

Variability and character association studies in rapeseed-mustard (*Brassica sp.*)

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ABSTRACT

Fifty four genotypes of rapeseed-mustard were evaluated during rabi season 2009-10 at Uttar Banga Krishi Viswavidyalaya, Pundibari, Cooch Behar, West Bengal for nine yield and its attributing traits. The genotypes were grouped into ten clusters based on D^2 values. The intra-cluster distance was highest in cluster-X and lowest in cluster-IV. The maximum inter-cluster distance was found between clusters-I and IX, followed by the distance between the clusters-I and V, clusters-III and IX and clusters-IX and X. Seed yield plant⁻¹ contributed the maximum to total divergence and some other traits with appreciable contribution were plant height, primary branches plant⁻¹, seeds siliqua⁻¹ at top and seeds siliqua⁻¹ at bottom. Significant varietal differences were observed for all the characters except siliqua on main raceme. The GCV was less than PCV for all the characters indicating considerable influence of the environment on their expression. High PCV and GCV were observed for secondary branches plant⁻¹ and siliqua on branches whereas, the remaining characters expressed low to medium GCV. High heritability along with high genetic advance as percentage of mean were exhibited by plant height, seed yield, secondary branches plant⁻¹, siliqua on branches and seeds siliqua⁻¹ at top of the plant indicating their control by additive gene action and chances of further improvement by selection. Among the yield attributing traits siliqua on main raceme was significantly correlated with seed yield both at genotypic and phenotypic level whereas, seeds siliqua⁻¹ at bottom was positively associated with seed yield only at the genotypic level. The highest direct effect at genotypic level on seed yield was equally exhibited by seeds siliqua⁻¹ at middle and secondary branches plant⁻¹.

Key words: Genetic advance, heritability, mustard, rapeseed

Rapeseed and mustard (*Brassica spp.*) are the second important oilseed crop of the country after soybean and plays a significant role in the Indian oil economy by contributing about 27% to the total oilseed production. In oilseed brassicas, the yield of the seed is the most, if not the only, important character. Seed yield, however, is a very complex entity, influenced by several components. For a rational approach to the improvement of yield, it is essential to have some information on the nature of inheritance and association between different yield components and their relative contributions to yield. The most important components are: the number of branches, siliqua per plant and 100-seed weight. Kumar *et al.* (1984) suggested that selection of component characters rather than yield itself can help substantially to increase seed yield in *Brassica*.

Plant genetic resources have an important role to play here as they provide the desired diversity for the different traits. A study of this genetic diversity among a set of genotypes in a germplasm enables a plant breeder to choose suitable parents and plan an appropriate hybridization programme. D^2 statistics (Mahalanobis, 1936) is a powerful tool in estimating genetic divergence among groups based upon multiple growth characters, assessing relative characters and assessing relative contribution of different components to total divergence (Bhatt, 1973).

The correlation analysis measures the existence of relationship between various plant characters and determines the component on which selection can be based for improvement in seed yield. Correlation of seed yield and its attributing traits is reflected from direct effect of that trait which will

contribute directly to improve seed yield. The present study was conducted to determine the extent of variability in yield and its attributing traits and investigate the direct and indirect effect of various yield components on seed yield of brassica through path coefficient analysis, for identification of traits that would be helpful for selection in segregating generations for high seed yield.

MATERIALS AND METHODS

A study was undertaken at the Instructional Farm of Uttar Banga Krishi Viswavidyalaya, Pundibari, Cooch Behar, West Bengal during rabi 2009-10. The experimental material in the present study consisted of 54 genotypes of rapeseed-mustard which were sown in RBD with three replications having inter-row spacing of 30 cm and within row spacing of 10 cm between plant to plant. Detailed observations were recorded for nine biometrical characters, viz., plant height (cm), primary branches plant⁻¹, secondary branches plant⁻¹, number of siliqua on main raceme, number of siliqua on branches, number of seeds siliqua⁻¹ at top, number of seeds siliqua⁻¹ at middle, number of seeds siliqua⁻¹ at bottom of the plant and seed yield (g plant⁻¹). The data were statistically analyzed for each character by analysis of variance from which different variance components were estimated. Divergence was studied by multivariate analysis using Mahalanobis D^2 Statistics and the genotypes were grouped into different clusters by employing Euclidean method as described by Rao (1952). Heritability estimates (broad sense) were computed by the formula suggested by Hanson *et al.* (1956) and expected genetic advance as percentage of mean were estimated

by the method suggested by Johnson *et al.* (1955). The coefficient of genetic variation were estimated by the method described by Burton (1952) while path analysis was carried out using the genotypic correlation coefficients to know direct and indirect effects of the components on yield as suggested by Wright (1921) and illustrated by Dewey and Lu (1959).

