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# Correlation and path coefficient studies for yield related traits in $F_2$ population of Indian mustard (*Brassica juncea* L)

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## Abstract

In the current investigation, 200 genotypes of Indian mustard underwent correlation analysis and path coefficient analysis to explore the cause-and-effect relationships with direct and indirect components. The $F_2$ population was resulted from crossing Pusa Mehak (Indian genotype) with Primus (East-European genotype) and selfing the $F_1$s. Correlation coefficients for yield-related traits indicated a significant positive correlation for all characters in association with yield per plant, except for plant height. In the path coefficient studies, with yield per plant as the dependent character and the remaining 12 yield-related traits as independent contributing characters, the analysis revealed a high order of direct effect on yield per plant, with harvest index (G= 0.46, P=0.41) having the highest impact, followed by biological yield (G= 0.38, P= 0.31), 1000-seed weight (G= 0.34, P= 0.32), average siliqua length (G= 0.28, P= 0.23), and number of seeds per siliqua (G= 0.24, P= 0.21). These characters were identified as major direct and indirect contributors to yield per plant in the $F_2$ population of Indian mustard. The variation in grain yield unexplained by the twelve traits was attributed to the residual effect (G= 0.24, P= 0.32), which is uncorrelated with other related factors in the study. The existence of two distinct gene pools in Indian mustard 'the East European and Indian gene pools' provided a valuable resource for breeding program aimed at reducing erucic acid quantity in Indian mustard while maintaining yield and adaptability. The complementary traits found in these gene pools can be effectively utilized to develop superior cultivars for future breeding programs.

***Keywords:*** *Brassica juncea, correlation coefficient, East-European genotype, Indian genotype, path coefficient analysis*

## Introduction

Indian mustard (*Brassica juncea* L., 2n=36, AABB genome) is a crucial oilseed crop in India, ranking second only to soybean in the oilseed hierarchy. The crop is predominantly cultivated in the north-western plains, central, and eastern regions of India, thriving in diverse agro-climatic conditions. Indian mustard is not only valued for its oil but also for its use as a condiment and its young leaves, which are consumed as leafy vegetables. The crop's resilience to drought and its moderate tolerance to saline soils make it an essential part of sustainable agriculture, especially in marginal areas. It is predominantly cultivated during the *Rabi* season**.** *Brassica juncea* comprises two distinct gene pools: the East European gene pool, characterized by low erucic acid, and the Indian gene pool, possessing undesirably high erucic acid content but exhibiting better yield under Indian subcontinent conditions, which were employed in this study for making crosses. The East European gene pool of Indian mustard primarily comprises cultivars developed in Eastern Europe, including countries like Russia and Ukraine. These cultivars are adapted to the temperate climates of Eastern Europe and exhibit traits such as cold tolerance, low erucic acid and high oil content. The East European gene pool is characterized by its genetic diversity, which includes alleles not commonly found in the Indian gene pool. The Indian gene pool consists of cultivars and landraces primarily developed and cultivated in India. This gene pool is adapted to the diverse agro-climatic conditions of India, including arid and semi-arid regions. Indian cultivars are known for their high yield potential, resistance to local pests and diseases, adaptability to low input conditions and high amount of erucic acid (Gupta *et al*., 2010). The utilization of East-European gene pool in breeding programs can contribute to the development of varieties with less erucic acid, improved yield stability and resilience to climate change. The integration of both the East European and Indian gene pools in breeding programs offers a comprehensive approach to enhancing the genetic base of Indian mustard.

The relative importance of different component characters concerning plant selection based on variability and interrelationships among genotypes' quantitative characters is achieved by correlation analysis. It helps to assess the strength and direction of the relationship between two traits. Positive and significant correlations among traits such as plant height, number of siliquae per plant, and seed yield suggest that these traits can be simultaneously improved through selection (Kumar and Singh, 2021). Path coefficient analysis emerges as a valuable tool for discerning the direct and indirect associations among diverse characters. The term "path coefficient" was coined by Wright in 1921 to denote the direct influence of one variable (cause) on another variable (effect), quantified by the standard deviation remaining in the effect after estimating the influence of all other possible paths except that of the cause. It disintegrates the correlation coefficients into direct and indirect effects, providing a clearer understanding of the cause-and-effect relationships and identifies traits with the most substantial direct influence on yield, guiding breeding programs more effectively (Kumar and Singh, 2021). Incorporating correlation and path coefficient analyses in breeding programs enhances the efficient use of genetic resources. By understanding the genetic architecture of yield-related traits, breeders can develop superior varieties with improved productivity and stability. This is particularly important for increasing genetic gains in Indian mustard and ensuring food security (Sharma and Gupta, 2022). For the present study, the $F_2$ segregating generation resulting from crosses of Indian and East European mustard was utilized for correlation analysis and path coefficient analysis.

