



CHARACTER ASSOCIATION AND PATH ANALYSIS STUDIES OF YIELD AND YIELD ATTRIBUTING TRAITS IN INDIAN MUSTARD (*BRASSICA JUNCEA* L. CZERN & COSS)

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Abstract

Mustard is one of the important oilseed crop produced worldwide. India is one of the leading producers of mustard crop but, despite having the third largest acreage its production remains stagnant. Therefore, intensive research is required for identification and selection of characters that contribute directly or indirectly to the increase in yield of the oilseed crop. In this context, the character association and path analysis studies were conducted during *Rabi* 2016-17 at Agricultural Research Farm, Institute of Agricultural Sciences, BHU, Varanasi. Thirty Indian mustard genotypes were sown under Randomized Block Design in three replications and observations were recorded on for eleven quantitative traits. Treatments mean sum of square for all traits were found significant except for main raceme length which shows presence of sufficient genetic variation among the genotypes tested. Highest estimate of heritability (broad sense) was observed for 1000 seed weight (94.40 %). Genetic advance for all the traits was in lower range except for number of siliqua per plant (41.605%). Genotypic correlation of five traits *viz.* plant height (0.6151), number of primary branches (0.4660), number of secondary branches (0.3829), length of main raceme (0.2979) and number of siliqua per plant (0.3230) showed positive and significant correlation with seed yield per plant whereas siliqua length (-0.3372) was found to be negatively and significantly correlated. Genotypic path coefficient analysis revealed positive direct effects on seed yield per hectare for plant height (2.3881), number of secondary branches (2.4428), siliqua length (0.1947) and seed yield/plant (0.1656). It can be concluded from the findings that plant height, number of secondary branches, siliqua length and seed yield/plant are reliable traits for selection of high yielding genotypes. Traits like number of siliqua/plant, 1000 seed weight, seed yield/plant and seed yield/ha showed high heritability hence give response for the selection. Number of siliqua per plant, 1000 seed weight and seed yield per plant showed moderate genetic advance which suggests that these traits may be helpful in improving the seed yield.

Key words: Indian mustard, correlation, path analysis, GCV and PCV.

Introduction

Indian mustard (*Brassica juncea* L.) commonly known as rai, raya or laha is important oil seed crop in India. It is second most important edible oilseed crop of India after groundnut. Mustard seed contains about 38 to 43 percent oil which is considered to be the healthiest and nutritious cooking medium (Patel *et al.*, 2012) as compared to other edible oils because it has lowest amount of harmful saturated fatty acids and adequate amount of linoleic and linolenic acid which are essential fatty acids (Porter and Crompton, 2008). India ranks third in terms of acreage (19.29%) after Canada (24.55%) and China (20.58%); however, it accounts for only 11.27% of total production next to China and Canada that contributes

nearly 22.08% and 21.77% of total production respectively (www.drmr.org.in). Mustard is produced in around 6.82 million tons from area of 5.76 million hectare in 2015-16, with the productivity of 1,184 kg/ha (Anonymous, 2016). The major Rapeseed-mustard growing states in India are Rajasthan (43% area), Uttar Pradesh (14%), Madhya Pradesh (11%) and Haryana (8%).

The assessment of parameters including phenotypic and genotypic coefficients of variation, heritability in broad sense, and genetic advance as % of mean is a pre-requisite for making effective selection (Manjunath *et al.*, 2017). An estimate of genetic advance along with heritability is helpful in assessing the reliability of character for selection (Meena *et al.*, 2017). The character showing

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high heritability along with low genetic advance can be improved by intermating superior genotypes of segregating population developed from combination breeding (Synrem *et al.*, 2014). The proper evaluation of important crop species helps in the identification and utilization of improved genotypes (Jan *et al.*, 2016). The present investigation was planned to access heritability, association between traits and defines suitable selection criteria for mustard yield improvement. Availability of sufficient genetic variability is very important in crop improvement programme. Therefore, it is essential for a breeder to measure the variability with the help of parameters like phenotypic coefficient of variation, genotypic coefficient of variation, heritability and genetic advance. Hence these parameters give the information regarding the availability of genetic variability for different characters in available germplasm which provides a strong basis for selection of desirable genotypes.

