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ESTIMATION OF MULTIVARIATE CORRELATION AND PATH COEFFICIENT ANALYSIS FOR YIELD AND ITS ASSOCIATED TRAITS AMONG MUTANTS OF INDIAN MUSTARD [*Brassica juncea* (L.) CZERN & COSS]

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ABSTRACT

An investigation was undertaken to study the correlation and path analysis of seventeen quantitative traits in 21 Indian mustard (*Brassica juncea* L.) mutant lines. It was conducted during *rabi* 2019-20 and *rabi* 2020-21 at Agricultural Research Farm, Institute of Agricultural Sciences, BHU, Varanasi. Genotypes were sown under randomized complete block design (RCBD) in 3 replications and observations were recorded for 17 quantitative traits for two consecutive years. The observations recorded were analysed using combined ANOVA. The results of combined ANOVA with genotypes as a source of variation for all the characters was found statistically significant. In case of genotype-environment interaction, it was found that (G×E) interaction was non-significant for all the traits except seeds per siliqua. Correlation study revealed genotypic correlation was statistically significant with a greater number of yield components along with higher magnitude and the traits plant height, days to flowering, length of main raceme, number of siliqua on main raceme, seed yield per plant, biological yield per plant, harvest index, test weight and chlorophyll content had positive correlation and traits number of primary branches and number of secondary branches exhibited negative correlation with yield per hectare. Path analysis showed that maximum positive direct effect was exerted on yield per hectare by seed yield per plant, number of siliqua on main raceme, plant height, number of secondary branches, length of main raceme, test weight and chlorophyll content. These findings have great potential to guide and improve selection and breeding programs focused on enhancing yield in Indian mustard.

Key words: genotypic and phenotypic correlation, path analysis, direct and indirect effects, mutant lines

Introduction

The genus *Brassica* belongs to the family Cruciferae and consists of some economically important species useful for various purposes. India's vegetable oil economy ranks fourth in the world, following the USA, China, and Brazil, accounting for about 20% of global oilseed production. The rapeseed-mustard crop group is the third most important oilseed crop after soybean and palm oil. Globally, India ranks second in terms of cultivation area, covering 6.70 million hectares, following China, and ranks third in production, with 8.50 million tonnes, after China and Canada (USDA, 2020-21). In rapeseed-mustard group of crops, Indian mustard occupies maximum area

(85-90%). Rajasthan stands in first place in production of mustard by 4.51 million tonnes on 2.72 million hectares of land followed by Madhya Pradesh with a production of 1.31 million tonnes and 0.77 million hectares area, in the year 2020 21 (Anonymous, 2021). The species such as *B. campestris*, *B. napus* and *B. juncea* are the allotetraploids from which edible oil is extracted. Their diploid progenitors are *B. nigra*, *B. napus* and *B. carinata* (Nagaharu, 1935). Rai (*B. juncea*) is a popular rapeseed and mustard variety among farmers because of its excellent yield and resistance to lodging, shattering, drought, heat, and disease, as well as saline sodic environments. *Brassica* also thrives in neglected areas

with issues such as soil acidity, low accessible nutrient content, poor drainage, drought, and topographical restrictions (Tripathi *et al.*, 2020).

Mustard is typically grown in temperate climates, but it can also be cultivated as a cold-weather crop in certain tropical and subtropical regions. Indian mustard thrives in a variety of environmental conditions, with annual rainfall ranging from 500 to 4,200 mm, temperatures between 6 and 27°C, and soil pH levels from 4.3 to 8.3. As a C₃ plant, rapeseed-mustard has an efficient photosynthetic response at temperatures of 15–20°C, achieving optimal CO₂ exchange within this range, which decreases at higher temperatures. Rai, a type of mustard, is primarily grown as a rainfed crop and shows moderate tolerance to soil acidity, favouring a pH of 5.5 to 6.8. It thrives in areas with hot days and cool nights and can withstand drought conditions fairly well. Mustard plants prefer well-drained sandy loam soil and have low water requirements (240–400 mm), making them suitable for rainfed cropping systems (Shekhawat *et al.*, 2012).

The primary goal of any crop improvement program is to increase the yield potential of the crop. To achieve this, different factors that influence seed yield are considered and analyzed thoroughly. The yield is complex character reliant on many other morphological traits which are also vastly influenced by the environment; henceforth direct selection for yield alone is inappropriate. It is necessary to examine the contribution of each of the trait in order to get trait having utmost influence on seed yield (Tuncturk and Ciftci, 2007). Hence, yield improvement can be done through selection of yield component traits. Yield component traits are highly associated among themselves and also with yield. Correlation is the measure of mutual relationship between two variables that measures the degree of closeness and the linear relationship between variables. But correlation predominantly doesn't satisfy the purpose of the breeders since it doesn't identify the characters having indirect effects on seed yield. In such circumstance path coefficient analysis created by Wright (1921) is utilized. Path coefficient analysis was used by plant breeders to help identify traits that could be useful as a selection criterion for improving crop yield (Moosavi *et al.*, 2013). Path coefficient analysis is a partial regression strategy that isolates correlation coefficient into direct and indirect effects for yield. Hence, the target of correlation and path coefficients was to evaluate the relationship among yield and yield contributing attributes and distinguishing traits those have the most direct and indirect effect on grain yield. Therefore, present study aimed to quantify the extent of associations between 17 quantitative traits

Table 1: List of genotypes taken under investigation.