RESULTS AND DISCUSSION

The analysis of variance revealed that the mustard genotypes differed significantly for all the traits except siliquae on main raceme (Table 1). Assessment of the phenotypic variability is a prerequisite of any breeding programme as to select desirable genotypes. A wide range of phenotypic variability was observed in almost all the characters studied. The estimates of range in variation, average mean performance, genotypic and phenotypic

coefficient of variation, heritability and genetic advance as percentage of mean are presented in table 1. The genotypic coefficient of variability measures and compares the range of genetic variability present in various characters. The genotypic coefficient of variation was less than that of phenotypic variation for all characters, indicating a considerable influence of environment on their expression. The phenotypic and genotypic coefficients of variation were high for secondary branches plant⁻¹ (54.03-37.39%) and siliqua on branches (45.36-31.38%) whereas the remaining characters exhibited low to medium genotypic coefficient of variation. Thus it may be concluded that high variability exists for seed yield contributing traits, offering opportunity for improvement through selection. Singh *et al.* (1997) recorded high PCV and GCV for characters like siliqua plant⁻¹ and seed yield.

Table 1: Genetic parameters for different characters of 54 genotypes of rapeseed-mustard

Characters	Mean	Range	Mean Square	SEm (±)	LSD (0.05)	CV	PCV	GCV	Heritability (Broad Sense)	GA as % of Mean
PH	121.96	74.6–180.6	2047.68**	4.58	12.84	6.50	22.07	21.09	0.91	41.52
PB/P	5.39	3.0–10.0	3.17**	0.61	1.70	19.48	24.83	15.39	0.38	19.66
SB/P	7.51	1.0–25.0	32.20**	1.69	4.74	39.00	54.03	37.39	0.48	53.30
Sili-M	39.01	0.0–59.0	55.08	3.90	-	17.33	17.91	4.53	0.06	2.36
Sili-B	139.72	13.0–332.0	7860.08**	26.42	74.07	32.75	45.36	31.38	0.48	44.72
Sd/S-T	12.69	2.0–41.0	36.84**	1.83	5.13	25.00	34.35	23.55	0.47	33.27
Sd/S-M	13.36	1.8–40.0	29.88**	2.23	6.25	28.89	33.38	16.71	0.25	17.24
Sd/S-B	14.25	2.2–36.0	35.26**	2.17	6.07	26.32	32.26	18.66	0.33	22.23
SdY/P	6.80	3.2–14.6	8.06**	0.68	1.91	17.31	27.93	21.92	0.62	35.44

*, ** Significant at 5% and at 1% probability level, respectively. PH=Plant height (cm), PB/P=Primary branches plant⁻¹, SB/P=Secondary branches/plant, Sili-M=Siliqua on main raceme, Sili-B=Siliqua on branches, Sd/S-T=Seeds siliqua⁻¹-Top, Sd/S-M=Seeds siliqua⁻¹-Middle, Sd/S-B=Seeds siliqua⁻¹-Bottom, SdY/P=Seed yield plant⁻¹ (g)

The high estimates of heritability are helpful as it enables the breeders to initiate the selection programme on phenotypic performance (Table 1). Heritability in broad sense includes both additive as well as epistatic gene effect, hence shall be reliable only if it is accompanied by high genetic advance (Singh *et al.*, 2009). In the present study, high heritability along with high genetic advance as percentage of mean was recorded for the characters like plant height, seed yield, secondary branches plant⁻¹, siliqua on branches and seed siliqua⁻¹ at top of the plant. Mandal and Khajuria (2000) reported high heritability coupled with high genetic advance for siliqua plant⁻¹, secondary branches plant⁻¹ and plant height in mustard.

