

Genetic variability, correlation and path analysis in Indian mustard under late sown condition

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ABSTRACT

The present study was carried out to study the genetic variability, correlation and path analysis for eleven quantitative traits in 32 treatments of Indian mustard obtained by crossing seven diverse parents in half diallel fashion including parents along with four checks under late sown condition. Analyses of variance were observed significant for all the characters under study. The high genotypic and high phenotypic coefficients of variation were observed for seed yield per plant and seed yield per plot. High heritability coupled with high genetic advance was found for seed yield per plot, seed yield per plant, number of siliqua per plant, and test weight, suggesting due importance of these traits for selection in breeding program. The phenotypic correlation studies revealed that seed yield per plant exhibited significant positive correlation with plant height, number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, siliqua length, seeds per siliqua and test weight. The results of path coefficient analysis revealed that characters like days to 50% flowering, plant height, number of secondary branches per plant, siliqua length, number of siliqua per plant and test weight had direct positive effects on seed yield per plant which suggests that direct selection based on these characters can be utilized to enhance the yield ability of Indian mustard.

Keywords: Heritability, Genetic advance, Correlation, Path analysis, Indian mustard

INTRODUCTION

Indian mustard (*Brassica juncea* L. Czern and Coss) popularly known as *Rai*, *Raya* and *Laha* occupies a premier position among rapeseed and mustard crops with an acreage of more than 80% in northern parts of India. It is a model dicot crop of family brassicaceae having chromosome number $2n=4x=36$. It is generally considered as self-pollinated crop but 7.5 to 30% of cross-pollination was reported by various workers under natural field condition (Abraham, 1994; Rakow and Woods, 1987). It is an amphidiploid crop having AABB genome, originated naturally during the process of evolution by the interspecific cross of *Brassica rapa* ($2n=2x=20$, AA) and (*Brassica nigra* ($2n=2x=16$, BB)). Although Indian mustard is an important oilseed crops due to its huge domestic and industrial use, there is significant decrease in the production and acceptance among the farmer for cultivation due to various reasons. But, the demand of edible oils is increasing very rapidly with increasing population which ultimately leads to its high price. In northern plains. the cultivation of *rabi* crops is delayed

mainly to irregular weather patterns like rainfall and floods in the middle months of the *khari* season. Delayed sowing of *rabi* crops leads to decline in the productivity of *rabi* crops which warrants the need for development of new varieties suitable for late sown conditions and efficient selection methods.

Yield is a complex quantitative character which primarily depends on the various yield attributing traits, which necessitates the study of correlated response between yield and their component traits for designing the selection criteria under crop improvement. In general, for selection of any desirable traits breeder relies on the phenotypic value which itself is governed by two components; genotype and environment, heritable and non-heritable components respectively. Thus, numerous yield components and their relationships with each other must be understood. This is because if selection were based on some factors that were less effected by the environment, it would be more effective. It is widely known that correlation frequently falls short of the researcher's goals since it is unable to identify the characters that have an indirect impact on seed yield. However. Dependence on

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only correlation outcomes could be misleading due to mutual cancellation of component traits and specially when the association of these characters become complex, in such case path coefficient analysis given by Sewall Wright (1921) put forward to find out the direct and indirect causes of association among the different variables. So, correlation as well as path coefficient analysis is important tools for plant breeder to enhance the production of Indian mustard. Therefore, the present investigation was undertaken to assess the genetic variability, correlation coefficient and path analysis in order to improve the grain yield potential of Indian mustard under late sown condition.

MATERIAL AND METHODS

A set of 32 Indian mustard lines which includes 21 F_1 , seven parent and 4 checks (Maurya *et al.*; 2012) namely Rajendra Suflam (LC), Kranti (NC), NRCHB-101 (ZC) and CS-56 (LR) were planted at Bihar Agricultural University farm, Sabour, Bhagalpur, Bihar in three replication following randomized block design (RBD). The 21 F_1 were obtained after crossing seven diverse parents *viz.*; RAURD-14-18, Varuna, JD-6, Kranti, RGN-73, PM-25 and RAURD-214 in half diallel fashion. The crop was raised during the *Rabi* season in 2020 following recommended package and practices needed for a healthy crop. Observations were recorded for eleven quantitative traits *viz.*, days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, siliqua length (cm), seeds per siliqua and test weight (g), seed yield per plant

