RESEARCH PAPER

Genetic variability and trait association studies in Indian mustard (*Brassica juncea*)

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Abstract : Thirty six Indian mustard genotypes were evaluated to estimate variability, heritability and genetic advance in yield and yield components at Anand Agricultural University (Gujarat). The experiment was conducted using a Randomized Complete Block Design with three replications. Significant genotypic variability among the test genotypes was observed for all traits studied. Higher values of phenotypic co-efficients of variation and genotypic co-efficients of variation were observed for number of secondary branches per plant, number of siliqua per plant and yield per plant indicating the existence of higher magnitude of variability among the test genotypes for effective selection in respect of the above characters. Higher heritability estimates values were recorded for number of siliqua per plant, yield per plant, number of seeds per siliqua, length of main branch, days to 50 per cent flowering, 1000 seed weight, number of secondary branches, Siliqua length, protein content and plant height, indicating these traits were less influenced by environmental factors and selection for them is fairly easy. Higher values of expected genetic advance as per cent of mean was recorded for yield per plant, number of siliqua per plant, number of secondary branches, number of seeds per siliqua, length of main branch, siliqua length, and 1000 seed weight, indicating that selection would be more useful to improve these traits. High heritability values coupled with high genetic advance was observed in case of number of siliqua per plant, plant height, length of main branch and yield per plant, indicating that selection for these traits would be effective in Indian mustard improvement. Inter-character association studies were also conducted. The characters which showed positive significant genotypic and phenotypic correlation with yield were plant height, length of main branch and number of siliqua per plant. These characters are playing important role in indirect selection for yield.

Key Words : Heritability, Indian mustard, Genetic advance, Genotypic variation, Phenotypic variation, Tomato, Yield

INTRODUCTION

Indian mustard [*B. juncea* (L.) Czern and Coss] is one of the most important oil seed crops of the country and it occupies considerably large acreage among the Brassica group of oil seed crops. India stands first both in acreage and production of rapeseed and mustard in Asia. Rapeseed and mustard is cultivated in an area of 6.30 million hectares with a production of 7.20 million metric tonnes and with an average yield of 1143 kg/ha (Anonymous, 2012). In India, mustard and rape seed are being grown largely in states like, Uttar Pradesh, Rajasthan, Haryana, Assam, Gujarat, Punjab, West Bengal and Madhya Pradesh.

The genetic variability is of great value while planning an efficient breeding programme for the improvement in any crop species like Indian mustard. Germplasm, the sum of

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variability present in any crop species and relatives, is important for exploitation to fulfill most of the changing needs for developing improved crop varieties. Variability for economic traits must exist in the working germplasm for profitable exploitation following recombination breeding and selection. Genetic diversity plays an important role in plant breeding because hybrid between lines of diverse origin generally display a great heterosis than those between closely related strains which permits to select the genetically divergent plants to obtain the desirable recombination of the segregating generation.

MATERIAL AND METHODS

The experimental material comprising of thirty six genotypes of Indian mustard were grown in Randomized Block Design with three replications at the research farm of B.A. College of Agriculture (Anand Agricultural University), Anand during *Rabi* season of 2012-13. Each genotype was sown in a plot consisting of single row of 5m length in three replications with inter and intra row spacing of 30cm×10cm. Recommended package of practices for Indian mustard were followed to raise a healthy crop. Data were recorded on five randomly selected competitive plants of each genotype in all

the replications for thirteen characters *viz.,* days to 50 per cent flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, length of main branch (cm), number of siliqua per plant, siliqua length (cm), number of seeds per siliqua, 1000 seed weight (g) and seed yield per plant (g). Oil and protein content were assessed from field harvested seed samples.

