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Association and causal relationship studies of yield and contributing traits in Indian Mustard (*Brassica juncea* L.)

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Abstract

Mustard is one of the important oilseed crop produced worldwide. India is one of the leading producers of mustard crop but, despite having the third largest acreage its production remains stagnant. Therefore, intensive research is required for identification and selection of characters that contribute directly or indirectly to the increase in yield of the oilseed crop. In this context, the character association and path analysis studies were conducted during Rabi 2024-25 at the SUB Agricultural Research Farm, affiliated with the School of Agriculture, Sanjeev Agrawal Global Educational University, Bhopal, Madhya Pradesh. Ten Indian mustard genotypes were sown under Randomized Block Design in three replications and observations were recorded on for eleven quantitative traits. Treatments mean sum of square for all traits were found significant except for main raceme length which shows presence of sufficient genetic variation among the genotypes tested. The highest estimates of heritability in broad sense were observed Number of siliqua/plant and 1000 seed weight showed 81.32, 94.40 percent of heritability. Genetic advance was highest for number of siliqua per plant (38.92%) and lowest for main raceme length (3.98%). Genotypic correlation of five traits *viz*. Results showed five traits were positively and significantly correlated with seed yield per plant *viz*. plant height (0.4987), number of primary branches (0.5734), number of secondary branches (0.4162), siliqua of main raceme (0.2249) and number of siliqua per plant (0.4175) showed positive and significant correlation with seed yield per plant. Path coefficient analysis revealed that plant height (1.2067) and secondary branches (0.7846) exerted the strongest positive direct effects on seed yield/plant, establishing them as major selection criteria in mustard breeding. Seed yield/plant (0.1424) and 1000-seed weight (0.1286) also showed positive contributions, though of lesser magnitude. Therefore, these traits should be prioritized for selection and breeding to enhance seed yield in mustard genotypes.

Keywords: Indian mustard, correlation, path analysis, GCV and PCV

Introduction

The global mustard production for 2022-23 reached approximately 11.35 million tonnes, with India contributing significantly at around 11.8 million tonnes, where Rajasthan, Uttar Pradesh, and Madhya Pradesh emerged as the top producing states, and the country's productivity averaged about 1,230 kg per hectare. Indian mustard (*Brassica juncea* L.), locally known as rai, raya, or laha, is a vital oilseed crop in India, ranking second only to groundnut in terms of importance among edible oilseeds. Mustard seeds contain approximately 38% to 43% oil, which is regarded as one of the healthiest cooking oils due to its low content of harmful saturated fats and balanced levels of essential fatty acids like linoleic and linolenic acids (Patel *et al*., 2012; Porter and Crompton, 2008). Globally, India holds the third position in mustard cultivation area, accounting for 19.29% of the total, following Canada (24.55%) and China (20.58%). However, it contributes only 11.27% to global production, whereas China and Canada account for 22.08% and 21.77%, respectively (www.drmr.org.in). (https://www.thehindubusinessline.com/) For the 2023-2024 crop year, India's rapeseed-mustard production reached a record high of 132.59 lakh tonnes from an area of 91.83 lakh hectares, resulting in an average productivity of 1443 kg/ha.

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This marked the first time rapeseed-mustard became the largest oilseed crop in India, with significant contributions from states like Rajasthan, Madhya Pradesh, Uttar Pradesh, Haryana, and West Bengal. The primary mustard-growing states include Rajasthan (43% of total area), Uttar Pradesh (14%), Madhya Pradesh (11%), and Haryana (8%). For effective crop improvement, understanding genetic variability is crucial. Parameters such as the phenotypic and genotypic coefficients of variation, heritability in the broad sense, and genetic advance as a percentage of the mean are essential tools for assessing selection potential (Manjunath *et al*., 2017) [15]. Heritability combined with genetic advance helps determine the reliability of traits for selection (Meena *et al*., 2017) [16]. Traits with high heritability but low genetic advance may be improved through intermating of elite genotypes from segregating populations (Synrem *et al*., 2014) [26]. Thorough evaluation of genetic material is necessary for identifying and utilizing improved varieties. This study aims to evaluate heritability, trait associations, and identify effective selection criteria to enhance yield in Indian mustard. The existence of adequate genetic variability within germplasm collections is fundamental for breeding programs. Estimating variability through statistical parameters provides a foundation for selecting desirable genotypes. However, yield-related traits often interact in complex ways, showing both direct and indirect effects on seed yield, making selection challenging. In such cases, path coefficient analysis becomes valuable, as it separates correlation coefficients into direct and indirect contributions. Therefore, combining character association and path analysis offers a comprehensive understanding of yield-contributing traits, aiding breeders in the selection of superior genotypes for further genetic improvement and conservation.