The 54 genotypes were grouped into 10 clusters on the basis of D² values (Table 2). Cluster-I consisted of the largest number of genotypes (21) followed by cluster-III with ten genotypes, cluster-II with nine genotypes and clusters IV, V, VI, VII, VIII,

IX and X with two genotypes each. Maximum inter-cluster distance was observed between clusters I and IX (104.60) followed by the distance between clusters I and V (94.31), clusters III and IX (87.07) and clusters IX and X (85.70), thus indicating maximum divergence between these clusters (Table 3). Minimum inter-cluster distance was observed between clusters IV and VI (8.10) indicating minimum divergence between these two clusters. Maximum intra-cluster divergence was recorded in cluster X (60.75) and minimum in cluster IV each with two genotypes. Cluster IX exhibited maximum siliqua on main raceme and seed yield plant⁻¹ (Table 4). Cluster VIII exhibited highest secondary branches plant⁻¹ and siliqua on branches whereas, cluster X exhibited highest seeds siliqua⁻¹ at top, seeds siliqua⁻¹ at middle and seeds siliqua⁻¹ at bottom. The highest value for primary branches plant⁻¹ was exhibited by cluster I.

Table 2: Distribution of 54 genotypes of mustard in different groups

Cluster No.	Total No. of Genotypes in each cluster	Name of the genotypes
I	21	YSB-95-5B, YSB-95-9B, YSB-95-4B, YSB-2, YSB-95-6B, B-9, YSB-95-11B, YSB-95-1B, NC-1, YSB-95-10B, TCN-39, TWC-3, TCN-30, TWB-19/86, TWB-27, TCN-40, TCN-38, B-54, TCN-36, TWB-14/86, TWB-872/2
II	9	Rajasthan Local, Varuna, Rajendra Swarna Sarson, Pundibari Local, Seeta (B-85), PT-507, PT-303, Pusa Bahar, Rajasthan Local Selection-1
III	10	TS-29, ORTM-7-2, Pusa Bold, Parbati, Pundibari Local-1, Pundibari Local-2, Chaita Local, Natabadi Local, Pusa Barani, A ₂ -10
IV	2	A ₂ -11, A ₂ -12
V	2	Rajasthan Local Selection-2, Bhagirathi Selection-1
VI	2	A ₂ -14, S-3
VII	2	Pusa Jaikissan, Kranti
VIII	2	T-6342, S-10
IX	2	Bhagirathi Selection-1, A ₂ -9
X	2	YSB-95-4B-Selection-1, A ₂ -13

Table 3: Average intra (diagonal) and inter (off-diagonal) cluster D² values of 54 genotypes of rape-mustard

Cluster No.	I	II	III	IV	V	VI	VII	VIII	IX	X
I	21.32	43.87	32.06	39.62	94.31	37.93	76.94	50.14	104.60	42.17
II		35.13	44.46	22.26	43.36	29.53	38.07	44.14	52.10	44.22
III			32.68	31.97	80.56	26.76	59.56	33.27	87.07	47.19
IV				3.75	27.73	8.10	21.04	16.91	32.57	39.96
V					3.96	49.53	10.00	55.42	8.46	69.36
VI						4.90	33.85	15.09	54.50	44.45
VII							10.20	38.77	17.05	53.58
VIII								19.45	54.98	61.91
IX									19.68	85.70
X										60.75

Table 4: Cluster means for nine yield and its attributing traits of mustard

Cluster No.	Characters									
	PH	PB/P	SB/P	Sili-M	Sili-B	Sd/S-TSd/S-MSd/S-B	SdY/P			
I	104.74	6.29	6.48	38.84	120.83	12.86	14.22	15.32	6.65	
II	135.29	4.96	5.48	36.63	107.85	11.93	13.00	13.74	6.27	
III	112.20	5.03	10.13	39.97	158.47	12.73	12.97	13.50	7.02	
IV	140.97	5.17	8.67	36.50	188.83	11.17	11.00	13.17	6.34	
V	170.40	4.67	6.67	43.50	163.50	12.67	13.00	12.83	8.14	
VI	131.21	4.33	10.33	35.00	176.83	11.33	12.50	11.17	4.99	
VII	156.50	3.67	6.83	42.67	161.17	15.00	12.67	12.33	8.08	
VIII	129.53	4.83	14.17	38.83	255.17	9.67	12.33	13.33	8.04	
IX	170.20	4.50	8.50	45.67	190.67	8.67	10.33	11.83	8.63	
X	124.40	4.83	4.17	38.67	89.83	21.67	16.33	19.83	6.31	
Population mean	121.96	5.39	7.51	39.01	139.72	12.69	13.36	14.25	6.80	
Percent Contribution to D²	13.00	10.90	2.66	1.47	1.61	10.55	5.17	13.84	40.81	

