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STUDY OF DIRECT AND INDIRECT EFFECT FOR SEED YIELD CHARACTERS OF INDIAN MUSTARD (*BRASSICA JUNCEA* L. CZERN AND COSS)

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ABSTRACT

Mustard (*Brassica juncea*), a member of the Brassicaceae family, is widely cultivated for its edible leaves, seeds, and oil. A recent study evaluated the genetic variability of twenty mustard genotypes during the *Rabi* season of 2022 at the central research farm of the Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology, and Sciences, Prayagraj. The experiment employed a Randomized Block Design with three replications. Plants were spaced 10 cm apart within rows, with 30 cm between rows. Data were collected from five randomly selected plants per genotype across all replications, assessing fourteen traits. Analysis of variance revealed significant differences among genotypes for all traits, highlighting genetic diversity. Strong correlations were observed between seed yield per plant and traits such as the number of primary and secondary branches and the harvest index at both phenotypic and genotypic levels. Path coefficient analysis identified the harvest index as the most influential factor directly affecting seed yield, followed by biological yield and the number of primary and secondary branches. These findings emphasize the importance of these traits in improving yield. To enhance mustard productivity, breeding programs should prioritize these key traits. By integrating them into selection criteria, high-yielding genotypes can be identified, enabling substantial advancements in mustard breeding. This study underscores the value of targeting specific morphological and physiological traits to maximize mustard crop yield through systematic breeding strategies.

Key words : Correlation coefficient, Mustard, Path coefficient analysis.

Introduction

By 2030, vegetable oil consumption in India is expected to exceed 20 kg per capita annually, necessitating significant growth in the oilseeds sector to meet this demand. With an estimated population of 1.276 billion, the country would require approximately 204 lakh tonnes of vegetable oils, translating to 680 lakh tonnes of oilseeds, assuming existing production ratios remain constant. As per Directorate of Oilseed Development, Ministry of Agriculture and Farmers Welfare, Government of India, 2020-21, achieving near self-sufficiency in vegetable oil production by the end of the XII Plan would necessitate producing 544 lakh tonnes of oilseeds. India, the fourth-largest player in the global vegetable oil economy after the USA, China and Brazil, devotes about 260 lakh hectares to oilseed cultivation, primarily on marginal, rain-dependent lands with limited water resources. Oilseeds occupy 13% of the gross cropped area, contribute 3% to the Gross National Product (GNP) and account for 10% of agricultural value, with 72% of cultivation occurring

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Abbreviation used : **PH:** Plant height; **NPB:** Number of primary branches; **NSB:** Number of secondary branches; **DF50:** Days to 50% flowering; **DM:** Days to maturity; **NSPP:** Number of siliquae per plant; **SL:** Siliquae length; **NSPS:** Number of seeds per siliquae; **MRL:** Main raceme length; **TW:** Test weight; **BY:** Biological yield; **HI:** Harvest index; **SYPP:** Seed yield per plant; **OC:** Oil content.