Different yield attributing traits very often exhibit varying degree of direct and/or indirect associations with seed yield as well as among themselves that create a complex situation to the breeder for making desirable selection. Therefore, path coefficient analysis could provide a more realistic picture of the interrelationship, as it partitions the correlation coefficient in direct and indirect effects of the variables. Thus, character association and path provide the information of yield contributing characters and breeder can practice selection using this information for the isolation of superior accession for gene bank.

Materials and method

The experiment was conducted during *Rabi* 2016-17 at Agricultural Research Farm, Institute of Agricultural Sciences, BHU, Varanasi. Thirty Indian mustard genotypes were sown under Randomized Block Design in three replications. The observations were recorded on five randomly selected plants for eleven traits *viz.* plant height (cm), number of primary branches/plant, number of secondary branches/plant, length of main raceme(cm), number of siliqua on main raceme, average siliqua length(cm), seeds/siliqua, number of siliqua/plant 1000 seed weight (g), seed yield/plant (gm) and seed yield/ hectare (kg).

Test of significance for each character were analyzed as per methodology advocated by Panse and Sukhatme (1967). Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated

by the formula given by Al-Jibouri *et al.*, (1958), heritability in broad sense (h^2) 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). The path analysis was carried out to know direct and indirect effects of the components on yield as suggested by Wright (1921) and illustrated by Dewey and Lu (1957).

Results and Discussion

ANOVA for randomized block design, carried out for eleven traits revealed significant differences for genotypes (treatments) except main raceme length (table 1). It indicates the presence of sufficient genetic variation among the genotypes tested for all the morphological traits. Replication MSS for number of siliqua/plant, 1000 seed weight, seed yield/ plant and seed yield/hectare were also found significant. This indicates the presence of differences in soil factors at the experimental location.

Mean, range, estimates of GCV, PCV, heritability and genetic advance for seed yield and component traits of Indian mustard is presented in table 2. Mean for plant height ranged from 196.20 (Vardan) cm to 147.17cm (RH 30), with average of 170.44, whereas mean for number of primary and secondary branches ranged from 10.97 (NDRE-8) to 5.57 (Pusa Bold) and 13.87 (RH 8812) to 6.97 (Ashirwad), having mean of 7.80 and 10.65, respectively. The mean for length of main raceme ranged from 63.63 (SEJ-2) to 46.17 (HUJM-9903), having mean of 54.61cm. The number of siliqua on main raceme had

Table 1: Analysis of variance for eleven yield attributing characters

Source of variation	Replication	Treatment	Error
Df	2	29	58
Plant height(cm)	172.054200	449.262474*	265.078167
No. of primary Branches	0.238778	4.239249*	2.135904
No. of secondary branches	5.884334	11.334426*	1.938586
Main receme length(cm)	85.086010	63.573891	40.635081
No. of siliqua on main receme	12.033770	66.158640*	37.508721
Siliqua length(cm)	0.371663	0.345481*	0.172290
Seeds/siliqua	0.424681	2.657489*	1.541097
No. of siliqua/plant	1500.750000*	6451.507977**	383.332263
1000 seed Wt. (gm)	0.067208*	1.026278**	0.019785
Seed yield/plant (gm)	9.529963*	7.889494**	2.280338
Seed yield/ha(kg)	414513.500000*	409225.765688**	116381.588293

Table 2: Estimates of genotypic (GCV) and phenotypic (PCV) co-efficient of variation, heritability (bs) and genetic advance (% of mean) for seed yield and component traits in Indian mustard