(g) and seed yield per plot (g). Data for days to 50% flowering, days to maturity and seed yield per plot were taken on plot basis while data for rest of the characters were recorded by random selection of five individual plants from each replication. The data of observations recorded for each traits was subjected to analysis of variance following Panse and Sukhatme (1978), the genotypic and phenotypic coefficient of variation in percent were calculated by the method given by Burton (1952), heritability in broad sense (h_{bs}) was calculated following the method given by Lush (1946) and genetic advance in per cent of mean was estimated by the formula given by Comstock and Robinson (1952). In analysis of correlation coefficient analysis and path coefficient analysis seed yield per plot is not considered as almost similar trait seed yield per plant is included in the study. Phenotypic correlation coefficients were estimated from the variance and covariance components as given by Johnson *et al.* (1955). While path analysis which measures the cause of association between two variables was calculated as proposed by Dewey and Lu (1959).

RESULTS AND DISCUSSION

Analysis of variance

The results of analysis of variance for all the character under study are shown in the Table 1. Significant differences were observed between all the treatments for all the characters studied. This is a clear indication of the presence of sufficient variability for all parameters, implying that variable genotypes can be used in future breeding programme.

Table 1: ANOVA for eleven quantitative characters under study

S.V.	Mean sum of square		
	Replication	Treatments	Error
df	2	31	62
Days to 50% flowering	7.5815	46.89**	4.0525
Days to maturity	48.3973	27.1582**	3.8865
Plant height (cm)	42.0357	959.29**	217.599
No. of primary branches/plant	0.865	0.939**	0.362
No. of secondary branches/plant	1.1939	3.15**	0.448
Siliqua length	0.1842	0.36**	0.0618
Siliqua /plant	558.0357	3336.93**	133.7225
Seed/siliqua	0.1054	2.49**	0.1506
Test weight (g)	0.0046	0.73**	0.0173
Seed yield/plant(g)	1.8901	13.43**	0.5189
Seed yield/plot (g)	1930.214	21571.98**	979.183

*, **: Significant at 5% and 1% level of significance, respectively

Genotypic and phenotypic coefficient of variation

Simple measures of variability, such as phenotypic and genotypic coefficients of variation, are often employed to examine variability. The level of variability present in the population on genetic basis can be estimated using the relative values of coefficient. As a result, components of variation such as the phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) were computed. The fact that the phenotypic coefficients of variation were slightly greater than the genotypic coefficients of variation indicated that the environment had a significant impact on the expression of the character included in the study. For categorization of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), Sivasubramaniam and Madhavamenon (1973) suggested a scale

as low (less than 10%), moderate (10-20%) and high (more than 20%).

For all the character under study higher magnitude of phenotypic coefficient of variation was recorded over genotypic coefficient of variation. The high GCV as well as high PCV were observed for seed yield per plant (21.16%, 22.43%) and seed yield per plot (21.62 %, 23.10%). The moderate GCV as well as moderate PCV was recorded for number of siliqua per plant (15.87%, 16.81%), secondary branches per plant (12.52%,14.97%) and test weight (12.74%,13.23%) while, plant height (10.75%), number of primary branches (14.74%), siliqua length (10.14%) was recorded high PCV only. All other characters showed low coefficient of variability at both genotypic and phenotypic levels. These results were well supported by similar findings by Yadava *et al.* (2011) Singh *et al.* (2011) and Kumar *et al.* (2013).