S. No	Name of entry/genotype	Source
1	TPM-1	BARC, Trombay.
2	TM-52	BARC, Trombay.
3	TM-53	BARC, Trombay.
4	TM-106	BARC, Trombay.
5	TM-108	BARC, Trombay.
6	TM-108-1	BARC, Trombay.
7	TM-117	BARC, Trombay.
8	TM-130	BARC, Trombay.
9	TM-134	BARC, Trombay.
10	TM-143	BARC, Trombay.
11	TM-172-1	BARC, Trombay.
12	TM-3	BARC, Trombay.
13	TM-179	BARC, Trombay.
14	TM-204	BARC, Trombay.
15	TM-217	BARC, Trombay.
16	TM-263-3	BARC, Trombay.
17	TM-258	BARC, Trombay.
18	TM-273	BARC, Trombay.
19	TM-276	BARC, Trombay.
20	TM-277	BARC, Trombay.
21	KRANTI	I. Ag. Sc BHU, Varanasi.

and yield, as well as the relationships among the traits themselves.

Materials and Methods

Plant material and experimental design

The experiment was conducted at Agriculture Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, UP, India during *rabi* 2019 and *rabi* 2020. The experimental materials consist of 20 mutants of Indian mustard which are derived from Bhabha atomic research centre (BARC) along with the national check Kranti (Table 1). The experimental materials were sown in same field at same location in two different years.

The Experimental Design was Randomized Block Design (RBD) with three replications. Each genotype was grown in five rows in 2019-20 and 2020-21 of 5m length in each replication, 30 cm of row-to-row distance and 10 cm of plant-to-plant distance within row was maintained. All the recommended agronomic package and practices were followed to raise a good crop.

Recording of observations

Data were recorded on 17 different traits namely plant height (PH), days to 50% flowering (DF), days to maturity (DM), number of primary branches (NPB), number of secondary branches (NSB), length of main raceme (LMR), number of siliquae on main raceme

Table 2: Combined/pooled ANOVA of two season for 17 characters in Indian mustard (*Brassicajuncea* L.).

source of variation	df	plant height (cm)	days to 50% flowering	days to maturity	no. of primary branch	no. of secondary branches	length of main raceme (cm)	no. of siliqua on main raceme	no. of siliqua per plant	siliqua length (cm)
replication within year	2	185.98	5.50	18.41	0.26	1.45	71.05*	0.49	1114.56	0.10
year	1	1334.19**	17.43**	12.72*	4.45**	111.12**	401.28**	46.30**	10719.17**	7.68**
year × genotypes	2	10.83	0.22	2.88	0.26	1.25	25.58	1.72	434.86	0.15
overall sum	5	345.56*	5.78	11.06	1.09**	23.30**	118.91**	10.15	2763.60**	1.63**
genotypes	20	1956.89**	203.60**	254.75**	1.34**	36.32**	433.57**	153.18**	13021.09**	0.61**
pooled error	100	137.76	11.91	45.89	0.23	1.92	15.28	14.85	752.09	0.14
C.D. 5%		13.44	3.95	7.76	0.55	1.59	4.48	4.41	31.41	0.42

source of variation	df	seeds per siliqua	seed yield per plant (g)	biological yield per plant (g)	harvest index	test weight (g)	yield per hectare (kg/ha)	canopy temperature deficit	chlorophyll content
replication within year	2	2.45	3.03	2.04	4.31	0.15	65228.61	0.43	22.60
year	1	27.79*	15.77**	145.75	11.74**	2.51**	322388.8**	14.91*	2.51
year × genotypes	2	5.20*	2.08	47.42	0.31	0.20	46707.70	0.12	4.77
overall sum	5	8.62**	5.19**	48.94	4.20	0.64**	109252.28**	3.67	11.45
genotypes	20	4.47**	14.64**	238.41**	35.40**	4.20**	309101.29**	6.28**	71.63**
pooled error	100	1.32	1.25	40.32	5.90	0.19	27539.72	0.89	10.17
C.D. 5%		1.31	1.28	7.27	2.78	0.50	190.09	0.53	3.65

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

(NSMR), number of siliquae per plant (NSPP), siliqua length (SL), seeds per siliqua (SPS), seed yield per plant (SYPP), biological yield per plant (BYPP), harvest index (HI), test weight (TW), seed yield per hectare (SYPH), canopy temperature deficit (CTD), chlorophyll content (CC). Five competitive plants were tagged randomly from each genotype in each replication for recording field observations for all the traits except for days to 50% flowering and days to maturity, which were observed on plot basis during both the years. Harvest index was calculated by dividing seed yield per plant by biological yield per plant.

Statistical analysis

The data recorded for each genotype at each environment were subjected to statistical analysis. The experimental data of two seasons was analysed using combined analysis technique to infer on the influence of year as random variable on the performance of the genotypes. The combined ANOVA technique was used to assess the statistical significance of varietal variances with respect to selected 17 characters/traits. Prior to the combined ANOVA, Bartlett's test was performed to verify the homogeneity of error variances for two seasons. Homogeneity of error variance tests were conducted to determine if data from individual environments (E) could

be pooled to evaluate $G \times E$ interaction using a combined ANOVA as per (Verma *et al.*, 1987). The Homogeneity of error variances were tested with F-test or the 'variance ratio' test as described by (Gomez and Gomez, 1984). For the combined analysis, variation was partitioned into relevant sources of variation to test for differences among genotypes and for the presence of $G \times E$ interaction. The phenotypic and genotypic correlation coefficients were estimated from the analysis of variance and covariance as suggested by Searle (1961). The significance of correlation coefficient was tested using t-test by comparing it with the table value of 'r' given by Fisher and Yates (1963) at (n-2) degrees of freedom. The direct and indirect effects both at genotypic and phenotypic level were estimated by taking yield per hectare as dependent variable using path coefficient analysis suggested by Wright (1921) and Dewey and Lu (1959).

