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Correlation and Path Coefficient Analysis for Seed Yield and Its Component Traits in Indian Mustard (*Brassica juncea L.*) under Western Uttar Pradesh Conditions

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Abstract
Although Indian mustard is a key oilseed crop in India, its per-hectare yield remains below the global average, primarily because seed production depends on numerous interacting traits. To address this, a field experiment was carried out during the *rabi* season at C.C.R.D. College in Muzaffarnagar. The aim was to explore how yield relates to its component traits and to pinpoint effective selection criteria for improving productivity under the specific conditions of Western Uttar Pradesh. Ten parent genotypes and forty-five F_1 hybrids were assessed for fifteen quantitative traits using a randomized block design with three replications. The genotypic correlation values were consistently higher than the phenotypic ones, revealing that most trait associations are largely influenced by genetic rather than environmental factors. Seed yield per plant displayed strong, positive associations with leaf area index, siliqua count per plant, biological yield, test weight, number of secondary branches, seeds per siliqua, harvest index, and main raceme length. On the other hand, flowering-related traits were negatively correlated with yield, highlighting the benefit of early-flowering genotypes. Path analysis further showed that leaf area index and siliquae per plant exerted the strongest direct effects on seed yield, followed by biological yield, test weight, secondary branches, seeds per siliqua, and harvest index. Collectively, these findings suggest that selecting genotypes with good canopy development, increased branching, high sink capacity, and heavier seeds can effectively raise seed yield in Indian mustard.

Keywords: Indian mustard, correlation, path analysis and quantitative traits

Introduction
Among the major oilseed crops grown across India, Indian mustard (*Brassica juncea* L.) holds a prominent place, especially in the northern plains, where it is vital for ensuring the country's edible oil supply. This crop accounts for a large share of total oilseed output and provides a primary livelihood source for farmers, particularly in areas like Western Uttar Pradesh. Recent figures show that rapeseed–mustard covers about 8.6 to 9.3 million hectares in India, with total production estimated between 12.6 and 13.2 million metric tons during the 2023–24 and 2024–25 growing seasons (USDA-FAS, 2024). Despite some gains in recent years, India's average crop productivity, roughly 1440–1460 kg per hectare, still falls short of the worldwide average (FAOSTAT, 2023). On a global scale, rapeseed–mustard is planted on around 44 million hectares, yielding close to 92 million tonnes, with an average productivity of about 1980–2070 kg per hectare (FAOSTAT, 2023). This indicates that India achieves only about 60–70% of the world average productivity, highlighting a substantial yield gap and emphasizing the need for genetic improvement and efficient breeding strategies (Kumar *et al*., 2025) [7]. Even though Indian mustard holds significant economic value, its yield continues to stay below achievable levels. This shortfall is largely attributed to the complicated manner in which seed yield is inherited and its reliance on many mutually influencing characteristics (Gupta *et al*., 2025) [6]. Seed yield in this crop is a quantitative attribute shaped by various morphological and physiological factors, such as plant stature, primary and secondary branch numbers, siliqua count per plant, seeds inside each siliqua, and seed weight.

These components often show varying levels of correlation both among themselves and with final seed yield, making direct selection less effective (Kaur *et al.*, 2025) [7]. Similar observations have emerged from broader *Brassica* improvement studies, where yield is determined by intricate interactions between component traits and environmental influences, thereby requiring the application of advanced biometrical tools for efficient selection. Correlation analysis helps estimate how strongly and in what direction yield is associated with its contributing traits. However, this method does not separate direct effects from indirect ones. Path coefficient analysis fills this gap by partitioning correlation coefficients into direct and indirect components, offering a clearer view of cause-and-effect connections among traits (Devi *et al.*, 2025) [2]. Research conducted across different environments has shown that traits like biological yield, harvest index, and number of siliquae per plant have strong direct impacts on seed yield, confirming their value as dependable selection criteria (Kumar *et al*., 2025) [7].

Moreover, the expression of both yield and its components is heavily affected by environmental conditions. Consequently, evaluating genotypes in a region-specific manner is crucial to identify stable, high-yielding traits suited to particular agro-climatic conditions. In Western Uttar Pradesh, where environmental fluctuations strongly influence crop performance, there is limited knowledge about how yield components interrelate in Indian mustard (Gadi *et al*., 2025) [5]. Therefore, the current study was carried out to examine the correlation and path coefficient relationships between seed yield and its component traits, aiming to determine effective selection criteria for yield improvement under the conditions prevailing in Western Uttar Pradesh.