Materials and Method: The experiment was carried out during the Rabi season of 2024–2025 at the SUB Agricultural Research Farm, affiliated with the School of Agriculture, Sanjeev Agrawal Global Educational University, Bhopal, Madhya Pradesh. Ten genotypes of Indian mustard were evaluated using a Randomized Block Design (RBD) with three replications. Data were collected from five randomly selected plants in each plot, focusing on eleven agronomic and yield-related traits: plant height (cm), number of primary and secondary branches per plant, main raceme length (cm), number of siliquae on the main raceme, average siliqua length (cm), number of seeds per siliqua, number of siliquae per plant, 1000-seed weight (g), seed yield per plant (g), and seed yield per hectare (kg). Statistical significance for each trait was analyzed following the procedure outlined by Panse and Sukhatme (1967) [18]. Estimates of the genotypic and phenotypic coefficients of variation (GCV and PCV) were calculated using the method described. Broad-sense heritability (h^2) was determined following the approach of Burton and De Vane (1953), while genetic advance, representing the expected genetic gain, was computed using the formula provided by Johnson *et al*. (1955). To assess the direct and indirect contributions of individual traits to seed yield, path coefficient analysis was conducted based on the method developed by Wright (1921) [28] and later elaborated by Dewey and Lu (1959) [5].

Results and Discussion

ANOVA for randomized block design, carried out for eleven traits revealed significant differences for genotypes (treatments) except main raceme length (table 1). It indicates the presence of sufficient genetic variation among the genotypes tested for all the morphological traits. Replication MSS for number of siliqua/plant, 1000 seed weight, seed yield/ plant and seed yield/hectare were also found significant. This indicates the presence of differences in soil factors at the experimental location.

Table 1: Analysis of variance for eleven yield attributing characters

Source of variation	Replication	Treatment	Error
Df	2	29	58
Plant Height (cm)	165.482316	462.781524*	259.347891
No. of Primary Branches	0.314562	4.582413*	2.042137
No. of Secondary Branches	6.107455	12.156229*	2.018625
Main Raceme Length (cm)	82.564128	69.248731	42.187436
No. of Siliqua on Main Raceme	14.205347	72.563821*	39.714258
Siliqua Length (cm)	0.402519	0.359781*	0.189432
Seeds/Siliqua	0.532144	2.812345*	1.482931
No. of Siliqua/Plant	1625.894000*	6710.482336**	412.274185
1000-Seed Weight (g)	0.071653*	1.134528**	0.021347
Seed Yield/Plant (g)	10.412538*	8.215649**	2.412836
Seed Yield/ha (kg)	398725.680*	421350.825**	118452.739

Table 2: Estimates of genotypic (GCV) and phenotypic (PCV) co-efficient of variation, heritability (bs) and genetic advance (% of mean) for seed yield and component traits in Indian mustard

Source of Variation	Plant Height (cm)	No. of Primary Branches	No. of Secondary Branches	Main Raceme Length (cm)	No. of Siliqua on Main Raceme	Siliqua Length (cm)	Seeds/Siliqua	No. of Siliqua/Plant	1000-Seed Weight (g)	Seed Yield/Plant (g)	Seed Yield/ha (kg)
Mean	162.35	6.92	11.48	51.87	42.73	5.41	14.22	192.65	4.83	8.65	2087.42
Min	142.67	5.21	8.42	44.36	34.12	4.63	12.05	124.88	3.72	6.12	1562.83
Max	185.42	9.83	14.26	61.29	55.64	6.02	16.12	276.41	6.28	13.54	3228.56
GCV	5.12	11.36	15.94	4.87	8.42	4.22	4.75	20.42	11.68	16.42	14.88
PCV	9.85	20.72	20.64	11.58	16.43	8.96	9.64	22.84	12.02	24.78	22.57
h^2 (Broad	21.4	27.35	59.25	18.42	23.65	28.14	21.76	81.32	92.25	47.36	46.52