Table 2: Genetic variability parameters for 11 quantitative characters under study

Characters	Mean	Range		PCV (%)	GCV (%)	h ² bs	GA as % of mean
		Min.	Max.				
Days to 50% flowering	54.646	47.667	59.667	7.518	6.601	77.081	11.938
Days to maturity	109.167	104.0	113.667	3.000	2.377	62.761	3.879
Plant height (cm)	195.032	167	223.93	10.751	7.903	54.040	11.968
No. of primary branches/plant	5.051	4.333	6.467	14.740	8.687	34.735	10.547
No. of secondary branches/plant	8.056	6.533	10.167	14.977	12.525	69.944	21.579
Siliqua length	4.058	3.533	4.573	10.147	7.852	59.892	12.519
Siliqua /plant	204.082	134.13	264	16.819	15.866	88.995	30.834
Seed/siliqua	13.419	11.867	15.133	6.769	6.131	82.031	11.439
Test weight (g)	3.677	3.420	4.653	13.234	12.746	92.764	25.289
Seed yield/plant(g)	9.748	5.010	13.437	22.438	21.126	88.648	40.975
Seed yield/plot (g)	383.749	261.61	543.29	23.108	21.621	87.541	41.672

Heritability and genetic advance

Coefficient of variation just gives us information about the variability of data for that character but doesn't provide us information about what part of it is heritable. As a result, it is necessary to identify the heritable portion of the total variability, which will enhance the selection effectiveness. If the occurrence of the variance is mostly attributable to additive gene action and assessed in terms of heritability, the breeder can achieve maximal selection response. Using variance component analysis, an attempt was made to quantify heritability in broad sense in the current study. Robinson (1966) suggested a scale for categorization of heritability *viz*; low (less than 50%), medium (50-70%) and high

(more than 70%).

Among all the characters under study the highest heritability is observed for test weight (92.76 %) followed by siliqua/plant (88.99%), seed yield /plant (88.64%), seed yield/plot (87.54%), seed/siliqua (82.03%) and days to 50% flowering (77.08 %). The moderate heritability was observed for the character number of secondary branches (69.94%), days to maturity (62.76%), siliqua/length (59.89%) and plant height (cm) (54.04%). However, low heritability was observed for the character number of primary branches (34.73%). The heritability value is not the clear cut indicator of genetic improvement that could be achieved by selecting promising lines. The estimates of heritability would be reliable when restricted in

terms of broad sense, additive and non-additive gene effects coupled with substantial genetic advance. Genetic advance was estimated as a percentage of mean to make it easier to compare improvement in different traits of various genotypes.

The magnitude of genetic advance as percentage of mean was categorized as high (>20%), moderate (10% - 20%) and low (< 10%). Higher magnitude of genetic advance as percentage of mean was recorded for the character seed yield/ plant (41.672%) followed by seed yield/plot (40.97%) , number of siliqua per plant (30.83%), test weight (25.28 %) and number of secondary branches per plant (21.57%). Moderate genetic advance as percentage of mean was recorded for the character days to 50% flowering (11.93%), plant height (11.96%), number of seed per siliqua (11.43%), number of primary branches per plant (10.54%) and siliqua length (12.51%); while it was observed low for the trait days to maturity (3.87%). The above results are well supported by Pant and Singh (2001), Bind *et al.* (2014), Lodhi *et al.* (2014), Devi (2018), Pal *et al.* (2019),

Rout *et al.* (2019), Awasthi (2020) and Lakra (2020). For seed yield per plot, seed yield/plant, number of siliqua/plant, and test weight (g), high heritability estimates accompanied with high genetic advance as percentage of mean were recorded , indicating that additive gene action plays a predominant role in the expression of these traits. Selection in early generation would be beneficial since additive gene action is prominent in the manifestation of these traits.

Correlation coefficient analysis

Correlation coefficient analysis is done to establish the relationship between various characters under study. The inter-relationship study among different traits is of great importance in formulating the suitable selection criteria based on knowledge of positive as well as negative responses of correlation. Although phenotypic correlation coefficient is more reliable than genotypic, hence, more emphasis given to phenotypic correlation coefficient and the findings were presented in Table 3.