## Materials and Methods

### Experimental material

The experimental setup involved $F_2$ individuals derived from a controlled cross between Pusa Mehak (Indian genotype) and Primus (European genotype). The resulting $F_2$ population consisted of 359 plants, with 200 plants selected for the study conducted during the *Rabi* 2019-20. These $F_2$ plants were systematically planted in a designated plot, covering 2.7 $m^2$ (3 m × 0.9 m) with four rows. Well-drained sandy loam soils with a pH of almost 7.0 with proper soil preparation involving deep ploughing followed by harrowing to create a fine seedbed was followed. The planting arrangement included a row-to-row distance of 30 cm and a plant-to-plant distance of 10 cm, achieved through thinning at 30 days post-sowing. Adhering to recommended agricultural practices, the experimental field received the prescribed fertilizer dosage (120 kg N + 40 kg $P_2O_5$ + 40 kg $K_2O$ per hectare), and irrigation was consistently applied at critical stages to optimize crop growth. Nitrogen was typically applied in two split doses: half at sowing and the remaining half at the rosette stage. Phosphorus and potassium were applied as a basal dose during sowing. Micronutrients such as sulphur (30 kg/ha) and boron (1.0 kg/ha) were applied for enhancing yield and oil quality. Integrated weed management practices, including pre-emergence herbicides like Pendimethalin (1 kg *a.i.*/ha) and mechanical weeding were followed. Hand weeding was typically performed 30-35 days after sowing to remove any emerging weeds. The crop was harvested by hand. After harvesting, the crop was allowed to dry in the field for a few days before threshing to separate the seeds from the siliquae.

### Correlation analysis

The significance of the phenotypic correlation coefficient was assessed against 'r' values in the 'r' table of Fisher and Yates (1938) for the degree of freedom calculated as (n2), where 'n' represents the number of treatments.

$$\text{Phenotypic correlation} = \frac{\text{Cov.xy(p)}}{[\text{Vx(p)Vy(p)}]}$$

$$\text{Genotypic correlation} = \frac{\text{Cov.xy(g)}}{[\text{Vx(p)Vy(p)}]}$$

Where, Cov.xy (p) = phenotypic covariance among traits x and y which was calculated as follows:
Cov.xy (p) = Cov.xy(e) Cov.xy(g)
Cov.xy (p) = genotypic covariance among traits x and y which was estimated as follows:
Cov.xy (g) = Cov.xy(p) - Conv.xy(e)
Vx (p) and Vy (p) = phenotypic variances for the traits x and y, respectively
Vx (g) and Vy (g) = genotypic variances for the traits x and y, respectively

### Path coefficient analysis

Path coefficient analysis was conducted following Dewey and Lu (1959). Grain yield per plant served as the dependent variable, influenced directly and indirectly by all twelve characters considered as independent variables.

## Results and Discussion

To investigate the correlation and evaluate the relative significance of traits in the selection program, correlation coefficients were computed at both genotypic and phenotypic levels for all possible pairs among the twelve traits (Table 1 and Table 2). The genotypic correlations, overall, displayed similar trends and slightly greater magnitudes than their phenotypic counterparts.

In the genotypic correlation (Table 1), the highest correlation was identified between yield per plant and harvest index (0.70**), as well as between yield per plant and 1000-seed weight (0.68**). This was followed by correlations between yield per plant and days to maturity (0.49**), yield per plant and the number of siliquae on the main shoot (0.46**), and yield per plant and the number of seeds per siliqua (0.43**).

In the phenotypic correlation (Table 2), the values obtained were generally lower than the genotypic correlations. The highest phenotypic correlation was found between yield per plant and 1000-seed weight (0.64**), followed by yield per plant and harvest index (0.59**), yield per plant and days to maturity (0.41**), yield per plant and the number of seeds per siliqua (0.41**), and the number of siliquae on the main shoot (0.36**).