Sense)											
Gen. Adv. as % of Mean (5%)	4.65	11.42	24.36	3.98	6.74	5.26	4.42	38.92	24.63	21.54	20.86

Mean, range, estimates of GCV, PCV, heritability and genetic advance for seed yield and component traits of Indian mustard is presented in table 2. Mean for plant height ranged from 185.42) cm to 142.67cm with average of 162.35, whereas mean for number of primary and secondary branches ranged from 9.83 to 5.21 and 14.26 to 8.42, having mean of 6.92 and 11.48, respectively. The mean for length of main raceme ranged from 61.29 to 44.36, having mean of 51.87cm. The number of siliqua on main raceme had mean values ranging from 55.64 to 34.12 with an average of 42.73, while siliqua length had mean values ranging from 6.02cm to 4.63cm, with an average of 5.41 cm. The mean values for number of seed per siliqua ranged from 16.12 to 12.05 with an average of 14.22. The mean for number of siliqua per plant was found to be 192.65 with maximum value of 276.41 and minimum value of 124.88. The mean for 1000 seed weight ranged from 6.28 to 3.72 with an average of 4.83. For seed yield per plant, maximum value was 13.54g whereas minimum was 6.12g with average of 8.65g. Seed yield per hectare recorded a mean of 2087.42 kg ranging from 3228,56 to 1562.83.The result was supported by Begum, (2018) [2]. The GCV ranged from 4.22 for siliqua length to 20.42 for number of siliqua per plant. GCV estimates for number of siliqua per plant (20.42) was in high range while it was in low range for traits like length of siliqua, main raceme length, plant height and seeds per siliqua. For traits like No. of Siliqua on Main Raceme, No. of Siliqua on Main Raceme, 1000 seed weight, seed yield per plant and seed yield per hectare GCV was in moderate range. The PCV ranged from 8.96 for siliqua length to 22.84 for No. of Siliqua/Plant. The PCV estimates were in high range for all the traits except plant height, Seeds/Siliqua which was in low range and 1000 seed weight which were in moderate range.

The highest estimates of heritability in broad sense were observed for 1000 seed weight (92.25%) while lowest was observed for main raceme length (18.42%). Number of siliqua/plant and 1000 seed weight showed 81.32, 94.40 percent of heritability, respectively which was in very high range. No. of Secondary Branches 59.25 Seed yield per plant (47.36) and seed yield per hectare (46.52) showed moderate heritability.

Expected genetic advance as percent of mean at 5% was highest for number of siliqua per plant (38.92%) and lowest for main raceme length (3.98%). Genetic advance for number of siliqua per plant (38.92), 1000 seed weight (24.63), No. of secondary branches (24.36) and seed yield per hectare (20.86) showed high genetic advance. Seeds/siliqua (4.42), siliqua length (5.26), No. of siliqua on main raceme (6.74), plant height (4.65) and main raceme length (3.98) were found in low range of genetic advance. Main raceme length has showed very low genetic advance. Similar findings were reported by Sharma and Yadav (2021), Ali *et al*. (2021) and Begum *et al* (2018) Chaubey *et al* (2022) [29, 1, 2, 3]. The traits number of siliquae per plant, 1000-seed weight, and number of secondary branches exhibited high heritability along with high genetic advance, indicating the involvement of additive gene action and the potential effectiveness of direct selection for improvement. In contrast, plant height, main raceme length, number of siliquae on the main raceme, average siliqua length, and seeds per siliqua displayed both low heritability and low genetic advance, suggesting strong environmental influence and limited scope for improvement through selection.

Table 3: Genotypic Correlation of Eleven Characters in Indian Mustard

Characters	**Plant Height**	**Primary Branches**	**Secondary Branches**	**Main Raceme Length**	**Siliquae on Main Raceme**	**Siliqua Length**	**Seeds/Siliqua**	**Siliquae/Plant**	**1000-Seed Weight**	**Seed Yield/Plant**
Plant Height	1.000	0.6124**	0.3985**	0.2853**	0.4528**	-0.3162*	-0.2285	0.5372**	-0.2044	0.4987**
Primary Branches		1.000	0.7248**	0.1649	0.3896**	-0.2681*	0.1062	0.4621**	-0.3126**	0.5734**
Secondary Branches			1.000	0.3186**	0.3411**	-0.4015**	0.1248	0.2863*	-0.2262*	0.4162**
Main Raceme Length				1.000	0.4025**	-0.3922**	-0.0547	0.6728**	-0.5181**	0.3147**
Siliquae on Main Raceme					1.000	-0.2562*	-0.1486	0.3025**	-0.4128**	0.2249*
Siliqua Length						1.000	0.6825**	-0.3148**	0.2941**	-0.2384*
Seeds/Siliqua							1.000	-0.0862	-0.2683*	0.0847
Siliquae/Plant								1.000	-0.2962**	0.4175**
1000-Seed Weight									1.000	-0.1984
Seed Yield/Plant										1.000
Seed yield/ha	0.3782	0.6245	0.3524	0.2886	0.0942	0.4127	0.0683	0.2648	0.1124	0.8462