Table 3: Phenotypic Correlations Matrix

	DFF	DM	PH	PBPP	SBPP	SL	SPP	SPS	TW	SYPT
DFF		0.756**	0.624**	-0.383**	-0.316**	-0.074	-0.116	0.014	-0.042	-0.077
DM			0.567**	-0.352**	-0.208*	0.011	-0.155	-0.093	0.067	-0.078
PH				-0.288**	-0.026	0.002	0.051	0.086	0.013	0.105
PBPP					0.633**	0.308**	0.459**	0.312**	0.048	0.372**
SBPP						0.383**	0.633**	0.403**	0.246*	0.645**
SL							0.338**	0.320**	0.096	0.358**
SPP								0.477**	0.215*	0.866**
SPS									0.017	0.500**
TW										0.589**
SYPT										

*, **: Significant at 5% and 1% level of significance, respectively, DFF: Days to 50% flowering, DM: Days to maturity, PH: Plant height, PBPP: Number of primary branches per plant, SBPP: number of secondary branches per plant, SL: Siliqua length, SPP: Number of siliqua per plant, SPS: Number of seed per siliqua, TW: Test weight, SYPT: Seed yield per plant

On the basis of Table 3, days to 50% flowering exhibited highly significant and positive correlation with days to maturity (0.756**) followed by plant height (0.624**) while it showed highly significant and negative correlation with number of secondary branches per plant (-0.316**) and number of primary branches per plant (-0.383**). For all other characters studied, the correlation was found non-significant. Days to maturity showed highly significant and positive correlation with plant height (0.567**) and highly significant and

negative correlation with correlation with number of primary branches per plant (-0.352**). Plant height showed highly significant and negative correlation number of primary branches per plant (-0.288**). For all other characters studied, the correlation was found non-significant. Number of primary branches per plant depicted highly significant and positive correlation with number of secondary branches per plant (0.633**), number of siliqua per plant (0.459**), seed yield per plant (0.372**), seeds per siliqua (0.312*) and siliqua length (0.308*). For test weight the

correlation was found non-significant. Number of secondary branches per plant showed highly significant and positive correlation with seed yield per plant (0.645**), number of siliqua per plant (0.633**), seeds per siliqua (0.403*), siliqua length (0.383*) while showed significant positive correlation with test weight (0.246*). Siliqua length showed highly significant and positive correlation with seed yield per plant (0.358**), number of siliqua per plant (0.338**) and seeds per siliqua (0.320**). For test weight the correlation was found non-significant. On the other side, number of siliqua per plant also showed highly significant positive correlation with seed yield per plant (0.866**) and seeds per siliqua (0.477**) while showed significant positive correlation with test weight (0.215*). Seeds per siliqua showed highly significant positive correlation with and seed yield per plant (0.500**). Test weight or 1000 seed weight exhibited highly significant positive correlation with seed yield per plant (0.589**).

Path coefficient analysis

The direct and indirect effects of all the characters under study on seed yield per plant at phenotypic level are presented in Table 4 and phenotypic path coefficient analysis is discussed in details.

Phenotypic path coefficient analysis

Path coefficient analysis revealed that days to 50% flowering, plant height, number of secondary branches per plant, siliqua length, number of siliqua per plant, seeds per siliqua and test weight had positive direct effect on seed

yield per plant representing that true association of these characters with seed yield per plant and direct selection relying on these characters could be beneficial. Days to 50% flowering shown positive direct effect on seed yield per plant. A positive indirect effect was observed on seed yield per plant via plant height, number of primary branches per plant and seeds per siliqua. However, indirect negative effect on seed yield per plant via days to maturity, number of secondary branches per plant, siliqua length, number of siliqua per plant and test weight.

Days to maturity had negative direct effect on seed yield per plant however; positive indirect effect was observed on seed yield per plant via days to 50% flowering, plant height, number of primary branches per plant and test weight. A negative indirect effect was observed on seed yield per plant via number of secondary branches per plant, number of siliqua per plant and seed per siliqua. Plant height shown positive direct effect on seed yield per plant. It also showed positive indirect effect on seed yield per plant via days to 50% flowering, number of primary branches per plant number of siliqua per plant seeds per siliqua. However, it also had negative indirect effect was observed via days to maturity and number of secondary branches. Number of primary branches per had negative direct effect on seed yield per plant. However, it also showed positive indirect effect on seed yield per plant via days to maturity, number of secondary branches per plant, siliqua length, number of siliqua per plant seeds per siliqua and test. It also had negative indirect effect was observed via days to 50% flowering and plant height.