under rainfed conditions, largely managed by small and marginal farmers. Key oilseeds grown in India include groundnut, rapeseed-mustard, soybean, sesame, sunflower, safflower and Niger; linseed and castor are the main non-edible oilseeds. Indian mustard (*Brassica juncea*), or rai, dominates the oilseed landscape, covering 70% of the rapeseed-mustard cultivation area. India leads globally in rapeseed-mustard production, contributing 27.5% of the cultivated area and 20% of global output, yet its productivity (900 kg/ha) falls short of the global average (1408 kg/ha). Mustard is India's second most important oilseed after groundnut, accounting for 25% of national oilseed production. In 2020–21, mustard was cultivated on 6.82 million hectares, yielding 10.95 million tonnes. Rajasthan, Haryana and Madhya Pradesh are the leading producers, with Rajasthan alone cultivating 3.08 million hectares and producing 4.20 million tonnes at a productivity rate of 1366 kg/ha. Uttar Pradesh follows with a productivity of 1605 kg/ha from 0.91 million hectares, producing 2.23 million tonnes (DES, 2021). Mustard seeds contain 36–48% oil and serve multiple purposes, including culinary uses in pickles and curries, as well as applications in biofuels, lubricants, and livestock feed. Mustard oil, favoured for cooking in northern India, is also a popular food preservative. The plant's green leaves and stems provide nutritional value as vegetables, while its foliage serves as quality fodder. Botanically classified as Brassica juncea, an annual self-pollinating amphidiploid (2n=4x=36), mustard has origins in Central Asia, including north-western India, and thrives in subtropical and temperate climates. Understanding the correlation between a characteristic, such as yield and other factors influencing yield components, would be advantageous for identifying suitable rice genotypes to serve as parent plants in breeding initiatives (Sreedhar and Reddy, 2019). It is a statistical measure which is used to find out the degree and direction of relationship between two or more variables. When change in one variable causes the change in another variable, the variables are said to be correlated. It distinguishes direct influences from indirect ones, providing essential insights for effective trait selection geared toward yield improvement (Talekar *et al.*, 2022). Character association studies provide information about traits that are positively correlated with each other and yield. Path analysis can partition these correlations into direct and indirect effects, offering additional insights and aiding in selection for yield improvement. Correlation estimates between yield and other traits are useful for selecting desired plant types and designing effective breeding programs. When changes in one variable cause changes in another, these variables are said to be correlated. Correlation coefficients measure the degree of genotypic or phenotypic association between two or more traits, forming the basis for selection. Path coefficient analysis, introduced by Wright (1921), is an important tool for partitioning the correlation coefficient into direct and indirect effects of variables on a dependent variable.

Materials and Methods

To comprehend the genetic variability, heritability, of Indian mustard genotypes, the current study, was conducted. The present investigation was done to understand the genetic variability, heritability present among Indian mustard genotypes. The investigation was carried out at Central Research Farm (CRF), Department of Genetics and Plant breeding, Sam Higginbottom University of Agriculture, Technology and Sciences (SHUATS), Prayagraj during the *Rabi* season of 2022. The experiment was set up using a Randomized Block Design (RBD) with three replications and 20 genotypes of mustard. The height of five randomly selected plants from each plot was measured in cm with help of meter scale from ground level to tip of the shoot at last harvest stage. The average of plant height of each replication of each treatment was recorded and subjected to statistical analysis. Number of primary and secondary branches per plant was counted at maturity stage. The average of number of secondary branches per plant from random five plants was taken of each replication. Days to 50% flowering was taken from sowing date to the stage when flowers emerged in 50 % of the plants in a row. The days taken from the date of sowing to the date of physiological maturity of the plants in whole plot were recorded as days to maturity. The number of siliquae per plant of 5 randomly selected plants were counted. Length of five different siliquae from five different plants were measured using scale and averaged. Length of five different raceme from five different plants were measured using scale and averaged and subjected for analysis for each genotype and replication. Harvest index was computed by using following formula as suggested by Singh and Stoskoff (1971). The harvest index was worked out by using following formula:

$$\text{Harvest index (\%)} = \frac{\text{Seed yield (g)}}{\text{Biological yield (g)}} \times 100$$

Oil content in 100-gram seed using Soxhlet apparatus. In this method fat is extracted, semi-continuously with an organic solvent. Solvent is heated and volatized then is condensed above the sample. Solvent drips onto sample and soaks it to extract the fat. At 15-20 minutes interval the solvent is siphoned to the heating flask, to start the process again (this process takes place in Soxhlet extractor). Fat content is measured by weight loss of sample *i.e.*, weight of fat removed. The data recorded, were subjected to statistical analysis. The Fisher and Yates, 1936 method was used to statistically analyse the data. Correlation was calculated using methods suggested by Al-Jibouri *et al.* (1958), while path coefficient analysis was worked out my method suggested by Dewey and Lu (1959).

