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Assessment of Genetic Variability, Heritability, Genetic Advance, Correlation and Path Coefficient for Seed Yield and its Component Traits in Indian Mustard [*Brassica juncea* (L.) Czern and Coss.]

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ABSTRACT

The study was conducted during the *rabi* season (October, 2021–March, 2022) at the crop research centre Sardar Vallabhbhai Patel University of Agriculture and Technology Meerut, Uttar Pradesh, India. The field experiment was conducted with 40 genotypes in randomized complete block design with three replications to assess the genetic variability, heritability, genetic advance, correlation, and path coefficient for seed yield and yield-related traits. The Indian mustard genotypes were evaluated for fourteen quantitative traits. The analysis of variance indicated highly significant variations among the genotypes. The highest estimate of GCV and PCV values were observed for grain yield plant^{-1}. The high level of heritability was recorded for grain yield plant^{-1}, biological yield plant^{-1}, siliquae on main axis, length of main axis, number of secondary branches plant^{-1}, siliqua length, days to 50% flowering, 1000 seed weight and number of seeds siliqua^{-1}. Grain yield plant^{-1}, biological yield plant^{-1}, number of secondary branches plant^{-1}, 1000 seeds weight, length of main axis, siliquae on main axis and siliqua length had the highest genetic advance. The seed yield plant^{-1} had a highly significant and positive association with biological yield plant^{-1}, number of secondary branches plant^{-1}, siliquae on main axis, number of primary branches plant^{-1}, siliqua length, number of seeds siliqua^{-1}, length of main axis and harvest index. Among fourteen characters studied the biological yield plant^{-1} recorded the maximum direct effect on seed yield plant^{-1} (both at genotypic and phenotypic levels). This indicated that yield improvement might be achieved by selection based on these traits.

KEYWORDS: Indian mustard, genetic variability, path coefficient, correlation coefficient

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1. INTRODUCTION

The oilseed crops play an important role in agriculture economy of our country. Indian mustard (*Brassica juncea* L.) is the most significant oilseed crop globally and in India, following groundnut (Gupta et al., 2022; Dwivedi et al., 2023; Kumar et al., 2024). It is an annual herbaceous crop commonly known as Rai/Raya/Laha in India (Patel et al., 2021; Kumar et al., 2023) and comes under the Cruciferae (Brassicaceae) family. Cytologically, *Brassica junceais* an amphidiploid (2n=36) resulting from a hybrid between *Brassica* species *i.e. Brassica nigra* (2n=16) and *Brassica compestris* (2n=20) (Nagaharu, 1935). Among the *Brassica* group, Indian mustard is one of the most significant oilseed crops grown in India (Chaurasiya et al., 2019; Meena et al., 2023). *Brassica juncea* accounts for over 80% of the overall production of rapeseed and mustard in the nation (Jat et al, 2019). It is a self-pollinated crop but 12–20% outcrossing also occurs (Nandi et al., 2021; Kumar et al., 2024). Mustard seeds contain about 3842% oil, which is golden yellow in color, aromatic and considered one of the most useful and nutritious cooking medium. Mustard cake is also highly nutritious, containing about 12% oil and 38–42% protein (Chaudhary et al., 2023). Its oil serves multiple functions, including cooking, frying, making pickles, medicinal use, hair oils, and applications in the tanning industry (Perween et al., 2024). The oil cake is utilized as feed for livestock and as fertilizer (Devi et al., 2024). This plant is thought to have originated in the Mediterranear area and has been grown for many countries. Although mustard is mainly grown in temperate climates, it is also cultivated as a cool-season crop in certain tropical and subtropical areas (Singh et al. (2020). Brown mustard prefers cool and moist growing conditions, usually with an average temperature between 15–25°C. Ideal growing conditions for mustard include sandy soils, and the plant can grow to a height of 60–70 cm or even taller (Sowmya et al., 2024). The major rapeseed-mustard growing countries are India, Canada, Pakistan, Bangladesh, and Sweden (Saha et al., 2024). It is predominantly grown in Rajasthan, Uttar Pradesh, Madhya Pradesh, Gujarat and Haryana in the country (Shyam et al., 2021). The India region has a production of rapeseed-mustard covering 8.06 mha, with a total yield of 11.75 mt and a productivity of 1458 kg ha^{-1}. In Uttar Pradesh, the area devoted to rapeseed and mustard production is 0.76 mha, with a total yield of 1.03 mt and a productivity of 1370 kg ha^{-1} (Anonymous, 2022). The production in country is not sufficient to meet the requirement. Therefore for the increasing population, it is essential to develop the high yielding varieties and enhance the yield and oil content in mustard. The area under mustard cultivation has meager and presently is not enough as per demand. The Indian genotypes have low productivity, requiring the breeding of varieties with high seed yields and high oil content. Genetic variability, heritability, genetic advance, correlation, and path analysis are crucial factors that influence crop improvement in Indian mustard (Tiwari et al., 2019). Several variables are studied in correlation, which gives an idea about indirect selection as well. Indirect selection is equally important in influencing the final product, and grain yield in any crop species. For this, path coefficient analysis has emerged as a very strong tool as it determines the direct and indirect causes of association giving the idea of specific forces that act to produce strong correlation and measures the relative importance of each causal factor. Keeping the above facts in mind, the current analysis aimed to assess genetic variability, heritability, correlation and path analysis of the degree of association and identify the direct and indirect effects of yield and its contributing characteristics.

