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Research Note

Genetic variability and trait associations for seed yield and related traits in Indian mustard (*Brassica juncea* L.)

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Abstract

An experiment was conducted using eighteen Indian mustard genotypes evaluated in a randomized block design with two replications. Analysis of variance revealed significant differences among genotypes for all characters studied, indicating the presence of substantial genetic variability. High genotypic and phenotypic coefficients of variation were recorded for 1000-seed weight, while moderate variability was observed for seed yield per plot, number of primary and secondary branches and seeds per siliqua. Seed yield exhibited strong positive correlations with days to 50% flowering, days to maturity, plant height, number of secondary branches, siliqua length, seeds per siliqua, 1000-seed weight, and number of siliquae per plant. Path coefficient analysis further identified days to 50% flowering, number of primary and secondary branches, siliqua length, seeds per siliqua, and 1000-seed weight as traits exerting positive direct effects on seed yield, suggesting their importance in selection strategies. Based on overall performance, the genotypes DRMR-1165-40, DRMR-IJ-31, DRMR-150-35, CS-60, RH-725, and Pusa Mustard-30 were found superior, with DRMR-1165-40 recording the highest seed yield. These genotypes may be utilized in future breeding programs to enhance the productivity of mustard.

Keywords: Mustard, GCV, PCV, heritability, correlation coefficient and path analysis**.**

Mustard (*Brassica* spp., 2n = 36) is one of the world's most important oilseed crops and among the earliest domesticated spice crops. It belongs to the family Brassicaceae and is predominantly self-pollinated, although natural out-crossing up to 30 % may occur depending on wind and insect activity. Being both photosensitive and thermosensitive, mustard is primarily cultivated as a *rabi* season crop under tropical and temperate environments. In India, it ranks second among edible oilseed crops after soybean.

The diverse agro-ecological conditions across India have facilitated the development and adoption of mustard varieties adapted to varied environments, contributing significantly to the "Yellow Revolution". Several species, including *Brassica juncea*, *B. napus*, *B. campestris*, *B. nigra* and *B. carinata*, are cultivated worldwide. Mustard seeds are rich in high-quality protein, particularly lysine and sulphur-containing amino acids (Sadeghi *et al.,* 2009). Moreover, *Brassica* crops are valued for vitamins, minerals and various therapeutic properties (Ildiko *et al.,* 2006). Beyond edible oil, mustard contributes to the Indian economy through its use as condiments, leafy vegetables and livestock feed.

During 2023–24, mustard cultivation in India covered approximately 9.25 million ha., producing 11.9 million tonnes, accounting for 19.8 % of global acreage and 9.8 % of global output (Anonymous, 2021–22). Genetic parameters such as heritability and genetic advance provide insights into the proportion of genetic variability that is transmissible to subsequent generations.

Similarly, correlation and path coefficient analyses help to identify traits with direct and indirect contributions to seed yield. High heritability coupled with high genetic advance generally indicates the predominance of additive gene action and greater effectiveness of selection (Devi *et al*., 2018).

Considering the economic importance of mustard and the scope for further genetic enhancement, the present investigation was undertaken to assess genetic variability, heritability, genetic advance, correlation and path coefficients for yield and yield-related traits in Indian mustard, with the aim of supporting future breeding strategies.

The present investigation was carried out during *rabi* 2024-25 at the Research Farm of Barrister Thakur Chhedilal College of Agriculture and Research Station, Bilaspur, under Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh. The experiment consisted of eighteen mustard varieties (**Table 1**) evaluated in a Randomized Block Design (RBD) with two replications. Each variety was sown in a plot measuring 1.60 m × 5.00 m (8.00 m²) with row x plant spacing is 30 x 10 cm. The crop was raised following the recommended package of practices, including timely irrigation, weed management, and fertilizer application. A fertilizer dose of 80:40:40 kg N, P_2O_5 and K_2O per hectare was applied to ensure uniform crop growth.

Observations were recorded on yield and yield-related traits. Five competitive plants were randomly selected from each replication for plant-based characters, and the mean values were used for statistical analysis. The statistical analysis is done through the open access software OPSTAT Sheoran *et al*. (1998). The study involved estimation of genetic variability, heritability, genetic advance, correlation coefficients and path analysis using standard biometrical procedures.

Variability among genotypes was assessed through analysis of variance (ANOVA) as described by Singh and Chaudhary (1985). Genotypic and phenotypic variances were estimated following Johnson *et al*. (1955). Phenotypic and genotypic coefficients of variation (PCV and GCV) were calculated using the method proposed by Burton (1952) and classified according to Sivasubramanian and Madhava Menon (1973). Heritability in the broad sense (h^2) was computed following Allard (1960). Genetic advance (GA) and genetic advance as percent of mean (GAM) were estimated using the procedure of Johnson *et al*. (1955).