Results and Discussion

Analysis of variance

For the experimental design, an analysis of variance was conducted on the mean sum squares data for 14 traits. The variance analysis for these traits is presented in Table 1. The analysis revealed highly significant differences (p = 0.01 & 0.05) among 20 genotypes for all studied traits, indicating substantial genetic variation within the Indian mustard germplasms. This also highlights the potential for genetic enhancement through selection. ANOVA allows researchers to determine if significant differences exist among various genotypes or treatments and to quantify the variation attributed to different factors. It compares the variability between groups, referred to as "treatments" or "factors," against the variability within each group. A significant disparity between group variability suggests that the traits being analyzed have a meaningful impact on mustard yield. The ANOVA findings pinpoint which traits most influence variations in grain yield, providing essential insights for optimizing cultivation practices, breeding strategies, and selecting the most promising genotypes to improve overall yield and quality. The analysis of variance and the data on various traits indicated significant differences among genotypes for all 14 traits, confirming that there is sufficient genetic variability to support a breeding program aimed at enhancing pod yield in Indian mustard. These findings are consistent with the research conducted by Yadav *et al.* (2020) and Nishad *et al.* (2022).

Table 1 : Analysis of Variance (ANOVA) for 14 characters in Mustard.

S. no.	Source	Mean Sum of Squares (MSS)		
		Replication	Treatment	Error
	Degrees of freedom	n=2	n=19	n=38
1.	Days to 50% flowering	0.60	9.719**	2.74
2.	Days to maturity	26.60	23.308*	9.86
3.	Number of Primary Branches	0.010	1.014**	0.02
4.	Number of secondary branches	0.3670	23.496**	0.96
5.	Siliqua length (cm)	0.2920	0.28**	0.10
6.	Number of siliquae per plant	546.7370	4040.128*	188.35
7.	Plant height (cm)	457.97	537.515**	128.85
8.	Test weight (g)	0.0160	0.238**	0.06
9.	Number of seeds per siliqua	0.0530	3.41*	0.91
10.	Main Raceme length (cm)	34.5330	28.888**	11.53
11.	Seed yield per plant (g)	0.0760	6.13*	0.30
12.	Biological yield (g)	6.1850	9.877**	3.49
13.	Harvest Index (%)	2.3560	134.463**	10.00
14.	Oil content (%)	0.5820	1.025**	0.29

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

Correlation matrix and path coefficient analysis

Due to its intricate and polygenic nature, yield selection benefits not only from measures of variability but also from association analyses, aiding in the identification of traits accountable for yield enhancement. Character association, determined through the correlation coefficient, stands as a significant biometric instrument for constructing a selection criterion, as it unveils the intensity of connections within a cluster of traits. The nature and degree of correlation between yield and other attributes aid in gauging the proportional impact of individual traits on yield enhancement, thus empowering breeders to pinpoint favourable traits crucial for augmenting yield. Understanding the correlation between a characteristic, such as yield, and other factors influencing yield components, would be advantageous for identifying suitable rice genotypes to serve as parent plants in breeding initiatives. It is a statistical measure, which is used to find out the degree and direction of relationship between two or more variables. When change in one variable causes the change in another variable, the variables are said to be correlated. This association between the attributes is measured as "Correlation coefficients". If the change is in same direction, the correlation is positive and if it is in opposite direction, the correlation is negative. The value is zero when two variables are not related. In plant breeding, study of correlation is essential because most of the traits such as yield are the end products of interaction of several genetic factors among themselves and their individual and combined interaction with environmental factors. Correlation forms the basis for selection index there by helping the plant breeder for the crop improvement Indirectly choosing for yield through yield components traits becomes feasible when the component traits exhibit high heritability and a positive correlation with yield (Asante *et al.*, 2019). Nevertheless, relying solely on correlation estimates does not always lead to an accurate understanding of the actual relationship between two variables, as it can sometimes be influenced by the presence of a third variable (Bello *et al.*, 2010). Path analysis holds significance as a statistical method employed in conjunction with correlation studies, aiming to establish causal relationships between variables. It distinguishes direct influences from indirect ones, providing essential insights for effective trait selection geared toward yield improvement (Talekar *et al.*, 2022). Path coefficient is defined as the ratio of the standard deviation of the effect due to a given cause to the total standard deviation of the effect. The path analysis is simply standardized partial regression coefficient analysis which may be useful in choosing the characters that have direct and indirect effect on yield. The correlation coefficient provides information about the degree of association between two characters. However, it is now known that almost all characters are polygenic and almost all genes are pleiotropic in action such that each gene, apart from its direct contribution to a particular character contributes to several other characters also. Therefore, correlation coefficient alone would not provide a clear picture about the contribution of a particular character. For example, the estimates of correlation coefficient between two characters may be positive but the direct effect of the characters to the correlation coefficient may be negative. In this case, indirect effects are the cause of correlation coefficient and have masked the direct effect of the character. In such instances, indirect effect should be taken into consideration in formulating a selection strategy.