*, ** Significant at 5% and at 1% probability level, respectively. PH=Plant height (cm), PB/P=Primary branches plant⁻¹, SB/P=Secondary branches/plant, Sili-M=Siliqua on main raceme, Sili-B=Siliqua on branches, Sd/S-T=Seeds siliqua⁻¹-Top, Sd/S-M=Seeds siliqua⁻¹-Middle, Sd/S-B=Seeds siliqua⁻¹-Bottom, SdY/P=Seed yield plant⁻¹ (g)

Table 5: Genotypic and phenotypic correlation between yield and its attributing traits in rape-mustard

Characters		PB/P	SB/P	Sili-M	Sili-B	Sd/S-T	Sd/S-M	Sd/S-B	SdY/P
PH	G	-0.67**	0.07	0.45**	0.38**	-0.26*	-0.30*	-0.36**	0.20
	P	-0.39**	0.07	0.13	0.29*	-0.15	-0.12	-0.19	0.13
PB/P	G		-0.34**	-0.28*	-0.51**	0.15	0.39**	0.58**	0.11
	P		0.05	0.25*	0.14	0.09	0.08	0.12	0.13
SB/P	G			0.06	0.87**	-0.42**	-0.59**	-0.51**	0.22
	P			0.30*	0.75**	-0.20*	-0.21*	-0.22	0.19
Sili-M	G				0.44**	-0.36**	-0.28*	-0.18	0.95**
	P				0.41**	-0.09	-0.13	-0.11	0.23*
Sili-B	G					-0.52**	-0.68**	-0.58**	0.18
	P					-0.24*	-0.32**	-0.27*	0.22
Sd/S-T	G						0.97**	0.55**	-0.01
	P						0.56**	0.44**	-0.02
Sd/S-M	G							0.69**	0.07
	P							0.62**	-0.01
Sd/S-B	G								0.31*
	P								0.20

Table 6: Direct (diagonal) and indirect effects of different attributing traits on seed yield in rape-mustard

Characters		PH	PB/P	SB/P	Sili-M	Sili-B	Sd/S-T	Sd/S-M	Sd/S-B	Correlation coefficient with SdY/P
PH	G	0.309	-0.208	0.021	0.138	0.117	-0.081	-0.093	-0.111	0.20
	P	0.196	-0.076	0.013	0.025	0.057	-0.030	-0.023	-0.037	0.13
PB/P	G	0.515	-0.764	0.256	0.213	0.390	-0.117	-0.295	-0.444	0.11
	P	-0.052	0.133	0.006	0.033	0.018	0.012	0.011	0.016	0.13
SB/P	G	0.262	-1.272	3.795	0.246	3.319	-1.604	-2.241	-1.947	0.22
	P	0.011	0.007	0.157	0.047	0.118	-0.032	-0.033	-0.034	0.19
Sili-M	G	0.804	-0.503	0.117	1.805	0.801	-0.658	-0.510	-0.333	0.95**
	P	0.016	0.032	0.038	0.129	0.053	-0.011	-0.017	-0.014	0.23*
Sili-B	G	-1.252	1.682	-2.884	-1.463	-3.297	1.700	2.235	1.900	0.18
	P	0.006	0.003	0.017	0.009	0.022	-0.005	-0.007	-0.006	0.22
Sd/S-T	G	0.819	-0.479	1.321	1.140	1.612	-3.125	-3.042	-1.710	-0.01
	P	0.004	-0.002	0.005	0.002	0.006	-0.024	-0.014	-0.011	-0.02
Sd/S-M	G	-1.147	1.468	-2.246	-1.074	-2.578	3.702	3.803	2.643	0.07
	P	0.020	-0.014	0.036	0.022	0.054	-0.096	-0.171	-0.107	-0.01
Sd/S-B	G	-0.112	0.181	-0.160	-0.058	-0.180	0.171	0.217	0.312	0.31*
	P	-0.073	0.047	-0.084	-0.042	-0.107	0.170	0.242	0.389	0.20

A comparison between cluster means for different characters revealed that the desirable characters (highest mean values) were distributed mainly in clusters VIII, IX and X with the exception being plant height and primary branches plant⁻¹, which were found to be highest in clusters I and V, respectively. The divergence between the clusters VIII and IX (54.98) and clusters VIII and X (61.91) was quite low, while on the other hand the divergence between the clusters IX and X (85.70) was appreciable though less than the most divergent ones. Also the character seed yield plant⁻¹ contributed maximum (40.81%) to the genetic divergence and cluster IX had exhibited the maximum for this trait. Therefore, breeding between the genotypes from clusters IX and X would give segregates with high seed yield. This is evidenced by the findings of Sarawgi *et al.* (1998) who were able to identify a few

elite genotypes from some of the clusters by considering the cluster mean and inter cluster distance. Thus from the cluster analysis the genotypes Bhagirathi Selection-2 and A₂-9 in cluster IX and YSB-95-4B-Selection-1 and A₂-13 in cluster X were found to be distinct with the desirable characteristics and may be incorporated in breeding programs to improve seed yield in rapeseed and mustard.