Genotypic and phenotypic correlation coefficients were computed according to the method of Miller *et al*. (1958). Path coefficient analysis was performed based on the approach originally proposed by Wright (1921) and later modified by Dewey and Lu (1959) to partition correlations into direct and indirect effects.

Analysis of variance: The analysis of variance (ANOVA) for eighteen mustard genotypes evaluated for ten quantitative traits (**Table 2**) revealed highly significant differences among genotypes for all characters studied,

Table 1. List of Indian mustard varieties under experimentation

S.No.	Name of genotype	Originating centre
1	DRMR-1165-40	ICAR-DRMR, Bharatpur
2	DRMR-150-35	ICAR-DRMR, Bharatpur
3	DRMR-IJ-31	ICAR-DRMR, Bharatpur
4	NRCHB-101	ICAR-DRMR, Bharatpur
5	BRIJRAJ	ICAR-DRMR, Bharatpur
6	RADHIKA	ICAR-DRMR, Bharatpur
7	NRCDR2	ICAR-DRMR, Bharatpur
8	RH-406	CCS HAU, Hisar
9	RH-725	CCS HAU, Hisar
10	RH-761	CCS HAU, Hisar
11	RH-749	CCS HAU, Hisar
12	CS-56	ICAR- CSSRI, Karnal
13	CS-60	ICAR- CSSRI, Karnal
14	PUSA MUSTARD-25	ICAR- IARI, New Delhi
15	PUSA MUSTARD-26	ICAR- IARI, New Delhi
16	PUSA MUSTARD-28	ICAR- IARI, New Delhi
17	PUSA MUSTARD-29	ICAR- IARI, New Delhi
18	PUSA MUSTARD-30	ICAR- IARI, New Delhi

Table 2. Analysis of variance (ANOVA) for different characters of mustard varieties

S.No.	Source of variation	Mean sum of square (MSS)		
		Replication	Treatment	Error
	Degree of freedom	1	17	17
1.	Days to 50% flowering	0.640	5.601**	2.396
2.	Days to maturity	3.674	68.126**	1.476
3.	Plant height	2.507	173.526**	15.689
4.	Number of primary branches	0.234	0.561**	0.222
5.	Number of secondary branches	0.934	3.925**	1.050
6.	Siliqua length	0.010	0.255*	0.106
7.	Number of seed/siliqua	0.490	3.387**	1.327
8.	1000 seed weight	0.018	1.833**	0.153
9.	Number of siliqua/plants	35.601	245.303**	23.880
10.	Seed yield/plot	44.667	3842.8**	1570.1

** Significant at 1% probability level, * Significant at 5% probability level

indicating the presence of substantial genetic variability in the experimental material. Pronounced variation was observed for seed yield per plot, number of siliquae per plant, plant height and days to maturity, suggesting that these traits are influenced by diverse genetic backgrounds. The availability of such variability offers considerable scope for effective selection and genetic improvement in Indian mustard.

Genetic Parameters of Variation: PCV values were slightly higher than GCV values for all the traits (**Table 3**), indicating minimal environmental influence and that phenotypic expression closely reflects underlying genetic differences. High GCV, PCV, heritability and genetic advance as percent of mean for 1000-seed weight, number of siliquae per plant and number of secondary branches per plant suggest that these traits are largely governed by additive gene action. This indicates that simple phenotypic selection would be effective for improving these characters, particularly in early segregating generations. Plant height and days to maturity exhibited high heritability but moderate genetic advance, suggesting the involvement of non-additive gene effects, which may reduce the efficiency of direct selection. Traits such as days to 50% flowering and siliqua length showed low variability and genetic advance, indicating limited scope for improvement through selection. These observations are in agreement with recent findings by Lakra *et al*. (2020) and Sachdeva *et al.* (2023).