Result and Discussion

Analysis of variance

The data pertaining to 17 characters was recorded for both the seasons. The preliminary analysis of variance was done separately for both season and the mean sum of square values indicated high significant difference among genotypes for all the characters in both the season. The Bartlett's test was found non-significant with 'F_{max}'

value less than three for all the characters. Hence, it was concluded that there existed homogeneity of error variances of seasons. Under homogeneity of error variances, unweighted combined ANOVA was carried out to assess significant mean difference of genotypes across characters. The results of combined ANOVA with genotypes as a source of variation for all the characters was found statistically significant which reflected the existence of sufficient variability among the genotypes (Table 2). The influence of season indicated by year as source of variation was found statistically significant for all the characters except biological yield per plant and chlorophyll content. Study by Iqbal *et al.*, (2014) showed non-significant G×E interaction for number of siliqua per plant, 1000 seeds weight and days to maturity. Kumari and Kumari (2018) and Mohan Rao and Kumari (2018) also studied influence of G×E effect in mustard. The interaction between genotypes and environment is hypothesized to influence phenotypic characters. This could be captured in interaction effect between genotypes and year. The interaction term was found non-significant for all the characters except seeds per siliqua. This indicated ranking of genotypes across seasons remained constant (Gomez and Gomez, 2010) for all the characters except seeds per siliqua.

Genotypic and phenotypic correlation coefficient

Association of yield per hectare with yield component traits

Seed yield is economical trait for almost all the crops. Thus, information on associated traits to seed yield is vital for selection procedures (Gangapur, 2008). Genotypic (r_g) and phenotypic correlation (r_{ph}) were presented in Table 4 and 3 respectively. The results showed that yield per hectare had highly significant ($p < 0.01$) positive correlations both at genotypic and phenotypic levels with plant height ($r_{ph} = 0.293$, $r_g = 0.396$), days to flowering ($r_{ph} = 0.352$, $r_g = 0.447$), length of main raceme ($r_{ph} = 0.468$, $r_g = 0.614$), number of siliqua on main raceme ($r_{ph} = 0.336$, $r_g = 0.535$), seed yield per plant ($r_{ph} = 0.999$, $r_g = 0.999$), biological yield per plant ($r_{ph} = 0.505$, $r_g = 0.692$), harvest index ($r_{ph} = 0.508$, $r_g = 0.602$), test weight ($r_{ph} = 0.547$, $r_g = 0.736$) and chlorophyll content ($r_{ph} = 0.528$, $r_g = 0.905$). and also, non-significant positive correlation with number of siliqua per plant, siliqua length and seeds per siliqua. And it had nonsignificant negative correlation at phenotypic level and significant negative correlation at genotypic level with number of primary branches ($r_{ph} = -0.041$, $r_g = -0.266$) and number of secondary branches ($r_{ph} = -0.237$, $r_g = -0.367$). Similarly, Mekonnen *et al.*, (2014) showed negative correlation of seed yield with days to flowering, number of pod per plant, number of seeds per pod and pod length at phenotypic level and,

Table 3: Phenotypic correlation coefficient among 17 characters studied among 21 genotypes of Indian mustard (*Brassica juncea* L.) pooled analysis of two years.

	PH	DF	DM	NPB	NSB	LMR	NSMR	NSPP	SL	SPS	SYPP	BYPP	HI	TW	CTD	CC
PH	1	0.494**	0.375**	-0.134	-0.209*	0.626**	0.616**	0.206*	0.072	-0.057	0.292**	0.233**	0.097	0.247**	-0.06	0.195*
DF		1	0.585**	-0.043	-0.122	0.361**	0.392**	0.017	-0.062	-0.053	0.354**	0.232**	0.117	0.345**	-0.224*	0.314**
DM			1	-0.087	-0.051	0.15	0.166	-0.039	-0.075	-0.305**	0.17	0.213*	-0.043	0.287**	-0.168	0.035
NPB				1	0.491**	-0.056	-0.057	0.225*	-0.0001	0.031	-0.033	-0.196*	0.163	-0.299**	-0.117	-0.183*
NSB					1	-0.179*	-0.11	0.378**	-0.026	-0.076	-0.232**	-0.197*	-0.064	-0.336**	-0.071	-0.245**
LMR						1	0.772**	0.365**	0.216*	-0.065	0.468**	0.366**	0.128	0.394**	0.054	0.314**
NSMR							1	0.495**	0.180*	-0.063	0.337**	0.226*	0.135	0.314**	0.018	0.371**
NSPP								1	0.095	0.037	0.228*	0.08	0.16	0.128	0.141	0.145
SL									1	0.188*	0.181*	0.082	0.098	0.167	0.127	-0.002
SPS										1	0.171	-0.123	0.303**	0.007	0.107	-0.001
SYPP											1	0.508**	0.506**	0.554**	0.151	0.531**
BYPP												1	-0.446**	0.364**	0.055	0.330**
HI													1	0.232**	0.135	0.219*
TW														1	0.279**	0.366**
CT															1	-0.107
CC																1
YH	0.293*	0.352**	0.17	-0.041	-0.237	0.468**	0.336**	0.222	0.183	0.171	0.9991**	0.505**	0.508**	0.547**	0.146	0.528**

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

Where,

PH = Plant height (cm), DF= Days to 50% flowering, DM= Days to maturity, NPB= Number of primary branches, NSB = Number of secondary branches, LMR= Length of main raceme (cm), NSMR = number of siliquae on main raceme, NSPP= Number of siliquae per plant, SL= Siliqua length (cm), SPS = Seeds per siliqua, SYPP= Seed yield per plant (g), BYPP = Biological yield per plant (g), HI= Harvest index, TW=Test weight (g), CTD= Canopy Temperature deficit, CC= Chlorophyll Content, YH = Yield (kg/ha).

Table 4: Genotypic correlation coefficient among 17 characters studied among 21 genotypes of Indian mustard (*Brassica juncea* L.) pooled analysis of two years.