Character association

In general, the genotypic correlation surpassed the phenotypic correlation, suggesting a fundamental link among various traits (Table 2). In the current study, the analysis of the Phenotypic Correlation coefficient showed that seed yield per plant had a highly significant and positive correlation with the number of primary branches (0.341*), the number of secondary branches (0.346*), and the harvest index (0.748**). Similarly, the Genotypic Correlation coefficient analysis indicated that seed yield per plant also displayed a highly significant and positive correlation with the number of primary branches (0.340*), the number of secondary branches (0.347**), and the harvest index (0.748**). These traits exhibited a robust positive correlation, highlighting their crucial role in influencing mustard seed yield. Consequently, even in the absence of direct selection for yield enhancement, efforts to improve one trait will inherently lead to the enhancement of the others. This aligns with previous research that found a significant and positive correlation

Table 2 : Correlation coefficient between yield and its attributing traits in 20 Mustard genotypes at phenotypic and genotypical level.

	Phenotypical (above diagonal) and Genotypical (below diagonal) Correlation Matrix													
Traits	**DF50**	**DM**	**NPB**	**NSB**	**SL (cm)**	**NSPP**	**PH (cm)**	**TW (g)**	**NSPS**	**MRL (cm)**	**BY (g)**	**HI (%)**	**OC (%)**	**SYPP**
DF50	**1.0000**	0.0918	0.465**	0.406*	0.1932	0.0869	0.2080	0.0145	0.0425	0.266*	-0.1949	0.2524	-0.1790	0.1199
DM	0.0935	**1.0000**	-0.0288	-0.1159	-0.0303	0.0028	-0.0943	-0.0755	0.1164	0.2258	-0.0357	-0.0568	0.0994	-0.0653
NPB	0.462**	-0.0340	**1.0000**	0.559**	0.2481	0.497**	0.459**	0.277*	0.2145	0.479**	-0.0349	0.388*	0.0723	0.340*
NSB	0.406*	-0.1167	0.558**	**1.0000**	0.1293	0.2099	0.334*	0.337*	0.2114	0.311*	-0.300*	0.532**	0.0619	0.347*
SL (cm)	0.1902	0.0325	0.2347	0.1199	**1.0000**	0.0123	0.1153	0.2048	0.1786	0.2422	-0.0912	0.0352	-0.0700	-0.0871
NSPP	0.0932	0.0038	0.491**	0.2122	0.0104	**1.0000**	0.290*	0.2359	0.308*	0.386*	0.0872	-0.0205	0.2435	0.0381
PH (cm)	0.1989	-0.1473	0.450**	0.329*	0.0493	0.282*	**1.0000**	0.1606	0.1649	0.1121	-0.1376	0.289*	0.1757	0.1974
TW (g)	0.0171	-0.0572	0.275*	0.335*	0.2132	0.2368	0.1411	**1.0000**	0.1627	0.2153	-0.0165	0.2500	-0.0178	0.2503
NSPS	0.0404	0.1083	0.2153	0.2105	0.1692	0.303*	0.1634	0.1604	**1.0000**	0.2406	-0.0372	0.347*	0.580**	0.2493
MRL (cm)	0.273*	0.2201	0.457**	0.308*	0.2296	0.400*	0.1050	0.2159	0.2248	**1.0000**	-0.1830	0.0979	0.0299	0.0357
BY (g)	-0.2030	-0.0568	-0.0285	-0.298*	-0.1057	0.0654	-0.1145	-0.0260	-0.0302	-0.2197	**1.0000**	-0.297*	-0.0857	0.1797
HI (%)	0.2491	-0.0588	0.389*	0.530**	0.0311	-0.0246	0.283*	0.2474	0.348*	0.0847	-0.283*	**1.0000**	0.0575	0.748**
OC (%)	-0.1877	0.0807	0.0759	0.0554	-0.0762	0.2164	0.1749	-0.0253	0.575**	-0.0200	-0.0464	0.0640	**1.0000**	0.0256
SYPP	0.1175	-0.0677	0.341*	0.346*	-0.0882	0.0345	0.1949	0.2477	0.2502	0.0265	0.1827	0.748**	0.0314	**1.0000**