Conducting a path coefficient analysis involved designating yield per plant as the dependent character and the remaining twelve traits (days to maturity, plant height, primary branches, secondary branches, average siliqua length, number of seeds per siliqua, 1000-seed weight, biological yield, harvest index, oil content, main shoot length, number of siliquae on main shoot) as independent contributing characters. The direct and indirect effects of different traits are presented in Table 3 and Table 4. The minimal direct effects observed for the remaining characters suggest that their contributions to yield per plant were negligible.

**Days to maturity**: The direct effect of days to maturity on yield per plant was positive (G= 0.21, P= 0.20), with indirect contributions through biological yield (G= 0.23, P= 0.20) and harvest index (G= 0.26, P= 0.24). Days to maturity contributed indirectly through all other traits positively except average siliqua length (G= -0.02, P= -0.03) and main shoot length (G= -0.01, P= -0.03).

**Plant height**: The direct effect of plant height on yield was negative (G= -0.05, P= -0.06) but minimal. Plant height contributed indirectly through all other traits positively except the number of seeds per siliqua (G= -0.01, P= -0.02) and oil content (G= -0.02, P= -0.04).

**Number of primary branches**: The direct effect of the number of primary branches was positive (G= 0.12, P=0.11), with indirect contributions through biological yield (G= 0.19, P= 0.17) and the number of secondary branches (G= 0.13, P= 0.11). The indirect effect of the number of primary branches through plant height and oil content was negative, while through the rest was positive.

**Number of secondary branches**: The direct effect of the number of secondary branches was positive (G= 0.10, P= 0.09), contributing indirectly through biological yield (G= 0.25, P= 0.21) and harvest index (G= 0.14, P= 0.10) positively. The indirect effect of the number of secondary branches through all traits was positive except the number of primary branches (G= -0.05, P= -0.06).

**Average siliqua length**: The direct effect of average siliqua length on yield was positive (G= 0.28, P= 0.23), with a negative indirect effect through plant height (G= -0.01, P= -0.02), the number of primary branches (G= -0.02, P= -0.03), and the number of siliquae on the main shoot (G= -0.01, P= -0.02).

**Number of seeds per siliqua**: The direct effect of the number of seeds per siliqua on yield per plant was positive (G= 0.24, P= 0.21), contributing indirectly through harvest index (G= 0.38, P= 0.32), 1000-seed weight (G= 0.24, P= 0.21), and biological yield (G= 0.22, P= 0.18) positively. The number of seeds per siliqua contributed indirectly positively through all other traits except the number of primary branches, number of secondary branches, and main shoot length.

**1000-seed weight**: The direct effect of 1000-seed weight on yield per plant was positive (G= 0.34, P= 0.32), with a high indirect effect through biological yield (G= 0.36, P= 0.23), harvest index (G= 0.31, P= 0.30), and oil content (G= 0.23, P= 0.15). 1000-seed weight contributed indirectly through all other traits positively.

**Biological yield**: The direct effect of biological yield on yield per plant was positive (G= 0.38, P= 0.31), with a negative indirect effect through days to maturity (G= -0.10, P= -0.11) and plant height (G= -0.01, P= -0.02). Biological yield contributed indirectly through all other traits positively.

**Harvest index** (HI): The direct effect of HI on yield per plant was positive (G= 0.46, P= 0.41), with indirect contributions through biological yield (G= 0.45, P= 0.43), 1000-seed weight (G= 0.35, P= 0.19), the number of seeds per siliqua (G= 0.21, P= 0.15), and the number of siliquae on the main shoot (G= 0.21, P= 0.20) positively. Harvest Index contributed indirectly positively through all other traits except plant height (G= -0.02, P= -0.03).

**Oil content**: The direct effect of oil content on yield was positive (G= 0.12, P= 0.11), with a negative indirect effect through plant height (G= -0.01, P= -0.02) and the number of seeds per siliqua (G= -0.04, P= -0.06).

**Main shoot length**: The direct effect of the main shoot length was positive (G= 0.10, P=0.07), with an indirect effect through days to maturity being negative (G= -0.02, P= -0.04) and the number of seeds per siliqua (G= -0.01, P= -0.03), while through the rest was positive.

**Number of siliquae on the main shoot**: The direct effect of the number of siliquae on the main shoot on yield was positive (G= 0.11, P= 0.10) but minimal, contributing indirectly through all other traits positively. The variation in grain yield unexplained by the twelve traits was considered to be due to the residual effect (G= 0.24, P= 0.32), which is uncorrelated with other related factors.