** Significant at 1% level, * - Significance at 5% level

Genotypic correlation of eleven characters in Indian mustard is presented in table 3. The correlation coefficients were classified as weak (0.7) on the basis of their absolute values (Dospekhov, 1984) [8]. Number of siliqua/plant showed significant and positive correlation with plant height (0.5372), number of primary branches (0.4621), number of secondary branches (0.2863), length of main raceme (0.6728) and number of siliqua on main raceme (0.3025) while siliqua length (-0.3148) showed significant negative correlation. Length of main raceme showed strong correlation with number of siliqua per plant, while plant height, number of primary branches, number of secondary branches, number of siliqua on main raceme and siliqua length showed moderate range of correlation with number of siliqua per plant. Number of seeds per siliqua showed weak correlation with this trait. The siliqua length was positively and significantly correlated with 1000 seed weight with genotypic correlation coefficient of 0.2941. Traits like plant height (-0.2044), number of primary branches (-0.3136), number of secondary branches (-0.2262) and number of siliqua per plant (-0.5181) were negatively and significantly correlated with 1000 seed weight. Traits like plant height, number of primary branches, number of secondary branches, number of siliqua on main raceme, siliqua length, seeds per siliqua and number of siliqua per plant were found to be in the moderate range of correlation coefficient while length of main raceme showed strong correlation with seed yield per plant. Results showed five traits were positively and significantly correlated with seed yield per plant *viz*. plant height (0.4987), number of primary branches (0.5734), number of secondary branches (0.4162), siliqua of main raceme (0.2249) and number of siliqua per plant (0.4175) while trait like siliqua length (-0.2384) was negatively and significantly correlated Positive association of seed yield/plant with primary branches/plant, secondary branches/plant, number of seeds/siliqua was also observed which was in agreement with that of the findings Choudhary *et al* (2023), Dipti *et al*. (2016) and Dixit *et al* (2019). Kumar, *et al*. (2016) [4, 6, 7, 12] observed positive association of seed yield/plant with length of main raceme. Similar results were observed by Dwivedi *et al*. (2023), Kumar *et al*. (2013) Kumar *et al*. (2020) [9, 11, 13]. Traits like plant height, number of primary branches, number of secondary branches, siliqua length, number of siliqua per plant, were found to be in the moderate range of correlation coefficient while length of main raceme and 1000 seed weight showed weak correlation with seed yield per plant.

Table 4: Phenotypic Correlation of Eleven Characters in Indian Mustard

Characters	Plant Height	Primary Branches	Secondary Branches	Main Raceme Length	Siliquae on Main Raceme	Siliqua Length	Seeds/Siliqua	Siliquae/Plant	1000-Seed Wt.	Seed Yield/Plant
Plant Height	1.000	0.2841*	0.1975	0.1634	0.3528**	-0.0824	-0.0426	0.3182**	-0.1763	0.2765*
Primary Branches		1.000	0.4026**	0.0925	0.2142*	-0.1048	0.1065	0.2916**	-0.2189*	0.2437*
Secondary Branches			1.000	0.2467*	0.1745	-0.1863*	0.0842	0.3271**	-0.1962*	0.3569**
Main Raceme Length				1.000	0.4183**	-0.0927	0.1524	0.2984**	-0.2867**	0.1143
Siliquae on Main Raceme					1.000	-0.0689	0.1275	0.1642	-0.2283*	0.1397
Siliqua Length						1.000	0.1846*	-0.2041*	0.1432	-0.2128*
Seeds/Siliqua							1.000	-0.0548	-0.1482	0.0635
Siliquae/Plant								1.000	-0.2641**	0.3982**
1000-Seed Weight									1.000	-0.1262
Seed Yield/Plant										1.000
Seed Yield/ha	0.1745	0.2136	0.3279	0.1242	0.1584	0.2465	0.0472	0.2865	0.0987	0.6248

