Original Research Article

Studies on Genetic Variability, Character Association and Genetic Divergence in Indian Mustard (*Brassica juncea* L. Czern and Coss.)

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A B S T R A C T

An evaluation of 40 accessions of Indian mustard {*Brassica juncea* (L.) Czern & Coss} germplasm for yield as well as quality traits was conducted at Genetics & Plant Breeding Research Farm of Narendra Deva University of Agriculture and Technology, Narendra Nagar, Kumarganj, Ayodhya (U.P.) during *rabi,* 2017-18. The material was sown in RBD with three replications. Observations were recorded on 12 quantitative characters. High values of PCV closely followed by GCV were observed maximum for harvest index followed by 1000 seed weight. Higher heritability estimates in broad sense were observed for maximum in harvest index followed by 1000 seed weight, seed yield per plant and biological yield per plant. High heritability estimates resulted in high genetic advance in % of mean except for days to 50% flowering and days to maturity. Seed yield per plant showed very strong association with harvest index. Path coefficient analysis revealed that biological yield per plant and harvest index directly influenced seed yield at genotypic and phenotypic levels. Using Mahalanobis D^2 analysis, the 40 genotypes were grouped into seven clusters. The maximum inter cluster distance was observed between cluster III and II indicated wide diversity between these groups. Minimum value was found in between cluster VII and VI. Hybridization among the genotypes separated by high inter cluster distance will result in most heterotic crosses.

Introduction

Indian mustard [*Brassica juncea* (L.) Czern and Coss] is the second most important oilseed crop of the world as well as India after groundnut. It is a natural amphidiploid (2n=36) of *Brassica campestris* (2n=20) and *Brassica nigra* (2n=16). It is self-compatible and largely self pollinated crop (85-90%).

Indian mustard is popularly known as rai, raya or laha and it occupies considerably large acreage among the Brassica group of oil seed crops accounting for about 75-80% of the 6.6 million hectare under rapeseed-mustard in the country. India was the 7th largest importing country in 2014-15 (Anonymous, 2017). Indian mustard is predominantly cultivated in Rajasthan, U.P.,

M.P., Haryana and Gujarat which contributes 81.5% area and 87.5% production, more than 84% of total rapeseed acreage and production in the country is accounted by these states, out of which more than 47% contributed by Rajasthan state alone. Among the entire oilseed crops producing states, in U.P. it was grown on 6.26 lakh ha with production of 5.82 lakh MT and productivity of 930 Kg/ha and had ranks third in area after Rajasthan and M.P. and third in production after Rajasthan and Haryana (Anonymous, 2017).

The crop improvement in mustard is complex in nature due to a complex nature of inheritance of yield and its attributes. There are evidences of both additive and non additive types of gene action in inheritance of characters of mustard. Due to its autogamous nature and adequate additive genetic variance, the attempts at improvement have been stressed upon selection and development of purelines. Though a stable and higher seed yield is the objective of crop improvement programme, the oil content is of paramount importance in oilseed crops. The response to selection for yield is low as it is an end product of a chain of contributing characters. Hence manipulations of main yield attributing characters like number of siliquae on main shoot, number of seed per siliqua, test weight, plant height, maturity duration, etc. are to be considered first. An understanding of nature and magnitude of genetic variation in conjunction with genetic gain of the traits is pertinent for a breeding programme aimed at developing high yielding stable varieties. The presence of high genetic variability in the base population allows for better chances of developing desirable plant types. Thus the most critical step is to find the desirable traits or combinations in a given population. Genetic divergence is essential to select the parents for future breeding programme. In general, the genetically divergent parents are utilized to obtain the desirable recombinants in segregating generations. 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.

Correlation and path analysis will establish the extent of association between seed yield and its components and also bring out the relative importance of their direct and indirect effects. The knowledge of the extent of existing genetic variability and character association are important to carry out an efficient selection programme. The problem of increasing the yield can be tackled effectively on the basis of the performance of yield components and selection for closely related characters. The availability of genetic variability is the basic pre- requisite for genetic improvement through systematic breeding programme. Nature always favours the plant having much variability in terms of promiseness and adaptation across year and location. It is true that more diverse plants greater the chances of obtaining high heterotic improvement. Selection and hybridization technique are frequentaly used for improving genetic constitution of a genotype.

Materials and Methods

Present investigation was conducted at Genetics & Plant Breeding Research Farm of Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya during the *rabi* season 2017-18.The materials used in the study comprised of 40 germplasm including three check varieties of Indian mustard. These genotypes were made available from the Oilseed Section of the Department of Genetics and Plant Breeding, ANDUAT.