2. MATERIALS AND METHODS

2.1. *Study site*

The study was conducted during the *rabi* season (October, 2021 to March, 2022) at the crop research centre Sardar Vallabhbhai Patel University of Agriculture and Technology Meerut, Uttar Pradesh, India. Geographically, Meerut was located at 28°57’ to 29°01’ North latitude 77°40’ to 77°45’ East longitude and an altitude of 277 m above MSL represented the Northwest Plain. The experiment was conducted in Randomized Complete Block Design (RCBD) in three replications. Each genotype was sown in four rows and each row length was 5.0 m. The present field experiment was conducted with 40 Indian mustard genotypes viz; DRMRCI-127, DRMR 2018-17, DRMRHT-1318, SKM-1728, SKM-1620, RGN-491, RGN-483, PBR-507, RH-1974, RH-1975, KMR-20-3, KMR-20-4, NPJ-241, NPJ-242, JM- 14-8, PR- 2017-5, PRB- 2012-3, TM-274, HUJM- 19-11, RMM- 19-18, ACNMM-23, ORM-2019-02, AKMS-20-1, BAUM-08-17, Kranti, RH-749, Giriraj, Pusa Mustard-26, RH-749-12-18, Laxmi-2, GM-2, KMR-19-3, Vaibhav, Rohini, Pusa Tarak, Azad, KMR-15-1, UJM-28, BR-40 and UJM-22 Spacing was 45×10 cm^2 maintained through proper thinning. All the recommended package of practices was followed during planting to raise a good crop.

2.2. *Method of data collection*

Five competitive plants were randomly selected from each plot for recording the observations of all quantitative characters except days to 50% flowering and days to maturity recorded based on the plot. The data wererecorded on 14 characters such as days to 50% flowering, days to maturity, plant height (cm), number of primary branches plant^{-1}, number of secondary branches plant^{-1}, siliquae on main axis, length of main axis (cm), siliqua length (cm), number of seeds siliqua^{-1}, 1000 seed weight (g), biological yield plant^{-1}

(g), harvest index (%), oil content (%) and seed yield plant^{-1}. The oil content wasestimated by using Fourier Transform Near-Infrared Reflectance Spectroscopy (FT-NIRS) at the Central Soil Salinity Research Institute, Karnal.The mean and analysis of variance (ANOVA) were determined according to the method outlined by Panse and Sukhatme (1954). The genotypic coefficient of variation (GCV) and Phenotypic coefficient of variation (PCV) are categorized as low (<10%), moderate (10-20%) and high (>20%) as recommended by Burton and Devane (1953).Heritability in a broad sense was categorized in three major groups low (<60%), Medium (60–80%) and High (>80%). Heritability and genetic advancewerecalculated according to Johnson et al.(1955).Correlations were estimated from the analysis of variance and covariance at the genotypic and phenotypic levels, according to AI-Jiobouri et al. (1958). An analysis of the path coefficient was conducted using the approach proposed by Wright (1921) and refined by Dewey and Lu (1959). Analysis of the path coefficient evaluated the direct and indirect effects of fourteen yield contributing characters on seed yield of Indian mustard.