	PH	DF	DM	NPB	NSB	LMR	NSMR	NSPP	SL	SPS	SYPP	BYPP	HI	TW	CTD	CC
PH	1	0.721**	0.639**	-0.260*	-0.2456	0.745**	0.706**	0.161	0.0012	-0.286*	0.390**	0.400**	0.1239	0.307*	0.0066	0.318*
DF		1	0.847**	-0.2259	-0.1959	0.437**	0.571**	-0.0149	-0.1821	-0.301*	0.446**	0.370**	0.1893	0.446**	-0.409**	0.502**
DM			1	-0.300*	-0.0938	0.285*	0.285*	-0.0806	-0.272*	-0.248*	0.307*	0.365**	0.0071	0.402**	-0.506**	0.392**
NPB				1	0.522**	-0.1447	-0.0697	0.2477	0.0111	-0.1834	-0.249*	-0.343**	0.0699	-0.489**	-0.212	-0.374**
NSB					1	-0.2316	-0.1457	0.487**	-0.1711	-0.0208	-0.359**	-0.269*	-0.1913	-0.391**	-0.2072	-0.403**
LMR						1	0.860**	0.362**	0.306*	-0.347**	0.612**	0.708**	0.0807	0.478**	0.0856	0.450**
NSMR							1	0.511**	0.2	-0.318*	0.529**	0.544**	0.1275	0.468**	0.0186	0.530**
NSPP								1	0.1301	-0.0493	0.1803	0.1545	0.0848	0.1766	0.298*	0.1947
SL									1	0.1393	0.284*	0.351**	0.031	0.311*	0.1973	0.137
SPS										1	0.0285	-0.1391	0.266*	0.0388	0.530**	0.0279
SYPP											1	0.698**	0.596**	0.739**	0.259*	0.902**
BYPP												1	-0.1699	0.614**	0.0142	0.747**
HI													1	0.296*	0.332**	0.376**
TW														1	0.443**	0.631**
CT															1	0.043
CC																1
YH	0.396**	0.447**	0.306*	-0.266*	-0.367**	0.614**	0.535**	0.1715	0.281*	0.0223	0.9997**	0.692**	0.602**	0.736**	0.259*	0.905**

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

Where,

PH = Plant height (cm), DF= Days to 50% flowering, DM= Days to maturity, NPB= Number of primary branches, NSB = Number of secondary branches, LMR= Length of main raceme (cm), NSMR = number of siliquae on main raceme, NSPP= Number of siliquae per plant, SL= Siliqua length (cm), SPS = Seeds per siliqua, SYPP= Seed yield per plant (g), BYPP = Biological yield per plant (g), HI= Harvest index, TW=Test weight (g), CTD= Canopy Temperature deficit, CC= Chlorophyll Content, YH = Yield (kg/ha).

with primary branches per plant and harvest index at genotypic level. Kumar *et al.*, (2016) and Sowmya *et al.*, (2024) showed positive correlation of seed yield with the 1000-seed weight, biological yield per plant and the harvest index both genotypic and phenotypic level. In a study Chaudhary *et al.*, (2023) showed Seed yield per plant had significant positive genotypic correlation with biological yield per plant, number of primary branches and seeds per siliqua. Similarly, Shekhawat *et al.*, (2014),

Kalyar and Salim (2015), Yadav *et al.*, (2023) showed significant association of seed yield per plant with siliqua per plant, test weight, days to 50 % flowering, main shoot length and plant height. Guguloth *et al.*, (2023) suggests more emphasis should be given to traits harvest index, siliqua/plant and biological yield for selection of genotypes since they exhibited positive significant correlation with seed yield/plant. Diagrammatic representation of phenotypic and genotypic correlation were shown in Fig. 1 and 3 respectively and also shaded

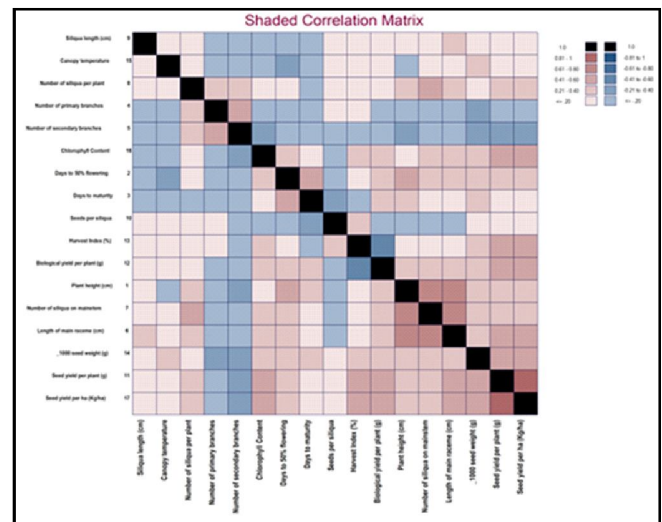
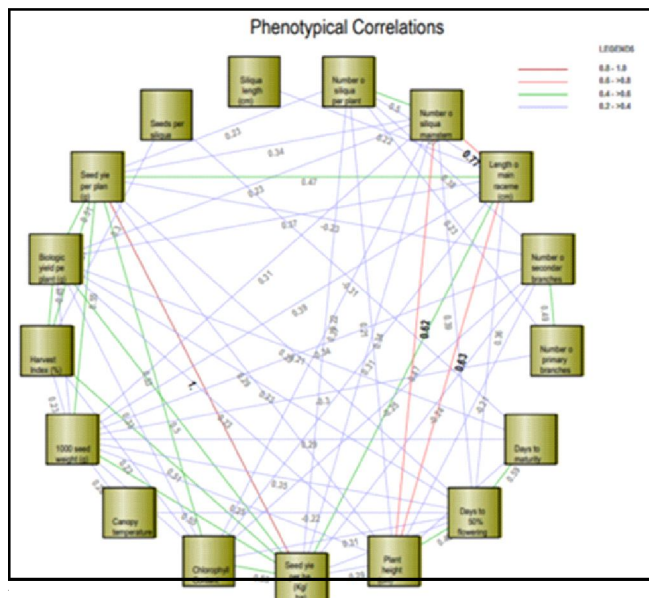


Fig. 2: Figure of phenotypic shaded correlation matrix

correlation matrices, simplifying the intensity of correlations among 17 characters were shown in Fig. 2 and 4 for both phenotypic and genotypic correlation respectively.

