



## Genetic parameters and character association of yield and its attributes in Indian mustard (*Brassica juncea* L.)

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### Abstract

Thirty eight genotypes of Indian mustard along with check Giriraj were evaluated in Randomized block design with three replications during *Rabi* 2016-17. The ANOVA suggested the existence of sufficient variability between genotypes and mean indicated that seed yield per plot showed highest performance followed by number of siliqua per plant and plant height. High heritability coupled with high genetic advance was found for days to 50% flowering, number of siliqua/plant, siliqua length, seeds/ siliqua, 1000-seed weight, seed yield/ plant, seed yield/plot, biological yield and seed yield (q/ha) suggesting presence of additive gene action for these traits hence direct selection for these traits may prove to be rewarding. Higher genotypic coefficient of variation coupled with higher phenotypic coefficient of variation was recorded for seeds/ siliqua. At genotypic level seed yield was positively correlated with plant height, number of secondary branches, number of siliqua/ plant, siliqua length, main raceme length, number of siliqua on main raceme, test weight, seed yield/plant, seed yield/ plot and biological yield therefore these traits can be considered for direct selection. At phenotypic level, path coefficient analysis revealed positive direct effect on seed yield (q/ha) for plant height, number of primary branches/ plant, number of secondary branches/ plant, siliqua length, seeds/ siliqua, main raceme length, number of siliqua on main raceme and number of siliqua/ plant. Since seed yield per plot and biological yield showed high heritability, high genetic advance and positive correlation with the seed yield (q/ha) which was supported by the path analysis, therefore, we can use these two traits as selection criteria in breeding programmes. RVM-2 (17.3 q/ha), RGN-73 (16.4 q/ha), JD-6 (16.2 q/ha), RGN-298 (15.9 q/ha) and RGN-48 (15.8 q/ha) were found better than Giriraj for seed yield.

**Keywords:** *Correlation, biological yield, heritability, Indian mustard, seed yield*

### Introduction

Indian mustard [*Brassica juncea* (L.) Czern & Coss.] is globally one of the most important oilseed crop grown in diverse agro-climatic conditions including irrigated or rainfed, timely or late sown and as a sole or mixed crop. India annually produces 6-8 million tonnes of mustard seed and ranks third in the world in production, having a market share of 11 per cent (USDA, 2018). It is one of the major sources of oil and oil meal in India. Hence, it is highly imperative to focus on increasing the seed yield through various breeding methodologies. The basic rationale in any crop improvement is to increase in yield potential of the crop. Yield being a complex character and a polygenic trait, is dependent on the various yield contributing traits and in order to study it properly, different factors affecting the seed yield must be considered and evaluated with regard to their contribution to seed yield (Yadav *et al.*, 2011 and Meena *et al.*, 2017). Availability of sufficient genetic variability is a basic requirement for a successful crop improvement programme. Therefore, it is essential for a plant breeder to measure the variability with the help of parameters like

phenotypic coefficient of variation, genotypic coefficient of variation, heritability and genetic advance.

Different components of seed yield very often exhibit varying degree of associations with seed yield as well as among themselves. In order to accumulate optimum combination of seed yield contributing characters in single genotype, it is essential to know the relationships among themselves. Further the seed yield is influenced by its various components directly and/or indirectly via other traits that create a complex situation before a 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 correlation provide the information of yield contributing characters and using this information a breeder can practice selection for the isolation of superior genotypes. Keeping this in view, present study was planned to estimate genetic parameter *viz.* variability, heritability and genetic advance for different quantitative characters, to estimate genotypic

and phenotypic correlation coefficient between seed yield and its contributing characters and to determine the direct and indirect effects of different characters on seed yield.

## Materials and Methods

The experiment was carried out during *Rabi* 2016-17 at Agricultural Research Farm, Institute of Agricultural Sciences, BHU, Varanasi, India. The experimental materials consisted of 38 genotype of *B. juncea* which were evaluated in Randomized Block Design (RBD) with three replications. For recording data, 5 plants were selected at random from each genotype in each replication. The observations were recorded for yield and 14 yield attributing traits *viz.*, plant height (cm), days to 50% flowering, number of primary branches/ plant, number of secondary branches/ plant, number of siliqua/ plant, length of siliqua (cm), number of seeds/ siliqua, main raceme length (cm), number of siliqua on main raceme, test weight (1000 seed weight in g), seed yield/ plant (g), seed yield/ plot (g), biological yield (g), yield (q/ha).