Source of variation	Plant height (cm)	No. of primary Branches	No. of secondary branches	Main receme length (cm)	No. of siliqua on main receme	Siliqua length (cm)	Seeds /siliqua	No. of siliqua /plant	1000 seed Wt. (gm)	Seed yield/ plant (gm)	Seed yield/ha (kg)
Mean	170.4421	7.8044	10.6500	54.6128	40.2611	5.1570	13.6481	204.1789	4.5141	7.9883	1971.1980
Min	147.1667	5.5667	6.9667	46.1667	32.2000	4.4667	11.3233	116.0000	3.5767	5.2233	1473.4670
Max	196.2000	10.9667	13.8667	63.6333	53.5667	5.7433	15.5333	279.7667	6.0133	13.0000	3383.2330
GCV	4.597	10.729	16.617	5.063	7.676	4.659	4.470	22.027	12.831	17.117	15.850
PCV	10.601	21.582	21.144	12.723	17.039	9.300	10.135	24.024	13.204	25.502	23.468
h² (Broad Sense)	18.80	24.70	61.80	15.80	20.30	25.10	19.50	84.10	94.40	45.10	45.60
Gen. Adv. as % of Mean 5%	4.107	10.987	26.903	4.151	7.123	4.808	4.061	41.605	25.686	23.668	22.052

Table 3: Genotypic Correlation of eleven characters in Indian Mustard

	Plant height (cm)	No. of primary Branches	No. of secondary branches (cm)	Main receme length receme	No. of siliqua on main	Siliqua length (cm)	Seeds /siliqua	No. of siliqua /plant	1000 seed Wt. (gm)	Seed yield/ plant
Plant height	1.0000	0.8762**	0.4559**	-0.1839	0.5622**	-0.5493**	-0.4446**	0.6306**	-0.3134**	0.6151**
No. of primary Branches		1.0000	0.8780**	0.0995	0.5893**	-0.4690**	0.0297	0.5094**	-0.5074**	0.4660**
No. of secondary branches			1.0000	0.3955**	0.3815**	-0.4749**	0.0821	0.2733**	-0.3163**	0.3829**
Main receme length				1.0000	0.4432**	-0.5627**	-0.0905	0.8096**	-0.7513**	0.2979**
No. of siliqua on main					1.0000	-0.3575**	-1.1731**	0.2970**	-0.5018	0.1702
Siliqua length receme						1.0000	0.8795**	-0.4620**	0.3508**	-0.3372**
Seeds/siliqua							1.0000	-0.1347	-0.3531**	-0.0948
No. of siliqua/plant								1.0000	-0.3219**	0.3230**
1000 seed Wt.									1.0000	-0.2012
Seed yield/plant										1.0000
Seed yield/ha	0.2928	0.6716	0.3283	0.3279	0.0517	-0.6893	-0.1025	0.2385	-0.0822	0.8374

** Significant at 1% level, * - Significance at 5% level

mean values ranging from 53.57 (RH 8812) to 32.20 (SEJ-2), with an average of 40.26, while siliqua length had mean values ranging from 5.74cm (Ashirwad) to 4.47cm (NDRE-8), with an average of 5.16cm. The mean values for number of seed per siliqua ranged from 15.53 (SEJ-2) to 11.32 (HUJM-05-03) with an average of 13.65. The mean for number of siliqua per plant was found to be 204.18 with maximum value of 279.77 (NDRE-8) and minimum value of 116.00 (DRMR-150-35). The mean for 1000 seed weight ranged from 6.01 (HUJM-07-06) to 3.58 (Kanti) with an average of 4.51g. For seed yield per plant, maximum value was 13.00g (Swarn Jyoti) whereas minimum was 5.22g (SEJ-2) with average of 7.99g. Seed yield per hectare recorded a mean of 1971.18 kg ranging from 3383.23 (NDRE-8) to 1473.47 (HUJM-9804).