Association among yield component traits

In comparison to phenotypic correlations, genotypic correlation coefficients were significant for the majority of characteristics. This reflects the influence of environment on the traits under study. When the magnitude of the correlation coefficients was taken into account, the genotypic correlation coefficients were slightly greater than the phenotypic correlation coefficients. This demonstrated that, despite the significant underlying relationship between the numerous character pairings investigated, the environment can influence how traits are expressed. Saini *et al.*, (2023) showed similar results while evaluating seven parents and their diallel crosses excluding reciprocals in mustard.

The trait plant height was positively and significantly associated with DF, DM, LMR, NSMR, BYPP, TW, CC and negatively and significantly associated with NPB and SPS both at phenotypic and genotypic level. At genotypic and phenotypic levels, days to 50% flowering was found significantly and positively correlated with DM, LMR, NSMR, BYPP, TW and CC. Many researchers have shown similar finding in their study (Gupta *et al.*, 2018; Devi, 2017; Rout *et al.*, 2018) and significantly negatively correlated with SPS and CTD. Similar finding was reported by Kalyar and Salim (2015).

At both genotypic and phenotypic levels, number of primary and secondary branches were found significantly

and positively associated with each other. The trait NPB was found significantly and negatively associated with BYPP, TW and CC. Both traits had positive association with NSPP. These results are in conformed with the study by Kerkhi *et al.*, (2018), Shekhawath *et al.*, (2014) and Yadav and Yadav (2020). The trait’s LMR and NSMR registered positive significant correlation with NSPP, SL, BYPP, TW and CC and significant negative correlation with SPS under both phenotypic and genotypic level. Similar results were reproduced in studies by Bind *et al.* (2014), Yadav and Yadav (2020) and Devi *et al.*, (2018) in mustard. NSPP had positive significant association with NSB, LMR, NSMR (Kerkhi *et al.*, 2018; Shekhawath *et al.*, 2014) and the association of SL with SPS and LMR was positive significant. Yadav and Yadav (2020) and Singh *et al.*, (2013) confirms these finding. SPS was found to have positive significant association with HI and negative significant association with LMR and NSMR. This result is in accordance with Gupta *et al.*, (2018), Devi *et al.*, (2018), Shekhawath *et al.*, (2014) but Rout *et al.*, (2018) and Kerkhi *et al.*, (2018) showed contradictory results.

Despite great yields, modern farmers now prefer bolded seed varieties that sells for a higher price in the market. As a result, in order to boost the boldness of mustard seed, traits related with TW were selected during the yield improvement programme. Characters that are positively related with TW are LMR, NSMR, BYPP and CC. this type of association was also seen in studies by Bind *et al.*, (2014) and Singh *et al.*, (2013). Therefore, these traits should be taken into account while selecting for improved mustard seed boldness while undertaking improvement of mustard seed yield and ideotype breeding. The relationship between chlorophyll content

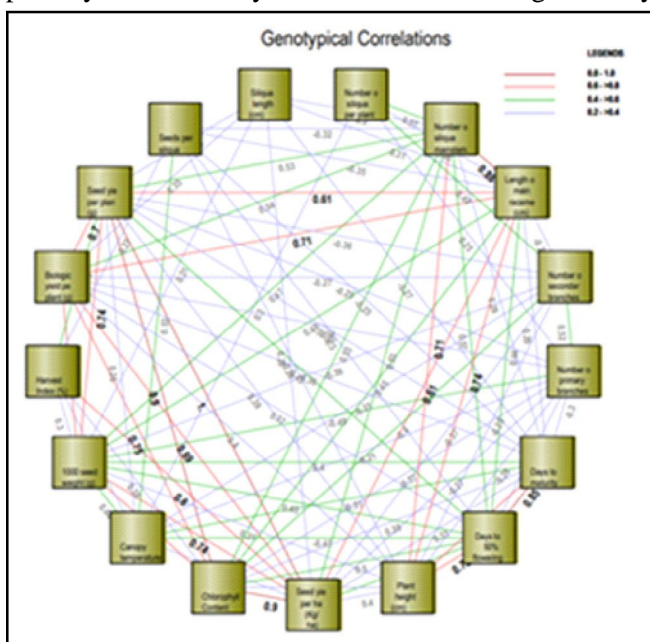


Fig. 3: Figure of genotypic correlation coefficient.

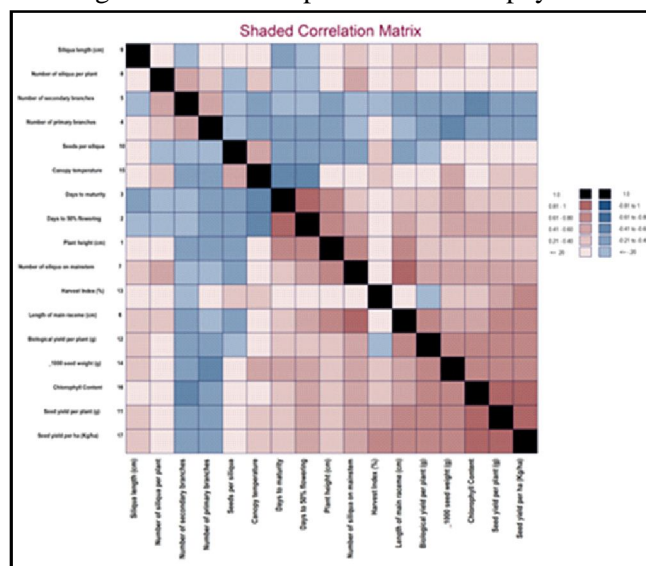


Fig. 4: Figure of genotypic shaded correlation matrix.

Table 5: Phenotypic direct and indirect effect among 17 characters studied among 21 genotypes of Indian mustard (*Brassica juncea* L.) pooled analysis of two years.