Materials and Methods

Site Description and Soil Properties

The field experiment was carried out at the research farm attached to C.C.R.D. College in Muzaffarnagar during the *rabi* (winter) season. The farm lies at 29°45' N latitude, 77°70' E longitude, at an elevation of 272 meters above sea level. This area falls within a subtropical climate zone, marked by a distinct winter season (October to March) with cool conditions (average minimum 6–7°C, average maximum 21–23°C) and occasional rain brought by western disturbances. The soil at the experimental site was sandy loam in texture, alkaline in reaction, low in organic carbon, and medium in available nitrogen, phosphorus, and potassium. It was well-drained and had moderate water-holding capacity.

Genetic Material and Experimental Layout

Ten Indian mustard accessions, used as parents, were obtained from the germplasm collection maintained at NBPGR, New Delhi. These were: Swarna, TERIGZ05, IC-491262, IC-491403, IC-491520, IC-491560, IC-520764, IC-521378, IC-546946, and Divya. These ten diverse genotypes were crossed in a diallel mating design (excluding reciprocals) during the *rabi* season of 2022–2023. The final experimental set included 55 treatment combinations (10 parents + 45 F_1 hybrids). The trial was arranged in a randomized block design (RBD) with three replications during the *rabi* season of 2023–2024. Each parent and F_1 hybrid was planted in a single row of 5 meters length, with rows spaced 45 cm apart. Within each row, plants were thinned to maintain a 15 cm spacing between plants. Standard agronomic practices were followed to ensure healthy crop growth. A uniform fertilizer dose of 60 kg nitrogen, 40 kg phosphorus pentoxide (P_2O_5), and 20 kg potassium oxide (K_2O) per hectare was applied at sowing. Irrigation and plant protection measures were carried out as needed.

Traits Measured

From each genotype within every replication, five competitive plants were chosen randomly to record data on the following quantitative characteristics: days to first flower (DFF), days to 50% flowering (DF50), days to maturity (DM), primary branches per plant (PB), secondary branches per plant (SB), plant height (PH), main raceme length (MRL), leaf area index (LAI), siliquae per plant (SP), seeds per siliqua (SS), thousand-seed weight (TSW), biological yield per plant (BY), seed yield per plant (SY), harvest index (HI), and oil content (OC).

Statistical Methods

Genotypic and phenotypic correlation coefficients among all pairs of traits were computed following standard methods. Path coefficient analysis was carried out using seed yield per plant as dependent (effect) variable, with other traits as independent (cause) variables, to partition correlations into direct and indirect effects. All the statistical computation were performed using standard biometrical procedures suggested by Searle (1961) [20] and Dewey and Lu (1959) [3] respectively.

Correlation Analysis

To understand relationships among traits, both phenotypic and genotypic correlation coefficients were calculated. Phenotypic correlation shows the observable association between characters, while genotypic correlation reflects the underlying genetic relationship after removing environmental effects. Comparing both levels helps clarify how traits depend on each other and guides selection decisions.

For any two traits, the correlation coefficient was derived by dividing their covariance by the square root of the product of their individual variances. Variance and covariance components were obtained from the analysis of variance and covariance tables. A t-test was then used to check whether the resulting correlations were statistically meaningful or simply due to chance.

Path Coefficient Analysis

Because correlation alone cannot tell whether a trait directly influences yield or acts through other traits, a path coefficient analysis was performed. This method splits the correlation between a given trait and seed yield into two parts: (1) the direct effect of that trait on yield, and (2) indirect effects flowing through other related traits. In this analysis, seed yield per plant was treated as the outcome (dependent) variable, while all other characters were considered as potential contributors (independent variables).

Additionally, a residual (unexplained) effect was estimated to assess how well the chosen set of traits accounted for variation in seed yield. A small residual value indicates that the traits included in the study explain most of the yield variability.

Residual Effect
A residual effect was estimated to determine how well the selected traits explained variation in seed yield. The residual value represents the contribution of other factors not included in the analysis. A small residual effect indicates that most of the variability in seed yield has been accounted for by the traits included in the study.

Results and Discussion
Correlation Patterns
The phenotypic and genotypic correlation coefficients among yield-related traits revealed meaningful interconnections. In almost all cases, genotypic correlations were larger than their phenotypic counterparts, indicating that environmental factors slightly masked the full expression of genetic associations. This pattern aligns with earlier observations by Patel *et al*. (2019) [16].