The mean value of each character genotype wise subjected to analysis of variance (ANOVA) following usual procedures (Panse and Sukhatme, 1967). The total phenotypic ( $\sigma^2 p$ ), genotypic ( $\sigma^2 g$ ) and error variance ( $\sigma^2 e$ ) were calculated using formula as suggested by Burton and Devane (1953). Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated using formula given by Burton (1952). The proportion of phenotypic and genotypic variances expressed in percentage known as the broad sense heritability was calculated utilizing the formula given by Johnson *et al.* (1955). Genetic advance and genetic advance as a percentage of mean was assessed as per scale given by Johanson *et al.* (1955). The correlation was estimated from the analysis of variance and co-various as suggested by Searle (1961). The significance of correlation co-efficient (r) was tested by comparing the observed value or correlation co-efficient with the tabulated value for (n-2) degree of freedom (Snedecar and Cochran, 1967). Path-coefficient analysis was done to partition the total correlation into direct and indirect effects due to the dependent variable. Wright (1934) suggested this analysis and it was further elaborated by Dewey and Lu (1959).

## Results and Discussion

Analysis of variance indicated highly significant differences for all the characters. Significant difference between treatments suggests variability among the genotypes, along with wide range of characters to select

for improvement. Treatments indicated highly significant difference for plant height and main raceme length and low significant for number of siliqua on main raceme and 1000- seed weight (Table 1).

Phenotypic coefficients of variation were higher than genotypic coefficient of variation for all the characters. Similar results were reported by Bind *et al.* (2014), Dewar *et al.* (2018), Iqbal *et al.* (2015), Meena *et al.* (2017) suggesting influence of environment. The values of GCV and PCV were found to be comparable for three traits *i.e.* plant height (GCV=10.4, PCV=11.2), siliqua length (GCV=11.3, PCV=12.0) and days to 50% flowering (GCV=10.8, PCV=11.3). Higher genotypic coefficient of variation coupled with higher phenotypic coefficients of variation was recorded for seeds per siliqua (GCV=30.5, PCV=32.6) (Table 2).

The high heritability coupled with high genetic advance was found for days to 50% flowering, number of siliqua/ plant, siliqua length, seeds/ siliqua, 1000 -seed weight, seed yield/ plant, seed yield/ plot, biological yield and seed yield (q/ha) (Table 2). Similar results were reported by Akbar *et al.* 2003, Singh, 2004, Neelam *et al.*, 2014, Uddin *et al.*, 1995, Pant & Singh, 2001, Acharya & Pati, 2008, Meena *et al.*, 2017 and Roy *et al.*, 2018 for various traits in Indian mustard.

The genotypic and phenotypic correlation coefficients are presented in Table 3 and Table 4, respectively. Seed yield (q/ha) showed significant positive correlation with number of secondary branches, seed yield/ plant, seed yield/ plot and biological yield. Biological yield was found to be significantly correlated with plant height, number of secondary branches and number of siliqua/ plant. Seed yield per plant showed positive correlation with plant height, number of siliqua/ plant, main raceme length and siliqua on main raceme. Test weight was positively correlated with siliqua length. Number of siliqua/ plant showed positive correlation with plant height only. On the other hand, plant height also showed positive correlation with traits as main raceme length, siliqua on main raceme, seed yield/ plant and biological yield. Number of seeds/ siliqua an important yield attributes showed positive correlation with days to 50% flowering, number of primary branches and siliqua length. Seed yield/ plant showed significant negative correlation with number of seeds/ siliqua and number of secondary branches. This implies that selection for seeds/ siliqua and number of secondary branches will not be reliable criteria for improvement of seed yield/ plant.