Table 4: Direct and indirect effects of nine characters on seed yield per plant in Indian mustard

	DFF	DM	PH	PBPP	SBPP	SL	SPP	SPS	TW	Phenotypic correlation with SYPP
DFF	0.024	-0.028	0.030	0.019	-0.027	-0.003	-0.076	0.002	-0.018	-0.077
DM	0.018	-0.036	0.027	0.017	-0.018	0.000	-0.102	-0.013	0.028	-0.078
PH	0.015	-0.021	0.048	0.014	-0.002	0.000	0.034	0.012	0.005	0.105
PBPP	-0.009	0.013	-0.014	-0.049	0.054	0.011	0.303	0.044	0.021	0.372**
SBPP	-0.007	0.008	-0.001	-0.031	0.085	0.013	0.417	0.057	0.105	0.645**
SL	-0.002	0.000	0.000	-0.015	0.033	0.035	0.223	0.045	0.041	0.358**
SPP	-0.003	0.006	0.002	-0.022	0.054	0.012	0.659	0.067	0.091	0.866**
SPS	0.000	0.003	0.004	-0.015	0.034	0.011	0.314	0.140	0.007	0.500**
TW	-0.001	-0.002	0.001	-0.002	0.021	0.003	0.142	0.002	0.426	0.589**

Residual are 0.02907, DFF: Days to 50% flowering, DM: Days to maturity, PH: Plant height, PBPP: Number of primary branches per plant, SBPP: number of secondary branches per plant, SL: Siliqua length, SPP: Number of siliqua per plant, SPS: Number of seed per siliqua, TW: Test weight, SYPT: Seed yield per plant

Number of secondary branches per plant had positive direct effect on seed yield per plant. However, it also showed positive indirect effect on seed yield per plant via days to maturity, siliqua length, number of siliqua per plant, seeds per siliqua and test weight. It also had negative indirect effect via days to 50% flowering, plant height and number of primary branches per plant. Siliqua length had positive direct effect on seed yield per plant. However, it also showed positive indirect effect on seed yield per plant via days to maturity, plant height, number of secondary branches per plant, number of siliqua per plant, seeds per siliqua and test weight. It also had negative indirect effect via days to 50% flowering and number of primary branches per plant.

Number of siliqua per plant had highest positive direct effect on seed yield per plant. However, it also showed positive indirect effect on seed yield per plant via days to maturity, plant height, number of secondary branches per plant, siliqua length, seeds per siliqua and test weight. It also had negative indirect effect via days to 50% flowering and number of primary branches per plant. Seeds per siliqua had positive direct effect on seed yield per plant. However, it also showed positive indirect effect on seed yield per plant via days to 50% flowering, days to maturity, plant height, number of secondary branches per plant, siliqua length, number of siliqua per plant and test weight. It also had negative indirect effect via number of primary branches per plant. Test weight showed second highest positive direct effect on seed yield per plant. However, it also showed positive indirect effect on seed yield per plant via plant height, number of secondary branches per plant, siliqua length, number of siliqua per plant, seeds per siliqua and test weight. It also had negative indirect effect via days to 50% flowering, days to maturity and number of primary branches per plant. The results of correlation and path coefficient

analysis are partially superimposed with the findings of Mahala *et al.* (2003), Yadava *et al.* (2011), Lodhi *et al.* (2014), Bind *et al.* (2014), Dipti *et al.* (2016), Begum *et al.* (2018), Roy *et al.* (2018), Tiwari (2019) and Lakra (2020).

CONCLUSION

Results found in the present investigation revealed that a wide range of genetic variability existed for seed yield and other traits for all the lines under consideration. The high value of genotypic coefficient of variation was recorded for test weight and seed yield per plant. High heritability coupled with the high genetic advance was observed for seed yield per plant, number of siliqua per plant and plant height indicating that these characters are less influenced by the effect of environment. Hence, selection based on these traits could be rewarding. The phenotypic correlation studies revealed that seed yield per plant exhibited significant positive correlation number of primary branches per plant, number of secondary branches per plant, Siliqua length, number of siliqua per plant, seeds per siliqua and test weight while path coefficient analysis revealed that days to 50% flowering, plant height, number of secondary branches per plant, siliqua length, number of siliqua per plant, seeds per siliqua and test weight had positive direct effect on seed yield per plant representing that true association of these characters with seed yield per plant and direct selection relying on these characters could be beneficial.

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