The GCV ranged from 4.47 for seeds per siliqua to

22.027 for number of siliqua per plant. GCV estimates for number of siliqua per plant (22.027) was in high range while it was in low range for traits like plant height, length of main raceme, number of siliqua on main raceme, siliqua length and seeds per siliqua. For traits like number of primary branches, number of secondary branches, 1000 seed weight, seed yield per plant and seed yield per hectare GCV was in moderate range. The PCV ranged from 9.30 for siliqua length to 25.50 for seed yield per plant. The PCV estimates were in high range for all the traits except siliqua length which was in low range and length of main raceme, number of siliqua on main raceme, number of seeds per siliqua and 1000 seed weight which were in moderate range.

The highest estimates of heritability in broad sense was observed for 1000 seed weight (94.40%) while lowest was observed for plant height (18.80%). Number of

Table 4: Phenotypic Correlation of eleven characters in Indian Mustard

	Plant height (cm)	No. of primary Branches	No. of secondary branches (cm)	Main raceme length	No. of siliqua on main	Siliqua length (cm)	Seeds /siliqua	No. of siliqua /plant	1000 seed Wt. (gm)	Seed yield/ plant (gm)
Plant height	1.0000	0.2316 *	0.2639 *	0.1456	0.3994 **	-0.0927	-0.0605	0.2832 **	-0.1515	0.2322*
No. of primary Branches		1.0000	0.3752 **	0.0658	0.1392	-0.1250	0.0979	0.2805 **	-0.2351 *	0.1937
No. of secondary branches			1.0000	0.2213 *	0.2062	-0.2124 *	-0.0197	0.3031 **	-0.2276 *	0.3740**
Main raceme length				1.0000	0.3985 **	-0.0748	0.1775	0.3169 **	-0.3119 **	0.0358
No. of siliqua on main raceme					1.0000	-0.0809	0.1131	0.1350	-0.2429 *	0.0811
Siliqua length						1.0000	0.1636	-0.2317 *	0.1304	-0.3337**
Seeds/siliqua							1.0000	-0.0767	-0.1351	-0.1077
No. of siliqua/plant								1.0000	-0.2734 **	0.3326**
1000 seed Wt.									1.0000	-0.1366
Seed yield/plant										1.0000
Seed yield/ha	0.1351	0.1247	0.2389	0.1051	0.1432	-0.2829	0.0551	0.1759	-0.0583	0.5721

** Significant at 1% level, * - Significance at 5% level

siliqua/plant and 1000 seed weight showed 84.10, 94.40 percent of heritability, respectively which was in very high range. Number of secondary branches per plant showed high heritability (61.80). Seed yield per plant (45.10) and seed yield per hectare (45.60) showed moderate heritability. Expected genetic advance as percent of mean at 5% was highest for number of siliqua per plant (41.605%) and lowest for number of seeds per siliqua (4.061%). Genetic advance for number of siliqua per plant (41.605), number of secondary branches (26.903), 1000 seed weight (25.686), seed yield per plant (23.668) and seed yield per hectare (22.052) showed high genetic advance. Number of siliqua on main raceme (7.123), siliqua length (4.808), length of main raceme (4.151), plant height (4.107) and number of seeds per siliqua (4.061) were found in low range of genetic advance. Plant height has showed very low genetic advance. Similar findings were reported by Singh *et al.* (2003), Arifullah *et al.*, 2013 and Singh *et al.* (2013). Number of siliqua per plant, 1000 seed weight and number of secondary branches showed high heritability accompanied with high genetic advance which suggests that heritability is due to additive gene effects and direct selection may be effective. Plant height (cm), length of main raceme(cm), number of siliqua on main raceme, average siliqua length (cm) and seeds/ siliqua showed low heritability with low genetic advance which suggests that traits are highly influenced by environment and selection will be ineffective.