The phenotypic as well as genotypic correlations between different pairs of traits are presented in Table 5. In general the values of correlation at genotypic level were higher than phenotypic correlations. This indicated little role of environment in the expression of genetic relationship on the phenotypes. In the present study siliqua on main raceme was positively and significantly correlated with seed yield plant⁻¹ at both genotypic and phenotypic level and seeds siliqua⁻¹ at bottom

showed significantly positive correlation with seed yield only at genotypic level.

The direct and indirect effects of different characters were worked out and are presented in Table 6. Among the characters studied, at genotypic level, number of seeds siliqua⁻¹ at middle exerted maximum direct effect on seed yield followed by secondary branches plant⁻¹ and siliqua on main raceme and at phenotypic level number of seeds siliqua⁻¹ at bottom exerted maximum direct effect on seed yield followed by plant height and secondary branches plant⁻¹. Thus, it may be concluded that characters such as secondary branches plant⁻¹, number of seeds siliqua⁻¹ at bottom and siliqua on main raceme deserve due attention while deciding selection strategy for improvement of seed yield. This is agreement in the findings of Somu (2001) and Srivastava and Singh (2002).

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REFERENCES

- Bhatt, G.M. 1973. Comparison of various methods of selecting parents for hybridization in common wheat. *Aust. J. Agri. Res.*, **24**: 457-64.
- Burton, G. W. 1952. Quantitative inheritance in grasses. *Proce. 6th Int. Cong.*, **1**: 277-83.
- Dewey, O. R. and Lu, K. H. 1959. A correlation and path coefficient analysis of components of crested wheat grass and production. *Indian J. Agron.*, **57**: 515-18.
- Hanson, C. H., Robinson, H. F. and Comstock, R. E. 1956. Biometric studies of yield in segregating population of Korean leopedeza. *Agron. J.*, **46**: 286-92.
- Johnson, H. W., Robinson, H. F. and Comstock, R. E. 1955. Estimates of genetic and environmental variability in soyabean. *Agron. J.*, **47**: 314-18.
- Kumar, P., Yadav, T. P. and Yadav, A. K. 1984. Association of seed yield and its component traits in the F₂ generation of Indian mustard. *Indian J. Agric. Sci.*, **54**: 604-07.
- Mahalanobis, P. C. 1936. On the generalized distance in statistics. *Proc. Nat. Inst. Sci. India*, **2**: 49-55.
- Mondal, S. K. and Khajuria, M. R. 2000. Genetic analysis for yield attributes in mustard. *Env. Ecol.*, **18**: 15-19.
- Panse, V. G. and Sukhatme, P. V. 1961. *Statistical Methods for Agricultural Workers*. ICAR, New Delhi.
- Rao, C. R. 1952. *Advance Statistical Methods in Biometrical Research*. John Wiley and Sons Inc., New York, p. 383
- Sarawgi, A. K., Rastogi, N. K. and Soni, D. K. 1998. Genetic diversity for grain quality parameters in traditional rice accessions from Madhya Pradesh. *Trop. Agric. Res. Extn.*, **1**: 103-06.
- Singh, D., Singh, M. and Kumar, K. 2009. Manifestation of genetic variability and correlation studies in seedling tree of walnut (*Juglans regia* L.). *Adv. Hort. Sci.*, **23**: 29-32.
- Singh, M., Singh, G. and Singh, M. 1997. Correlation and path analysis in Indian mustard (*Brassica juncea* L.) under mid hills of sikkim. *J. Hill Res.*, **10**: 10-12.
- Somu, G. 2001. Genetic divergence in Indian mustard (*Brassica juncea* L. Czern and Coss.). *M. Sc. (Agri.) Thesis*, Univ. Agric. Sci., Bangalore (India).
- Srivastava, M. K. and Singh, B. P. 2002. Correlation and path analysis in Indian mustard (*Brassica juncea* L. Czern and Coss.). *Crop Res.*, **23**: 517-21.
- Wright, S. 1921. Correlation and causation. *J. Agric. Res.*, **20**: 557-85.