Seed yield per plant showed consistently strong and positive correlations with several component traits, evident at both the phenotypic and genotypic levels. Phenotypically, the highest positive association was with leaf area index (r = 0.790), followed closely by siliquae per plant (r = 0.786), biological yield (r = 0.677), test weight (r = 0.629), secondary branches (r = 0.611), seeds per siliqua (r = 0.396), harvest index (r = 0.341), main raceme length (r = 0.265), and primary branches (r = 0.217). Genotypically, the pattern was similar: leaf area index (r = 0.814), siliquae per plant (r = 0.797), biological yield (r = 0.675), secondary branches (r = 0.644), test weight (r = 0.642), seeds per siliqua (r = 0.411), harvest index (r = 0.350), main raceme length (r = 0.274), and primary branches (r = 0.245**). The fact that these relationships held across both levels suggests these traits are dependable indicators of seed yield and can be employed effectively in selection programs. Comparable findings have been reported by Prasad and Patil (2018) [19], Nandi *et al.* (2021) [15], and Chaudhary *et al.* (2023) [1] regarding positive associations of biological yield, primary branches, and seeds per siliqua with seed yield.

In contrast, flowering-related traits displayed significant negative correlations with seed yield. Days to first flowering was inversely associated with yield (phenotypic r = -0.352, genotypic r = -0.360), and days to 50% flowering followed the same trend (phenotypic r = -0.311, genotypic r = -0.320). This implies that genotypes which flower earlier tend to achieve higher yields, possibly due to better alignment of reproductive growth with available resources. Similar negative links between flowering time and seed yield were noted by Meena *et al.* (2024) [14]. However, Lakra *et al.* (2020) [12] reported a positive association between days to 50% flowering and yield, highlighting that the phenology–yield relationship may shift depending on environment and genetic background. Days to maturity, meanwhile, showed only a very weak positive link with seed yield at both levels (phenotypic r = 0.005**, genotypic r = 0.007), indicating that maturity duration has almost no meaningful effect on productivity. This finding is partly supported by recent work in Indian mustard; for example, Perween *et al.* (2025) [18] found that days to maturity had a positive but relatively minor direct impact compared to major yield components like secondary branches and siliquae per plant. Similarly, Kumar *et al.* (2024) [7] observed a positive correlation but secondary importance for days to maturity.

Path Coefficient Results
Because correlation does not reveal whether a trait exerts its own direct influence or works through others, path analysis was performed at both the phenotypic and genotypic levels. As Dewey and Lu (1959) [3] noted, this method separates correlation coefficients into direct and indirect components. The residual effects were low, 0.0255 for phenotypic and 0.0145 for genotypic analysis, meaning the selected traits collectively explained most of the variation in seed yield. The smaller genotypic residual points to stronger genetic control over these traits.

Phenotypic Direct and Indirect Effects
Leaf area index (direct effect = 0.790) and number of siliquae per plant (0.786) had the largest positive direct effects on seed yield, highlighting the importance of photosynthetic capacity and reproductive sink size in determining yield. Other traits also showed notable direct contributions: biological yield (0.677), test weight (0.629), secondary branches (0.611), seeds per siliqua (0.396), harvest index (0.341), main raceme length (0.265), and primary branches (0.217). These results are in line with Meena *et al.* (2024), who concluded that biological yield and siliqua number are key direct drivers of seed yield in mustard. Days to first flowering (-0.352) and days to 50% flowering (-0.311) showed negative direct effects, reinforcing the advantage of early flowering. Oil content also had a slight negative direct effect (-0.120), suggesting that simultaneous improvement in yield and oil content may require careful, balanced selection. Similar negative relationships between delayed flowering and yield have been observed by Yadava *et al*. (2016) [22], Patel *et al.* (2018) [19]. Additionally, leaf area index and siliquae per plant contributed indirectly through biological yield, further amplifying their total influence.