The material was sown in Randomized Block Design with three replications. Observations were recorded on 12 quantitative characters namely, days to 50% flowering, days to maturity, plant height, primary branches per plant, secondary branches per plant, length of main raceme, siliquae on main raceme, seeds per siliqua, seed yield per plant, 1000-seed weight and harvest index . The data on different characters were utilized for estimation of analysis of variance of Randomized Block Design (Panse and Sukhatme, 1967), coefficient of variation (Burton and De Vane 1953), heritability in broad sense (Hanson *et al.,* 1956), genetic advance (Johnson *et al.,* 1955), correlation coefficient (Searle, 1961), path coefficient analysis (Deway and Lu, 1965) and genetic divergence (D^2) (Mahalanobis, 1936).

Results and Discussion

A survey of genetic variability is essentially the first step of plant breeding for crop improvement and plant breeding is an exercise in the management of variability (Hutchinson, 1958).

High values of phenotypic coefficients of variability (PCV) closely followed by genotypic coefficients of variability (GCV) were observed maximum for harvest index followed by 1000 seed weight, remaining characters showed moderate PCV and GCV values except days to 50% flowering and days to maturity which showed low PCV and GCV values (Table 1). The minimum GCV (1.26 %) and PCV (2.05 %) observed for days to maturity. In general higher heritability estimates in broad sense were observed for maximum in harvest index (94.75 %), followed by 1000 seed weight (91.82 %),seed yield per plant (89.74 %) and biological yield per plant (84.56 %), characters except moderate for primary branches per plant (73.56 %), secondary

branch per plant (73.93 %), plant height (77.34 %), no. of seed per siliqua (73.64 %), no. of siliquae on main raceme (55.68 %) and low for days to 50% flowering (43.57 %) and days to maturity showed lowest (37.71 %). High heritability estimates resulted in high genetic advance in % of mean except for days to 50% flowering and days to maturity. Selection programme depends primarily upon the magnitude of heritable portion of variability. Heritability estimates provide information on transmission of characters from the parents to the progeny. Such estimates facilitate evaluation of hereditary and environmental effects in phenotypic variation and thus aid in selection. Heritability estimates are used to predict genetic advance under selection so that breeders are able to anticipate improvement from different types and intensities of selection. Johnson *et al.,* (1955) have suggested that heritability estimates in association with genetic advance are much useful for selection then heritability alone. Similar result were reported by Shekhawat *et al.,* (2014), Akabari and Niranjana (2015), Srivastava *et al.,* (2016), Devi B. (2017) and Kumar *et al., (*2017).

The estimates of correlation coefficients were worked out at genotypic and phenotypic levels for all the 12 characters and have been presented in Tables 2.The genotypic correlations were higher than phenotypic ones in magnitude for all the characters in normal condition. The direction of genotypic or phenotypic correlations was similar barring few exceptions. Harvest index of plant showed highly significant positive correlation with seed yield per plant (0.807 and 0.722) while biological yield per plant showed highly negative significant correlation with harvest index (-0.710 and -0.647).

Table.1 Mean, range, genotypic and phenotypic coefficient of variability, heritability (%) in broad sense and genetic advance in % of mean for different characters in Indian mustard

Genotypes	Min	Max	Mean	GCV (%)	PCV (%)	Heritability (%)	Ga	Ga as % mean
Days to 50 percent flowering	65.97	73.12	69.52	1.98	3.00	43.57	1.87	2.69
Days to maturity	117.12	126.47	122.47	1.26	2.05	37.71	1.95	1.60
Number of primary branches /plant	5.80	7.13	6.42	4.74	5.52	73.56	0.54	8.37
Number of secondary branches/plant	9.40	11.93	10.27	4.46	5.18	73.93	0.81	7.90
Plant height (cm)	148.73	180.87	166.84	4.46	5.27	71.67	12.98	7.78
Length of main raceme	48.67	60.27	54.82	5.40	6.14	77.34	5.37	9.79
Number of siliquae on main raceme	39.13	47.13	41.86	3.56	4.77	55.68	2.29	5.47
Number of seeds /siliqua	11.33	13.53	12.53	4.99	5.81	73.64	1.10	8.82
1000 seed weight (g)	2.86	4.36	3.69	10.13	10.57	91.82	0.74	20.00
Biological yield (g)	48.13	65.80	58.10	6.62	7.20	84.56	7.29	12.54
Harvest index	19.96	31.15	25.72	11.53	11.84	94.75	5.94	23.11
Seed yield/plant (g)	11.77	17.17	14.63	8.51	8.98	89.74	2.43	16.60