Genotypic correlation of eleven characters in Indian mustard is presented in table 3. The correlation coefficients were classified as weak (<0.3), moderate

(0.3-0.7) and strong (>0.7) on the basis of their absolute values (Dospikhov, 1984). Number of siliqua/plant showed significant and positive correlation with plant height (0.6306), number of primary branches (0.5094), number of secondary branches (0.2733), length of main raceme (0.8096) and number of siliqua on main raceme (0.2970) while siliqua length (-0.4620) showed significant negative correlation. Length of main raceme showed strong correlation with number of siliqua per plant, while plant height, number of primary branches, number of secondary branches, number of siliqua on main raceme and siliqua length showed moderate range of correlation with number of siliqua per plant. Number of seeds per siliqua showed weak correlation with this trait. The siliqua length was positively and significantly correlated with 1000 seed weight with genotypic correlation coefficient of 0.3508. Traits like plant height (-0.3134), number of primary branches (-0.5074), number of secondary branches (-0.3163), length of main raceme (-0.7513), number of siliqua on main raceme (0.5018), seeds per siliqua (-0.3531) and number of siliqua per plant (-0.3219) were negatively and significantly correlated with 1000 seed weight. Traits like plant height, number of primary branches, number of secondary branches, number of siliqua on main raceme, siliqua length, seeds per siliqua and number of siliqua per plant were found to be in the moderate range of correlation coefficient while length of main raceme showed strong correlation with seed yield per plant. Results showed five traits were positively and significantly correlated with seed yield per plant *viz.* plant height (0.6151), number of primary branches (0.4660), number of secondary branches (0.3829), length of main

Table 5: Genotypic path coefficient of ten yield components to seed yield/plant in Indian Mustard

	Plant height (cm)	No. of primary Branches	No. of secondary branches (cm)	Main raceme length raceme	No. of siliqua on main	Siliqua length (cm)	Seeds /siliqua	No. of siliqua /plant	1000 seed Wt. (gm)	Seed yield/plant (gm)
Plant height	2.3881	2.0924	1.0888	-0.4392	1.3427	-1.3118	-1.0619	1.5058	-0.7484	1.4690
No. of primary Branches	-3.1885	-3.6390	-3.1951	-0.3622	-2.1446	1.7068	-0.1082	-1.8539	1.8463	-1.6957
No. of secondary branches	1.1137	2.1448	2.4428	0.9662	0.9319	-1.1600	0.2005	0.6676	-0.7727	0.9354
Main raceme length	0.0165	-0.0089	-0.0355	-0.0898	-0.0398	0.0505	0.0081	-0.0727	0.0675	-0.0267
No. of siliqua on main raceme	-0.2229	-0.2336	-0.1512	-0.1757	-0.3964	0.1417	0.4650	-0.1177	0.1989	-0.0675
Siliqua length	-0.1069	-0.0913	-0.0924	-0.1095	-0.0696	0.1947	0.1712	-0.0899	0.0683	-0.0656
Seeds/siliqua	0.0190	-0.0013	-0.0035	0.0039	0.0502	-0.0377	-0.0428	0.0058	0.0151	0.0041
No. of siliqua/plant	-0.0654	-0.0529	-0.0284	-0.0840	-0.0308	0.0479	0.0140	-0.1038	0.0334	-0.0335
1000 seed wt.	0.2373	0.3842	0.2395	0.5689	0.3800	-0.2656	0.2673	0.2437	-0.7572	0.1524
Seed yield/plant	0.1019	0.0772	0.0634	0.0493	0.0282	-0.0558	-0.0157	0.0535	-0.0333	0.1656
Seed yield/ha	0.2928	0.6716	0.3283	0.3279	0.0517	-0.6893	-0.1025	0.2385	-0.0822	0.8374
Partial R ²	0.6993	-2.4439	0.8021	-0.0294	-0.0205	-0.1342	0.0044	-0.0247	0.0623	0.1387

raceme (0.2979) and number of siliqua per plant (0.3230) while trait like siliqua length (-0.3372) was negatively and significantly correlated. Positive association of seed yield/plant with primary branches/plant, secondary branches/plant, number of seeds/siliqua was also observed which was in agreement with that of the findings Ramanjaneyulu and Giri (2007), Verma *et al.* (2008) and Singh & Singh (2010). Singh *et al.* (2003) observed positive association of seed yield/plant with length of main raceme. Similar results were observed by Singh *et al.* (2009), Arifullah *et al.* (2013) and Lohia *et al.* (2013). Traits like plant height, number of primary branches, number of secondary branches, siliqua length, number of siliqua per plant, were found to be in the moderate range of correlation coefficient while length of main raceme and 1000 seed weight showed weak correlation with seed yield per plant.