Table 3 : Direct and Indirect effects of yield attributing traits on seed yield at phenotypic level.

	Phenotypical (above diagonal) and Genotypical (below diagonal) Correlation Matrix													
Traits	**DF50**	**DM**	**NPB**	**NSB**	**SL (cm)**	**NSPP**	**PH (cm)**	**TW (g)**	**NSPS**	**MRL (cm)**	**BY (g)**	**HI (%)**	**OC (%)**	**SYPP**
DF50	**-0.007**	-0.001	-0.003	-0.003	-0.001	-0.001	-0.001	-0.000	-0.000	-0.002	0.001	-0.002	0.001	0.120
DM	-0.001	**-0.007**	0.000	0.001	0.000	0.003	0.001	0.001	-0.001	-0.002	0.000	0.000	-0.001	-0.065
NPB	0.008	-0.001	**0.017**	0.010	0.004	0.008	0.008	0.005	0.004	0.008	-0.001	0.007	0.001	0.340*
NSB	-0.003	0.001	-0.004	**-0.008**	-0.001	-0.002	-0.003	-0.003	-0.002	-0.002	0.002	-0.004	-0.001	0.347*
SL (cm)	-0.017	0.003	-0.022	-0.011	**-0.088**	-0.001	-0.010	-0.018	-0.016	-0.021	0.008	-0.003	0.006	-0.087
NSPP	-0.001	0.001	-0.007	-0.003	-0.000	**-0.013**	-0.004	-0.003	-0.004	-0.005	-0.001	0.000	-0.003	0.038
PH (cm)	0.000	-0.000	0.000	0.000	0.000	0.000	**0.001**	0.000	0.000	0.000	-0.000	0.000	0.000	0.197
TW (g)	0.001	-0.004	0.015	0.019	0.011	0.013	0.009	**0.055**	0.009	0.012	-0.001	0.014	-0.001	0.250
NSPS	-0.003	-0.009	-0.016	-0.016	-0.013	-0.023	-0.012	-0.012	**-0.075**	-0.018	0.003	-0.026	-0.043	0.249
MRL (cm)	0.016	0.013	0.028	0.018	0.014	0.023	0.007	0.013	0.014	**0.059**	-0.011	0.006	0.002	0.036
BY (g)	-0.087	-0.016	-0.016	-0.134	-0.041	0.039	-0.061	-0.007	-0.017	-0.081	**0.445**	-0.132	-0.038	0.180
HI (%)	0.223	-0.050	0.343	0.470	0.031	-0.018	0.255	0.221	0.307	0.087	-0.262	**0.885**	0.051	0.748**
OC (%)	-0.009	0.005	0.004	0.003	-0.004	0.013	0.009	-0.001	0.030	0.002	-0.004	0.003	**0.051**	0.026

Residual: 0.50

Table 4 : Direct and Indirect effects of yield attributing traits on seed yield at genotypic level.