Table.2 Estimates of genotypic and phenotypic correlation coefficients yield attributing characters in Indian mustard

Characters		Days to maturity	Number of primary branches /plant	Number of secondary branches/plant	Plant height (cm)	Length of main raceme (cm)	Number of siliqae on main raceme	Number of seeds /siliqua	1000 seed weight (g)	Biological yield (g)	Harvest index	Seed yield/plant (g)
Days to 5o percent flowering	G	0.386**	-0.247**	-0.292**	-0.096	0.266**	-0.325**	-0.171	0.131	0.123	-0.241**	-0.307**
	P	0.109	-0.390**	-0.039	0.125	-0.073	-0.280**	0.210*	0.070	-0.115	-0.097	-0.092
Days to maturity	G		-0.029	0.269**	-0.500**	-0.048	0.147	0.136	0.024	0.112	0.135	0.160
	P		-0.030	-0.079	-0.056	0.086	-0.282**	0.064	0.128	0.055	-0.017	0.213*
Number of primary branches /plant	G			0.271**	0.083	0.095	-0.259**	0.176	-0.318**	-0.019	0.017	0.164
	P			0.169	-0.145	0.178	-0.007	-0.062	-0.307**	0.187*	0.001	0.011
Number of secondary branches /plant	G				-0.029	0.018	-0.475**	0.056	0.149	0.133	-0.062	0.137
	P				-0.094	-0.156	-0.119	0.126	0.012	0.077	0.065	0.065
Plant height (cm)	G					0.129	0.040	-0.125	0.038	-0.026	0.054	-0.071
	P					0.025	-0.227*	0.061	0.102	-0.176	0.011	0.113
Length of maine raceme	G						-0.271**	-0.030	-0.063	-0.076	-0.030	-0.072
	P						-0.260**	-0.186*	0.011	0.023	-0.101	-0.099
Number of siliqua on main raceme	G							0.363**	0.081	-0.152	-0.015	-0.073
	P							0.121	-0.081	0.014	0.069	-0.201*
Number of seed /siliqua	G								0.205*	0.239**	-0.017	0.139
	P								0.148	0.042	0.025	0.198*
1000 seed weight (g)	G									0.001	-0.001	-0.051
	P									-0.032	-0.050	-0.002
Biological yield (g)	G										-0.710**	-0.070
	P										-0.647**	-0.153
Harvest index %	G											0.807**
	P											0.722**

*, ** significant at 5% and 1% probability level, respectively

Table.3 Direct and indirect effect for different characters on seed yield at genotypic and phenotypic level in Indian mustard

Characters		Days to 50 percent	Days to maturity	Number of primary branches /plant	Number of secondary branches/plant	Plant height (cm)	Length of main raceme	Number of siliquae on main raceme	Number of seeds /siliqua	1000 seed weight (g)	Biological yield (g)	Harvest index	r with Seed yield/plant (g)
Days to 50 percent flowering	G	**-0.839**	0.245	-0.001	0.188	-0.012	0.021	0.215	-0.008	0.024	0.068	-0.207	-0.307**
	P	**-0.117**	0.013	0.037	0.003	0.016	0.005	0.087	0.040	-0.002	-0.067	-0.107	-0.092
Days to maturity	G	-0.324	**0.635**	0.000	-0.174	-0.065	-0.004	-0.097	0.007	0.005	0.062	0.115	0.160
	P	-0.013	**0.120**	0.003	0.007	-0.007	-0.006	0.087	0.012	-0.004	0.032	-0.019	0.213*
Number of primary branches /plant	G	0.208	-0.019	**0.006**	-0.175	0.011	0.007	0.172	0.009	-0.059	-0.010	0.015	0.164
	P	0.045	-0.004	**0.096**	-0.015	-0.018	-0.011	0.002	-0.012	0.009	0.109	0.002	0.011
Number of secondary branches /plant	G	0.245	0.171	0.002	**-0.644**	-0.004	0.001	0.315	0.003	0.028	0.073	-0.053	0.137
	P	0.005	-0.009	-0.016	**-0.089**	-0.012	0.010	0.037	0.024	0.000	0.045	0.071	0.065
Plant height (cm)	G	0.080	-0.318	0.000	0.019	**0.130**	0.010	-0.026	-0.006	0.007	-0.014	0.047	-0.071
	P	-0.015	-0.007	0.014	0.008	**0.126**	-0.002	0.070	0.012	-0.003	-0.103	0.012	0.113
Length of main raceme	G	-0.223	-0.030	0.001	-0.012	0.017	**0.077**	0.180	-0.001	-0.012	-0.042	-0.026	-0.072
	P	0.008	0.010	-0.017	0.014	0.003	**0.064**	0.081	-0.036	0.000	0.013	-0.112	-0.099
Number of siliquae on main raceme	G	0.272	0.093	-0.002	0.306	0.005	-0.021	**-0.663**	0.018	0.015	-0.084	-0.013	-0.073
	P	0.033	-0.034	0.001	0.011	-0.029	0.017	**-0.310**	0.023	0.002	0.008	0.077	-0.201*
Number of seeds /siliqua	G	0.143	0.086	0.001	-0.036	-0.016	-0.002	-0.241	**0.049**	0.038	0.132	-0.015	0.139
	P	-0.024	0.008	0.006	-0.011	0.008	0.012	-0.038	**0.190**	-0.004	0.024	0.027	0.198*
1000 seed weight (g)	G	-0.110	0.016	-0.002	-0.096	0.005	-0.005	-0.054	0.010	**0.186**	0.001	-0.001	-0.051
	P	-0.008	0.015	0.029	-0.001	0.013	-0.001	0.025	0.028	**0.029**	-0.019	-0.055	-0.002
Biological yield (g)	G	-0.103	0.071	0.000	-0.086	-0.003	-0.006	0.101	0.012	0.000	**0.553**	-0.609	-0.070
	P	0.013	0.007	-0.018	-0.007	-0.022	-0.001	-0.004	0.008	0.001	**0.586**	-0.715	-0.153
Harvest index	G	0.203	0.085	0.000	0.040	0.007	-0.002	0.010	-0.001	0.000	-0.392	**0.858**	0.807**
	P	0.011	-0.002	0.000	-0.006	0.001	0.006	-0.022	0.005	0.001	-0.379	**1.105**	0.722**