** Significant at 1% level, * - Significance at 5% level

Phenotypic correlation of siliqua per plant (0.3182) number of primary branches (0.2916), number of secondary branches (0.3271), length of main raceme (0.2984) was positively correlated (Ali *et al*., 2021) [1]. Traits like siliqua length (-0.2041) and number of siliqua per plant (-0.0548) were negatively and significantly correlated with 1000 seed weight. Traits like plant height (-0.1763), seeds per siliqua and seed yield per plant were negatively correlated with 1000 seed weight. Traits like plant height, number of primary branches, number of secondary branches, number of siliqua on main raceme, siliqua length, seeds per siliqua, number of siliqua per plant and seed yield per plant were found to be in weak correlation coefficient while length of main raceme showed moderate correlation with seed yield per plant.

Three traits were positive significantly correlated with seed yield per plant *viz*. plant height (0.2765), number of secondary branches (0.2437) number of secondary branches (0.3569) and siliqua/plant (0.3982) while trait like siliqua length (-0.2128) and 1000 seed weight was negative significantly correlated. Traits like plant height, number of primary branches, length of main raceme, number of siliqua on main raceme, number of seeds per siliqua and 1000 seed weigh were found to have weak correlation coefficient while number of secondary branches, siliqua length and number of siliqua per plant showed moderate correlation with seed yield per plant. Parallel verdicts were also reported by Singh *et al*. (2011) Singh *et al*. (2010) Verma *et al* (2017) [20, 25, 24]

The phenotypic correlation table indicated that yield per hectare was positively correlated with plant height (0.1745), number of primary branches (0.2136), number of secondary branches (0.3279), length of main raceme (0.1242), number of siliqua on main raceme (0.1584) and seeds per siliqua (0.2465), number of siliqua per plant (0.0472) and seed yield per plant (0.2865) while 1000 seed weight (-0.0987) was negatively correlated with seed yield per hectare. All the traits showed weak correlation with seed yield per plant, except seed yield per plant which had moderate correlation with this trait. In general, the values of genotypic correlations were higher than their phenotypic correlations indicating the inherent association among the traits. Similar findings were also reported by Dwivedi *et al.*, 2023, Lodhi *et al*. (2014), Patel *et al*. (2019) and Roy *et al*. (2018) Shekhawat *et al*. (2014) Shrivastava *et al*. (2023) [9, 14, 21, 22, 19]. The genotypic correlation coefficients of traits such as plant height, number of primary and secondary branches per plant, main raceme length, number of siliquae on the main raceme, average siliqua length, and 1000-seed weight with seed yield per plant were higher than their corresponding phenotypic correlations, indicating a strong genetic relationship. However, the lower phenotypic values suggest environmental factors had a diminishing effect. Conversely, the phenotypic correlation coefficients for number of seeds per siliqua and number of siliquae per plant were higher than their genotypic counterparts, implying that their association with seed yield per plant was influenced not only by genetic factors but also by favourable environmental conditions.

Table 5: Genotypic Path Coefficient of Ten Yield Components to Seed Yield/Plant in Indian Mustard

Characters	Plant Height	Primary Branches	Secondary Branches	Main Raceme Length	Siliquae on Main Raceme	Siliqua Length	Seeds/Siliqua	Siliquae/Plant	1000-Seed Wt.	Seed Yield/Plant
Plant Height	1.8742	1.5263	0.9425	-0.3154	1.1826	-1.0257	-0.8421	1.2348	-0.5632	1.2067
Primary Branches	-2.6348	-2.9845	-2.1873	-0.2897	-1.8264	1.2843	-0.0742	-1.5648	1.4267	-1.2948
Secondary Branches	0.8745	1.8543	2.1682	0.8326	0.7682	-0.9456	0.1843	0.5428	-0.5341	0.7846
Main Raceme Length	0.0256	-0.0128	-0.0293	-0.0734	-0.0325	0.0428	0.0095	-0.0652	0.0548	-0.0223
Siliquae on Main Raceme	-0.1785	-0.1946	-0.1384	-0.1442	-0.3286	0.1186	0.3924	-0.0985	0.1562	-0.0534
Siliqua Length	-0.0826	-0.0732	-0.0745	-0.0943	-0.0562	0.1642	0.1387	-0.0768	0.0625	-0.0587
Seeds/Siliqua	0.0224	-0.0028	-0.0047	0.0042	0.0386	-0.0328	-0.0415	0.0064	0.0128	0.0051
Siliquae/Plant	-0.0586	-0.0473	-0.0218	-0.0726	-0.0253	0.0436	0.0124	-0.0942	0.0285	-0.0271
1000-Seed Weight	0.1985	0.3261	0.1845	0.4367	0.3186	-0.2182	0.1985	0.1857	-0.6421	0.1286
Seed Yield/Plant	0.0867	0.0654	0.0528	0.0441	0.0262	-0.0487	-0.0134	0.0453	-0.0287	0.1424
Seed yield/ha	0.3145	0.5426	0.2982	0.2428	0.0826	· -0.2862	· -0.0864	0.2148	· -0.0983	0.7562