Higher value of genotypic correlation coefficient than

Table 1: Analysis of variance for 14 yield characters in Indian mustard

Characters/ Mean sum of square	PH	DTF 50%	NPB	NSB	NSP	SL	SS	MRL	NSMR	TGW	SYP1	SYP	BYP	SY
Replication (d.f.=2)	721.4**	2.6	1.95**	1.92	6912.2	0.06	4.58	84.7**	44.2*	0.4*	10.5**	1641	141.9**	0.3
Treatment (d.f.=37)	1238.6**	94.4**	1.34**	3.38**	10129.9**	0.9**	54.9**	188.4**	81.5**	0.9**	10.8**	11553.7**	160.1**	15.5**
Error (d.f.=74)	65.4	2.9	0.38	1.3	1425.9	0.03	2.47	5.3	13.5	0.1	1.6	902.6	16.3	1.2

Where, \*\*significant at 1% level of significance, \*significant at 5% level of significance, (PH)=Plant height(cm), (DTF 50%)=Days to 50% flowering, (NPB)=No. of primary Branches, (NSB)=No. of secondary branches, (NSP)=No. of siliqua/plant, (SL)=siliqua length(cm), (SS)=seeds/siliqua, (MRL)=main raceme length(cm), (NSMR)=No. of siliqua on main raceme, (TGW)=1000 seed Wt. (gm), (SYP1)=seed yield/plot(gm), (SYP)=seed yield/plot(gm), (BYP)=biological yield (gm), (SY)=seed yield (q/ha).

Table 2: Estimate of genetic parameters for 14 quantitative characters studied among 38 genotypes of Indian mustard

Characters	PH	DTF 50%	NPB	NSB	NSP	SL	SS	MRL	NSMR	TGW	SYP1	SYP	BYP	SY
GCV (%)	10.4	10.8	9.7	9.5	19.2	11.3	30.5	8.8	10	11.9	15.9	16.2	15.2	16.8
PCV (%)	11.2	11.3	14.4	16.3	23.5	12	32.6	11.2	12.7	14	19.8	18.2	17.6	18.9
h <sup>2</sup> (%)	85	91	45	34	67	88	87	62	62	72	64	79	74	79
GA	37.7	10.8	0.78	1.0	90.8	1.04	8.06	7.8	7.7	0.91	2.8	109.6	12.3	4

GA as % of Mean 19.9 21.3 13.4 11.5 32.4 22 58.9 14.3 16.4 21 26.3 29.9 27.1 30.8  
 Where, (PH)=Plant height (cm), (DTF 50%)=Days to 50% flowering, (NPB)=No. of primary Branches, (NSB)=No. of secondary branches, (NSP)=No. of siliqua/plant, (SL)=siliqua length(cm), (SS)=seeds/siliqua, (MRL)=main raceme length (cm), (NSMR)=No. of siliqua on main raceme, (TGW)=1000 seed Wt. (gm), (SYP1) seed yield/plot (gm), (SYP)=seed yield/plot(gm), (BYP)=biological yield (gm), (SY)=seed yield (q/ha).

Table 3: Genotypic correlation coefficient among 14 quantitative characters studied among 38 genotype of Indian mustard

Characters	PH	DTF 50%	NPB	NSB	NSP	SL	SS	MRL	NSMR	TGW	SYP1	SYP	BYP
PH	1.00												
DTF 50%	0.09	1.00											
NPB	-0.032	-0.189*	1.00										
NSB	-0.185*	0.199*	-0.284**	1.00									
NSP	0.383**	-0.139	-0.039	0.292**	1.00								
SL	-0.247**	-0.02	-0.185*	-0.317**	-0.599**	1.00							
SS	-0.472**	0.206*	0.386**	-0.009	-0.716**	0.38**	1.00						
MRL	0.287**	-0.250**	-0.257**	-0.056	0.310**	-0.196*	-0.453**	1.00					
NSMR	0.395**	-0.137	-0.050	-0.219*	0.601**	-0.649**	-0.562**	0.598**	1.00				
TGW	-0.137	0.035	-0.107	-0.227**	-0.362**	0.583**	-0.015	-0.309**	-0.655**	1.00			
SYP1	0.470**	-0.130	-0.073	-0.156*	0.378**	-0.127	-0.464**	0.334**	0.287**	0.040	1.00		
SYP	0.136	-0.280**	-0.317**	0.173	0.067	0.145	-0.322**	0.102	-0.111	0.277**	0.232**	1.00	
BYP	0.469**	-0.05	-0.019	0.223**	0.683**	-0.283**	-0.597**	0.384**	0.420**	-0.035	0.760**	0.181*	1.00
SY	0.147	-0.393	-0.196	0.198	0.096	0.058	-0.281	0.131	0.008	0.122	0.214	0.945	0.182

