ANALYSIS IN GENOTYPES OF INDIAN MUSTARD (*Brassica juncea L. czern & coss*)

GREESH KUMAR SINGH*, YOGESH PANDEY AND LOKENDRA SINGH

Department of Genetics and Plant Breeding,
C.S. Azad .Univ. of Ag. & Tech., Kanpur 208 002, U.P., INDIA
e-mail: Greeshsingh88@gmail.com

ABSTRACT

The present investigation comprised of seven strains / varieties and their twenty one F_1 crosses developed in a diallel mating design was carried out for evaluation of eleven characters viz. Days to flowering, days to maturity, plant height, length of main raceme, number of siliquae/ plant, number of seeds/ siliqua, number of primary branches/ plant, number of secondary branches/ plant, 1000 seed weight, oil content and seed yield/ plant. Analysis of variance revealed significant differences among the genotypes for all the characters. In general, PCV was higher than GCV for almost all the characters. High heritability coupled with genetic advance over mean was observed for test weight. In general, genotypic correlation coefficients were higher than phenotypic ones for all the traits, indicating environmental influence on the expression of these traits. Seed yield per plant had positive correlation with number of siliquae per plant, test weight while seed yield per plant had negative association with number of primary branches per plant both at genotypic and phenotypic levels. Highest direct effect was obtained by number of secondary branches per plant followed by day to maturity, test weight and oil content on seed yield.

INTRODUCTION

The genetic variability is of great value while planning an efficient breeding programme for the improvement in any crop species like Indian mustard. Indian mustard (*Brassica juncea*) belongs to the family cruciferae. Cytologically, *Brassica juncea* is an amphidiploid (2n = 36) derived from interspecific cross of *Brassica nigra* (2n = 16) and *Brassica campestris* (2n = 20). Rapeseed-mustard productivity in the country is much lower [1145-kg /ha] than the World's average (1451kg/ha). Indian mustard [*Brassica Juncea* (L)] is the second largest oil seed crop in India after groundnut, which received great attention of breeders for its genetic improvement, as it has greater production potential under varying environment. 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 (Singh, 1983) which permits to select the genetically divergent plants to obtain the desirable recombination of the segregating generation. Multivariate analysis is a useful tool in quantifying the degree of divergence between biological population at genotypic level and to assess relative contribution of different components to the total divergence both at intra- and intercluster levels (Jatasra and Parada, 1978; Zahan *et al.*, 2008). Therefore, the present study was undertaken to identify divergent parents for hybridization program, which would provide superior segregates in mustard genotypes.

MATERIALS AND METHODS

The experimental material comprising seven morphologically diverse parents/strains viz, Maya, Basanti, RLM198, Urvashi, Pusa-Jaikisan, Arawali, Pusa-Basant and their twenty one cross combinations developed using half diallel mating design during Rabi season 2012-13. Twenty one hybrids along with seven parents were evaluated for eleven characters in a Randomized complete Block Design with three replicatins during Rabi 2012-13 at Oilseed Research Farm, Kalyanpur of C.S.Azad University of Agriculture and Technology, Kanpur. Each treatment was planted in a single row of five meter length. Row to row and plant to plant spacing was kept of 45 x 20 cm. All recommended agronomic practices were adopted for raising a good crop. The observations were recorded on five randomely taken plants from each plot replication wise for characters, viz., days to flowering, days to maturity, plant height, primary branches/ plant, secondary branches/ plant, length of main raceme, siliquae/ plant, seeds/ siliqua, 1000-seed weight, seed yield/ plant and oil content in seeds which was estimated by NMR (New Port Analyzer MK 111A). Test of significance for each character were analyzed as per methodology advocated by Panse and Sukhatme (1961). Phenotypic coefficient of variation (PCV) and Genotypic coefficient of variation (GCV) were calculated by the formula given by Burton (1952), heritability in broad sense (h2) by Burton and De Vane (1953) and genetic advance *i.e.* the expected genetic gain were calculated by using the procedure proposed by Johnson *et al*. (1955) and Robinson (1963) correlations and path coefficient analysis were computed to determine the inter relationship among these traits and their

direct and indirect contribution to seed yield as suggested by Johnson *et al.* (1955) and Dewey and Lu (1959).