Partial R²:0.6124. The genotypic path coefficient analysis (table 5) revealed that plant height (1.8742), number of secondary branches (2.1682), siliqua length (0.1682) and seed yield/ plant (0.1424) 1000 seed weight (0.1286) showed positive direct effects on seed yield per hectare while number of primary branches (-2.9845), main raceme length (-0.0734), number of siliqua on main raceme (-0.3286), seeds/siliqua (-0.0415), number of siliqua/plant (-0.0942) and 1000 seed weight (-0.6421) showed negative direct effects on seed yield per hectare. Yadav *et al* (2021), Yadav *et al*. (2015) and Roy *et al*. (2018) [29, 30, 19] also observed positive direct effect for plant height, number of secondary branches and seeds/siliqua. Selection based on the traits with positive direct effect may help in improvement of seed yield while selection based on traits with negative direct effect may be ineffective. Number of secondary branches has highest direct effect on seed yield per hectare. Indirect effect of number of siliqua/plant, 1000 seed weight and seed yield/plant was 0.2148, -0.0983 and 0.7562 respectively on seed yield per hectare.

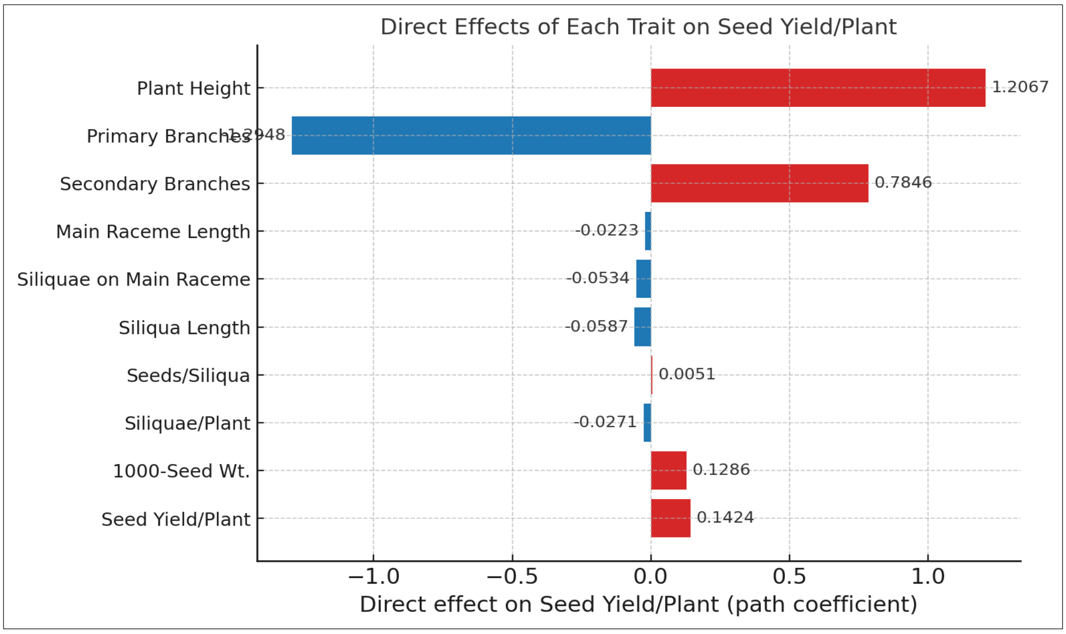
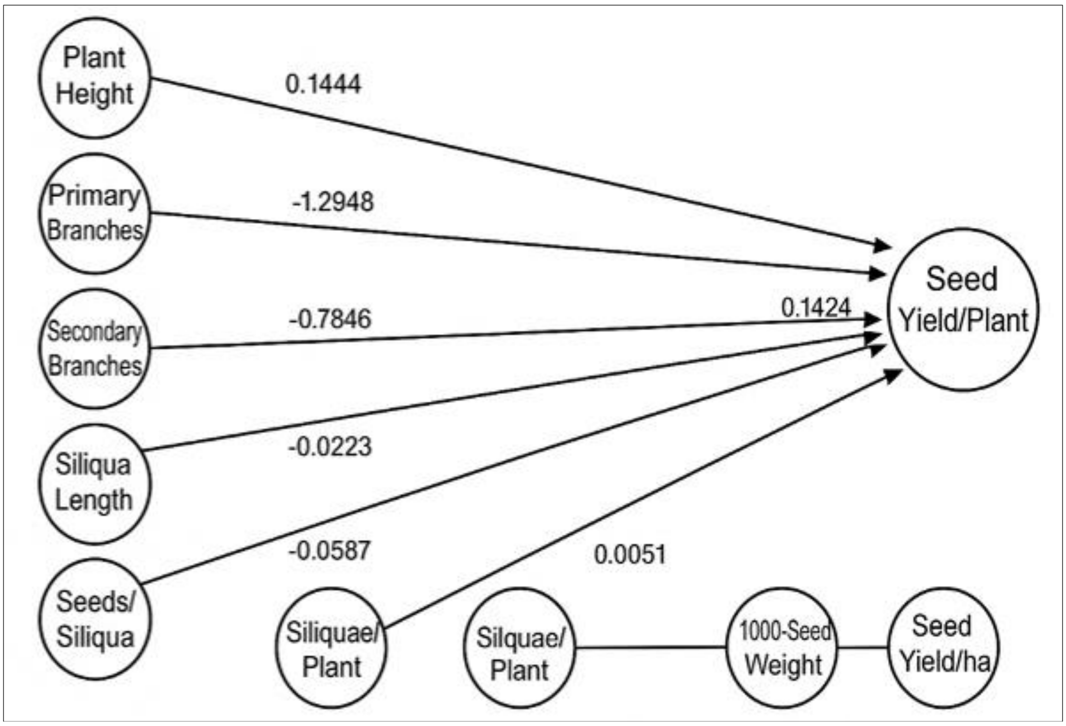
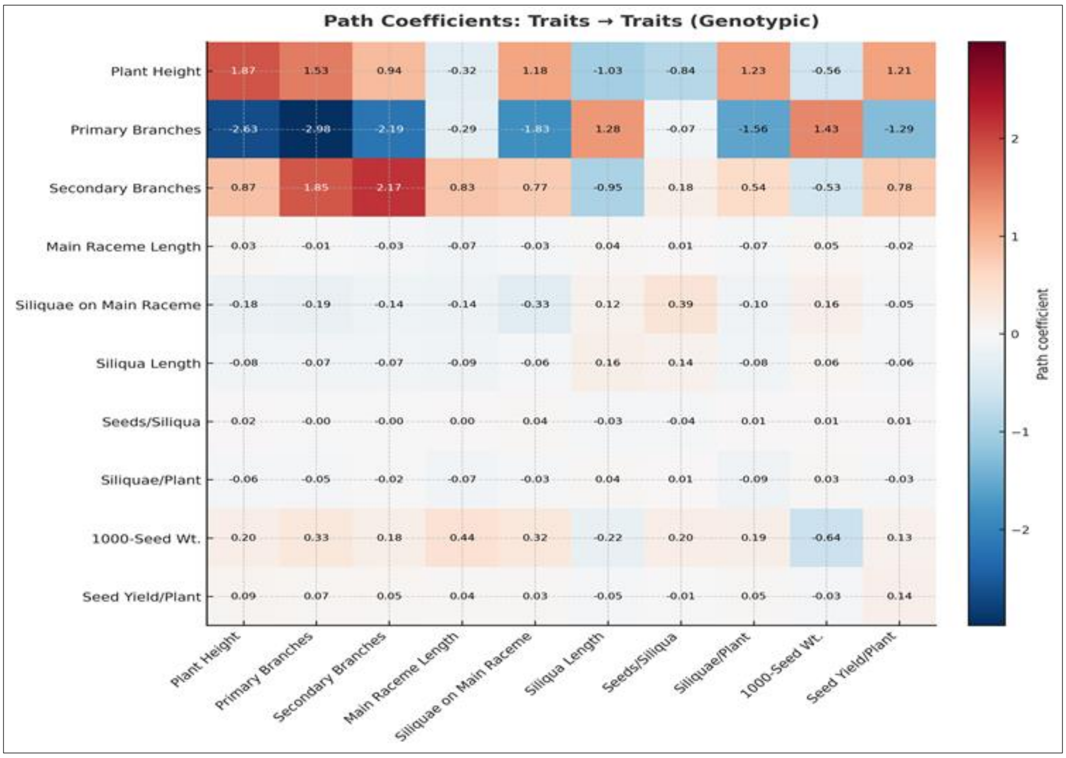


