



International Journal of Research in Agronomy

E-ISSN: 2618-0618
P-ISSN: 2618-060X
© Agronomy
NAAS Rating (2026): 5.20
www.agronomyjournals.com
2026; 9(8): 1476-1482
Received: 06-05-2026
Accepted: 13-06-2026

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Studies on genetic variability, correlation and path coefficient analysis in Indian mustard (*Brassica juncea* L.)

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DOI: <https://www.doi.org/10.33545/2618060X.2026.v9.i8s.6445>

Abstract

The present investigation entitled “Studies on Genetic Variability, Correlation and Path Coefficient Analysis in Indian Mustard (*Brassica juncea* L.)” was conducted during Rabi 2025–26 using 27 Indian mustard genotypes to assess the genetic variability, the nature and magnitude of association between seed yield and component characters and direct and indirect effects of component traits on seed yield. The analysis of variance revealed significant differences among genotypes for all 12 characters studied, indicating substantial genetic variability and considerable scope for selection and improvement. The mean performance and range showed wide variation for all the characters studied indicating presence of wide variability. The phenotypic coefficient of variation (PCV%) is higher than genotypic coefficient of variation (GCV%) for all the characters indicating the influence of environment on character expression. Genotypic coefficient of variation was highest for seed yield per plot (20.79%) and seed yield per plant (20.78%) whereas the lowest was observed for days to maturity (1.06%) followed by plant height (4.39%). High heritability was recorded for seed yield per plot (98.34%), seed yield per plant (98.16%), number of primary branches (97.40%), number of secondary branches (93.98%) and siliquae per plant (92.53%). High heritability coupled with high genetic advance as per cent of mean for primary branches, secondary branches, siliquae per plant, seed yield per plant and seed yield per plot indicated the predominance of additive gene action and effectiveness of selection. Genotypic correlations were generally higher than phenotypic correlations. Seed yield per plant showed highly significant positive association with seed yield per plot (1.0000 at genotypic level). Path analysis revealed the highest positive direct effect of seed yield per plot (1.1049), followed by secondary branches (0.0358), days to 50% flowering (0.0254) and length of main branch (0.0105). On the basis of the study it was concluded that the selection on the basis of seed yield/plant (g) followed by number of primary branches per plant, number of secondary branches/plant and number of siliquae per plant are most effective in Indian mustard.

Keywords: Indian mustard, *Brassica juncea*, genetic variability, heritability, genetic advance, correlation, path coefficient

1. Introduction

Indian mustard (*Brassica juncea* L. Czern. & Coss.) is one of the most important *rabi* oilseed crops cultivated in India and occupies a prominent position in the national oilseed economy. The crop is valued primarily for its edible oil, but its seeds are also used as condiments, animal feed and in several industrial applications. Indian mustard is an amphidiploid species with an AABB genome ($2n = 36$) belonging to the family Brassicaceae. It is predominantly self-pollinated, although a certain degree of natural cross-pollination occurs through insect activity (Tiwari *et al.*, 2025; Yadav *et al.*, 2024) [20, 21]. The seed contains appreciable amounts of oil and protein, making mustard an important crop for nutritional and edible-oil security (Chaudhary *et al.*, 2023) [4].

India is one of the leading producers of rapeseed–mustard globally. During 2025–26, mustard was cultivated on approximately 94.27 lakh hectares in India, producing about 13.68 million tonnes with an average productivity of 1460 kg ha⁻¹ (MoAFW, 2025-26) [14]. Rajasthan is the leading mustard-producing state, contributing substantially to the country's total production. The crop is widely cultivated in districts such as Alwar, Bharatpur, Bikaner, Churu, Ganganagar, Hanumangarh, Jaipur, Jaisalmer, Jodhpur and Nagaur (Directorate of Agriculture, Rajasthan,

2023) [8]. Despite its considerable production, the productivity of Indian mustard remains lower than its potential because of genetic, environmental and agronomic constraints.