The genotypic correlation study indicated that yield per hectare was positively and significantly correlated with plant height (0.2928), number of primary branches (0.6716), number of secondary branches (0.3283), length of main raceme (0.3279) and number of siliqua per plant (0.2385) and seed yield per plant (0.8374) while siliqua length (-0.6893) was significantly and negatively correlated with seed yield per hectare. Traits like plant height, number of siliqua on main raceme, number of seeds per siliqua, number of siliqua per plant 1000 seed weight showed weak correlation with seed yield per plant, on the other hand seed yield per plant had strong correlation with this trait, while number of primary branches, number of secondary branches, length of main raceme and siliqua

length were found to be in the moderate range of correlation coefficient.

Number of siliqua per plant showed positive significant phenotypic correlation with plant height (0.2832), number of primary branches (0.2805), number of secondary branches (0.3031), length of main raceme (0.3169) and seed yield per plant (0.3326), while siliqua length (-0.2317) and 1000 seed weight (-0.2734) showed significant and negative correlation. Traits like number of secondary branches, length of main raceme and seed yield per plant showed moderate range of correlation with number of siliqua per plant while Plant height, number of primary branches, number of siliqua on main raceme, siliqua length, seeds per siliqua and 1000 seed weight showed weak correlation with number of siliqua per plant.

Phenotypic correlation of siliqua length (0.1304) with 1000 seed weight was positively correlated. Traits like number of primary branches (-0.2351), number of secondary branches (-0.2276), length of main raceme (-0.3119), number of siliqua on main raceme (-0.2429) and number of siliqua per plant (-0.2734) were negatively and significantly correlated with 1000 seed weight. Traits like plant height (-0.1515), seeds per siliqua and seed yield per plant were negatively correlated with 1000 seed weight. Traits like plant height, number of primary branches, number of secondary branches, number of siliqua on main raceme, siliqua length, seeds per siliqua, number of siliqua per plant and seed yield per plant were found to be in weak correlation coefficient while length of main raceme showed moderate correlation with seed yield per plant.

Three traits were positive significantly correlated with seed yield per plant *viz.* plant height (0.2322), number of secondary branches (0.3740) and number of siliqua per plant (0.3326) while trait like siliqua length (-0.3337) was negative significantly correlated. Traits like plant height, number of primary branches, length of main raceme, number of siliqua on main raceme, number of seeds per siliqua and 1000 seed weigh were found to have weak correlation coefficient while number of secondary branches, siliqua length and number of siliqua per plant showed moderate correlation with seed yield per plant.

The phenotypic correlation table indicated that yield per hectare was positively correlated with plant height (0.1351), number of primary branches (0.1247), number of secondary branches (0.2389), length of main raceme (0.1051), number of siliqua on main raceme (0.1432) and seeds per siliqua (0.0551, number of siliqua per plant (0.1759) and seed yield per plant (0.5721) while siliqua length (-0.2829) and 1000 seed weight (-0.0583) were negatively correlated with seed yield per hectare. All the traits showed weak correlation with seed yield per plant, except seed yield per plant which had moderate correlation with this trait. In general, the values of genotypic correlations were higher than their phenotypic correlations indicating the inherent association among the traits. Similar findings were also reported by Shah *et al.* (2002), Singh *et al.* (2003) and Joshi *et al.* (2009).