	PH	DF	DM	NPB	NSB	LMR	NSMR	NSPP	SL	SPS	SYPP	BYPP	HI	TW	CTD	CC
PH	-0.0007	-0.0004	-0.0003	0.0001	0.0002	-0.0005	-0.0005	-0.0002	-0.0001	0.0001	-0.0002	-0.0002	-0.0001	-0.0002	0.000	-0.0001
DF	-0.002	-0.004	-0.0023	0.0002	0.0005	-0.0014	-0.0016	-0.0001	0.0002	0.0002	-0.0014	-0.0009	-0.0005	-0.0014	0.0009	-0.0013
DM	0.001	0.0016	0.0028	-0.0002	-0.0001	0.0004	0.0005	-0.0001	-0.0002	-0.0008	0.0005	0.0006	-0.0001	0.0008	-0.0005	0.0001
NPB	0.0016	0.0005	0.001	-0.0116	-0.0057	0.0007	0.0007	-0.0026	0.0001	-0.0004	0.0004	0.0023	-0.0019	0.0035	0.0014	0.0021
NSB	0.0008	0.0005	0.0002	-0.0019	-0.0038	0.0007	0.0004	-0.0014	0.0001	0.0003	0.0009	0.0008	0.0002	0.0013	0.0003	0.0009
LMR	0.0014	0.0008	0.0003	-0.0001	-0.0004	0.0022	0.0017	0.0008	0.0005	-0.0001	0.001	0.0008	0.0003	0.0009	0.0001	0.0007
NSMR	0.0011	0.0007	0.0003	-0.0001	-0.0002	0.0014	0.0018	0.0009	0.0003	-0.0001	0.0006	0.0004	0.0002	0.0006	0.0001	0.0007
NSPP	-0.0005	0.0001	0.0001	-0.0005	-0.0009	-0.0009	-0.0012	-0.0023	-0.0002	-0.0001	-0.0005	-0.0002	-0.0004	-0.0003	-0.0003	-0.0003
SL	0.0002	-0.0002	-0.0002	0.0001	-0.0001	0.0006	0.0005	0.0002	0.0026	0.0005	0.0005	0.0002	0.0003	0.0004	0.0003	0.0001
SPS	0.0001	0.0001	0.0003	0.0001	0.0001	0.0001	0.0001	0.0001	-0.0002	-0.001	-0.0002	0.0001	-0.0003	0.0001	-0.0001	0.0001
SYPP	0.2979	0.3613	0.1732	-0.0343	-0.2363	0.4772	0.3439	0.2326	0.1845	0.1744	0.965	0.5173	0.5161	0.5643	0.1542	0.5409
BYPP	-0.0029	-0.0029	-0.0026	0.0024	0.0024	-0.0045	-0.0028	-0.001	-0.001	0.0015	-0.0063	-0.0123	0.0055	-0.0045	-0.0007	-0.0041
HI	-0.0006	-0.0007	0.0003	-0.001	0.0004	-0.0008	-0.0008	-0.001	-0.0006	-0.0019	-0.0032	0.0028	-0.0063	-0.0015	-0.0008	-0.0014
TW	-0.0032	-0.0045	-0.0037	0.0039	0.0043	-0.0051	-0.0041	-0.0017	-0.0022	-0.0001	-0.0071	-0.0047	-0.003	-0.0129	-0.0036	-0.0047
CT	0.0003	0.0012	0.0009	0.0006	0.0004	-0.0003	-0.0001	-0.0008	-0.0007	-0.0006	-0.0008	-0.0003	-0.0007	-0.0015	-0.0054	0.0006
CC	-0.0013	-0.002	-0.0002	0.0012	0.0016	-0.002	-0.0024	-0.0009	0.0001	0.0001	-0.0034	-0.0021	-0.0014	-0.0024	0.0007	-0.0064
YH	0.293*	0.352**	0.17	-0.0415	-0.2377	0.468**	0.336**	0.2225	0.1831	0.1718	0.998**	0.505**	0.508**	0.547**	0.1465	0.528**

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

Where,

PH = Plant height (cm), DF= Days to 50% flowering, DM= Days to maturity, NPB= Number of primary branches, NSB = Number of secondary branches, LMR= Length of main raceme (cm), NSMR = number of siliquae on main raceme, NSPP= Number of siliquae per plant, SL= Siliqua length (cm), SPS = Seeds per siliqua, SYPP= Seed yield per plant (g), BYPP = Biological yield per plant (g), HI= Harvest index, TW=Test weight (g), CTD= Canopy Temperature deficit, CC= Chlorophyll Content, YH = Yield (kg/ha).

(CC) and test weight (TW) can be explained by the fact that higher chlorophyll levels improve the fixation of CO₂ and water into glucose, leading to an increased rate and extent of net photosynthesis in plants. This increased photosynthetic activity directs more photosynthates towards the sink (seeds), thereby increasing seed weight.

Biological yield plays a crucial role in boosting mustard seed production. Since biological yield is closely associated with seed yield, selecting genotypes with

higher biological yields is essential for increasing production. Through the characters like PH, LMR, NSMR, TW and CC, indirect selection could be done to increase the biological yield since these traits are significantly positively associated with biological yield (Gupta *et al.*, 2018; Kerkhi *et al.*, 2018; and Devi *et al.*, 2018). The harvest index is determined by the ratio of economic yield to biological yield. Consequently, economic yield is expected to positively correlate with the harvest index, while total accumulated biomass should show a negative correlation (Gangapur, 2008). Similar results were observed in this study. The harvest index showed a significant positive correlation with SPS, TW, and CC and a significant negative correlation with BYPP. These findings align with those of Gupta *et al.*, (2018) and Devi (2017).