Data collected for each trait were subjected to analysis of variance for Randomized Complete Block Design as suggested by Panse and Sukhatme (1957). To estimate the extent of variability, genotypic and phenotypic co-efficients of variability were estimated according to the method suggested by Burton (1952). The broad sense heritability and genetic advance as per cent of mean were calculated as proposed by Jonson *et al.* (1955). Phenotypic and genotypic correlation co-efficients for seed yield were calculated for each pair of traits as described by Singh and Choudhary (1977).

RESULTS AND DISCUSSION

The result on analysis of variance using Randomized Complete Block Design revealed that the genotypes exhibited highly significant differences for all the characters studied

Table 1 : Analysis of variances in Randomized Complete Block Design for thirteen characters in some Indian mustard genotypes

Sources	d.f.	DF	DM	PH	PB/P	SB/P	LMB	NS/P	SL	NS/S	TSW	Y/P	OC	PC
Replication	2	21.79**	27.84	366.20	1.39*	1.48	23.92	2626.10	0.06	0.28	0.01	9.79	0.06	0.57
Genotypes	36	68.25**	48.46**	1014.56**	1.80**	66.09**	656.96**	58469.48**	1.13**	10.67**	0.88**	264.56**	3.49*	7.64**
Error	70	3.66	11.61	144.49	0.37	4.19	26.24	1144.47	0.08	0.40	0.05	6.83	2.10	0.89
CV (%)		3.78	2.97	5.76	8.26	9.18	4.04	6.12	5.69	4.07	4.85	7.70	4.52	3.89

DF = Days to 50 % flowering, DM = Days to maturity, PH = Plant height (cm), PB/P = Primary branches/pl., SB/P = Secondary branches/pl., LMB = Length of main branch, NS/P = No. of siliquae/pl., SL = Siliqua length (cm), NS/S = No. of seeds/siliqua, TSW = Thousand seed weight (g), Y/P = Yield/pl.(g), OC = Oil content (%), PC = Protein content (%).
* and ** indicate significance of values at P=0.05 and 0.01, respectively

Table 2 : Estimates of mean, range of mean, genotypic (GCV) and phenotypic (PCV) co-efficient of variation, genotypic, phenotypic and environmental variances, Heritability in broad sense (h^2b), genetic advance (GA) and genetic advance as per cent of mean (GAM) for different characters of mustard genotypes

Sr. No.	Character	Range Min.	Range Max.	Mean	V_g	V_e	V_p	GCV	PCV	Hari.	GA	GAM
1.	Days to 50 % flowering	38.33	57.33	50.650	21.530	3.660	25.190	9.161	9.909	85.470	8.837	17.447
2.	Days to maturity	103.67	122.33	114.740	12.283	11.610	23.893	3.055	4.260	51.409	5.177	4.512
3.	Plant height (cm)	162.80	238.93	208.640	290.023	144.490	434.513	8.162	9.991	66.747	28.661	13.737
4.	No. of primary branches	5.00	8.83	7.320	0.477	0.370	0.847	9.432	12.570	56.299	1.067	14.579
5.	No. of secondary branches	8.30	29.00	22.310	20.633	4.190	24.823	20.360	22.332	83.121	8.531	38.239
6.	Length of main branch (cm)	95.67	152.60	126.800	210.240	26.240	236.480	11.435	12.128	88.904	28.163	22.211
7.	No. of siliqua per plant	264.53	970.57	552.480	19108.337	1144.470	20252.807	25.020	25.759	94.349	276.597	50.065
8.	Siliqua length (cm)	4.23	7.86	5.120	0.350	0.080	0.430	11.555	12.807	81.395	1.100	21.475
9.	No. of seeds per siliqua	12.33	20.60	15.370	3.423	0.400	3.823	12.038	12.722	89.538	3.607	23.465
10.	1000 seed weight (g)	3.68	5.66	4.700	0.277	0.050	0.327	11.191	12.161	84.694	0.997	21.217
11.	Yield per plant (g)	15.79	56.12	33.980	85.910	6.830	92.740	27.277	28.341	92.635	18.377	54.082
12.	Oil content (%)	30.73	34.37	32.070	0.463	2.100	2.563	2.123	4.992	18.075	0.596	1.859
13.	Protein content (%)	23.82	29.79	26.260	2.250	0.890	3.140	5.712	6.748	71.656	2.616	9.961