\*\*significant at 1% level of significance; \*significant at 5% level of significance

Where, (PH)=Plant height (cm), (DTF 50%)=Days to 50% flowering, (NPB)=No. of primary Branches, (NSB)=No. of secondary branches, (NSP)=No. of siliqua/plant, (SL)=siliqua length(cm), (SS)=seeds/siliqua, (MRL)=main raceme length (cm), (NSMR)=No. of siliqua on main raceme, (TGW)=1000 seed Wt. (gm), (SYP1) seed yield/plot (gm), (SYP)=seed yield/plot(gm), (BYP)=biological yield (gm), (SY)=seed yield (q/ha).

Table 4: Phenotypic correlation coefficient among 14 quantitative characters studied among 38 genotypes of Indian mustard

Characters	PH	DTF 50%	NPB	NSB	NSP	SL	SS	MRL	NSMR	TGW	SYP1	SYP	BYP
PH	1.00	0.067	0.031	-0.067	0.331**	-0.241**	-0.385**	0.199*	0.322**	-0.126	0.387**	0.119	0.396**
DTF 50%		1.00	-0.134	-0.077	-0.144	0.006	0.171	-0.170	-0.132	0.063	-0.098	-0.246**	-0.069
NPB			1.00	0.035	0.083	-0.127	0.255**	-0.156	0.036	-0.077	0.022	-0.145	-0.008
NSB				1.00	0.395**	-0.174	-0.006	0.042	-0.017	-0.168	-0.052	0.157	0.227*
NSP					1.00	-0.492**	-0.540**	0.262**	0.535**	-0.269**	0.365**	0.120	0.568**
SL						1.00	0.293**	-0.156	-0.502**	0.501**	-0.077	0.117	-0.226*
SS							1.00	-0.356**	-0.399**	-0.02	-0.344**	-0.256**	-0.462**
MRL								1.00	0.505**	-0.173	0.232*	0.116	0.278**
NSMR									1.00	-0.492**	0.241**	-0.0007	0.353**
TGW										1.00	0.0409	0.240*	-0.052
SYP1											1.00	0.199*	0.562**
SYP												1.00	0.217*
BYP													1.00
SY	0.124	-0.330	-0.040	0.188	0.166	0.067	-0.234	0.178	0.082	0.141	1.212	0.872	0.209

\*\*significant at 1% level of significance; \*significant at 5% level of significance

Where, (PH)=Plant height (cm), (DTF 50%)=Days to 50% flowering, (NPB)=No. of primary Branches, (NSB)=No. of secondary branches, (NSP)=No. of siliqua/plant, (SL)=siliqua length(cm), (SS)=seeds/siliqua, (MRL)=main raceme length (cm), (NSMR)=No. of siliqua on main raceme, (TGW)=1000 seed Wt. (gm), (SYP1) seed yield/plot (gm), (SYP)=seed yield/plot(gm), (BYP)=biological yield (gm), (SY)=seed yield (q/ha).