The productivity of mustard is a complex quantitative character controlled by several genes and strongly influenced by environmental conditions. A narrow genetic base, genotype $\times$ environment interaction, moisture stress, temperature fluctuations and biotic stresses further contribute to yield instability (Akkenapally and Chetariya, 2022; Redu and Singh, 2024) [1, 18]. Seed yield is determined by the combined expression of several yield-attributing characters, including plant height, number of primary and secondary branches, number of siliquae per plant, siliqua length, number of seeds per siliqua, 1000-seed weight, biological yield and harvest index. Consequently, selection based solely on seed yield may not always be effective because yield is highly influenced by environmental variation and the interaction of several component traits (Gupta *et al.*, 2025; Devi, 2018) [6, 9]. Genetic variability is the fundamental prerequisite for successful crop improvement. The presence of sufficient variability among genotypes provides opportunities for selection and recombination of desirable characters through breeding programmes. Assessment of variability using genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance helps in understanding the relative contribution of genetic and environmental factors to the expression of different traits. Generally, higher PCV than GCV indicates the influence of environmental factors, whereas traits exhibiting comparatively high GCV and PCV possess greater potential for genetic improvement through selection (Meena and Bishnoi, 2023; Akkenapally and Chetariya, 2022) [1, 12]. High heritability coupled with high genetic advance is particularly useful because it suggests a substantial contribution of additive gene effects and greater effectiveness of selection for the concerned character (Yadav *et al.*, 2024; Chaudhary *et al.*, 2023) [4, 21].

Correlation analysis is an important biometrical technique used to determine the degree and direction of association between yield and its component characters. Knowledge of the correlation among different traits is essential for identifying characters that can be effectively used as indirect selection criteria for improving seed yield. A positive and significant correlation between a particular character and seed yield indicates that improvement in that character may contribute to increased productivity. In Indian mustard, significant positive associations of seed yield with characters such as number of branches per plant, number of siliquae per plant, siliqua length, seeds per siliqua, biological yield and harvest index have been reported by several researchers (Singh *et al.*, 2024; Akkenapally and Chetariya, 2022; Gupta *et al.*, 2025) [1, 9, 19]. However, correlation coefficients alone do not provide information regarding whether an observed association is due to a direct influence of a trait on yield or is the result of indirect effects through other characters.

Path coefficient analysis, therefore, provides additional information by partitioning correlation coefficients into direct and indirect effects. It helps identify the characters that exert the greatest direct influence on seed yield and consequently provides a more reliable basis for selection. Traits showing high positive direct effects on seed yield can be given greater emphasis in breeding programmes, even when their simple correlation with yield is influenced by other associated characters. Previous studies have identified biological yield, harvest index, number of siliquae per plant, seeds per siliqua, siliqua length and branching traits as important contributors to seed yield in Indian mustard (Singh *et al.*, 2024; Yadav *et al.*, 2024) [19, 21].

The simultaneous assessment of genetic variability, heritability, genetic advance, correlation and path coefficients provides a comprehensive understanding of the inheritance and interrelationship of important quantitative traits. Such information is particularly valuable for identifying superior genotypes and determining appropriate selection criteria for mustard improvement. Therefore, the present investigation was undertaken to assess the genetic variability, heritability, genetic advance, correlation and path coefficient relationships among yield and its contributing traits in Indian mustard (*Brassica juncea* L.), with the objective of identifying important traits that could be effectively utilized for the selection and development of high-yielding mustard genotypes.

2. Materials and Methods

The present investigation entitled “Studies on Genetic Variability, Correlation and Path Coefficient Analysis in Indian Mustard (*Brassica juncea* L.)” was conducted during the Rabi season of 2025–26 at the Agricultural Research Farm, School of Agriculture, Suresh Gyan Vihar University, Jaipur, Rajasthan. A total of 27 Indian mustard genotypes were evaluated under field conditions in a Randomized Block Design (RBD) with three replications. Each genotype was sown in 6 rows at a spacing of 45 cm $\times$ 15 cm in a separate plot under uniform agronomic and crop-management practices so that the observed differences among genotypes could primarily be used for estimating genetic variability and trait associations.

Observations were recorded on five randomly selected plants from each genotype in each replication. The randomly selected plants were tagged and observations were recorded on 12 quantitative characters, viz., days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, length of main branch (cm), number of siliquae per plant, length of siliqua (cm), number of seeds per siliqua, seed yield per plant (g), seed yield per plot (kg) and 1000-seed weight (g).

2.4 Statistical analysis

The mean data recorded for 12 quantitative characters were subjected to statistical analysis of variance to determine the significance of differences among genotypes for each character. The analysis of variance was carried out following the procedure for Randomized Block Design as suggested by Panse and Sukhatme (1967) [16]. The phenotypic and genotypic components of variance were estimated by the method suggested by Burton (1952) [2]. Broad-sense heritability (%) was estimated by adopting the formula suggested by Hanson *et al* (1956) [10]. Genetic advance (GA) and genetic advance as percentage of mean (GAM) were estimated by using the method suggested by Johanson *et al.* (1955) [11].