(Table 1). This suggested that adequate scope is available for selection of superior genotypes aimed at enhancing genetic yield potential of *Brassica juncea.*

Genetic parameters (Table 2) were studied to examine genetic worth of yield and yield contributing traits, based on genetic variability estimates *viz.,* mean, range, phenotypic co-efficient of variation (PCV), genotypic co-efficient of variation (GCV), heritability (h²), genetic advance (GA) and genetic advance as per cent of mean (GAM). It was observed that all the characters studied exhibited wide range of variation, with most pronounced range for most of traits except oil and protein content reflecting narrow range of variation. Higher estimates of phenotypic co-efficient of variation than genotypic co-efficient of variation for all the traits reflected influence of environmental factor on these traits with variable influence.

The estimates of phenotypic co-efficient of variation and genotypic co-efficient of variation were high for number of secondary branches, number of siliqua per plant and seed yield per plant, was earlier reported by Kardam and Singh (2005). It was interesting to note that the smallest differences were observed between PCV and GCV values of characters such as days to 50 per cent flowering, days to maturity, length of main branch (cm), number of siliqua per plant and number of seeds per siliqua, suggesting lesser influence of environmental factors on their expression. Relatively higher differences between PCV and GCV values were recorded with respect to characters like plant height, number of primary branches per plant, number of secondary branches per plant, siliqua length, 1000 seed weight, seed yield per plant, oil content and protein content. The results revealed that these characters were more influenced by environmental factors than rest of the characters

Table 3 : Genotypic and phenotypic correlation between various characters in Indian mustard (8 Parents)

Sr. No.	Characters		DF	DM	PH	PB/P	SB/P	LMB	NS/P	SL	NS/S	TSW	Y/P	OC	PC
1.	DF	rg	1	0.728*	0.529	0.687	0.442	0.084	0.666	-0.865**	-0.295	0.099	0.462	0.841**	0.490
		rp		0.544**	0.449*	0.531**	0.368	0.060	0.475*	-0.773**	-0.262	0.104	0.332	0.217	0.310
2.	DM	rg		1	0.549	0.601	0.698	0.454	0.257	-0.793*	-0.628	0.612	0.084	0.991**	0.317
		rp			0.335	0.480*	0.630**	0.342	0.261	-0.714**	-0.514*	0.507*	0.150	0.301	0.225
3.	PH	rg			1	0.953**	0.947**	0.848**	1.111**	-0.766*	-0.908**	0.926**	1.194**	-0.328	-0.320
		rp				0.484*	0.626**	0.593**	0.625**	-0.636**	-0.666**	0.453*	0.506*	-0.123	-0.230
4.	PB/P	rg				1	0.694	0.470	0.815*	-0.869**	-0.702	0.573	0.612	-0.147	-0.064
		rp					0.634**	0.395	0.726**	-0.658**	-0.484*	0.409*	0.538**	-0.089	-0.174
5.	SB/P	rg					1	0.884**	0.626	-0.736*	-0.961**	0.885*	0.674	0.385	-0.305
		rp						0.807**	0.647**	-0.687**	-0.853**	0.795**	0.654**	0.117	-0.320
6.	LMB	rg						1	0.471	-0.362	-0.924**	1.00**	0.735**	0.047	-0.269
		rp							0.421*	-0.314	-0.824**	0.882**	0.592**	-0.133	-0.223
7.	NS/P	rg							1	-0.792*	-0.674	0.433	0.891**	-0.625	-0.311
		rp								-0.708**	-0.561**	0.342	0.842**	-0.132	-0.276
8.	SL	rg								1	0.667	-0.449	-0.536	-0.382	-0.017
		rp									0.653**	-0.371	-0.429*	-0.071	0.028
9.	NS/S	rg									1	-0.961**	-0.720*	0.189	0.276
		rp										-0.825**	-0.523**	0.130	0.265
10.	TSW	rg										1	0.537	-0.129	-0.182
		rp											0.521**	-0.057	-0.194
11.	Y/P	rg											1	-0.539	-0.287
		rp												-0.046	-0.244
12.	OC	rg												1	0.398
		rp													0.272
13.	PC	rg													1
		rp													