Table 5: Genotypic direct and indirect effect of 14 characters of yield of seed yield (q/ha) in Indian mustard

Characters	PH	DTF 50%	NPB	NSB	NSP	SL	SS	MRL	NSMR	TGW	SYP1	SYP	BYP
PH	0.0109	0.0010	-0.0004	-0.0020	0.0042	-0.0027	-0.0051	0.0031	0.0043	-0.0015	0.0051	0.0015	0.005
DTF 50%	-0.0158	-0.1669	0.0317	-0.0333	0.0233	0.0034	-0.0344	0.0418	0.0229	-0.0060	0.0218	0.0468	0.008
NPB	0.0027	0.0157	-0.0825	0.0235	0.0033	0.0153	-0.0319	0.0212	0.0041	0.0089	0.0060	0.0262	0.002
NSB	0.0334	-0.0360	0.0513	-0.1805	-0.0528	0.0572	0.0017	0.0102	0.0397	0.0411	0.0283	-0.0312	-0.040
NSP	-0.0563	0.0206	0.0058	-0.0430	-0.1470	0.0882	0.1054	-0.0456	-0.0884	0.0533	-0.0556	-0.0099	-0.101
SL	0.0406	0.0034	0.0305	0.0520	0.0984	-0.1642	-0.0624	0.0322	0.1066	-0.0957	0.0210	-0.0239	0.047
SS	-0.0351	0.0153	0.0287	-0.0007	-0.0532	0.0282	0.0743	-0.0337	-0.0418	-0.0012	-0.0345	-0.0240	-0.044
MRL	-0.0164	0.0143	0.0146	0.0032	-0.0177	0.0112	0.0258	-0.0569	-0.0341	0.0176	-0.0191	-0.0058	-0.022
NSMR	-0.0586	0.0203	0.0074	0.0325	-0.0891	0.0962	0.0833	-0.0887	-0.1481	0.0970	-0.0426	0.0164	-0.062
TGW	0.0343	-0.0089	0.0267	0.0566	0.0902	-0.1450	0.0039	0.0768	0.1630	-0.2487	-0.0101	-0.0691	0.009
SYP1	-0.1027	0.0285	0.0160	0.0342	-0.0825	0.0279	0.1013	-0.0731	-0.0627	-0.0088	-0.2182	-0.0507	-0.166
SYP	0.1373	-0.2815	-0.3182	0.1736	0.0679	0.1460	-0.3235	0.1027	-0.1113	0.2787	0.2330	1.0030	0.180
BYP	0.1722	-0.0184	-0.0073	0.0818	0.2507	-0.1041	-0.2190	0.1409	0.1541	-0.0131	0.2788	0.0658	0.367
SY	0.1465	-0.3926	-0.1957	0.1980	0.0957	0.0576	-0.2806	0.1310	0.0082	0.1217	0.2140	0.9451	0.182
Partial R <sup>2</sup>	0.0016	0.0655	0.0162	-0.0357	-0.0141	-0.0095	-0.0208	-0.0075	-0.0012	-0.0303	-0.0467	0.9479	0.067

Residual effect =SQRT (0.2603)

Where, (PH)=Plant height (cm), (DTF 50%)=Days to 50% flowering, (NPB)=No. of primary Branches, (NSB)=No. of secondary branches, (NSP)=No. of siliqua/plant, (SL)=siliqua length(cm), (SS)=seeds/siliqua, (MRL)=main raceme length (cm), (NSMR)=No. of siliqua on main raceme, (TGW)=1000 seed Wt. (gm), (SYP1) seed yield/plot (gm), (SYP)=seed yield/plot(gm), (BYP)=biological yield (gm), (SY)=seed yield (q/ha)

Table 6: Phenotypic direct and indirect effect of 14 characters of yield of seed yield (q/ha) in Indian mustard