Genotypic and phenotypic correlation coefficients were calculated among the 12 characters were computed utilizing respective component of variance and co-variance by following formula suggested by Miller *et al.* (1958) [13]. Path coefficient analysis was carried out following the approach of Dewey and Lu (1959) [7] to partition the correlation coefficients into direct and indirect effects of different characters on seed yield per plant. Seed yield per plant was considered the dependent variable, while the remaining yield-associated traits were considered independent variables. Both genotypic and phenotypic path analyses were performed. The magnitude and direction of direct effects were used to identify traits having the greatest contribution to seed yield, while indirect effects were used to understand the contribution mediated through other component characters.

3. Results and Discussion

3.1 Analysis of Variance

The analysis of variance (Table-1) revealed significant differences among the 27 Indian mustard genotypes for all the twelve characters studied, indicating the presence of substantial genetic variability in the experimental material. Significant genotypic variation provides an opportunity for effective selection of superior genotypes and is a prerequisite for successful genetic improvement. Similar significant variation among Indian mustard genotypes for yield and its component traits has been reported by Yadava *et al.* (2011), Chakraborty *et al.* (2021) and Chaudhary *et al.* (2023) [3, 4, 22].

3.2 Mean Performance of Genotypes

The mean performance and range of 27 genotypes were given in Table-2. The perusal of Table-2 reveals that a considerable variation were present among the genotypes for all the characters. Days to 50% flowering ranged from 44.67 (Bio-902) to 52.00 (Jaipur Local) days, with a mean of 48.01 days. Days to maturity ranged from 129.67 to 139.33 days, with a mean of 133.80 days. Plant height varied from 175.67 cm (Bio-902) to 208.00 cm (Maya) with a mean of 193.27. The number of primary branches ranged from 3.37 (Jaipur local) to 7.23 (Pusa Bold). The lowest (9.90) and highest (16.23) number of secondary branches per plant were observed in Navgold and Pusa Bold, respectively. The length of main branch ranged from 64.57 cm (KDR1019) to 81.80 cm (Pusa Tarak). The lowest and highest number of siliqua/plant, length of siliqua, seed yield per plant, seed yield/plot were observed in Jaipur local and Giriraj, respectively. The number of seeds/siliqua ranged from 12.13 (NPJ 153) to 17.27 (Giriraj). The 1000-seed weight ranged from 4.13 g (Jaipur Local) to 5.38 g (Maya).

The observed variation among genotypes indicates the diverse genetic constitution of the material and provides scope for identifying superior genotypes for different breeding objectives. Similar wide variation in flowering, maturity, plant height and seed-related traits has been reported in Indian mustard germplasm by Yadava *et al.* (2011) [22].

3.3 Genetic Variability

The estimates of PCV were higher than GCV for all the characters (Table 3), indicating the influence of environmental factors on the expression of traits. However, the relatively narrow differences between GCV and PCV for primary branches, secondary branches, siliqua per plant, seeds per siliqua, seed yield per plant and seed yield per plot indicated comparatively lower environmental influence and greater contribution of genetic factors.

The highest GCV was recorded for seed yield per plot (20.79%), followed by seed yield per plant (20.78%). Moderate GCV was observed for primary branches per plant (13.91%), secondary branches per plant (11.84%) and siliqua per plant (10.35%), while comparatively low GCV was recorded for 1000-seed weight (5.85%), plant height (4.39%), days to 50% flowering (3.10%) and days to maturity (1.06%).

The high GCV for seed yield and its associated traits indicates greater scope for selection and improvement. Similar findings have been reported by Pal *et al.* (2019) [15], who observed substantial variability for seed yield and yield-contributing traits in Indian mustard.

3.4 Heritability and Genetic Advance

Very high broad-sense heritability (Table 3) was observed for seed yield per plot (98.34%), seed yield per plant (98.16%),

primary branches per plant (97.40%), secondary branches per plant (93.98%), number of siliqua per plant (92.53%), number of seeds per siliqua (91.22%), siliqua length (86.71%), 1000-seed weight (83.15%) and length of main branch (81.23%). Plant height showed high heritability (67.62%), whereas days to 50% flowering had moderate heritability (48.97%) and days to maturity showed low heritability (16.40%).