Genotypic Direct and Indirect Effects
The genotypic path analysis mirrored the phenotypic results but with slightly larger direct effect magnitudes, indicating strong genetic determination. Major direct contributors were leaf area index (0.814), siliquae per plant (0.797), biological yield (0.675), test weight (0.642), secondary branches (0.644), seeds per siliqua (0.411), harvest index (0.350), and main raceme length (0.274). The consistency across both levels increases confidence in using these traits for selection. As Kumar *et al.* (2024) [8] stated, siliquae per plant, biological yield, and test weight have strong direct effects and should be emphasized during selection, a conclusion fully supported here. Days to first flowering (-0.360) and days to 50% flowering (-0.320) again had negative direct effects at the genotypic level, confirming that early-maturing genotypes hold higher genetic potential for yield. Similar conclusions for days to 50% flowering were drawn by Lavanya *et al.* (2022) [13], who stressed the value of early flowering in mustard breeding.

Table 1: Phenotypic correlation among yield and yield attributes for 15 characters of 55 genotypes in Indian mustard

Characters	Days to First flowering	Days to 50% flowering	Days to maturity	No pri. branches per plant	No sec. branches per plant	Plant height (cm)	Length of main raceme (cm)	Leaf area index	No siliquae per plant	No of seeds /siliqua	Test weight (g)	Harvest index (%)	Oil content (%)	Biological yield (g/plant)	Seed yield (g/plant)
DF1	1.000	0.807**	0.217**	0.156*	-0.117	-0.081	-0.188*	-0.209**	-0.351**	-0.419**	-0.045	-0.088	0.028	-0.223**	-0.352**
DF2			0.338**	0.029	-0.179*	-0.140	-0.265**	-0.211**	-0.310**	-0.372**	-0.002	-0.010	0.056	-0.241**	-0.311**
DM				0.155*	0.053	0.051	0.066	0.094	0.005	0.018	0.071	-0.324**	-0.153*	0.290**	0.005
NPB					0.700**	0.137	0.141	0.267**	0.092	0.032	0.259**	0.060	-0.081	0.147	0.217**
NSB						0.137	0.225**	0.550**	0.452**	0.217**	0.426**	0.338**	-0.101	0.265**	0.611**
PH							0.095	-0.173*	-0.113	0.374**	-0.110	-0.040	-0.001	0.023	0.024
LMR								0.148	0.085	0.245**	0.246**	0.033	-0.007	0.255**	0.265**
LAI									0.661**	0.245**	0.553**	0.212**	-0.227**	0.569**	0.790**
NSP										0.245**	0.157*	0.198*	-0.247**	0.556**	0.786**
NSS											-0.044	0.060	-0.094	0.330**	0.396**
TW												0.338**	0.093	0.360**	0.629**
HI													0.066	-0.389**	0.341**
OC														-0.155*	-0.120
BYP															0.677**
SYP															1.000

*, ** significant at 5% and 1% level, respectively

Table 2: Genotypic correlation among yield and yield attributes for 15 characters of 55 genotypes in Indian mustard

Characters	Days to First flowering	Days to 50% flowering	Days to maturity	No pri. branches per plant	No sec. branches per plant	Plant height (cm)	Length of main raceme (cm)	Leaf area index	No siliquae per plant	No of seeds /siliqua	Test weight (g)	Harvest index (%)	Oil content (%)	Biological yield (g/plant)	Seed yield (g/plant)
DF1	1.000	0.818**	0.219**	0.186*	-0.115	-0.083	-0.194*	-0.214**	-0.356**	-0.474**	-0.040	-0.090	0.024	-0.230**	-0.360**
DF2			0.342**	0.035	-0.194*	-0.144	-0.272**	-0.216**	-0.315**	-0.442**	0.007	-0.012	0.073	-0.250**	-0.320**
DM				0.177*	0.055	0.052	0.068	0.106	0.005	0.027	0.082	-0.337**	-0.184*	0.299**	0.007
NPB					0.772**	0.148	0.148	0.303**	0.102	0.033	0.317**	0.061	-0.082	0.175*	0.245**
NSB						0.142	0.239**	0.599**	0.469**	0.257**	0.481**	0.358**	-0.133	0.280**	0.644**
PH							0.097	-0.182*	-0.114	0.427**	-0.116	-0.041	0.002	0.022	0.024
LMR								0.150	0.086	0.279**	0.265**	0.031	-0.009	0.265**	0.274**
LAI									0.686**	0.249**	0.580**	0.222**	-0.266**	0.586**	0.814**
NSP										0.279**	0.165*	0.200**	-0.279**	0.565**	0.797**
NSS											-0.070	0.068	-0.097	0.346**	0.411**
TW												0.357**	0.104	0.364**	0.642**
HI													0.088	-0.388**	0.350**
OC														-0.192*	-0.142
BYP															0.675**
SYP															1.000