Correlation Coefficient analysis: The genotypic and phenotypic correlation coefficients among ten quantitative traits in mustard are presented in **Table 4**. Seed yield per plot exhibited a strong, positive, and significant association with days to 50 % flowering (r_9 = 0.874; r_p = 0.565**), days to maturity (r_9 = 0.993**; r_p = 0.591**), number of secondary branches per plant (r_9 = 0.905**; r_p = 0.866**), siliqua length (r_9 = 0.525**; r_p = 0.521**), number of seeds

Table 3. Genetic parameter's for different quantitative characters of Mustard

S.No.	Traits	Mean	Range		GCV (%)	PCV (%)	h^2 (bs) (%)	GA	GAM (%)
			Minimum	Maximum					
1	Days to 50% flowering	41.52	38.2	44.6	3.04	4.81	40.08	1.65	3.97
2	Days to maturity	120.27	107.2	135.1	4.80	4.90	95.75	11.63	9.67
3	Plant height (cm)	180.72	162.3	200	4.91	5.38	83.41	16.71	9.24
4	Number of primary branches	5.33	4.2	6.3	7.71	11.72	43.32	0.55	10.46
5	Number of secondary branches	13.57	9.7	16.3	8.83	11.61	57.79	1.87	13.82
6	Siliqua length (cm)	5.09	4.4	6.2	5.35	8.34	41.12	0.36	7.07
7	Number of seed/siliqua	13.32	10.0	16.2	7.61	11.51	43.70	1.38	10.37
8	1000 seed weight (g)	4.26	3.0	6.9	21.47	23.35	84.55	1.73	40.68
9	Number of siliqua/plants	126.81	108.2	145.1	8.29	9.14	82.25	19.65	15.49
10	Seed yield/plot (g)	378.22	304.4	480.2	8.91	13.75	41.99	45.01	11.9

Table 4. Genotypic and phenotypic correlation matrix (Above diagonal Phenotypic and below diagonal Genotypic)

Character	Days to 50% flowering	Days to maturity	Plant height	Number of primary branches	Number of secondary branches	Siliqua length	Number of seed/siliqua	1000 seed weight	Number of siliqua/plants	Seed yield/ plot
Days to 50% flowering	**1**	0.447**	0.061	0.221	0.633**	0.322	0.465**	0.412*	0.126	0.565**
Days to maturity	0.701**	**1**	0.353*	0.065	0.664**	0.271	0.244	0.213	0.023	0.591**
Plant height	-0.099	0.377*	**1**	-0.194	0.181	-0.216	0.345*	-0.026	-0.030	0.255
Number of primary branches	0.565**	0.172	-0.312	**1**	-0.061	0.222	-0.175	-0.248	-0.338*	0.089
Number of secondary branches	0.823**	0.927**	0.097	-0.111	**1**	0.482**	0.430**	0.516**	0.283	0.866**
Siliqua length	0.587**	0.449**	-0.450**	0.462**	0.359*	**1**	0.315	0.203	0.096	0.521**
Number of seed/siliqua	0.012	0.358*	0.527**	-0.289	0.548**	0.619**	**1**	0.251	0.300	0.399*
1000 seed weight	0.664**	0.227	-0.090	-0.328	0.613**	0.232	0.422*	**1**	0.572**	0.439**
Number of siliqua/plants	0.095	-0.025	-0.045	0.359*	0.461**	-0.025	0.313	0.667**	**1**	0.226
Seed yield/plot	0.874**	0.993**	0.333*	0.061	0.905**	0.525**	0.788**	0.551**	**0.541****	1

** significant at 1% probability level, * significant at 5% probability level

Table 5. Direct and indirect effects of yield component on seed yield in mustard (Genotypic path matrix)

Character	Days to 50% flowering	Days to maturity	Plant height	Number of primary branches	Number of secondary branches	Siliqua length	Number of seed/siliqua	1000 seed weight	Number of siliqua/ plants	Genotypic correlation with seed yield
Days to 50% flowering	**0.746**	-3.386	0.075	1.051	5.064	-1.576	0.034	-0.955	-0.179	0.874**
Days to maturity	0.523	**-4.830**	-0.287	0.320	5.704	-1.206	1.048	-0.326	0.046	0.993**
Plant height	-0.073	-1.819	**-0.762**	-0.580	0.598	1.209	1.547	0.129	0.084	0.333*
Number of primary branches	0.421	-0.830	0.237	**1.860**	-0.683	-1.242	-0.848	0.471	0.675	0.061
Number of secondary branches	0.613	-4.476	-0.074	-0.206	**6.155**	-0.965	1.607	-0.881	-0.868	0.905**
Siliqua length	0.437	-2.168	0.343	0.859	2.210	**-2.688**	1.816	-0.333	0.047	0.525**
Number of seed/siliqua	0.008	-1.726	-0.402	-0.537	3.372	-1.663	**2.934**	-0.606	-0.589	0.788**
1000 seed weight	0.495	-1.094	0.068	-0.609	3.771	-0.622	1.236	**-1.439**	-1.255	0.551**
Number of siliqua/plants	0.070	0.118	0.034	-0.667	2.840	0.067	0.919	-0.960	**-1.882**	0.541**

** significant at 1% probability level, * significant at 5% probability level; Residual effects = 0.6251

Table 6. Direct and indirect effects of yield component on seed yield in mustard (Phenotypic path matrix)