Genetic advance (Table 3) ranged from 0.54 to 55.50, with the highest value recorded for number of siliqua per plant (55.50), followed by plant height (14.38) and length of main branch (8.87). Genetic advance as percentage of mean was highest for seed yield per plot (42.45%), followed by seed yield per plant (42.42%), primary branches per plant (28.29%), secondary branches per plant (23.65%) and siliqua per plant (20.50%).

High heritability coupled with high genetic advance as percentage of mean for primary branches, secondary branches, siliqua per plant, seed yield per plant and seed yield per plot suggested the predominance of additive gene action. Therefore, direct selection based on these traits may be effective for genetic improvement. Similar conclusions have been reported by Yadava *et al.* (2011) [22], who emphasized the usefulness of heritability and genetic advance estimates for identifying effective selection criteria in Indian mustard.

3.5 Correlation Coefficient Analysis

Genotypic correlation coefficients (Table 4) were generally higher than the corresponding phenotypic correlations (Table 5), indicating that the associations among the traits were predominantly genetic and were comparatively less affected by environmental variation.

Days to 50% flowering showed significant positive association with days to maturity ($r_g = 0.7122$; $r_p = 0.5554$) and plant height ($r_g = 0.5036$; $r_p = 0.2982$). Days to maturity showed a highly significant positive correlation with plant height at the genotypic level ($r_g = 0.9236$) and was also positively associated with siliqua length, seeds per siliqua, seed yield per plant and seed yield per plot.

The strongest positive association with seed yield per plant was observed for seed yield per plot ($r_g = 1.0000$; $r_p = 0.9919$). Similarly, number of siliqua per plant showed a highly significant positive correlation with seed yield per plant ($r_g = 0.8497$; $r_p = 0.8029$), siliqua length showed a positive association ($r_g = 0.8522$; $r_p = 0.7836$) and number of seeds per siliqua also exhibited a highly significant positive association ($r_g = 0.8156$; $r_p = 0.7688$).

These positive associations suggest that improvement in important yield components may contribute to improvement in seed yield. Similar positive associations of seed yield with siliqua per plant, secondary branches, seeds per siliqua and other yield components have been reported by Chaurasiya *et al.* (2019) and Yadava *et al.* (2011) [5, 22].

3.6 Path Coefficient Analysis

Path coefficient analysis was employed to separate the direct and indirect contributions of individual characters towards seed yield per plant. At the genotypic level (Table 6), the highest positive direct effect was recorded for seed yield per plot (1.1049), followed by secondary branches per plant (0.0358), days to 50% flowering (0.0254), length of main branch (0.0105) and 1000-seed weight (0.0084). In contrast, negative direct effects were observed for siliqua length (-0.0617), seeds per siliqua (-0.0279), primary branches (-0.0255), siliqua per plant (-0.0241), plant height (-0.0239) and days to maturity (-0.0172).

Length of main branch exhibited a positive direct effect (0.0105) and a strong positive correlation with seed yield per plant (0.8369 at genotypic level). Number of siliquae per plant showed a negative direct effect at the genotypic level (-0.0241), but its overall correlation with seed yield was highly positive (0.8497), mainly because of strong indirect effects through seed yield per plot. Similarly, siliqua length and seeds per siliqua showed negative direct effects but strong positive correlations with seed yield, indicating that their positive associations were primarily mediated through other component traits.

The results indicate that correlation alone may not always provide a reliable basis for selection because a high positive correlation can result from indirect effects. Therefore, traits showing positive correlation together with appreciable positive direct effects, particularly secondary branches per plant, length of main branch, 1000-seed weight and seed yield per plot, should receive greater consideration in selection programmes. Comparable findings emphasizing path analysis for identifying effective yield components in Indian mustard have been reported by Yadava *et al.* (2011) and Perween *et al.* (2025) [17, 22].

Conclusion

The study of 27 Indian mustard genotypes revealed substantial genetic variability for all 12 characters. High GCV and PCV were recorded for seed yield per plant and seed yield per plot, while very high heritability coupled with high genetic advance for primary branches, secondary branches, siliquae per plant and seed yield indicated the predominance of additive gene action and good prospects for selection. Genotypic correlations were generally stronger than phenotypic correlations. Seed yield per plant showed strong positive associations with seed yield per plot, number of siliquae per plant, siliqua length and seeds per siliqua. Path analysis identified seed yield per plot, secondary branches per plant, length of main branch and 1000-seed weight as important traits based on their positive direct effects.

Overall, selection for higher seed yield should give particular emphasis to primary and secondary branching, number of siliquae per plant, length of main branch, 1000-seed weight and other yield-related traits. Superior genotypes identified in the study can be utilized as promising breeding material for developing high-yielding Indian mustard varieties.