Correlation of plant height, number of primary branches/plant, number of secondary branches/plant, length of main raceme, number of siliqua on main raceme, average siliqua length, 1000- seed weight with seed yield/plant showed higher values of genotypic correlation coefficient than the phenotypic correlation coefficient, this suggests that there is strong genetic association between these traits with seed yield per plant but phenotypic values were lessen by significant interaction of environment. Number of seeds per siliqua and number of siliqua per plant had higher values of phenotypic correlation coefficient than the genotypic correlation coefficient, this shows that association between these two traits with seed yield per plant is not only due to genes but also due to favourable environment.

The genotypic path coefficient analysis (table 5) revealed that plant height (2.3881), number of secondary branches (2.4428), siliqua length (0.1947) and seed yield/plant (0.1656) showed positive direct effects on seed yield per hectare while number of primary branches (-3.6390), main raceme length (-0.0898), number of siliqua on main raceme (-0.3964), seeds/siliqua (-0.0428), number of siliqua/plant (-0.1038) and 1000 seed weight (-0.7572) showed negative direct effects on seed yield per hectare.

Srivastava and Singh (2002), Panth *et al.* (2002) and Marjanovic *et al.* (2007) also observed positive direct effect for plant height, number of secondary branches and seeds/siliqua. Selection based on the traits with positive direct effect may help in improvement of seed yield while selection based on traits with negative direct effect may be ineffective. Number of secondary branches has highest direct effect on seed yield per hectare. Indirect effect of number of siliqua/plant, 1000 seed weight and seed yield/plant was 0.2385, -0.0822 and 0.8374, respectively on seed yield per hectare.

Conclusion

Based on the above findings, it can be concluded that traits such as plant height, number of secondary branches, siliqua length and seed yield/plant should be considered selection of high yielding genotypes. Traits like number of siliqua/plant, 1000 seed weight, seed yield/plant and seed yield/ha showed high heritability hence give positive response for the selection. Number of siliqua per plant, 1000 seed weight and seed yield per plant showed moderate genetic advance which suggests that these traits may prove to be helpful in improving the seed yield. The above suggested traits can be efficiently used for improvement of seed yield.

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References

- Al-Jibouri, H.A., P.A. Miller and H.F. Robinson (1958). Genotype and environmental variances and co-variance in upland cotton cross of interspecific origin. *Agron J.*, **50**:633-637.
- Anonymous, (2016). Directorate of Economics and Statistics, Department of Agriculture and Cooperation. 4th Advance Estimates.
- Arifullah, M., M. Munir, A. Mahmood, K.S. Ajmal and F. Hassanul (2013). Genetic analysis of some yield attributes in Indian mustard (*Brassica juncea* L.). *Afri. J. Pl. Sc.*, **7**(6): 219-226.
- Burton, G.W. and E.H. Devane (1953). Estimating heritability in tall Fescue (*Festuca arundinacea*) from replicated clonal martial. *Agron J.*, **45**: 478-481.
- Dewey, D.R. and K.H. Lu (1957). A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agron J.*, **51**: 515-518.
- Dospikhov, B.A. (1984). Field experimentation. Statistical