DF = Days to 50 % flowering, DM = Days to maturity, PH = Plant height (cm), PB/P = Primary branches/pl., SB/P = Secondary branches/pl., LMB = Length of main branch, NS/P = No. of siliquae/pl., SL = Siliqua length (cm), NS/S = No. of seeds/siliqua, TSW = Thousand seed weight (g), Y/P = Yield/pl.(g), OC = Oil content (%), PC = Protein content (%).
* and ** indicate significance of values at P=0.05 and 0.01, respectively

studied.

The heritability estimate was more than 50 per cent for all the characters considered in this study (Table 2) except for oil content. Very high values of heritability estimates were recorded for characters like number of siliqua per plant (94.35 %), yield per plant (92.64 %), number of seeds per siliqua (89.54 %), length of main branch (88.90 %), days to 50 per cent flowering (85.47 %), 1000 seed weight (84.69 %), number of secondary branches (83.12 %) and siliqua length (81.40 %) indicating the possibility of improvement through selection.

The expected genetic advance as per cent of mean from selecting the top 5 per cent of the genotypes ranged from 1.86 per cent for oil content to 54.08 per cent for yield per plant (Table 2). This indicated that selecting the top 5 per cent of the base population would result an increase of 1.86 per cent for oil content to 54.08 per cent for yield per plant over the base population mean. Higher values of expected genetic advance as per cent of mean was recorded for yield per plant, number of siliqua per plant, no. of secondary branches, number of seeds per siliqua, length of main branch, siliqua length and 1000 seed weight, indicating that selection would be more useful to improve these traits.

Keeping in view that consideration of heritability and genetic advance together prove more useful in predicting the resultant effect of selection on phenotypic expression of character (Johnson et al., 1955) four characters were identified viz., number of siliqua per plant, plant height, length of main branch and yield per plant which have high heritability values coupled with high genetic advance. These characters reflected greater contribution of additive genetic component which may be exploited in selection in early segregating generations for the development of Indian mustard genotypes. The findings of Mahla et al. (2003), Singh (2004), Kumar and Mishra (2007) were in accordance with the present investigation. The result of this study indicated that selection for number of seeds per siliqua, days to 50 per cent flowering, 1000 seed weight, number of secondary branches, siliqua length and protein content would be less effective as compared to selection for the characters that showed high heritability and high genetic advance in this crop improvement programme.

The characters which showed positive and significant genotypic and phenotypic correlation with yield were plant height, length of main branch and number of siliqua per plant (Table 3). These characters are very important in indirect selection for yield. Similar observations were made by Shalini (1998), Somu (2001), Bikram Singh (2004), Dastidar and Patra (2004), Rai et al. (2005) and Tusar et al. (2006). In addition, traits like number of primary branches, number of secondary branches and test weight expressed positive significant correlation at phenotypic level only. The trait viz., number of seeds per siliqua was negatively correlated with yield at genotypic and phenotypic levels, whereas siliqua length was negatively correlated with yield at phenotypic level only. In case of oil content, the significantly and positively correlated characters were days to 50 per cent flowering and days to maturity. So, oil content will be more in late varieties of mustard. Except these two traits no association between oil content and any of the other characters was observed. In the present investigation dwarfness was considered as a desirable trait, but plant height was positively correlated with yield. In such cases optimum plant height is preferred. In some cases the value of exceeded unity. Such higher correlation co-efficient arises due to highly selective material or sampling error.

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