In the present investigation, correlation analyses

Table 1: Genotypic correlations among different yield and yield attributes for 200 $F_2$ plants

| Character | Days to maturity | Plant height | Primary branches | Secondary branches | Siliqua length | Seeds / siliqua | 1000 - seed weight | Biological yield | Harvest index | Oil content | Main shoot length | Siliquae on main shoot | Yield/ plant |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Days to maturity | 1 | -0.04 | 0.43** | 0.13** | 0.20** | 0.19** | 0.39** | 0.47** | 0.49** | 0.14** | 0.15** | 0.12** | 0.49** |
| Plant height | | 1 | 0.19** | 0.23** | 0.11** | 0.08 | 0.11** | 0.17** | -0.04 | -0.06 | 0.29** | 0.12** | -0.07 |
| Primary branches | | | 1 | 0.38** | 0.29** | -0.05 | 0.18** | 0.24** | 0.27** | 0.04 | 0.18** | 0.21** | 0.24** |
| Secondary branches | | | | 1 | 0.32** | -0.08 | 0.17** | 0.25** | 0.22** | 0.10** | 0.23** | 0.19** | 0.30** |
| Siliqua length | | | | | 1 | 0.28** | 0.18** | 0.25** | 0.22** | 0.05 | 0.24** | 0.26** | 0.31** |
| Seeds/ siliqua | | | | | | 1 | 0.23** | 0.31** | 0.30** | 0.28** | 0.03 | 0.08 | 0.43** |
| 1000-seed weight | | | | | | | 1 | 0.48** | 0.49** | 0.26** | 0.07 | 0.13** | 0.68** |
| Biological yield | | | | | | | | 1 | 0.20** | 0.21** | 0.13** | 0.20** | 0.31** |
| Harvest index | | | | | | | | | 1 | 0.23** | 0.16** | 0.19** | 0.70** |
| Oil content | | | | | | | | | | 1 | 0.04 | 0.07 | 0.29** |
| Main shoot length | | | | | | | | | | | 1 | 0.24** | 0.20** |
| Siliqua on main shoot | | | | | | | | | | | | 1 | 0.46** |
| Yield/ plant | | | | | | | | | | | | | 1 |

The sign of genotypic correlation was tested using t test (two-tail). The degree of freedom used is (genotypes*replication) – 2.

Table 2: Phenotypic correlation correlations among different yield and yield attributes for 200 $F_2$ plants

| Character | Days to maturity | Plant height | Primary branches | Secondary branches | Siliqua length | Seeds / siliqua | 1000 - seed weight | Biological yield | Harvest index | Oil content | Main shoot length | Siliquae on main shoot | Yield/ plant |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Days to maturity | 1 | -0.06 | 0.40** | 0.11** | 0.18** | 0.14** | 0.33** | 0.42** | 0.46** | 0.11** | 0.12** | 0.11** | 0.41** |
| Plant height | | 1 | 0.14** | 0.19** | 0.10** | 0.07 | 0.10** | 0.15** | -0.06 | -0.08 | 0.24** | 0.11** | -0.09 |
| Primary branches | | | 1 | 0.34** | 0.25** | -0.04 | 0.13** | 0.23** | 0.23** | 0.03 | 0.13** | 0.20** | 0.23** |
| Secondary branches | | | | 1 | 0.29** | -0.09 | 0.16** | 0.23** | 0.20** | 0.10** | 0.21** | 0.15** | 0.26** |
| Siliqua length | | | | | 1 | 0.24** | 0.16** | 0.22** | 0.21** | 0.04 | 0.22** | 0.23** | 0.29** |
| Seeds/ siliqua | | | | | | 1 | 0.22** | 0.28** | 0.28** | 0.24** | 0.02 | 0.06 | 0.41** |
| 1000-seed weight | | | | | | | 1 | 0.43** | 0.42** | 0.24** | 0.06 | 0.12** | 0.64** |
| Biological yield | | | | | | | | 1 | 0.18** | 0.20** | 0.12** | 0.18** | 0.27** |
| Harvest index | | | | | | | | | 1 | 0.22** | 0.13** | 0.15** | 0.59** |
| Oil content | | | | | | | | | | 1 | 0.03 | 0.05 | 0.23** |
| Main shoot length | | | | | | | | | | | 1 | 0.22** | 0.19** |
| Siliqua on main shoot | | | | | | | | | | | | 1 | 0.36** |
| Yield/ plant | | | | | | | | | | | | | 1 |

The sign of phenotypic correlation was tested using t test (two-tail). The degree of freedom used is (genotypes*replication) – 2.