3. RESULTS AND DISCUSSION

3.1. *Analysis of variance*

The genotypes were compared using analysis of variance to test for differences in all the studied characteristics. The result from the analysis of variance (ANOVA) indicated highly significant variations among the genotypes (Table 1). Comparable finding were also documented by Jat et al. (2019), Gupta et al. (2022) and Meena et al. (2023).

Table 1: ANOVA for fourteen characters of forty genotypes in Indian mustard

Source of variance	DF	50F	DM	PH	NPB	NSB	SMA
Replication	2	3.61	23.43	52.38	0.23	2.13	0.10
Treatment	39	21.31**	44.64**	316.30**	1.37**	16.08**	115.71**
Error	78	1.25	4.34	44.90	0.11	0.66	2.90
Total	119	7.86	17.87	133.97	0.53	5.74	39.82

Table 1: continue...

Source of variance	LMA	SL	NSPS	1000 SW	BYP	HI	OC	GYP
Replication	6.87	0.34	0.10	0.12	0.93	6.12	0.76	2.12
Treatment	307.81**	1.78**	5.89**	1.75**	491.13**	17.36**	4.89**	41.76**
Error	8.83	0.07	0.37	0.10	8.97	2.34	0.50	0.74
Total	106.78	0.64	2.17	0.64	166.85	7.32	1.94	14.21

50F: Days to 50% flowering; DM: Days to maturity; PH: Plant height (cm); NPB: Number of primary branches plant^{-1}; NSB: Number of secondary branches plant^{-1}; SMA: Siliquae on main axis; LMA: Length of main axis; SL: Siliqua length (cm); NSPS: Number of seeds siliqua^{-1}; 1000 SW: 1000 seed weight (g); BYP: Biologicalyield plant^{-1} (g); HI: Harvest index (%); OC: Oil content (%); SYP: Seed yield plant^{-1} (g); *, **: Significant at (*p*: 0.05) and (*p*: 0.01) level; respectively

3.2. *Genotypic and phenotypic coefficient of variation*

The calculated mean, range, PCV and GCV for various characters studied were presented in Table 2. The values of PCV were greater than the values of GCV for all the traits, suggesting that the expression of traits was influenced by the environment. High GCV and PCV values were observed for grain yield plant^{-1} (20.63%) and grain yield plant^{-1} (21.18). However, moderate GCV and PCV were observed for biological yield plant^{-1} (17.96%), number of secondary branches plant^{-1} (17.77%), 1000 seeds weight (14.37%), length of main axis (12.51%), siliquae on main axis (11.64), siliqua length (11.50), number of primary branches plant^{-1} (10.88%) and number of seeds siliqua^{-1} (10.52%). Similar results in mustard have also been reported by Kumar et al. (2023), Soumya et al. (2023), and Chaudhary et al. (2023).

3.3. *Heritability and genetic advance*

The knowledge of heritability helped to assess the merits and demerits of a particular trait as it enabled the plant breeder to decide the course of selection procedures to be followed under a given situation. The estimation of heritability in a broad sense were work out for all the 14 characters and laid out in Table 2. The perusal of the data revealed this investigation the heritability ranged from 66.83 to 94.86. Number of primary branches plant^{-1} (79.03%), days to maturity (75.59%), oil content (74.49%), harvest index (68.17%) and plant height (66.83%) revealed moderate level of heredity in a broad sense. The high level of heritability was recorded for grain yield plant^{-1} (94.86%), biological yield plant^{-1} (94.71%), siliquae on main axis (92.84%), length of main axis (91.86%), number of secondary branches plant^{-1} (88.65%), siliqua length (88.38%), days to 50% flowering

Table 2: Mean, range, GCV (%), PCV(%), heritability (%) and genetic advance (GA) for fourteen characters in Indian mustard