RESULTS AND DISCUSSION

Analysis of variance revealed that treatments/genotypes had considerable amount of genetic variation for all the characters studied. Phenotypic coefficient of variation values were slightly higher than genotypic coefficient of variation values for all the traits except number of primary branches per plant (Table-1) which indicated a little bit influence of environment on these traits expression Highest PCV and GCV was observed for number of secondary branches per plant followed by test weight, hence selection for these traits may be effective. High values of heritability coupled with high genetic advance in parent over mean were found for test weight while estimates of moderate heritability and while rest of the genetic advance were found for number of seeds per siliqua, was earlier reported by Kardam and Singh (2005)

Heritability

The estimates of heritability (narrow sense) were computed for eleven characters. As per classification high heritability were recorded for plant height (81.86), test weight (46.26), oil content (46.02), length of main raceme (43.29), days to flowering (41.81), and days to maturity (40.50). Medium heritability were recorded for seed yield per plant (22.71),

number of primary branches per plant (15.41), number of secondary branches per plant (19.78), number of siliquae per plant (19.24) and number of seed per siliqua (16.69). The findings of Singh (2004), Kumar and Mishra (2007), Kumar *et al.* (2013) were in accordance with the present investigation.

Genetic Advance:

The genetic advance in percent over mean for all the characters ranged from 1.81 to 62.52. Highest value of genetic advance over mean was found for number of secondary branches per plant (62.52) followed by test weight (33.81), number of seeds per siliqua (21.24), days to maturity (9.92), plant height (9.85), length of main raceme (8.47), seed yield per plant (6.72), days to flowering (6.10), oil content (3.58) and number of primary branches per plant (3.61). Minimum value of genetic advance was observed for number of siliqua per plant. Similar Results were also reported by Kardam and Singh (2005), Kumar *et al.* (2013) and Vermai *et al.* (2016).

Correlation coefficient:

Correlation coefficients for various pairs of characters are presented in Table-2. Perusal of table revealed that in general genotypic correlations were higher as compared to phenotypic correlations indicating much influence of environmental factors on the expression of these characters. Testing of significance of correlation coefficients was done at phenotypic level and the values of genotype correlation equal to as higher than significant values of phenotypic correlation were

Table 1: Estimates of mean, range, phenotypic and genotypic coefficient of variation, heritability and genetic advance for eleven characters in Indian mustard

characters	Mean	Range	PCV	GCV	Heritability (% n.s.)	Genetic advance	% Genetic advance
Days to flowering	75.57	71.00-79.00	3.72	3.32	41.81	4.52	6.1
Days to maturity	133.81	121.67-155.00	5.07	4.94	40.5	12.73	9.92
Plant height	163.65	146.00-181.30	4.68	4.61	81.86	16.12	9.85
Length of main raceme	78.71	69.60-82.60	4.58	4.34	43.29	6.88	8.47
Number of siliquae/ plant	311.42	258.00-330.00	9.45	9	19.24	5.64	1.81
Number of seed/ siliqua	12.66	11.00-14.67	12.29	10.79	16.69	2.69	21.24
Number of primary branches/ plant	7.47	7.00-8.00	9.58	11.67	15.41	0.27	3.61
Number of secondary branches/ plant	16.09	10.33-21.33	28.08	27.48	19.78	10.06	62.52
Test weight	4.82	3.00-6.20	17.47	16.45	46.26	1.63	33.81
Oil content(%)	40.15	38.97-41.67	2.2	1.95	46.02	1.46	3.58
Seed yield/plant	25.71	23.00-27.67	8.44	5.24	22.71	1.78	6.72

Table 2: Genotypic (lower diagonal) and phenotypic (upper diagonal) correlation coefficient among 11 attributes in 7 x 7 diallel cross in Indian mustard.