- procedures. Mir Publishers, Moscow.
- Jan, S.A., Z.K. Shinwari and M.A. Rabbani (2016). Morpho-biochemical evaluation of *B. rapa* sub-species for salt tolerance. *Genetika*, **8**: 323-338.
- Johnson, H.W., H.F. Robinson and R.E. Comstock (1955). Estimates of genetic and environmental variability in soybean. *Agron J.*, **47**: 314-318.
- Joshi, V., H.C. Pathak, J.B. Patel and S. Haibatpure (2009). Genetic variability, correlation and path analysis over environments in mustard. *GAU Res. J.*, **34(1)**: 14-19.
- Lohia, R.S., R.K. Singh and M. Singh (2013). Studies on genetic variability, heritability and character association in Indian mustard [*Brassica juncea* (L.) Czern & Coss]. *Progressive Res. J.*, **8(1)**: 75-77.
- Manjunath, H., D.S. Phogat, P. Kumari and D. Singh (2017). Genetic analysis of seed yield and yield attributes in Indian mustard [*B. juncea* (L.) Czern and Coss.]. *Elect. J. Plant Breed.*, **8**: 182-186.
- Marjanovic, J.A., R. Marinkovic, A. Mijic, M. Jankulovska and C. Zdunic (2007). Interrelationship between oil yield and other quantitative traits in rapeseed (*Brassica napus* L.). *Central European Agri.*, **8(2)**: 165-170.
- Meena, H.S., A. Kumar, V.V. Singh, P.D. Meena, B. Ram and S. Kulshrestha (2017). Genetic variability and interrelation of seed yield with contributing traits in Indian mustard (*B. juncea*). *J. Oilseed Brassica*, **8**: 131-137.
- Panse, V.G. and P.V. Sukhatme (1967). Statistical Methods of Agricultural Workers. 2nd Endorsement, ICAR Publication, New Delhi, India, pp: 381.
- Panth, S.C., P. Singh, R. Kumar, S. Mishra, S.P. Singh and S. Mishra (2002). Correlation and path analysis in Indian mustard. *Plant Archives*, **2(2)**: 207-211.
- Patel, A.M., D.B. Prajapati and D.G. Patel (2012). Heterosis and combining ability studies in Indian mustard (*B. juncea* L.). *Ind. J. Sci. Res. Tech.*, **1**: 38-40.
- Porter, P. and D. Crompton (2008). Canola. In: Varietal trial results. Minnesota Agricultural Experiment Station, University of Minnesota, Saint Paul, Minnesota, USA. p. 52-53.
- Ramanjaneyulu, A.V. and G. Giri (2007). Correlation and path coefficient analysis in Indian mustard [*Brassica juncea* (L.) Czern & Coss]. *J. Res. ANGRAU*, **35**: 107-110.
- Shah, P., G. Tiwari and A.S. Gontia (2002). Correlation studies in Indian mustard [*Brassica juncea* (L.) Czern and Coss]. *Agric. Sci. Dig.*, **22(2)**: 79-82.
- Singh, M., M. Rao, Rajshekhar and R.K. Dixit (2009). Genetic variability and character association in Indian mustard (*Brassica juncea*). *J. Oilseeds Res.*, **26**: 56-57.
- Singh, M., R.L. Srivastava, L. Prasad and R.K. Dixit (2003). Correlation and path analysis in Indian mustard (*Brassica juncea*). *J. Adv. Plant Sci.*, **16**: 311-316.
- Singh, R.K., R.S. Lohia and M. Singh (2013). Study of gene action on inheritance of seed yield and its contributing traits in Indian mustard [*Brassica juncea* (L.) Czern & Coss]. *Progressive Res. J.*, **8(1)**: 78-81.
- Singh, S.K. and A.K. Singh (2010). Inter-relationship and path analysis for seed yield in Indian mustard. *Ind. J. Ecol.*, **37**: 8-12.
- Srivastava, M.K. and R.P. Singh (2002). Correlation and path analysis in Indian mustard [*Brassica juncea* (L.) Czern & Coss]. *Crop. Res.*, **23(3)**: 517-521.
- Synrem, G.J., N.R. Rangare, I. Myrthong and D.M. Bahadure (2014). Variability studies in Intra specific crosses of Indian mustard [*B. juncea* (L.) Czern and Coss.] genotypes. *IOSR J. Agric. Vet. Sci.*, **7**: 29-32.
- Verma, R., R. Sharma and S.K. Sharma (2008). Association studies among yield and its component characters in Indian mustard [*Brassica juncea* (L.) Czern & Coss]. *Ind. J. Genet. Plant Breed.*, **68**: 87-89.
- Wright, S. (1921). Correlation and causation. *J. Agric. Res.*, **20**: 557-585.