Characters	PH	DTF 50%	NPB	NSB	NSP	SL	SS	MRL	NSMR	TGW	SYP1	SYP	BYP
PH	0.0218	0.0015	0.0007	-0.0015	0.0072	-0.0053	0.0044	0.0044	0.0070	-0.0028	0.0085	0.0026	0.0087
DTF 50%	-0.0072	-0.1077	0.0144	-0.0083	0.0156	-0.0007	-0.0185	0.0183	0.0142	-0.0068	0.0106	0.0265	0.0075
NPB	0.0021	-0.0093	0.0693	0.0024	0.0058	-0.0088	0.0177	-0.0108	0.0025	-0.0054	0.0015	-0.0101	-0.0006
NSB	-0.0056	0.0065	0.0030	0.0840	0.0332	-0.0146	-0.0006	0.0035	-0.0015	-0.0141	-0.0044	0.0132	-0.0191
NSP	-0.0063	0.0028	-0.0016	-0.0076	-0.0191	0.0094	0.0103	-0.005	-0.0102	0.0051	-0.0070	-0.0023	-0.0109
SL	-0.0059	0.0002	-0.0031	-0.0043	-0.0120	0.0245	0.0072	-0.0038	-0.0123	0.0123	-0.0019	0.0029	-0.0055
SS	-0.0030	0.0013	0.002	-0.0001	-0.0042	0.0023	0.0079	-0.0028	-0.0031	-0.0002	-0.0027	-0.0020	-0.0036
MRL	0.0092	-0.0079	-0.0072	0.0019	0.0121	-0.0072	-0.0165	0.0462	0.0233	-0.0080	0.0107	0.0054	0.0129
NSMR	0.0201	-0.0082	0.0023	-0.0011	0.0333	-0.0313	-0.0249	0.0315	0.0623	-0.0307	0.0151	0.0000	0.0220
TGW	0.0018	-0.0009	0.0011	0.0025	0.0039	-0.0073	0.0003	0.0025	0.0072	-0.0146	-0.0006	-0.0035	0.0008
SYP1	0.0160	-0.0041	0.0009	-0.0022	0.0151	-0.0032	-0.0142	0.0096	0.0100	0.0017	0.0413	0.0082	0.0232
SYP	0.1002	-0.2071	-0.1229	0.1325	0.1018	0.0986	-0.2162	0.0976	-0.0006	0.2020	0.1674	0.8415	0.1827
BYP	-0.0188	0.0033	0.0004	-0.0108	-0.0269	0.0107	0.0219	-0.0132	-0.0167	0.0025	-0.0266	-0.0103	-0.0473
SY	0.1244	-0.3296	-0.0404	0.1876	0.1657	0.0669	-0.2340	0.1780	0.0822	0.1410	0.2118	0.8721	0.2089
Partial R <sup>2</sup>	0.0027	0.0033	-0.0028	0.0157	-0.0032	0.0016	-0.0018	0.0082	0.0051	-0.0021	0.0087	0.7339	-0.0099

Residual effect =SQRT (0.4563)

Where, (PH)=Plant height (cm), (DTF 50%)=Days to 50% flowering, (NPB)=No. of primary Branches, (NSB)=No. of secondary branches, (NSP)=No. of siliqua/plant, (SL)=siliqua length(cm), (SS)=seeds/siliqua, (MRL)=main raceme length (cm), (NSMR)=No. of siliqua on main raceme, (TGW)=1000 seed Wt. (gm), (SYP1) seed yield/plot(gm), (SYP)=seed yield/plot(gm), (BYP)=biological yield (gm), (SY)=seed yield (q/ha).

phenotypic correlation coefficient suggests that there is strong genetic association between two correlated characters but the lesser phenotypic value is due to significant interaction of environment. In general higher values of genotypic correlation coefficient were observed as compared to phenotypic correlation coefficient for all important yield attributing traits. Seed yield (q/ha) showed higher genotypic correlation than phenotypic correlation for number of secondary branches, seed yield per plant, seed yield per plot and biological yield. Similarly, seed yield per plant exhibited higher genotypic correlation coefficient than phenotypic correlation coefficient for traits such as plant height, number of siliqua per plant, main raceme length and number of siliqua on main raceme. Similar results were reported by Bind *et al.* (2014) for seed yield per plant; Lodhi *et al.* (2014) for siliqua length, number of seeds/ siliqua and seed yield/ plant; Mohan *et al.* (2017) for biological yield, harvest index, 1000-seed weight and oil content; Bineeta Devi (2018) for biological yield per plant and siliqua on main raceme and Dawar *et al.* (2018).