*, ** significant at 5% and 1% level, respectively

Table 3: Direct and indirect effects of phenotypic path coefficient for 15 characters of 55 genotypes in Indian mustard

Characters	Days to First flowering	Days to 50% flowering	Days to maturity	No pri. branches per plant	No sec. branches per plant	Plant height (cm)	Length of main raceme (cm)	Leaf area index	No siliquae per plant	No of seeds /siliqua	Test weight (g)	Harvest index (%)	Oil content (%)	Biological yield (g/plant)	Seed yield (g/plant)
DF1	-0.0046	0.0101	-0.0128	-0.0093	-0.0130	-0.0049	0.0003	-0.0071	-0.1416	-0.0550	-0.0148	-0.0197	0.0002	-0.0798	-0.352**
DF2	-0.0037	0.0125	-0.0199	-0.0018	-0.0199	-0.0085	0.0005	-0.0072	-0.1252	-0.0488	-0.0007	-0.0023	0.0004	-0.0861	-0.311**
DM	-0.0010	0.0042	-0.0587	-0.0093	0.0059	0.0031	-0.0001	0.0032	0.0019	0.0024	0.0232	-0.0724	-0.0010	0.1038	0.005
NPB	-0.0007	0.0004	-0.0091	-0.0600	0.0777	0.0083	-0.0002	0.0091	0.0373	0.0042	0.0845	0.0135	-0.0005	0.0527	0.217**
NSB	0.0005	-0.0022	-0.0031	-0.0420	0.1111	0.0083	-0.0004	0.0187	0.1825	0.0284	0.1392	0.0755	-0.0007	0.0948	0.611**
PH	0.0004	-0.0018	-0.0030	-0.0082	0.0152	0.0606	-0.0002	-0.0059	-0.0456	0.0491	-0.0359	-0.0089	0.0000	0.0082	0.024
LMR	0.0009	-0.0033	-0.0039	-0.0085	0.0250	0.0058	-0.0017	0.0050	0.0345	0.0322	0.0803	0.0073	0.0000	0.0914	0.265**
LAI	0.0010	-0.0026	-0.0056	-0.0160	0.0611	-0.0105	-0.0003	0.0340	0.2667	0.0322	0.1805	0.0474	-0.0015	0.2038	0.790**
NSP	0.0016	-0.0039	-0.0003	-0.0055	0.0502	-0.0069	-0.0001	0.0225	0.4035	0.0321	0.0512	0.0443	-0.0016	0.1991	0.786**
NSS	0.0019	-0.0047	-0.0011	-0.0019	0.0241	0.0227	-0.0004	0.0083	0.0988	0.1313	-0.0142	0.0135	-0.0006	0.1182	0.396**
TW	0.0002	0.0000	-0.0042	-0.0155	0.0473	-0.0067	-0.0004	0.0188	0.0632	-0.0057	0.3266	0.0755	0.0006	0.1290	0.629**
HI	0.0004	-0.0001	0.0190	-0.0036	0.0375	-0.0024	-0.0001	0.0072	0.0799	0.0079	0.1104	0.2235	0.0004	-0.1392	0.341**
OC	-0.0001	0.0007	0.0090	0.0049	-0.0112	0.0000	0.0000	-0.0077	-0.0996	-0.0124	0.0305	0.0148	0.0065	-0.0555	-0.120
BYP	0.0010	-0.0030	-0.0170	-0.0088	0.0294	0.0014	-0.0004	0.0193	0.2244	0.0433	0.1177	-0.0869	-0.0010	0.3580	0.677**

Residual effect: 0.0255, Diagonal value indicates direct effect; Values right and left indicates indirect effect

*, ** significant at 5% and 1% level, respectively

Table 4: Direct and indirect effects of genotypic path coefficient for 15 characters of 55 genotypes in Indian mustard

