1573	0.4167**	0.187	0.094	0.00
6.	No. of primary branches/plant							0.181	-0.035	0.1618	0.1722	0.1953	0.0271	0.042
7.	No. of Secondary branches/plant								0.327**	0.2026	0.2512*	0.052	-0.028	-0.4019**
8.	Silique length(cm)									0.2408	-0.268	0.4314**	0.3472**	-.575**
9.	No. of Seeds/ siliqua										-0.017	0.098	-0.163	-0.1402
10.	Total Silique /plant											-0.049	0.071	-0.1644
11.	1000-seed weight (gm)												0.4633**	0.0293
12.	Seed yield/plant (g)													-0.0988
13.	Oil content (%)													

Table 3: Clustering pattern of 64 genotypes of Indian mustard on the basis of D² values

Cluster Number	Genotypes	Number of genotypes in each cluster
Cluster-I	RKM-1 (Kota, Rajasthan), PHJO 2-40-2 (PSCPL, Haryana), PRB-2006-18, PRQ-2005, P-R-2004-2, Kranti, PAB-9511, (Pantnagar, UK), NDR-05-1, NDYR-32 (Faizabad, UP), RGN-142 (Navgaon, Rajasthan), Vardan (Kanpur, UP), RH-9811(Hisar, Haryana), RM-2 (Rallies India), RH-0115 (Hisar, Haryana).	14
Cluster-II	RB-50 (Bawal, Haryana), NDR-03-6 (Faizabad, UP), PBR-283 (Ludhiana, Panjab), PRB-2006-11, PRB-2006-7, PRB-2006-2, PRB-2006-8, PRB-2006-8, PR-2006-18, PWR-9541, PR-2003-30 (Pantnagar, UK), RK-04-4 (Kanpur, UP), RH-0213 (Hisar, Haryana).	13
Cluster-III	SKM-401, SKM-425 (S.K. Nagar, Gujrat), RL -2106 (Ludhiyana, Punjab), ORY(M) 15-2-2 (Bhubneswar, Orissa), JMWR-941-1-2, JMM-18, JMMWR-93-38 (Morena, Rajasthan), RH-04-1, RH-0121, RH-05-1 (Hisar, Haryana), JS-21, PBG-1986, JS-19, SEJ-2 (IARI, New Delhi), Rohini (Kanpur, UP), PAB-9534 (Pantnagar, UK), BPR-560 (Bharatpur, Rajasthan).	17
Cluster-IV	JKMS-2, JK Kriti (J.K. Seeds Hyderabad, AP), HUJM-03-03 (Varanasi, UP), CS-609-B-10 (Karnal, Haryana).	4
Cluster-V	Maya (Kanpur, UP), 45-J-21 (Ghaziabad, UP), HUJM-03-01 (Varanasi, UP), RM-105 (Jodhpur, Rajasthan), NDRE-2010 (Faizabad, UP), PRB-2006-12 (Pantnagar, UK).	6
Cluster-VI	Radha (Agra, UP), RH-011(Hisar, Haryana), PRB-2006-3, PRB-2006-17, PRB-2006-5 (Pantnagar, UK).	5
Cluster-VII	RGN-145 (Sriganganagar, Rajsthan), Kanti (Kanpur, UP), NDRE-4 (Faizabad, UP), NPJ-108, JD-6 (IARI, New Delhi).	5

Table 4: Cluster Mean Values for Various Characters of Indian mustard (*Brassica juncea*)

S. No.	Characters	Clusters						
		I	II	III	IV	V	VI	VII
1.	Days to flowering	56.83	56.23	54.51	57.08	40.89	56.60	48.27
2.	Days to maturity	135.07	134.36	134.82	133.92	132.56	135.53	130.53
3.	Plant height (cm)	185.21	190.60	182.19	193.18	182.26	179.09	156.61
4.	Length of main raceme (cm)	53.71	67.86	54.62	67.36	56.05	58.03	63.90
5.	Siliquae on main raceme	35.07	39.41	34.53	50.53	32.71	34.12	32.40
6.	Number of primary branches/plant	4.31	4.69	5.09	6.44	5.32	5.64	4.32
7.	Number of secondary branches/plant	7.52	5.28	4.41	9.17	6.98	7.81	6.87
8.	Silique length(cm)	4.96	5.30	4.53	5.42	4.91	6.05	4.98
9.	Number of seeds/silique	13.24	13.16	13.56	14.81	14.43	14.99	13.19
10.	Number of siliquae/plant	197.23	186.16	177.94	232.63	208.69	185.05	163.00
11.	1000–seeds weight (g)	3.68	4.00	3.58	3.58	3.65	3.99	3.32
12.	Seed yield/plant (g)	5.36	0.16	6.60	11.99	4.62	17.68	7.39
13.	Oil content (%)	39.35	39.91	40.18	39.54	39.34	39.31	40.34

Table 5: Contribution of Different Characters towards Diversity of genotypes in Indian mustard

Sr. No.	Characters	% Contribution
1.	Days to flowering	19.94
2.	Days to maturity	13.89
3.	Plant height (cm)	13.68
4.	Length of main raceme (cm)	10.96
5.	Siliquae on main raceme	8.33
6.	Number of primary branches/plant	7.52
7.	Number of secondary branches/plant	5.56
8.	Siliqua length(cm)	4.90
9.	Number of seeds/siliqua	4.43
10.	Total siliqua/plant	3.50
11.	1000 – seed weight (gm)	2.72
12.	Seed yield/plant (g)	2.59
13.	Oil content (%)	1.88

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