Table 1: Analysis of variance for different characters of Indian mustard

S. No.	Characters	Replications (df=2)	Genotypes (df=26)	Error (df=52)
1	Days to 50% flowering	0.05	8.93**	2.30
2	Days to maturity	2.37	16.36*	10.30
3	Plant height (cm)	8.63	250.78**	34.52
4	Number of primary branches per plant	0.09	1.90**	0.02
5	Number of secondary branches per plant	0.15	8.56**	0.18
6	Length of main branch (cm)	0.67	73.68**	5.27
7	Number of siliquae per plant	19.42	2417.27**	63.38
8	Length of siliqua (cm)	0.03	0.36**	0.02
9	Number of seeds per siliqua	0.01	6.07**	0.19
10	Seed yield per plant (g)	0.07	41.27**	0.26
11	Seed yield per plot (Kg)	0.01	2.38**	0.01
12	1000-seed weight (g)	0.03	0.27**	0.02

* Significant at the 5% level and ** Significant at the 1% level.

Table 2: Mean performance of 27 Indian mustard genotypes during Rabi, 2025-26

S. No.	Genotypes	DF	DM	PH	NPBPP	NSBPP	LMB	NSPP	LS	NSPS	SYPP	SYPT	1000S W
G ₁	Navgold	47.67	132.33	185.67	6.07	9.90	72.63	287.67	4.53	14.67	16.87	4.05	4.60
G ₂	Vardan	47.67	134.00	187.67	6.30	14.80	69.23	240.00	4.77	15.13	18.10	4.34	4.81
G ₃	Pusa bold	49.00	136.33	206.00	7.23	16.23	77.00	306.67	5.23	16.80	23.17	5.56	5.23
G ₄	Pusa Agarni	46.33	131.33	181.00	6.03	14.40	74.13	259.67	4.63	15.27	16.13	3.87	4.95
G ₅	Rohani	47.33	132.33	186.33	5.80	14.73	65.20	277.00	4.63	15.43	17.33	4.16	4.72
G ₆	Kranti	48.33	134.33	193.00	6.10	14.97	66.77	224.33	5.10	14.70	16.20	3.89	5.30
G ₇	Bio-902	44.67	129.67	175.67	5.33	13.30	70.00	274.33	4.53	16.07	17.10	4.10	5.03
G ₈	KDR-1019	49.00	136.00	199.67	5.10	15.17	64.57	273.67	4.93	13.07	15.10	3.62	4.72
G ₉	JPN-2	48.00	134.33	194.33	6.20	15.30	68.47	256.00	4.63	14.43	14.07	3.37	4.95
G ₁₀	CS-52	48.33	132.67	190.33	4.37	14.70	65.00	256.00	5.10	13.40	13.20	3.17	5.23
G ₁₁	RB-50	46.00	131.00	181.67	4.83	11.83	71.30	239.33	4.50	15.57	12.77	3.06	4.42
G ₁₂	SKM-904	47.00	132.33	187.33	5.63	13.43	68.73	230.67	4.43	13.93	12.57	3.01	4.95
G ₁₃	RL-1359	50.33	136.33	202.33	5.30	13.70	73.67	292.67	5.10	14.70	20.10	4.82	5.07
G ₁₄	NPJ-153	48.00	132.67	191.33	6.43	14.33	72.73	263.67	4.47	12.13	15.27	3.67	4.78
G ₁₅	RH-749	50.00	137.33	206.33	7.07	15.43	76.87	302.67	5.20	16.53	23.33	5.60	5.10
G ₁₆	RGN-298	48.67	134.67	198.00	5.93	13.97	74.90	284.67	5.13	16.13	19.47	4.67	5.03
G ₁₇	RH-91	49.33	134.00	195.33	5.83	15.00	70.47	280.67	4.83	14.43	16.10	3.86	5.11
G ₁₈	RH-51	46.67	132.33	187.67	5.60	13.90	71.93	256.00	4.47	13.13	13.43	3.23	4.80
G ₁₉	RM-51	49.00	135.33	201.33	5.80	13.63	77.00	292.67	5.03	15.07	20.10	4.82	5.12
G ₂₀	Pusa Mahak	46.67	132.00	200.00	5.73	15.50	77.87	296.33	5.20	16.77	21.23	5.10	5.03
G ₂₁	Pusa Tarak	46.00	132.33	201.67	6.00	14.23	81.80	298.33	5.43	16.53	22.20	5.33	4.71
G ₂₂	Urvashi	49.00	136.00	203.33	5.67	15.67	80.10	303.33	5.40	17.00	23.07	5.54	5.27
G ₂₃	Ashirwad	47.67	132.33	192.67	5.23	13.80	71.40	269.67	5.03	16.03	20.13	4.83	4.71
G ₂₄	JM-1	46.67	132.00	185.33	4.60	10.93	69.87	224.67	4.63	13.67	15.27	3.67	4.52
G ₂₅	Maya	51.33	137.67	208.00	6.07	15.93	76.03	297.00	5.13	15.13	22.20	5.33	5.38
G ₂₆	Giriraj (Check)	45.67	131.67	199.67	6.30	16.20	80.27	311.00	5.43	17.27	23.57	5.65	5.26