	PATH matrix of Seed yield per plant (g)													
Traits	**DF50**	**DM**	**NPB**	**NSB**	**SL (cm)**	**NSPP**	**PH (cm)**	**TW (g)**	**NSPS**	**MRL (cm)**	**BY (g)**	**HI (%)**	**OC (%)**	**SYPP**
DF50	**-0.008**	-0.001	-0.004	-0.003	-0.002	-0.001	-0.002	-0.000	-0.000	-0.002	0.002	-0.002	0.002	0.118
DM	0.000	**0.003**	-0.000	-0.000	0.000	0.001	-0.001	-0.000	0.000	0.001	-0.000	-0.000	0.000	-0.068
NPB	0.001	-0.000	**0.003**	0.002	0.001	0.001	0.001	0.001	0.001	0.001	-0.000	0.001	0.000	0.341*
NSB	-0.003	0.001	-0.004	**-0.007**	-0.001	-0.001	-0.002	-0.002	-0.001	-0.002	0.002	-0.004	-0.000	0.346*
SL (cm)	-0.015	-0.003	-0.019	-0.010	**-0.081**	-0.001	-0.004	-0.017	-0.014	-0.019	0.009	-0.003	0.006	-0.088
NSPP	0.000	0.001	0.002	0.001	0.002	**0.005**	0.001	0.001	0.001	0.002	0.000	-0.000	0.001	0.035
PH (cm)	-0.002	0.001	-0.004	-0.003	-0.000	-0.002	**-0.009**	-0.001	-0.001	-0.001	0.001	-0.003	-0.002	0.195
TW (g)	0.001	-0.003	0.016	0.019	0.012	0.013	0.008	**0.057**	0.009	0.012	-0.002	0.014	-0.001	0.248
NSPS	-0.003	-0.008	-0.016	-0.016	-0.013	-0.022	-0.012	-0.012	**-0.074**	-0.017	0.002	-0.026	-0.043	0.250
MRL (cm)	0.020	0.016	0.033	0.022	0.017	0.029	0.008	0.016	0.016	**0.073**	-0.016	0.006	-0.002	0.027
BY (g)	-0.089	-0.025	-0.013	-0.130	-0.046	0.029	-0.050	-0.011	-0.013	-0.096	**0.437**	-0.124	-0.020	0.183
HI (%)	0.220	-0.052	0.344	0.469	0.028	-0.022	0.250	0.219	0.308	0.075	-0.250	**0.885**	0.057	0.748**
OC (%)	-0.006	0.003	0.003	0.002	-0.003	0.007	0.006	-0.001	0.019	-0.001	-0.002	0.002	**0.033**	0.031