Path coefficient analysis revealed that highest positive direct effect on seed yield (q/ha) was exhibited by seed yield/ plot followed by biological yield, seeds/ siliqua and plant height. Negative direct effect on seed yield was recorded for day to 50% flowering, number of primary branches/ plant, number of secondary branches/ plant, number of siliqua/ plant, siliqua length, main raceme length, number of siliqua on main raceme, test weight and seed yield/ plant at genotypic level (Table 5). At phenotypic level path coefficient analysis revealed that highest positive direct effect on seed yield (q/ha) was exhibited by plant height, number of primary branches/ plant, number of secondary branches/ plant, siliqua length, seeds/ siliqua, main raceme length, number of siliqua on main raceme, number of siliqua/ plant and seed yield/ plot. Negative direct effect on seed yield (q/ha) was recorded for day to 50% flowering, number of siliqua/ plant, test weight and biological yield (Table 6). Genotypic and phenotypic residual effect values were 0.2603 and 0.463 respectively.

Traits like number of secondary branches per plant, number of siliqua per plant, siliqua length, seeds per siliqua, main raceme length, number of siliqua on main raceme, test weight, seed yield per plant showed positive correlation was due to indirect effect and hence during selection, the selection pressure should be given on the trait that exhibit indirect effects. The high positive direct effect on seed yield results are in accordance with results reported by Yadav *et al.* (2011), Bind *et al.* (2014) for biological yield/ plant; Lodhi *et al.* (2014) for seed yield/

plant, Bineeta (2018) for 50 % flowering; Dawar *et al.* (2018) for (g) for siliqua/ plant, plant height, 1000-seed weight; Rout *et al.* (2018) for harvest index and biological yield/ plant; Roy *et al.* (2018) for oil content, leaf area index.

## Conclusion

The variability judged from mean, range and coefficient of variation (CV), was found adequate for all the characters. Direct selection can be followed for traits such as number of siliqua per plant, seeds per siliqua, 1000 - seed weight, seed yield per plant, seed yield per plot, biological yield and seed yield (q/ha) since high values of heritability in broad sense coupled with high genetic advance were recorded for these characters, which is an indication additive gene effects. For characters showing low heritability values, indirect selection can be practised which will eventually improve their heritability. The comparison of mean indicated that among all the traits studied seed yield/ plot showed highest performance followed by number of siliqua per plant and plant height. At genotypic level seed yield was positively correlated with plant height, number of secondary branches, number of siliqua/ plant, siliqua length, main raceme length, number of siliqua on main raceme, test weight, seed yield/ plant, seed yield/ plot and biological yield, therefore these traits can be considered for direct selection. Results of path analysis concluded that traits such as biological yield, seeds/ siliqua and plant height can be regarded as a selection criteria since they showed high positive correlation coefficient and high positive direct effect on seed yield.

Genotypes such as RVM-2 (17.3 q/ha), RGN-73 (16.4 q/ha), JD-6 (16.2 q/ha), RGN-298 (15.9 q/ha) and RGN-48 (15.8 q/ha) were found better than Giriraj (check genotype) for seed yield. Higher genotypic coefficient of variation coupled with higher phenotypic coefficient of variation was recorded for seeds/ siliqua. Seed yield/ plot and biological yield showed high heritability, high genetic advance and positive correlation with the seed yield (q/ha) which was supported by path analysis, we can use these traits as the selection criteria in further breeding programme. The traits like number of siliqua/ plant, siliqua length, test weight and seed yield/ plant can also be considered for practicing selection and selection pressure can be applied on these traits exhibiting high heritability, high genetic advance and were positively correlated with seed yield.

## References

- Acharya NN and Patil P. 2008. Genetic variability, correlation and path analysis in Indian mustard (*B. juncea* L.). *Env Eco* **26**: 2165-2168.