Path coefficient analysis

Correlation coefficients only show the relationship between traits, while path coefficients break down these relationships into the direct and indirect effects of various yield parameters on yield. Seed yield is affected by numerous interconnected components, each of which can directly influence seed yield or have indirect effects through other components not captured by correlation analyses. Path analysis, initially introduced by Wright (1921) and later refined by Dewey and Lu (1957), is an

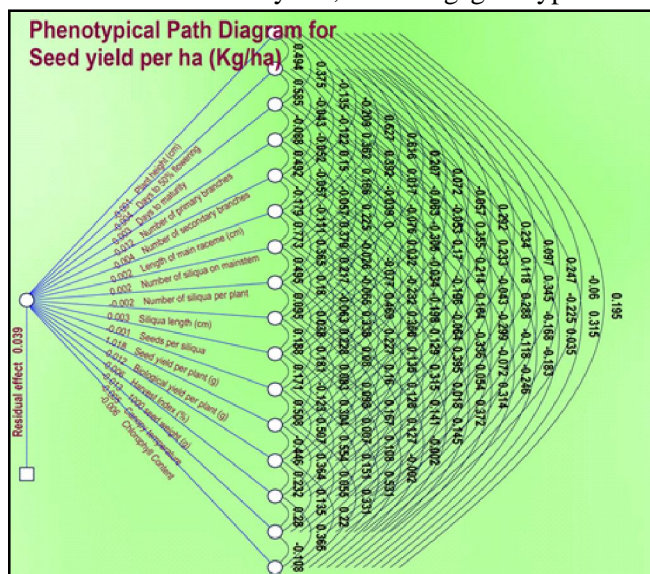


Fig. 5: Figure of phenotypic path coefficient analysis.

Table 6: Genotypic direct and indirect effect among 17 characters studied among 21 genotypes of Indian mustard (*Brassica juncea* L.) pooled analysis of two years.

	PH	DF	DM	NPB	NSB	LMR	NSMR	NSPP	SL	SPS	SYPP	BYPP	HI	TW	CTD	CC
PH	0.033	0.0238	0.0211	-0.0086	-0.0081	0.0246	0.0233	0.0053	0.0001	-0.0094	0.0129	0.0132	0.0041	0.0101	0.0002	0.0105
DF	-0.0554	-0.0769	-0.0651	0.0174	0.0151	-0.0336	-0.0439	0.0011	0.014	0.0231	-0.0343	-0.0285	-0.0145	-0.0343	0.0315	-0.0386
DM	0.0083	0.011	0.013	-0.0039	-0.0012	0.0037	0.0037	-0.001	-0.0035	-0.0032	0.004	0.0047	0.0001	0.0052	-0.0066	0.0051
NPB	0.008	0.0069	0.0092	-0.0306	-0.016	0.0044	0.0021	-0.0076	-0.0003	0.0056	0.0076	0.0105	-0.0021	0.015	0.0065	0.0114
NSB	-0.0072	-0.0058	-0.0028	0.0154	0.0295	-0.0068	-0.0043	0.0144	-0.005	-0.0006	-0.0106	-0.0079	-0.0056	-0.0115	-0.0061	-0.0119
LMR	-0.0325	-0.0191	-0.0125	0.0063	0.0101	-0.0437	-0.0376	-0.0158	-0.0134	0.0152	-0.0268	-0.031	-0.0035	-0.0209	-0.0037	-0.0197
NSMR	0.054	0.0437	0.0218	-0.0053	-0.0111	0.0658	0.0765	0.0391	0.0153	-0.0243	0.0405	0.0416	0.0097	0.0358	0.0014	0.0406
NSPP	-0.0072	0.0007	0.0036	-0.011	-0.0217	-0.0161	-0.0227	-0.0444	-0.0058	0.0022	-0.008	-0.0069	-0.0038	-0.0078	-0.0132	-0.0087
SL	0.0001	-0.0004	-0.0006	0.0001	-0.0004	0.0007	0.0005	0.0003	0.0023	0.0003	0.0006	0.0008	0.0001	0.0007	0.0004	0.0003
SPS	0.0042	0.0044	0.0036	0.0027	0.0003	0.0051	0.0046	0.0007	-0.002	-0.0146	-0.0004	0.002	-0.0039	-0.0006	-0.0078	-0.0004
SYPP	0.4062	0.4648	0.3192	-0.2589	-0.3734	0.6377	0.5507	0.1877	0.2962	0.0297	1.0413	0.7271	0.6205	0.7692	0.2695	0.9395
BYPP	-0.0202	-0.0187	-0.0184	0.0173	0.0136	-0.0358	-0.0275	-0.0078	-0.0177	0.007	-0.0353	-0.0506	0.0086	-0.0311	-0.0007	-0.0378
HI	-0.0014	-0.0022	-0.0001	-0.0008	0.0022	-0.0009	-0.0015	-0.001	-0.0004	-0.0031	-0.0069	0.002	-0.0115	-0.0034	-0.0038	-0.0043
TW	0.0014	0.002	0.0018	-0.0022	-0.0018	0.0022	0.0021	0.0008	0.0014	0.0002	0.0034	0.0028	0.0013	0.0045	0.002	0.0029
CT	-0.0001	0.0048	0.0059	0.0025	0.0024	-0.001	-0.0002	-0.0035	-0.0023	-0.0062	-0.003	-0.0002	-0.0039	-0.0052	-0.0117	-0.0005
CC	0.0052	0.0082	0.0064	-0.0061	-0.0066	0.0073	0.0086	0.0032	0.0022	0.0005	0.0147	0.0122	0.0061	0.0103	0.0007	0.0163
YH	0.396**	0.447**	0.306*	-0.266*	-0.367**	0.614**	0.535**	0.1715	0.281*	0.0223	0.9997	0.692**	0.602**	0.736**	0.259*	0.905**

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

Where,

PH = Plant height (cm), DF= Days to 50% flowering, DM= Days to maturity, NPB= Number of primary branches, NSB = Number of secondary branches, LMR= Length of main raceme (cm), NSMR = number of siliquae on main raceme, NSPP= Number of siliquae per plant, SL= Siliqua length (cm), SPS = Seeds per siliqua, SYPP= Seed yield per plant (g), BYPP = Biological yield per plant (g), HI= Harvest index, TW=Test weight (g), CTD= Canopy Temperature deficit, CC= Chlorophyll Content, YH = Yield (kg/ha).

effective tool for identifying these direct and indirect relationships and highlighting the relative importance of each component in seed yield. In this study, the cause-and-effect relationships between yield and seventeen yield components were analyzed to understand their developmental connections. The results of the path coefficient analysis at both genotypic (Table 6) and phenotypic levels (Table 5) are presented.