Characters	Mean	Range		Heritability (h^2) (%)	GA	GA as % mean	GCV (%)	PCV (%)
		Min.	Max.					
Days to 50% flowering	54.2	48.0	59.7	84.26	4.89	9.02	4.77	5.20
Days to maturity	142.6	136.3	149.3	75.59	6.56	4.60	2.57	2.96
Plant height (cm)	205.9	180.2	222.2	66.83	16.02	7.78	4.62	5.65
No. of primary branches plant^{-1}	6.0	4.6	7.3	79.03	1.19	19.93	10.88	12.24
No. of secondary branches plant^{-1}	12.8	7.8	16.5	88.65	4.40	34.47	17.77	18.88
Siliquae on main axis	52.7	40.8	64.5	92.84	12.17	23.11	11.64	12.08
Length of main axis	79.8	64.2	110.1	91.86	19.71	24.70	12.51	13.05
Siliqua length (cm)	6.6	4.9	8.5	88.38	1.46	22.27	11.50	12.23
Number of seeds siliqua^{-1}	12.9	8.7	16.1	83.43	2.55	19.79	10.52	11.51
1000 seeds weight (g)	5.2	3.6	7.0	84.20	1.40	27.17	14.37	15.66
Biological yield plant^{-1} (g)	70.6	48.9	102.5	94.71	25.42	36.01	17.96	18.46
Harvest index (%)	25.4	19.5	32.7	68.17	3.81	14.98	8.81	10.67
Oil content (%)	38.6	35.5	40.4	74.49	2.15	5.57	3.14	3.63
Grain yield plant^{-1} (g)	17.9	11.4	26.8	94.86	7.42	41.40	20.63	21.18

(84.26%), 1000 seeds weight (84.20%) and number of seeds siliqua^{-1} (83.43%).

The data of genetic advance as a percentage of the mean are presented in Table 2. The estimated genetic advance expressed as a percent of the mean varied from 4.60% to 41.40%. Days to 50 % flowering (9.02%), days to maturity (4.60%), plant height (7.78%) and oil content (5.57%) exposed low genetic advance as a percent of the mean (<10%). Number of primary branches plant^{-1} (19.93%), number of seeds siliqua^{-1} (19.79%) and harvest index (14.98%) showed moderate genetic advance as a percent of the mean (10–20%). Grain yield plant^{-1} (41.40%), biological yield plant^{-1} (36.01%), number of secondary branches plant^{-1} (34.47%), 1000 seeds weight (27.17%), length of main axis (24.70%), siliquae on main axis (23.11%) and siliqua length (22.27%) had the highest genetic advance as a percent of mean (>20).These outcomes were strongly backed by comparable result from Meena et al. (2023), Kumar et al. (2023) and Devi et al. (2024).

3.4. Correlation coefficients

The main objective must be to find and choose superior genotypes with desirable characteristics from a wide range of breeding materials to properly exploit the available variability. In the current analysis, the correlation coefficient was estimated among fourteen traits at genotypic and phenotypic levels. To study the association between various quantitative characters and their relative importance in selection, the correlation coefficient estimated at the genotypic and phenotypic levels, and the values were presented in Table 3. The seed yield plant^{-1} had a highly significant and positive association with biological yield plant^{-1} (0.904), number of secondary branches plant^{-1} (0.825), siliquae on main axis (0.800), number of primary branches plant^{-1} (0.767), siliqua length (0.680), number of seeds siliqua^{-1} (0.616), length of main axis (0.576) and harvest index (0.499). The character 1000 seed weight (0.202) had also recorded a positive and significant correlation with seed yield plant^{-1}. The characters oil content (0.110), days to 50% flowering (0.050) and plant height (0.035) revealed positive but non-significant correlation with seed yieldplant^{-1}. The character days to maturity (-0.063) expressed negative and non-significant associations with seed yield plant^{-1} at the genotypic level. Seed yield plant^{-1} had a positive and highly significant correlation with biological yield plant^{-1} (0.862), siliquae on main axis (0.748), number of secondary branches plant^{-1} (0.746), number of primary branches plant^{-1} (0.676), siliqua length (0.621), number of seed siliqua^{-1} (0.546), length of main axis (0.541) and harvest index (0.495). Whereas 1000 seed weight (0.189) had a positive and significant correlation with seed yield plant^{-1}, on the other hand oil content (0.062), days to 50% flowering (0.059) and plant height (0.053) had positive but non-significant correlation with seed yield plant^{-1}. Negative non-significant correlation exhibited by days to maturity (-0.035) at the phenotypic level. Similar result of correlation coefficients have also been reported by Chaudhary et al. (2023), Dwivedi et al. (2023), and Kumar et al. (2024).