Table 3: Path coefficient (genotypic) showing direct and indirect effects of yield related traits in 200 $F_2$ plants

| Character | Days to maturity | Plant height | Primary branches | Secondary branches | Siliqua length | Seeds / siliqua | 1000 - seed weight | Biological yield | Harvest index | Oil content | Main shoot length | Siliquae on main shoot | Yield/ plant |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Days to maturity | 0.21 | 0.00 | 0.04 | 0.00 | -0.02 | 0.02 | 0.10 | 0.23 | 0.26 | 0.11 | -0.01 | 0.12 | 0.22** |
| Plant height (cm) | -0.01 | -0.05 | 0.03 | 0.00 | 0.02 | -0.01 | 0.00 | 0.02 | 0.07 | -0.02 | 0.02 | 0.00 | 0.00 |
| Primary branches | 0.00 | -0.01 | 0.12 | 0.13 | 0.02 | 0.03 | 0.03 | 0.19 | 0.11 | -0.04 | 0.02 | 0.01 | 0.10 |
| Secondary branches | 0.00 | 0.00 | -0.05 | 0.10 | 0.01 | 0.03 | 0.02 | 0.25 | 0.14 | 0.01 | 0.04 | 0.03 | 0.23** |
| Siliqua length (cm) | 0.00 | -0.01 | -0.02 | 0.00 | 0.28 | 0.23 | 0.09 | 0.44 | 0.22 | 0.00 | 0.01 | -0.01 | 0.34** |
| Seeds per siliqua | 0.09 | 0.01 | -0.01 | -0.12 | 0.00 | 0.24 | 0.24 | 0.22 | 0.38 | 0.10 | -0.01 | 0.03 | 0.35** |
| 1000-seed weight (g) | 0.00 | 0.00 | 0.01 | 0.01 | 0.05 | 0.13 | 0.34 | 0.36 | 0.31 | 0.23 | 0.00 | 0.12 | 0.42** |
| Biological yield | -0.10 | -0.01 | 0.02 | 0.01 | 0.03 | 0.22 | 0.21 | 0.38 | 0.45 | 0.14 | 0.02 | 0.11 | 0.31** |
| Harvest index | 0.00 | -0.02 | 0.01 | 0.12 | 0.06 | 0.21 | 0.35 | 0.45 | 0.46 | 0.13 | 0.06 | 0.21 | 0.38** |
| Oil content | 0.00 | -0.01 | 0.01 | 0.00 | 0.03 | -0.04 | 0.28 | 0.12 | 0.11 | 0.12 | 0.03 | 0.12 | 0.13 |
| Main shoot length (cm) | -0.02 | 0.00 | 0.03 | 0.02 | 0.01 | -0.01 | 0.01 | 0.01 | 0.02 | 0.01 | 0.10 | 0.13 | 0.11 |
| Siliqua on main shoot | 0.00 | 0.01 | 0.02 | 0.03 | 0.00 | 0.00 | 0.13 | 0.11 | 0.23 | 0.11 | 0.12 | 0.11 | 0.22** |

**p>0.05

Table 4: Path coefficient (phenotypic) showing direct and indirect effects of yield related traits in 200 $F_2$ plants