- Akbar M, Mahmood T, Yaqub M, Anwar M, Ali M, and Iqbal N. 2003. Variability, correlation and path coefficient studies in summer mustard (*B. juncea* L.). *Asian J Plant Sci* **2**: 696-698.
- Bind D, Singh D and Dwivedi VK. 2014. Genetic variability and character association in Indian mustard [*B. juncea* (L.) Czern & Coss.]. *Agri Sc Digest* **34**: 183-188.
- Burton GW and Devane EH. 1953. Estimating heritability in tall fescue (*F. arundinacea*) from replicated clonal material 1. *Agro J* **45**: 478-481.
- Burton GW. 1952. Quantitative inheritance in grasses. *Proc. 6<sup>th</sup> Intl Grassland Cong* **1**: 277-283.
- Devi Bineeta. 2018. Studies on correlation and path analysis in Indian mustard (*Brassica juncea* L.) in agro-climatic condition of Jhasi (U.P.). *J Pharmacog Phytochem* **7**: 1678-1681.
- Dewar S, Kumar N and Mishra SP. 2018. Genetic variability, correlation, path coefficient analysis in the Indian mustard [*B. juncea* (L.) Czern & Coss.]. *Int J Curr Micro Appl Sci* **7**: 883-890.
- Fisher RA. 1936. The use of multiple measurements in taxonomic problems. *Ann Eugenics* **7**: 179.
- Iqbal AM, Shikari AB, Ashaq H and Dar ZA. 2015. Genetic variability *B. rapa* var. Brown sarson for maturity, yield and yield attributing traits. *Env Ecol* **33**: 267-270.
- Johanson HW, Robinson HF and Comstock RE. 1955. Estimates of genetic and environmental variability in Soyabean. *Agron J* **47**: 314-315.
- Lodhi B, Thakral NK, Avtar R and Singh A. 2014. Genetic variability, character association and path analysis in Indian mustard (*B. juncea* L.). *J Oilseed Brassica* **5**: 26-31.
- Meena HS, Kumar A, Singh VV, Meena PD, Ram B and Kulshrestha S. 2017. Genetic variability and interrelation of seed yield with contributing traits in Indian mustard (*B. juncea*). *J Oilseed Brassica* **8**: 131-137.
- Mohan S, Yadav RK, Tomar A and Singh M. 2017. Utilization of selection parameter for seed yield and its contributed traits in Indian mustard [*B. juncea* (L.) Czern & Coss.]. *Pharma Innov J* **6**: 306-309.
- Neelam S, Jedeja GC and Jogendra S. 2014. Genetic variability for yield and its components in Indian mustard [*B. juncea* (L.) Czern & Coss.]. *Elect J Plant Breed* **5**: 117-119.
- Panase VG and Sukhatme PV. 1967. Statistical methods for research workers. *ICAR, New Delhi*, 220-40.
- Pant SC and Singh P. 2001. Genetic variability in Indian mustard. *Agri Sci Digest* **21**: 28-30.
- Rout S, Kerkhi SA and Chauhan C. 2018. Character association and path analysis among yield components in Indian mustard [*B. juncea* (L.) Czern & Coss.]. *Int J Curr Micro Appl Sci* **7**: 50-55.
- Roy RK, Kumar A, Kumar S, Kumar A and Kumar RR. 2018. Correlation and path analysis in Indian mustard (*B. juncea* (L.) Czern & Coss.) under late sown condition. *Env Ecol* **36**: 247-254.
- Searle SR. 1965. The value of indirect selection: I. Mass selection. *Biometrics*: 682-707.
- Singh B. 2004. Character association and path analysis under dry land condition in Indian mustard (*B. juncea* L.). *Cruciferae Newsl* **25**: 99-100.
- Snedecor GW. 1967. Statistical methods. NY George W. Snedecor and William G. Cochran. Iowa State University Press.
- Uddin MJ, Chowdhury MAZ and Mia MFU. 1995. Genetic variability, character association and path analysis in Indian mustard [*B. juncea* (L.) Czern & Coss.]. *Ann Ban Agri* **5**: 51-54.
- USDA, 2018. National Agricultural Statistics Service, Acreage report.
- Wright S. 1921. Correlation and causation. *J Agril Res* **20**: 557-585.
- Yadava DK, Giri SC, Vignesh M, Vasudev S, Yadav AK, Dass B and Prabhu KV. 2011. Genetic variability and trait association studies in Indian mustard (*B. juncea* L.). *Indian Agri Sci* **81**: 712.