Character	Days to 50% flowering	Days to maturity	Plant height	Number of primary branches	Number of secondary branches	Siliqua length	Number of seed/ siliqua	1000 seed weight	Number of siliqua/ plants	Phenotypic correlation with seed yield
Days to 50% flowering	**-0.019**	-0.026	0.013	0.036	0.492	0.056	-0.019	0.025	0.003	0.565**
Days to maturity	-0.008	**-0.060**	0.078	0.010	0.517	0.047	-0.010	0.013	0.000	0.591**
Plant height	-0.001	-0.021	**0.224**	-0.032	0.141	-0.038	-0.014	-0.001	-0.000	0.255
Number of primary branches	-0.004	-0.003	-0.043	**0.167**	-0.047	0.039	0.007	-0.015	-0.010	0.089
Number of secondary branches	-0.011	-0.039	0.040	-0.010	**0.779**	0.085	-0.017	0.032	0.008	0.866**
Siliqua length	-0.005	-0.016	-0.048	0.037	0.375	**0.177**	-0.013	0.012	0.002	0.521**
Number of seed/siliqua	-0.008	-0.014	0.077	-0.029	0.335	0.055	**-0.041**	0.015	0.008	0.399*
1000 seed weight	-0.007	-0.012	-0.005	-0.041	0.401	0.035	-0.010	**0.062**	0.017	0.439**
Number of siliqua/ plants	-0.002	-0.001	-0.004	-0.056	0.220	0.017	-0.012	0.035	**0.030**	0.226

** significant at 1% probability level, * significant at 5% probability level; Residual effect =0.1899

per siliqua (r_9 = 0.788**; r_p = 0.399*), 1000-seed weight (r_9 = 0.551**; r_p = 0.439**), and number of siliquae per plant (r_9 = 0.541**; r_p = 0.226). These associations indicate that simultaneous improvement in these traits is likely to enhance seed yield and that they may serve as reliable selection criteria in mustard breeding programmes.

The strong positive correlations observed in this study are consistent with earlier reports by Sowmya *et al.* (2024), Sachdeva *et al.* (2023) and Ghosh *et al.* (2023) for mustard, Comparable correlation patterns in oilseed crops have also been documented in oilseed sesame study by Disowja *et al.* (2020). Similar supportive evidence recorded by Nirmala *et al.* (2023) further validates the stability of these trait relationships across diverse genetic backgrounds and environments.

Path Coefficient Analysis: Path coefficient analysis (**Table 5 & 6**) partitioned the genotypic correlations into direct and indirect components. The results revealed that the number of secondary branches per plant exerted the highest positive direct effect on seed yield, followed by number of seeds per siliqua, number of primary branches, days to 50% flowering, and number of siliquae per plant. Moderate to low direct effects were recorded for 1000-seed weight, plant height, siliqua length, and days to maturity. The traits exhibiting strong positive direct effects contribute substantially to yield determination and should therefore be prioritized in selection and hybridization programmes. The prominence of number of secondary branches and seeds per siliqua in influencing seed yield aligns with reports by Choudhary *et al.* (2023) and Lavanya *et al.* (2022). Similar direct contributions of primary branches and days to 50% flowering have been documented by Ghosh *et al.* (2023), Lakra *et al.* (2020), and Saiyad *et al.* (2020) in mustard. Positive direct effects of number of siliquae per plant corroborate the findings of Lavanya *et al.* (2022). Nirmala *et al.* (2023) have similarly emphasized the importance of branching traits and seed-setting attributes in determining yield in mustard crop.

The present investigation revealed that high to moderate GCV and PCV values for seed yield per plot, 1000-seed weight, and number of primary and secondary branches suggested considerable inherent variability. Seed yield exhibited strong positive associations with days to maturity, number of secondary branches, number of seeds per siliqua, 1000-seed weight, and siliqua length, identifying them as key selection indices for yield enhancement. Path coefficient analysis further confirmed the direct contribution of number of secondary branches, seeds per siliqua, and days to maturity towards seed yield, emphasizing their importance in selection-oriented breeding programs. The predominance of black and dark-brown seed coat types across genotypes also indicated underlying genetic diversity that can be further exploited in quality and nutrition-oriented breeding. Among the evaluated genotypes, DRMR-1165-40, DRMR-IJ-31, DRMR-150-35, CS-60, RH-725, and PUSA MUSTARD-30 performed superiorly, with DRMR-1165-40 recording the highest seed yield. These genotypes could be used as potential donors in future breeding programs aimed at improving yield and productivity in Indian mustard.

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