Characters	Days to First flowering	Days to 50% flowering	Days to maturity	No pri. branches per plant	No sec. branches per plant	Plant height (cm)	Length of main raceme (cm)	Leaf area index	No siliquae per plant	No of seeds /siliqua	Test weight (g)	Harvest index (%)	Oil content (%)	Biological yield (g/plant)	Seed yield (g/plant)
DF1	0.0287	0.0018	-0.0141	-0.0185	-0.0157	-0.0043	0.0021	0.0015	-0.1696	-0.0848	-0.0170	-0.0118	-0.0001	-0.0578	-0.360**
DF2	0.0235	0.0022	-0.0221	-0.0035	-0.0266	-0.0075	0.0030	0.0015	-0.1500	-0.0791	0.0029	-0.0016	-0.0003	-0.0628	-0.320**
DM	0.0063	0.0008	-0.0644	-0.0176	0.0075	0.0027	-0.0008	-0.0008	0.0022	0.0048	0.0348	-0.0443	0.0007	0.0750	0.007
NPB	0.0053	0.0001	-0.0114	-0.0995	0.1058	0.0076	-0.0016	-0.0022	0.0484	0.0059	0.1341	0.0080	0.0003	0.0438	0.245**
NSB	-0.0033	-0.0004	-0.0035	-0.0768	0.1371	0.0073	-0.0026	-0.0043	0.2234	0.0461	0.2033	0.0472	0.0005	0.0702	0.644**
PH	-0.0024	-0.0003	-0.0034	-0.0147	0.0195	0.0517	-0.0011	0.0013	-0.0541	0.0765	-0.0491	-0.0054	0.0000	0.0056	0.024
LMR	-0.0056	-0.0006	-0.0044	-0.0147	0.0328	0.0050	-0.0110	-0.0011	0.0412	0.0500	0.1122	0.0041	0.0000	0.0665	0.274**
LAI	-0.0061	-0.0005	-0.0068	-0.0302	0.0821	-0.0094	-0.0017	-0.0072	0.3268	0.0446	0.2454	0.0292	0.0010	0.1471	0.814**
NSP	-0.0102	-0.0007	-0.0003	-0.0101	0.0643	-0.0059	-0.0010	-0.0049	0.4764	0.0500	0.0697	0.0263	0.0011	0.1420	0.797**
NSS	-0.0136	-0.0010	-0.0017	-0.0033	0.0353	0.0221	-0.0031	-0.0018	0.1329	0.1791	-0.0297	0.0090	0.0004	0.0868	0.411**
TW	-0.0012	0.0000	-0.0053	-0.0316	0.0659	-0.0060	-0.0029	-0.0042	0.0786	-0.0126	0.4228	0.0470	-0.0004	0.0914	0.642**
HI	-0.0026	0.0000	0.0217	-0.0061	0.0491	-0.0021	-0.0003	-0.0016	0.0952	0.0122	0.1510	0.1316	-0.0003	-0.0974	0.350**
OC	0.0007	0.0002	0.0119	0.0082	-0.0182	0.0001	0.0001	0.0019	-0.1331	-0.0174	0.0442	0.0116	-0.0039	-0.0482	-0.142
BYP	-0.0066	-0.0006	-0.0192	-0.0174	0.0383	0.0011	-0.0029	-0.0042	0.2694	0.0619	0.1538	-0.0510	0.0008	0.2511	0.675**

Residual effect: 0.0145, Diagonal value indicates direct effect; Values right and left indicates indirect effect

*, ** significant at 5% and 1% level, respectively

Conclusion

This study demonstrated that seed yield in Indian mustard is shaped by multiple interconnected morphological and physiological traits. Genotypic correlations were consistently stronger than phenotypic ones, confirming that most trait associations are under genetic control, though environment slightly dampens their visible expression. Correlation analysis identified leaf area index, siliquae per plant, biological yield, test weight, secondary branches, seeds per siliqua, harvest index, and main raceme length as having consistently strong positive links with seed yield at both levels. Conversely, days to first flower and days to 50% flower were negatively correlated with yield, favouring early-flowering types. Days to maturity had only a negligible association, suggesting little direct role in yield improvement. Path analysis further clarified these relationships by separating direct from indirect contributions. Leaf area index and siliquae per plant emerged as the most influential traits with the largest direct positive effects on seed yield. Biological yield, test weight, secondary branches, seeds per siliqua, and harvest index also made substantial direct contributions. The low residual effects at both levels confirmed that the included traits captured nearly all the variability in seed yield. Negative direct effects of flowering traits again emphasized the benefit of earliness. Taken together, the evidence from correlation and path analyses indicates that seed yield improvement can be achieved most effectively by selecting simultaneously for canopy development, branching capacity, reproductive sink size, and seed weight. These traits can serve as reliable selection criteria in breeding programs aimed at developing high-yielding Indian mustard varieties.

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