G ₂₇	Jaipur local (Check)	52.00	139.33	176.67	3.37	10.13	64.93	210.67	4.27	12.47	12.23	2.94	4.13
	Mean	48.01	133.80	193.27	5.70	14.12	72.33	270.72	4.88	15.02	17.79	4.27	4.92
	SEm (±)	0.88	1.85	3.39	0.07	0.24	1.33	4.60	0.08	0.25	0.29	0.07	0.08
	CD (5%)	2.49	5.26	9.63	0.21	0.69	3.76	13.04	0.22	0.71	0.83	0.19	0.21
	CD (1%)	3.31	7.01	12.83	0.28	0.92	5.01	17.38	0.29	0.95	1.10	0.25	0.28
	CV (%)	3.16	2.40	3.04	2.27	3.00	3.17	2.94	2.70	2.89	2.84	2.69	2.63
	Range	44.67-52.00	129.67-139.33	175.67-208.00	3.37-7.23	9.90-16.23	64.57-81.80	210.67-311.00	4.27-5.43	12.13-17.27	12.23-23.57	2.94-5.65	4.13-5.38

DF: Days to 50% flowering, DM: Days to maturity, PH: Plant height (cm), NPBPP: Number primary branches per plant, NSBPP: Number secondary branches per plant, LMB: Length of main branch (cm), NSPP: Number of siliqua per plant, LS: Length of siliqua (cm), NSPS: Number of seeds per siliqua, SYPP: Seed yield per plant (g), SYPPT: Seed yield per plot (Kg) and 1000SW: 1000-seed weight (g).

Table 3: Estimates the genetic variability, heritability and genetic advance as per cent (%) of mean of 27 Indian mustard genotypes

Trait	Mean	Range		GCV (%)	PCV (%)	Heritability% (BS)	Genetic Advance	GA as % of Mean
		Min.	Max.					
Days to 50% flowering	48.01	44.67	52.00	3.10	4.42	48.97	2.14	4.46
Days to maturity	133.80	129.67	139.33	1.06	2.62	16.40	1.19	0.89
Plant height (cm)	193.27	175.67	208.00	4.39	5.34	67.62	14.38	7.44
Number of primary branches per plant	5.70	3.37	7.23	13.91	14.10	97.40	1.61	28.29
Number of secondary branches per plant	14.12	9.90	16.23	11.84	12.22	93.98	3.34	23.65
Length of main branch (cm)	72.33	64.57	81.80	6.60	7.33	81.23	8.87	12.26
Number of siliqua per plant	270.72	210.67	311.00	10.35	10.76	92.53	55.50	20.50
Length of siliqua (cm)	4.88	4.27	5.43	6.88	7.39	86.71	0.64	13.21
Number of seeds per siliqua	15.02	12.13	17.27	9.32	9.76	91.22	2.75	18.34
Seed yield per plant (g)	17.79	12.23	23.57	20.78	20.98	98.16	7.55	42.42
Seed yield per plot (Kg)	4.27	2.94	5.65	20.79	20.96	98.34	1.81	42.45
1000-seed weight (g)	4.92	4.13	5.38	5.85	6.41	83.15	0.54	10.99

Table 4: Genotypic correlation among 12 characters in 27 Indian mustard genotypes during *Rabi* season, 2025-26