Fig 1: Direct influence of each yield component trait





	Plant Height	Primary Branches	Secondary Branches	Main Raceme Length	Siliquae on Main Raceme	Siliqua Length	Seeds/Siliqua	Siliquae/Plant	1000-Seed Wt.	Seed Yield/Plant
Plant Height	1.87	1.53	0.94	-0.32	1.18	-1.03	-0.84	1.23	-0.56	1.21
Primary Branches	-2.63	-2.98	-2.19	-0.29	-1.83	1.28	-0.07	-1.56	1.43	-1.29
Secondary Branches	0.87	1.85	2.17	0.83	0.77	-0.95	0.18	0.54	-0.53	0.78
Main Raceme Length	0.03	-0.01	-0.03	-0.07	-0.03	0.04	0.01	-0.07	0.05	-0.02
Siliquae on Main Raceme	-0.18	-0.19	-0.14	-0.14	-0.33	0.12	0.39	-0.10	0.16	-0.05
Siliqua Length	-0.08	-0.07	-0.07	-0.09	-0.06	0.16	0.14	-0.08	0.06	-0.06
Seeds/Siliqua	0.02	-0.00	-0.00	0.00	0.04	-0.03	-0.04	0.01	0.01	0.01
Siliquae/Plant	-0.06	-0.05	-0.02	-0.07	-0.03	0.04	0.01	-0.09	0.03	-0.03
1000-Seed Wt.	0.20	0.33	0.18	0.44	0.32	-0.22	0.20	0.19	-0.64	0.13
Seed Yield/Plant	0.09	0.07	0.05	0.04	0.03	-0.05	-0.01	0.05	-0.03	0.14

Fig 2: Path coefficient trait heat map

Path coefficient analysis quantifies the direct influence of each yield component trait on seed yield/plant. From the figure 1: Path coefficient analysis revealed that plant height (1.2067) and secondary branches (0.7846) exerted the strongest positive direct effects on seed yield/plant, establishing them as major selection criteria in mustard breeding. Seed yield/plant (0.1424) and 1000-seed weight (0.1286) also showed positive contributions, though of lesser magnitude. Seeds/siliqua (0.0051) had negligible influence. Among negative contributors, primary branches (–1.2948) exerted the highest adverse effect, indicating resource competition. Other traits like siliqua length, siliquae on main raceme, siliquae/plant, and raceme length had minor negative roles. Overall, taller plants with more secondary branches and heavier seeds are key for yield improvement.

Conclusion

Founded on the verdicts above, it can be settled that traits such as plant height, number of secondary branches, siliqua length, and seed yield per plant should be prioritized in selecting high-yielding genotypes. Traits like the number of siliqua per plant, 1000 seed weight, seed yield per plant, and seed yield per hectare exhibit high heritability, signifying a positive response to selection. Furthermore, the number of siliqua per plant, 1000 seed weight, and seed yield per plant show moderate genetic advancement, suggesting their potential in improving seed yield. These identified traits can be effectively utilized to enhance seed yield improvement.

This study enhances our knowledge of the intricate interrelationships among agronomic traits that determine yield in Indian mustard. Recognizing traits with notable direct and indirect influences on yield enables breeders to focus on them while developing superior, high-yielding varieties. In addition, the outcomes provide important guidance for future research aimed at maximizing yield potential and improving overall productivity in Indian mustard.

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