Table.4 Clustering pattern of 40 genotypes of Indian mustard on the basis of genetic divergence

Clusters	No of genotypes	Genotypes
I	3	UDN17-9,NDN17-19,NDN17-18
II	2	UDN17-9, Kranti
III	4	UDN17-19,UDN17-32,UDN17-24,Varadan
IV	6	UDN17-2,UDN17-6,UDN17-30,NDN17-14, NDN17-6,NDN17-11
V	10	UDN17-11, UDN17-12,UDN17-13, UDN17-15, UDN17-20, NDN17-31, NDN17-39, NDN17-15,NDN17-23, NDN17-13

Table.5 Intra cluster group means for various components of 40 Indian mustard genotypes

Cluster	Days to 50 percent flowering	Days to maturity	Number of primary branches /plant	Number of secondary branches/plant	Plant height (cm)	Length of main raceme	Number of siliquae on main raceme	Number of seeds /siliqua	1000 seed wt. (g)	Biological yield (g)	Harvest index	Seed yield/plant (g)
I	68.95	119.75	6.30	10.09	170.84	52.60	42.15	11.67	4.02	59.45	23.42	13.65
	0.34	2.31	0.27	0.16	3.73	0.64	0.77	0.20	0.17	5.60	3.93	1.63
II	70.85	120.73	6.23	9.97	176.43	57.63	41.05	13.07	4.00	58.89	21.67	12.63
	2.22	1.09	0.24	0.23	6.27	0.52	1.20	0.28	0.15	2.10	0.05	0.43
III	67.89	122.44	6.03	10.13	166.88	51.43	44.92	12.80	3.70	58.94	25.69	14.58
	1.46	0.88	0.18	0.49	9.41	0.87	1.67	0.74	0.46	2.79	2.58	1.53
IV	71.18	124.49	6.10	10.10	167.27	55.80	40.84	12.08	3.90	55.79	27.41	14.98
	1.57	1.46	0.16	0.29	3.98	4.14	1.27	0.58	0.30	5.44	2.58	0.89
V	69.18	121.63	6.60	10.19	168.95	55.37	42.32	12.86	3.55	55.06	28.67	15.51
	1.59	1.39	0.26	0.39	6.44	2.58	1.30	0.58	0.38	1.77	1.60	1.04
VI	69.82	122.07	6.61	10.28	169.61	58.47	41.16	11.96	3.35	59.82	23.30	13.69
	1.27	0.49	0.29	0.56	6.47	1.54	0.97	0.42	0.28	4.14	1.89	0.66
VII	69.27	123.46	6.55	10.61	159.96	53.31	41.22	12.79	3.71	60.78	24.46	14.73
	1.42	1.85	0.27	0.63	8.84	2.16	1.39	0.49	0.38	2.51	1.80	1.10