Trait	DF	DM	PH	NPBPP	NSBPP	LMB	NSPP	LS	NSPS	SYPP	SYPPT	1000SW
DF	1	0.7122 *	0.5036 **	-0.1199	0.0416	-0.1040	0.0681	0.2041	-0.2999	0.1355	0.1320	0.1019
DM		1	0.9236 **	0.0443	0.2363	0.0826	0.2012	0.4179 *	-0.1857	0.3883 *	0.4178 *	0.2063
PH			1	0.5772 **	0.7040 **	0.6560 **	0.7720 **	0.9015 **	0.4614 *	0.8135 **	0.8080 **	0.7045 **
NPBPP				1	0.6130 **	0.5449 **	0.5740 **	0.3979 *	0.4866 *	0.5836 **	0.5822 **	0.5709 **
NSBPP					1	0.3328	0.5337 **	0.6634 **	0.4309 *	0.5333 **	0.534 **	0.8069 **
LMB						1	0.7695 **	0.6661 **	0.7370 **	0.8369 **	0.8368 **	0.4262 *
NSPP							1	0.7221 **	0.6735 **	0.8497 **	0.8486 **	0.5718 **
LS								1	0.6945 **	0.8522 **	0.8460 **	0.6960 **
NSPS									1	0.8156 **	0.8132 **	0.4518 *
SYPP										1	1.0000 **	0.5552 **
SYPPT											1	0.5535 **
1000SW												1

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

DF: Days to 50% flowering, DM: Days to maturity, PH: Plant height (cm), NPBPP: Number primary branches per plant, NSBPP: Number of secondary branches per plant, LMB: Length of main branch (cm), NSPP: Number of siliqua per plant, LS: Length of siliqua (cm), NSPS: Number of seeds per siliqua, SYPP: Seed yield per plant (g), SYPPT: Seed yield per plot (Kg) and 1000SW: 1000-seed weight (g).

Table 5: Phenotypic correlation among 12 characters in 27 Indian mustard genotypes during *Rabi* season, 2025-26

Trait	DF	DM	PH	NPBPP	NSBPP	LMB	NSPP	LS	NSPS	SYPP	SYPPT	1000SW
DF	1	0.5554 **	0.2982 **	-0.0668	0.0538	-0.1286	0.0314	0.0352	-0.2342 *	0.0794	0.0858	0.1044
DM		1	0.2611 *	-0.0305	0.0821	-0.0300	0.0686	0.1390	-0.0910	0.1658	0.1433	0.0713
PH			1	0.4691 **	0.6101 **	0.5203 **	0.6617 **	0.7229 **	0.3609 **	0.6609 **	0.6690 **	0.5142 **
NPBPP				1	0.5895 **	0.4849 **	0.5455 **	0.3552 **	0.4686 **	0.5658 **	0.5660 **	0.5124 **
NSBPP					1	0.3102 **	0.5113 **	0.6076 **	0.3984 **	0.5154 **	0.5107 **	0.7127 **
LMB						1	0.6861 **	0.5849 **	0.6099 **	0.7461 **	0.7480 **	0.3336 **
NSPP							1	0.6550 **	0.6147 **	0.8029 **	0.8036 **	0.4898 **
LS								1	0.6222 **	0.7836 **	0.7930 **	0.5795 **
NSPS									1	0.7688 **	0.7701 **	0.3934 **
SYPP										1	0.9919 **	0.5008 **
SYPPT											1	0.4992 **
1000SW												1

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

DF: Days to 50% flowering, DM: Days to maturity, PH: Plant height (cm), NPBPP: Number primary branches per plant, NSBPP: Number of secondary branches per plant, LMB: Length of main branch (cm), NSPP: Number of siliqua per plant, LS: Length of siliqua (cm), NSPS: Number of seeds per siliqua, SYPP: Seed yield per plant (g), SYPPT: Seed yield per plot (Kg) and 1000SW: 1000-seed weight (g).

Table 6: Genotypic path coefficient analysis showing direct and indirect effects for seed yield per plant during Rabi, 2025-26