At genotypic level, traits plant height, days to maturity, number of secondary branches, number of siliqua on main raceme, siliqua length, seed yield per plant, test weight and chlorophyll content exhibited positive direct effect on yield. And negative direct effect was observed for the traits like days to 50% flowering, number of primary branches, length of main raceme, number of siliquae per plant, seeds per siliqua and biological yield, HI and CTD. At phenotypic level traits DM, LMR, NSMR, SL and SYPP exhibited positive direct effect on yield and remaining traits exhibited negative direct effect. Similar results were presented by many researchers Priyamedha *et al.*, (2013) evaluated one hundred ten early generation (F₃) lines of Indian mustard derived from 5 crosses and showed that number of secondary branches per plant, number of siliquae on main shoot and total siliquae per plant had positive and direct effect on seed yield per plant, indicating that indirect selection for these traits in early

generations would be effective in improving seed yield. According to study by Shekhawat *et al.*, (2014) and Kalyar and Salim *et al.*, (2015) seeds per siliqua, 1000-seed weight and number of siliqua per plant had direct positive effects on seed yield per plant. Saini *et al.*, (2023), Yadav *et al.*, (2023) and Kumar *et al.*, (2023) also showed positive direct effect of traits DM, NSB, TW, PH on seed yield. LMR and DF were having negative direct effect on seed yield in study conducted by Rathore

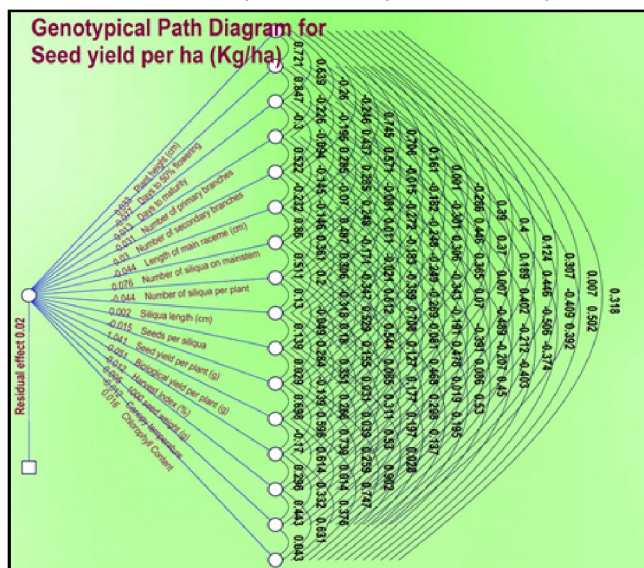


Fig. 6: Figure of genotypic path coefficient analysis.

(2023) and Saini *et al.*, (2023). Negative direct effect of biological yield was reported by Maurya *et al.*, (2019). Positive direct effect of BYPP and SPS was reported by Choudhary *et al.*, (2023) and Rathore (2023). The results suggest that direct selection should be done in breeding programme for increasing the yield for the above traits like LMR, NSMR, SL, TW and SYPP since these characters exhibited positive direct effect and significant positive correlation with yield per hectare.

PH, LMR and NSMR exhibited negative indirect effects on yield via DF, NSPP, BYPP, HI, TW, CC and positive indirect effect via remaining traits. DF exhibited negative indirect effects on yield via DM, SL, BYPP, HI, TW, CC and positive indirect effect via remaining traits. NPB and NSB showed positive indirect effect on yield via PH, DF, BYPP, TW and negative indirect effects via remaining traits. NSPP showed positive indirect effect on yield via LMR, NSMR, SL, SPS, SYPP and negative indirect effects via remaining traits. SPS exhibited positive indirect effect on yield via PH, DF, SL, SYPP, BYPP, CC and negative indirect effects via remaining traits. BYPP showed negative indirect effects on yield via PH, DF, NSPP, TW, CTD, CC and positive indirect effects via remaining traits. HI showed positive indirect effect on yield via NSB, LMR, NSMR, SL, SYPP, BY and negative indirect effects via remaining traits. TW showed negative indirect effects on yield via PH, DF, NSPP, BYPP, HI, CTD, CC and positive indirect effects via remaining traits. The current results are in concordance with previous studies by Singh *et al.*, (2013), Bind *et al.*, (2014), Shekhawat *et al.*, (2014), Kumar *et al.*, (2016), Rout *et al.*, (2018), Saini *et al.*, (2023) and Sowmya *et al.*, (2024).

Conclusion

The correlation coefficient is a valuable tool for identifying relationships between pairs of individual traits. However, it's crucial to understand that a dependent trait like grain yield is not the result of a single characteristic. Instead, it is a complex outcome shaped by the combined interactions of various interconnected component traits. Any change in one of these component traits can potentially disrupt the entire framework of interrelationships. In our study, path analysis helped unravel the complexity of these associations and provided a clearer understanding of how individual component traits influence grain yield. Based on the above findings, it can be concluded that to improve yield and developing a biological model of mustard that is expected to perform predictably, traits like main raceme length, number of siliqua on main raceme, seed yield per plant, biological yield per plant, harvest index, test weight, and chlorophyll

content should be prioritised. Since these traits showed strong positive association with yield per hectare.

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