Characters	Days to flowering	Days to maturity	Plant height (cm)	Length of main raceme	Number of siliquae /plant	Number of seeds /siliqua	Number of primary branches / plant	Number of secondary branches / plant	1000-Seed weight (g)	Oil content	Seed yield/ plant
Days to flowering	Rgrp	0.273*	0.057	-o.341**	0.126	-0.142	0.006	0.117	0.015	-0.341**	-0.014
Days to maturity	0.223	rgrp	0.057	-0.15	0.164	-0.091	0.252*	0.221	-0.025	-0.342**	0.148
Plant height(cm)	0.269*	0.319*	Rgrp	0.101	0.058	-0.088	-0.031	-0.181	-0.026	-0.146	0.193
Length of main raceme	-0.112	0.073	0.353**	rgrp	0.089	-0.133	-0.019	-0.126	-0.141	0.19	0.195
Number of siliquae /plant	0.332**	0..412**	-0.111	0.60**	rgrp	-0.224	0.257*	-0.036	-0.205	-0.192	0.409**
Number of seeds /siliqua	0.187	0.491**	0.055	0.818**	0.484**	rgrp	-0.169	-0.124	0.115	0.095	0.2
Number of primary branches/ plant	-0.570**	0.167	0.781**	-1.779**	1.500**	-1.308**	rgrp	0.94	-0.142	0.001	-0.15
Number of secondary branchs/plant	0.152	0.269*	0.428**	0.624**	0.414**	-1.295**	0.967**	rgrp	-0.039	-0.262*	0.583**
1000-Seed weight(g)	-0.337**	0.06	0.360**	0.133	0.19	0.21	0.526**	0.578**	rgrp	0.255**	0.370**
Oil content	-0.371**	-0.489**	0.194	-o.005	-0.077	-0.04	0.306**	0.282*	0.358**	rgrp	0.173
Seed yield / plant (g)	0.188	0.223	0.319**	0.353**	0.609**	0.484**	-1. 308**	0.967**	0.578**	0.358**	Rgrp

Table 3: Path Coefficient analysis for Eleven characters towards Seed Yield in Indian Mustard

Characters	Direction	Days to flowering	Days to maturity	Plant height (cm)	Length of main raceme	Number of siliquae /plant	Number of seeds /siliqua	Number of primary branches /plant	Number of secondary branches /Plant	1000-seed weight (gm)	Oil content	Seed yield as correlated
Days to flowering	P	-0.333	0.145	0.003	-0.002	0.137	-0.03	0.001	0.067	0.013	-0.015	-0.014
	G	-0.226	0.174	0.015	0.006	0.033	0.002	-0.007	0.211	0.012	-0.032	0.188**
Days to maturity	P	-0.163	0.295	0.006	-0.002	0.101	-0.014	0.001	0.044	-0.092	-0.027	0.148
	G	-0.12	0.328	0.028	0.014	0.022	0.001	-0.02	0.125	-0.079	-0.075	0.223**
Plant height (cm)	P	-0.044	0.077	0.022	0.001	0.123	-0.039	-0.001	0.072	0.016	-0.033	0.193*
	G	-0.033	0.088	0.103	-0.009	0.028	0.002	0.006	0.22	0.014	-0.099	0.319**
Length of main raceme	P	0.031	-0.034	0.002	0.018	-0.029	-0.002	-0.006	0.11	0.091	0.014	0.195*
	G	0.012	-0.037	0.007	-0.124	-0.007	0	0.028	0.351	0.084	0.039	0.353**
Number of siliquae/ plant	P	-0.144	0.094	0.008	-0.002	0.315	-0.061	0.007	0.164	0.029	-0.002	0.409**
	G	-0.111	0.109	0.042	0.014	0.067	0.003	-0.056	0.511	0.031	-0.001	0.609**
Number of seeds/ siliqua	P	-0.106	0.044	0.009	0	0.205	-0.093	-0.005	0.097	0.052	-0.003	0.200*
	G	-0.101	0.061	0.05	-0.007	0.055	0.004	0.053	0.339	0.044	-0.016	0.484**
Number of primary branches/ plant	P	0.006	-0.003	0	0.002	-0.033	-0.007	-0.069	-0.038	-0.007	0	-0.15
	G	0.043	-0.187	0.017	-0.097	-0.106	0.005	0.035	-1.06	0.049	-0.008	-1.308
Number of secondary branches/ plant	P	-0.079	0.046	0.005	0.007	0.182	-0.032	0.009	0.283	0.143	0.018	0.583**
	G	-0.058	0.05	0.028	-0.053	0.042	0.001	-0.046	0.819	0.123	0.062	0.967**
1000-seed weight (gm)	P	-0.015	-0.092	0.001	0.005	0.031	-0.016	0.002	0.137	0.296	0.021	0.370**
	G	-0.11	-0.11	0.006	-0.045	0.009	0.001	0.007	0.431	0.233	0.057	0.578**
Oil content	P	0.065	-0.105	-0.01	0.003	-0.01	0.004	0	0.068	0.082	0.075	0.173*
	G	0.036	-0.122	-0.05	-0.024	0	0	-0.001	0.251	0.066	0.203	0.358**