Residual: 0.507

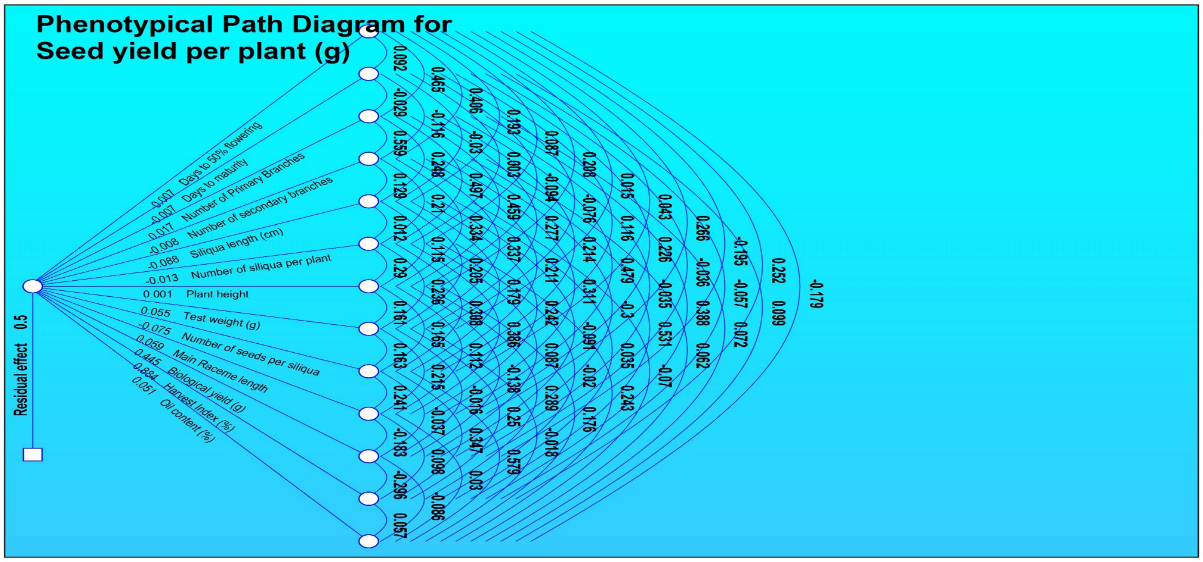

Fig. 1 : Phenotypic path diagram for seed yield per plant.

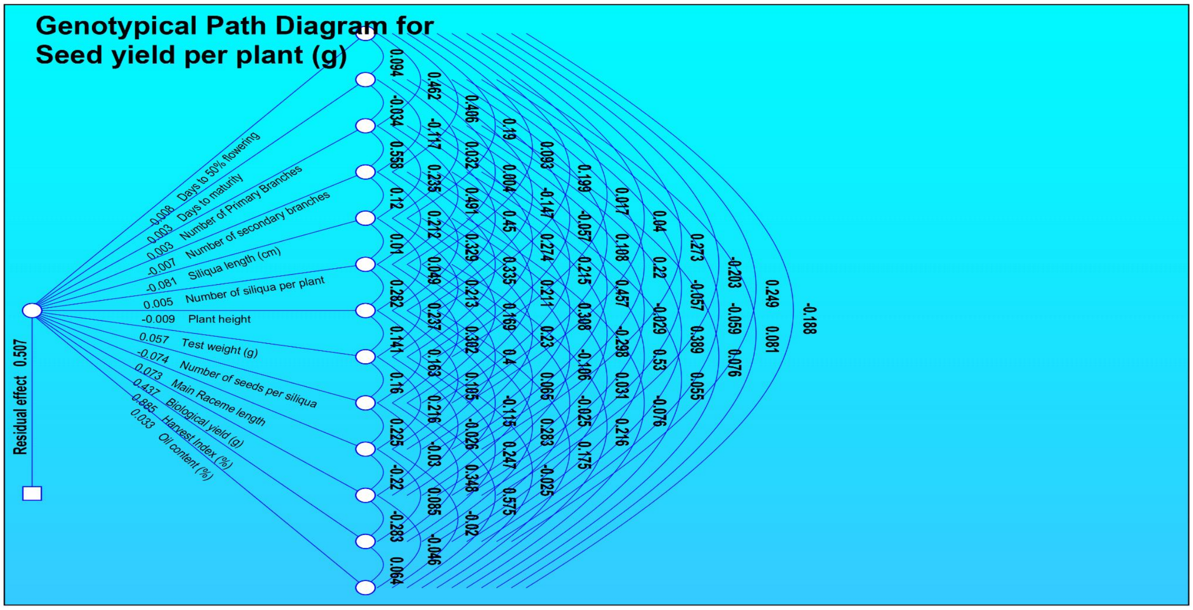

Fig. 2 : Genotypic path diagram for seed yield per plant.

between grain yield and associated traits.