The genotypic correlation coefficient values generally exceeded the phenotypic value. This indicated that

Table 3: Genotypic and phenotypic correlation coefficient among fourteen characters in Indian mustard

Characters		DM	PH	NPB	NSB	SMA	LMA	SL	NSPS	1000 SW	BYP	HI	OC	SYP
50F	G	0.611**	0.699**	0.267**	0.043	0.231*	0.259**	-0.039	0.208*	-0.170	0.127	-0.132	-0.016	0.050
	P	0.507**	0.560**	0.259**	0.035	0.200*	0.213*	-0.047	0.162	-0.132	0.125	-0.094	-0.034	0.059
DM	G		0.471**	-0.032	-0.132	-0.030	0.050	-0.206*	0.077	0.029	-0.017	-0.081	0.024	-0.063
	P		0.283**	0.033	-0.068	-0.051	0.041	-0.181*	0.071	0.029	0.021	-0.084	-0.029	-0.035
PH	G			0.267**	0.108	0.284**	0.154	0.125	0.117	-0.487**	0.129	-0.180*	-0.041	0.035
	P			0.193*	0.038	0.212*	0.125	0.095	0.067	-0.284**	0.092	-0.055	-0.036	0.053
NPB	G				0.684**	0.723**	0.398**	0.571**	0.429**	-0.055	0.674**	0.419**	-0.289**	0.767**
	P				0.589**	0.611**	0.353**	0.486**	0.335**	-0.035	0.588**	0.317**	-0.260**	0.676**
NSB	G					0.619**	0.427**	0.697**	0.538**	0.316**	0.733**	0.448**	0.109	0.825**
	P					0.567**	0.396**	0.617**	0.461**	0.248**	0.683**	0.309**	0.073	0.746**
SMA	G						0.596**	0.484**	0.392**	0.015	0.726**	0.403**	0.105	0.800**
	P						0.559**	0.428**	0.357**	-0.002	0.683**	0.312**	0.077	0.748**
LMA	G							0.470**	0.279**	0.231*	0.576**	0.185*	0.374**	0.576**
	P							0.435**	0.232*	0.221*	0.531**	0.160	0.313**	0.541**
SL	G								0.512**	0.121	0.707**	0.141	0.123	0.680**
	P								0.438**	0.101	0.636**	0.123	0.078	0.621**
NSPS	G									0.249**	0.647**	0.096	0.151	0.616**
	P									0.196*	0.570**	0.082	0.129	0.546**
1000 SW	G										0.127	0.259**	0.296**	0.202*
	P										0.100	0.231*	0.218*	0.189*
BYP	G											0.085	0.154	0.904**
	P											-0.008	0.113	0.862**
HI	G												-0.033	0.499**
	P												-0.049	0.495**
OC	G													0.110
	P													0.062

*, ** significant at p=0.05 and p=0.01 level, respectively

strong intrinsic associations were somewhat masked at the phonotypic level due to environmental effects. Seed yield plant^{-1}showed a significant correlation in a positive direction with biological yield plant^{-1}, number of secondary branches plant^{-1}, siliquae on main axis, number of primary branches plant^{-1}, siliqua length, length of main axis and harvest index at both genotypic and phenotypic level. This could be because of the linkage of genes determining these characteristics. Thus, it might be indirect that selection supported by any one of these characters either alone or together, would help to identify high-yielding genotypes.

3.5. *Path coefficient*

The path coefficient took into account the cause-and-effect relationship between the variables which was unique in partitioning the association into direct and indirect effects through other dependent variables. The seed yield plant^{-1} was a dependent character and it was the output of direct and indirect effects of independent characters. The direct and indirect contribution of each character toward seed yield plant^{-1} is presented in Table 4. At the genotypic level among the fourteen characters studied the biological yield plant^{-1} recorded maximum direct effect (0.8281) on seed yield plant^{-1}. The number of seeds siliqua^{-1} (0.0393), length of main axis (0.0171), number of secondary branches plant^{-1} (0.0155), siliqua length (0.078), siliquae on main axis (0.0074) also revealed a positive direct effect on seed yield plant^{-1}. Whereas, 1000 seed weight (-0.0412), plant height (-0.0244), number of primary branches plant^{-1} (-0.0120), oil content (-0.0114), days to maturity (-0.0023) and days to 50% flowering had negative direct effects on seed yield plant^{-1}. Biological yield plant^{-1}showed a positive indirect effect viaharvest index, number of seeds siliqua^{-1}, number of secondary branches plant^{-1}, length of main axis, siliqua length, siliquae on main axis and days to maturity on seed yield plant^{-1}. These results generally align with several previous reports Gupta et al. (2022), Kumar et al. (2023), and Chaudhary et al. (2024).