Residual P = 0.5357 ,G = -0.0155 ,* , ** Significant 5 and 1 Percent levels, respectively.

considered to be significant. At phenotypic level most of the values were negative. So association between characters has been described at genotypic level. Seed yield per plant had positive and significant association with plant height length of main raceme, number of siliquae per plant, number of seeds per siliquae, number of secondary branches per plant, 1000 seed weight and oil content. At phenotypic level seed yield showed positive and non-significant correlation with days to maturity and number of siliquae per plant. 1000 seed weight and number of secondary branches per plant were positively and significantly correlated with plant height, number of primary branches per plant and oil content at genotypic level suggested by Singh et al. (1996), Khayat et al. (2012) and Hasan et al. (2014). Number of primary branches was positively correlated with number of siliquae per plant and plant height. Bolder seed size was found to be associated with higher oil extraction was also reported by earlier studies of Shekhawat et al. (2014).

PATH COEFFICIENT

Path coefficient analysis has been given in Table-3. Perusal of table-3 revealed that number of secondary branches per plant exerted highest positive (0.819) direct effect followed by days to maturity (0.328), 1000-seed weight (0.233) and oil content (0.203) on seed yield per plant at genotypic level reported by singh and singh (1997). These characters also exhibited higher positive direct effect on seed yield at phenotype level. Days to flowering exerted negative direct on seed yield at both genotypic and phenotypic levels. Length of main raceme, number of siliquae, number of seeds per siliqua, 1000-seed and oil content showed higher indirect effects on seed yield through number of secondary branches per plant. Number of secondary branches per plant and oil content showed higher indirect effect through 1000-seed weight in comparison to other traits on seed yield. Almost all these traits had positive relationship among themselves as well as with seed yield. Hence, it could be concluded that due emphasis should be given on one or more of these traits during selection process.

Importances of these traits in the form of major yield components reflected through inter relationship analysis as well as path analysis. The similar results were also obtained by Gangapur et al. (2009), Singh and Singh (2010), Hasan et al. (2014), Mekonnen et al. (2014) and Rout et al. (2018).

REFERENCES

Burton, G. W. 1952. Quantitative inheritance of grasses. Proc 6th Int, *Grassland Congress*. **1:** 277-283.

Burton, G. W. and De Vane, E. H. 1953. Estimating heritability in all fescue (Festuca arundinacea) from replicated clonal material. *Agron. J.* **45:** 478-481.

Dewey, O. R. and Lu, K. H. 1959. Correlation and path coefficient analysis of component of crested wheat grass seed production. *J Agron.* **57:** 515-518.

Gangapur, D. R., Prakash, B. G., Salimath, P. M., Ravikumar, R. L. and Rao, M. S. L. 2009. Correlation and path analysis in Indian mustard [Brassica juncea (L.) Czern and Coss]. *Karnataka J. Agric. Sci.* **22(5):** 971-97.

Hasan, Ejaz-Ul, Mustafa, H. S. B., Bibi, T. and Mahmood, T. 2014. Genetic variability, correlation and path analysis in advanced lines of rapeseed (Brassica napus L.) for yield components. *Cercetari Agronomice in Moldova*. **97(1):** 71-79.