The genetic correlation coefficient was found to be greater than the corresponding phenotypic correlation coefficient for many traits, a finding that aligns with earlier research by Roy *et al.* (2011). In addition, significant and positive correlations between the phenotypic correlation coefficient and seed yield per plant in relation to plant height were reported by Yadav and Pandey (2016), Laghari *et al.* (2020), Lavanya *et al.* (2022) and Meena *et al.* (2022). Similar conclusions were drawn regarding the number of primary branches, number of secondary branches, main raceme length, and harvest index by the same authors. These traits exhibit a significant correlation at both genetic and phenotypic levels, suggesting that improvements in one trait can lead to enhancements in the other. This approach allows for the selection of a single trait rather than relying on the correlated trait, which may not always be prioritized. The significant correlation observed primarily at the genotypic level indicates that environmental factors may obscure these relationships. Therefore, when aiming to improve seed yield per plant, it is essential to consider the number of primary branches, number of secondary branches, main raceme length, and harvest index.

Direct and Indirect effect

Path coefficient analysis was conducted with seed yield per plant as the dependent variable to differentiate the correlation coefficient into direct and indirect effects, thereby determining the impact of various traits on seed yield. The analysis showed a relationship between seed yield and the magnitude and direction of the direct effects of these traits (Tables 3 and 4; Figs. 1 and 2). Consequently, it is logical to expect that selecting traits with strong positive direct effects will lead to a notable increase in seed yield. In this study, at the phenotypic level, the harvest index (0.885) and biological yield (0.445) exhibited the highest positive direct effects on seed yield, while the number of primary branches showed a minimal positive effect (0.017). Conversely, the number of secondary branches had a negative direct effect on seed yield (-0.008). The residual component of the phenotypic path analysis revealed that these fourteen traits accounted for 50% of the variability in seed yield. At the genotypic level, the harvest index (0.885) and biological yield (0.437) again demonstrated the highest positive direct effects on seed yield, with the number of primary branches showing a negligible positive effect (0.003) and the number of secondary branches reflecting a negative direct effect (-0.007). The residual component of the genotypic path analysis indicated that these fourteen traits accounted for 49.9% of the variability in seed yield. Similar findings have been documented by previous researchers, including Rathod *et al.* (2014), Hasan *et al.* (2014), Yadav and Pandey (2018), Laghari *et al.* (2020), Lavanya *et al.* (2022) and Meena *et al.* (2022).

Path analysis revealed that the significant direct influence of certain traits was a key factor in the strong positive correlation of other traits with seed yield per plant (g). This analysis highlighted that biological yield per plant, the count of primary branches, the count of secondary branches, and the harvest index all exerted both direct and indirect impacts on seed yield. The positive relationships among these traits stemmed from their indirect effects via biological yield per plant and harvest index, as well as their direct effects at the genotypic level on seed yield. Consequently, seed yield was predominantly influenced by both direct and indirect effects related to the harvest index, primary branches, secondary branches, and biological yield per plant. Therefore, selecting for these traits is likely to be effective in enhancing the seed yield of mustard. The low residual effect noted in the path analysis suggests that the traits examined in this study accounted for the majority of the influences on seed yield in mustard.

Conclusion

Analysis of variance showed significant variation among different genotypes for all characters studied. The study also demonstrated a positive and significant correlation between seed yield per plant and key traits such as the number of primary branches, secondary branches, and harvest index at both phenotypic and genotypic levels. Path coefficient analysis revealed that harvest index, followed by biological yield, number of primary branches, and number of secondary branches, exhibited direct effects on seed yield at both levels of analysis. These findings suggest that these traits have a substantial influence on yield improvement. Therefore, during selection for mustard breeding, particular attention should be given to these characters to enhance seed yield per plant. Incorporating these traits into breeding strategies could lead to significant improvements in mustard productivity, making them critical for selecting high-yielding genotypes. Overall, this research highlights the importance of specific morphological and physiological traits that can be effectively targeted for boosting mustard crop yield potential through systematic breeding efforts.

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Conflict of interest

The authors declare no competing interests.

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