At the phenotypic level biological yield plant^{-1} (0.8458) had the highest positive direct effect on seed yield plant^{-1} followed by harvest index (0.4991), number of seeds siliqua^{-1} (0.0250), length of main axis (0.0141), number of primary branches plant^{-1} (0.0087) and siliqua length (0.0067). The direct effect of the remaining characters on seed yield plant^{-1} was negative and very low in degree. Positive and indirect effect of biological yield plant^{-1} vianumber of seeds siliqua^{-1}, length of main axis, number of primary branches plant^{-1} and siliqua length on seed yield plant^{-1}. However, siliquae on main axis, harvest index, 1000 seed weight, number of secondary branches plant^{-1}, oil content, days to 50% flowering, days to maturity and plant height revealed negative indirect effects on seed yield plant^{-1}. Gupta et al. (2022), Kumar et al. (2023) and Chaudhary et al. (2024) also find these results.

The examination of different characteristics included biological yield plant^{-1} and harvest index had high positive direct effect followed by number of seeds siliqua^{-1}, length

Table 4: Direct and indirect impacts of component characters on grain yield in Indian mustard at the genotypic and phenotypic

Characters		50F	DM	PH	NPB	NSB	SMA	LMA
50F	G	-0.00010	-0.0014	-0.0171	-0.0032	0.0007	0.0017	0.0045
	P	-0.0031	-0.0059	-0.0008	0.0023	-0.0001	-0.0015	0.0030
DM	G	-0.00006	-0.0023	-0.0115	0.0004	-0.0020	-0.0002	0.0009
	P	-0.0016	-0.0117	-0.0004	0.0003	0.0003	0.0004	0.0006
PH	G	-0.00007	-0.0011	-0.0244	-0.0032	0.0017	0.0021	0.0027
	P	-0.0017	-0.0033	-0.0014	0.0017	-0.0001	-0.0016	0.0018
NPB	G	-0.00003	0.0001	-0.0065	-0.0120	0.0106	0.0054	0.0068
	P	-0.0008	-0.0004	-0.0003	0.0087	-0.0022	-0.0045	0.0050
NSB	G	0.00003	0.0003	-0.0027	-0.0082	0.0155	0.0046	0.0073
	P	-0.0001	0.0008	-0.0001	0.0051	-0.0038	-0.0042	0.0056
SMA	G	-0.00002	0.0001	-0.0069	-0.0087	0.0096	0.0074	0.0102
	P	-0.0006	0.0006	-0.0003	0.0053	-0.0022	-0.0074	0.0079
LMA	G	-0.00003	-0.0001	-0.0038	-0.0048	0.0066	0.0044	0.0171
	P	-0.0007	-0.0005	-0.0002	0.0031	-0.0015	-0.0041	0.0141
SL	G	0.00004	0.0005	-0.0031	-0.0069	0.0108	0.0036	0.0081
	P	0.0001	0.0021	-0.0001	0.0042	-0.0023	-0.0032	0.0061
NSPS	G	-0.00002	-0.0002	-0.0029	-0.0052	0.0083	0.0029	0.0048
	P	-0.0005	-0.0008	-0.0001	0.0029	-0.0018	-0.0026	0.0033
1000 SW	G	0.00002	-0.0001	0.0119	0.0007	0.0049	0.0001	0.0040
	P	0.0004	-0.0003	0.0004	-0.0003	-0.0009	0.0000	0.0031
BYP	G	-0.00001	0.0000	-0.0032	-0.0081	0.0113	0.0054	0.0099
	P	-0.0004	-0.0003	-0.0001	0.0051	-0.0026	-0.0051	0.0075
HI	G	0.00001	0.0002	0.0044	-0.0051	0.0069	0.0030	0.0032
	P	0.0003	0.0010	0.0001	0.0027	-0.0012	-0.0023	0.0022
OC	G	0.00001	-0.0001	0.0010	0.0035	0.0017	0.0008	0.0064
	P	0.0001	0.0003	0.0001	-0.0023	-0.0003	-0.0006	0.0044

Table 4: Continue...