Trait	DF	DM	PH	NPBPP	NSBPP	LMB	NSPP	LS	NSPS	SYPT	1000SW	SYPP
DF	0.0254	-0.0294	-0.0121	0.0031	0.0015	-0.0011	-0.0016	-0.0126	0.0084	0.1497	0.0009	0.1320
DM	0.0435	-0.0172	-0.0221	-0.0011	0.0085	0.0009	-0.0048	-0.0258	0.0052	0.4291	0.0017	0.4178 *
PH	0.0128	-0.0159	-0.0239	-0.0147	0.0252	0.0069	-0.0186	-0.0556	-0.0129	0.8988	0.0059	0.8080 **
NPBPP	-0.0030	-0.0008	-0.0138	-0.0255	0.0219	0.0057	-0.0138	-0.0246	-0.0136	0.6448	0.0048	0.5822 **
NSBPP	0.0011	-0.0041	-0.0169	-0.0156	0.0358	0.0035	-0.0128	-0.0409	-0.0120	0.5892	0.0068	0.5340 **
LMB	-0.0026	-0.0014	-0.0157	-0.0139	0.0119	0.0105	-0.0185	-0.0411	-0.0206	0.9247	0.0036	0.8368 **
NSPP	0.0017	-0.0035	-0.0185	-0.0146	0.0191	0.0081	-0.0241	-0.0446	-0.0188	0.9389	0.0048	0.8486 **
LS	0.0052	-0.0072	-0.0216	-0.0101	0.0237	0.0070	-0.0174	-0.0617	-0.0194	0.9416	0.0059	0.8460 **
NSPS	-0.0076	0.0032	-0.0110	-0.0124	0.0154	0.0077	-0.0162	-0.0429	-0.0279	0.9011	0.0038	0.8132 **
SYPT	0.0034	-0.0067	-0.0195	-0.0149	0.0191	0.0088	-0.0204	-0.0526	-0.0228	1.1049	0.0047	1.0041 **
1000SW	0.0026	-0.0035	-0.0169	-0.0145	0.0289	0.0045	-0.0138	-0.0430	-0.0126	0.6134	0.0084	0.5535 **

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

DF: Days to 50% flowering, DM: Days to maturity, PH: Plant height (cm), NPBPP: Number primary branches per plant, NSBPP: Number of secondary branches per plant, LMB: Length of main branch (cm), NSPP: Number of siliqua per plant, LS: Length of siliqua (cm), NSPS: Number of seeds per siliqua, SYPP: Seed yield per plant (g), SYPT: Seed yield per plot (Kg) and 1000SW: 1000-seed weight (g).

Table 7: Phenotypic path coefficient analysis showing direct and indirect effects for seed yield per plant during Rabi, 2025-26

Trait	DF	DM	PH	NPBPP	NSBPP	LMB	NSPP	LS	NSPS	SYPT	1000SW	SYPP
DF	0.0391	-0.0192	0.0027	-0.0017	-0.0014	-0.0011	0.0004	0.0022	-0.0061	0.0722	-0.0012	0.0858
DM	0.0217	-0.0346	0.0023	-0.0008	-0.0022	-0.0003	0.0008	0.0088	-0.0024	0.1507	-0.0008	0.1433
PH	0.0117	-0.0090	0.0089	0.0122	-0.0161	0.0044	0.0074	0.0455	0.0094	0.6006	-0.0060	0.6690 **
NPBPP	-0.0026	0.0011	0.0042	0.0260	-0.0155	0.0041	0.0061	0.0224	0.0122	0.5141	-0.0060	0.5660 **
NSBPP	0.0021	-0.0028	0.0055	0.0153	-0.0263	0.0026	0.0057	0.0383	0.0103	0.4683	-0.0083	0.5107 **
LMB	-0.0050	0.0010	0.0047	0.0126	-0.0082	0.0085	0.0077	0.0369	0.0158	0.6780	-0.0039	0.7480 **
NSPP	0.0012	-0.0024	0.0059	0.0142	-0.0135	0.0058	0.0112	0.0413	0.0159	0.7296	-0.0057	0.8036 **
LS	0.0014	-0.0048	0.0065	0.0092	-0.0160	0.0049	0.0074	0.0630	0.0161	0.7121	-0.0068	0.7930 **
NSPS	-0.0092	0.0031	0.0032	0.0122	-0.0105	0.0052	0.0069	0.0392	0.0259	0.6986	-0.0046	0.7701 **
SYPT	0.0031	-0.0057	0.0059	0.0147	-0.0136	0.0063	0.0090	0.0494	0.0199	0.9087	-0.0058	0.9919 **
1000SW	0.0041	-0.0025	0.0046	0.0133	-0.0188	0.0028	0.0055	0.0365	0.0102	0.4551	-0.0117	0.4992 **

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

DF: Days to 50% flowering, DM: Days to maturity, PH: Plant height (cm), NPBPP: Number primary branches per plant, NSBPP: Number of secondary branches per plant, LMB: Length of main branch (cm), NSPP: Number of siliqua per plant, LS: Length of siliqua (cm), NSPS: Number of seeds per siliqua, SYPP: Seed yield per plant (g), SYPT: Seed yield per plot (Kg) and 1000SW: 1000-seed weight (g).

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