Jatasra, D. S. and R. S. Parada. 1978. Genetic divergence in wheat under different environmental conditions. *Cereal Res. Comm.* **6:** 307-317.

Johnson, H. W., Robinson, H. F. and Comstock, R. E. 1955. Genotypic and phenotypic correlations in soybean and their implications in selection. *Agron. J.* **47:** 477-483.

Kardam, D. K. and Singh, V. V. 2005. Correlation and path analysis in Indian mustard grown under rainfed condition. *J. Spices and Aromatic crops*. **14(1):** 56-60.

Khayat, M., Lack, S. and Karami, H. 2012. Correlation and path analysis of traits affecting grain yield of canola (Brassica napus L.) varieties. *J. Basic. Appl. Sci. Res.* **2(6):** 5555- 5562.

Kumar, B., Pandey, A. and Singh, S. K. 2013. Genetic diversity for

agro-morphological and oil quality traits in Indian mustard (B.juncea L. CZERN& COSS). *The Bioscan.* **8(3):**771-775.

Kumar, S. and Misra M. N. 2007. Study on genetic variability, heritability and genetic advance in population in Indian mustard (Brassica juncea L. Czern and Coss). *Int. J. Plant Sci.* **2(1):** 188-190.

Mahla, H. R., Jambhulkar, S. J., Yadav, D. K. and Sharma, R. 2003. Genetic variability, correlation and path analysis in Indian mustard (Brassica juncea L. Czern and Coss). *Indian J. Gen. Plant Breed.* **63:** 171-172.

Mekonnen, T. W., Wakjira, A. and Genet, T. 2014. Correlation and path coefficient analysis among yield component traits of Ethiopian mustard (Brassica carinata a. Brun) at Adet, Northwestern, Ethiopia. *J. Plant Sci..* **2(2):** 89-96.

Panse,V.G. and Shukhatme,P.V. 1961. Statistical methods for agriculture workers. 2nd Edn ICAR, New Delhi p.361.

Robinson, H. F. 1963. Statistical Genetics and Plant Breeding NAS-NRC. Washington Publ. **982:** 429-438

Shekhawat, N., Jadeja, G.C., Singh, J. and Shekhawat, R.S. 2014. Character association studies among yield and its component characters in Indian mustard (*B.juncea* L. Czern & Coss). *The Bioscan.*

9(2):685-688.

Sanghamitra Rout, S. A. Kerkhi and Charupriya Chauhan. 2018. Character Association and Path Analysis among Yield Components in Indian Mustard (*Brassica juncea* (L.) Czern and Coss). *Int.J.Curr.Microbiol.App.Sci.* **7(01):** 50-55.

Singh, B. 2004. Character association and path analysis under dry land condition in Indian mustard (*Brassica juncea* L. Czern and Coss). Cruciferae Newsletter. **25:** 99-100.

Singh, J. N., Yadav, M. C. and Sheik, L. A. 1996. Genetical studies for yield and oil content in *Brassica juncea. J. Genet.* **56:** 299-304.

Singh, M. and Singh, G. 1997. Correlation and path analysis in Indian mustard (*B. juncea* L.) under mid hills of Sikkim. *J Hill Res.* (India), **10(1):**10-12.

Singh, R. S., Chauhan, R. A. and Singh, O. N. 1983. Heterobilities in relation to *Per se* performance and effect of general combining ability in rai, Pl. Breeding Abst.**54:** 526-1984.

Vermai, U., Thakral, N. K. and Neeru. 2016. Genetic diversity analysis in Indian mustard (*Brassica juncea* (L.) Czern and Coss). I*nternational J. Applied Mathematics & Statistical Sciences (IJAMSS).* **6(2):** 2319-3980.

Zahan, M. I., Bhuiyan, M. S. R. and Hossain, M. S. 2008. Genetic divergence in Oleiferous Brassica species. *J. Sher-e-Bangla Agric. Univ.* **2(1):**1-6.