Characters	SL	NSPS	1000 SW	BYP	HI	OC	SYP
50F	-0.0004	0.0082	0.0070	0.1050	-0.0555	0.0002	0.050
	-0.0003	0.0041	0.0022	0.1056	-0.0470	0.0004	0.059
DM	-0.0019	0.0030	-0.0012	-0.0137	-0.0340	-0.0003	-0.063
	-0.0012	0.0018	-0.0005	0.0181	-0.0417	0.0003	-0.035
PH	0.0011	0.0046	0.0201	0.1071	-0.0756	0.0005	0.035
	0.0006	0.0017	0.0046	0.0780	-0.0277	0.0004	0.053
NPB	0.0052	0.0169	0.0023	0.5584	0.1765	0.0033	0.767**
	0.0032	0.0084	0.0006	0.4975	0.1580	0.0026	0.676**
NSB	0.0063	0.0212	-0.0130	0.6067	0.1886	-0.0012	0.825**
	0.0041	0.0116	-0.0041	0.5775	0.1541	-0.0007	0.746**
SMA	0.0044	0.0154	-0.0006	0.6013	0.1695	-0.0012	0.800**
	0.0028	0.0089	0.0000	0.5779	0.1559	-0.0008	0.748**
LMA	0.0043	0.0110	-0.0095	0.4771	0.0779	-0.0043	0.576**
	0.0029	0.0058	-0.0036	0.4490	0.0798	-0.0032	0.541**
SL	0.0090	0.0201	-0.0050	0.5851	0.0593	-0.0014	0.680**
	0.0067	0.0110	-0.0016	0.5376	0.0614	-0.0008	0.621**
NSPS	0.0046	0.0393	-0.0103	0.5359	0.0404	-0.0017	0.616**
	0.0029	0.0250	-0.0032	0.4818	0.0408	-0.0013	0.546**
1000 SW	0.0011	0.0098	-0.0412	0.1053	0.1091	-0.0034	0.202*
	0.0007	0.0049	-0.0163	0.0842	0.1151	-0.0022	0.189*
BYP	0.0064	0.0254	-0.0052	0.8281	0.0358	-0.0018	0.904**
	0.0042	0.0143	-0.0016	0.8458	-0.0040	-0.0011	0.862**
HI	0.0013	0.0038	-0.0107	0.0705	0.4210	0.0004	0.499**
	0.0008	0.0021	-0.0038	-0.0068	0.4991	0.0005	0.495**
OC	0.0011	0.0059	-0.0122	0.1272	-0.0137	-0.0114	0.110
	0.0005	0.0032	-0.0036	0.0952	-0.0246	-0.0102	0.062

50F: Days to 50% flowering; DM: Days to maturity; PH: Plant height (cm); NPB: Number of primary branches plant^{-1}; NSB: Number of secondary branches plant^{-1}; SMA: Siliquae on main axis; LMA: Length of main axis; SL: Siliqua length (cm); NSPS: Number of seeds siliqua^{-1}; 1000 SW: 1000 seed weight (g); BYP: Biologicalyield plant^{-1} (g); HI: Harvest index (%); OC: Oil content (%); SYP: Seed yield plant^{-1} (g); Residual effect : 0.00188; *, ** significant at p: 0.05 and p: 0.01 level; respectively

of main axis and siliqua length at both genotypic and phenotypic levels on seed yield plant^{-1}. So, direct selection of genotypes for seed yields plant^{-1} over and done with biological yield plant^{-1} and harvest index could be effective. Based on path analysis it was identified that biological yield plant^{-1} and harvest index are the important direct yield contributing characters, these characters were also found to be useful for indirect contributors via each other. Biological yield plant^{-1} and harvest index appeared as the most important indirect yield components. The characters cited above, merit due consideration at the time of planning the selection strategy aimed at developing high-yielding lines in mustard.

4. CONCLUSION

The ANOVA showed highly significant differences among the genotypes for all the characters studied. High heritability and genetic advance estimates were obtained for different characters. This designated the lesser effect of the environment on these traits. So, the utilization of these characteristics for selection could be beneficial for enhancing the mustard crop. The coefficient of correlation studies exposed higher genotypic correlation values than the corresponding phenotypic correlation values indicating the existence of strong inherent association among the various traits.

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