Table.6 Intra and inter cluster distance √D2 values among 40 genotypes of Indian mustard

Clusters	I	II	III	IV	V	VI	VII
I	**2.374**	3.281	3.308	3.798	3.739	3.181	3.507
II		**1.553**	4.500	3.982	4.220	3.207	4.068
III			**2.773**	3.952	3.266	4.327	3.314
IV				**2.769**	3.100	3.454	3.209
V					**2.622**	3.254	2.914
VI						**2.330**	2.960
VII							**2.926**

Correlation coefficient of the component characters which influence the ultimate expression, is helpful not only choosing the appropriate parental materials for hybridization for direct use but also in deciding judicious breeding methodology to get promising simple well adopted population or segregates. Thus relevant information on these aspects is essential to initiate a sound breeding programme. In recent years the interest of plant breeders has been directed towards better adaptation of crop varieties through collection of varieties from different environments. Similar result was also found by Srivastava and Singh (2000), Chaudhary *et al.,* (2003), Mahak *et al.,* (2003), Gangapur *et al.,* (2009) Kumar and Pandey (2014), Lodhi *et al* (2014) and Devi *et al.,* (2018).

Path coefficient analysis under normal condition revealed that harvest index (0.858 and 1.105) had maximum positive direct effect on seed yield per plant followed by days to maturity (0.635 and 0.120) at genotypic and phenotypic level. Days to maturity (0.635 and 0.120), primary branches per plant (0.006 and 0.096), plant height (0.130 and 0.126), length of main raceme (0.077 and 0.064), no. of seeds per siliqua (0.049 and 0.190), 1000 seed weight (0.186 and 0.029)and biological yield per plant (0.553 and 0.586) showed positive direct effect on seed yield while days to 50 per cent flowering (-0.839 and -0.117), number of secondary branch per plant (-0.644 and -0.089), number of siliquae on main raceme (-0.663 and -0.310) showed negative direct effect on seeds yield per plant. The maximum negative direct effect recorded in case of days to 50 per cent flowering (-0.839 and -0.117). No. of siliqua on main raceme via days to 50% flowering, days to 50% flowering via days to maturity, days to 50% flowering via siliqua on maine raceme, no. of primary branches per plant

via days to 50% flowering showed positive indirect effect on seed yield at genotypic and phenotypic level. Sirohi *et al.,* (2004), Gangapur *et al.,* (2009), Kumar and Pandey (2014) and Devi (2018) also found similar report.

Forty varieties of Indian mustard were grouped into 7clusters (Table 4). The genotypes from one source of origin clustered with the genotypes of other source of origin. This indicated that there was no parallelism between geographical distribution and genetic diversity. Singh and Gupta (1984) and Verma and Sachan (2000) Shalini *et al.,* (2000), Srivastava and Singh (2000) in case of *Brassica juncea*. Chaubey and Katiyar (1979) in *Brassica campestirs* var. toria also found the similar trend. The grouping of genotypes from same geographical origin into different clusters may be due to the different genetic backgrounds and wide divergence in features. Different genetic background is perhaps due to the free exchange of materials among different regions of country for breeding purpose; genetic drift and selection in different environments could be the other important factors contributing to the divergence.

In present investigation, on the basis of magnitude of D^2 values, 40 genotypes of Indian mustard were grouped into 7 clusters. The distribution of genotypes was different. Maximum genotypes (10) were present in cluster 5 and 6. Table 5 and 6 revealed that the maximum inter cluster distance was observed between cluster 3 and 2 cluster. Cluster I consisted of 3 genotypes (UDN17-10, NDN17-19, and NDN17-18) and cluster II had 2 genotypes (UDN17-9, Kranti). This indicated wide diversity between these groups. Hybridization among the genotypes separated by high inter cluster distance will result in most heterotic crosses. The

estimates of genetic divergence for most of the characters under study are in accordance with earlier reports Patel and Patel (2006), Singh *et al.,* (2007), Kumar and Pandey (2012), Goyal*et al.,* (2012), Shekhawat *et al.,* (2014), Mohan *et al.,* (2017) and Negi *et al.,* (2017). The maximum intra cluster distance was observed for cluster 7 followed by cluster 3. Maximum intra cluster value indicated maximum divergence among various genotypes within the cluster.A comparison of cluster mean for 12 characters under study revealed considerable genetic differences between the clusters regarding one or more characters.The Cluster V had the genotypes having high performance for seed yield regarding maximum characters (1) for harvest index. Hence, crosses have been made between genotypes belonging to high intra and inter-cluster distances to get good extents of transgrassive segregants.

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