| Character | Days to maturity | Plant height | Primary branches | Secondary branches | Siliqua length | Seeds / siliqua | 1000 - seed weight | Biological yield | Harvest index | Oil content | Main shoot length | Siliquae on main shoot | Yield/ plant |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Days to maturity | 0.20 | 0.00 | 0.03 | 0.00 | -0.03 | 0.01 | 0.09 | 0.20 | 0.24 | 0.10 | -0.03 | 0.10 | 0.20** |
| Plant height (cm) | 0.00 | -0.06 | 0.02 | 0.00 | 0.01 | -0.02 | 0.00 | 0.02 | 0.04 | -0.04 | 0.01 | 0.00 | 0.00 |
| Primary branches | 0.00 | -0.02 | 0.11 | 0.11 | 0.01 | 0.02 | 0.02 | 0.17 | 0.10 | -0.06 | 0.01 | 0.00 | 0.08 |
| Secondary branches | 0.00 | 0.00 | -0.06 | 0.09 | 0.00 | 0.02 | 0.02 | 0.21 | 0.10 | -0.02 | 0.03 | 0.02 | 0.20** |
| Siliqua length (cm) | 0.00 | -0.02 | -0.03 | 0.00 | 0.23 | 0.22 | 0.03 | 0.41 | 0.19 | 0.00 | 0.00 | -0.02 | 0.32** |
| Seeds per siliqua | 0.06 | 0.00 | 0.00 | -0.14 | 0.00 | 0.21 | 0.21 | 0.18 | 0.32 | 0.07 | -0.04 | 0.02 | 0.31** |
| 1000-seed weight (g) | 0.00 | 0.00 | 0.00 | 0.01 | 0.03 | 0.11 | 0.32 | 0.23 | 0.30 | 0.15 | 0.00 | 0.11 | 0.39** |
| Biological yield | -0.11 | -0.02 | 0.01 | 0.01 | 0.01 | 0.21 | 0.20 | 0.31 | 0.42 | 0.12 | 0.01 | 0.10 | 0.25** |
| Harvest index | 0.00 | -0.03 | 0.01 | 0.10 | 0.03 | 0.15 | 0.19 | 0.43 | 0.41 | 0.11 | 0.04 | 0.20 | 0.31** |
| Oil content | 0.00 | -0.02 | 0.00 | 0.00 | 0.02 | -0.06 | 0.15 | 0.10 | 0.10 | 0.11 | 0.02 | 0.11 | 0.10 |
| Main shoot length (cm) | -0.04 | 0.00 | 0.03 | 0.01 | 0.00 | -0.03 | 0.00 | 0.00 | 0.00 | 0.00 | 0.07 | 0.10 | 0.10 |
| Siliqua on main shoot | 0.00 | 0.00 | 0.02 | 0.02 | 0.00 | 0.00 | 0.10 | 0.10 | 0.14 | 0.10 | 0.11 | 0.10 | 0.21** |

**p>0.05

revealed the highest correlations between yield per plant and harvest index (G= 0.70**, P= 0.59**) and yield per plant with 1000-seed weight (G= 0.68**, P= 0.64**). These results are consistent with previous findings reported by Dwivedi *et al*. (2023), Bhupendra *et al*. (2021), Yadav *et al*. (2021), Rout *et al*. (2019), Kumar *et al*. (2016), Singh *et al*. (2010) and Mahla *et al*. (2003).

In the path coefficient analyses, with yield per plant as the dependent character and all other residual 12 character percentages as independent contributing characters, harvest index (G= 0.46, P=0.41), biological yield (G= 0.38, P= 0.31), and 1000-seed weight (G= 0.34, P= 0.32) exhibited a high direct effect on yield per plant, followed by average siliqua length (G= 0.28, P= 0.23) and number of seeds per siliqua (G= 0.24, P= 0.21). These characters were identified as major direct and indirect contributors to yield per plant in Indian mustard. Similar results have been reported by Dwivedi *et al*. (2023), Bhupendra *et al*. (2021), Yadav *et al*. (2021), Dipti and Priyanka (2016), Kumar *et al.* (2016), Singh *et al*. (2010), and Mahla *et al*. (2003). This study contributes to the understanding of correlations among different yield-related traits in a large segregating population and the determination of each trait's contribution to yield.

## Conclusion

The correlation analyses revealed strong positive correlations between yield per plant and traits such as harvest index and 1000-seed weight, both at the genotypic and phenotypic levels. These findings align with previous research, reinforcing the importance of these traits in determining yield in Indian mustard. The path coefficient analysis further elucidated the direct and indirect effects of different traits on yield per plant. Harvest index, biological yield, and 1000-seed weight emerged as major contributors to yield per plant, highlighting their significance in breeding programs aimed at enhancing yield in Indian mustard. Specifically, the high path coefficient values for these traits indicate their substantial direct effects on yield, making them critical targets for selection. Additionally, average siliqua length and the number of seeds per siliqua exhibited considerable direct effects on yield per plant. These traits, while perhaps less frequently emphasized in breeding programs, demonstrated significant potential in yield determination and thus warrant inclusion in selection criteria. The identification of these secondary traits as important yield determinants offers new avenues for breeding strategies, potentially leading to more comprehensive approaches to yield improvement. Overall, this study contributes to a better understanding of the complex interplay between various agronomic traits and yield in Indian mustard. By identifying traits with significant direct and indirect effects on yield, breeders can prioritize these traits in selection programs to develop high-yielding varieties. Moreover, the findings of this study can inform future research efforts aimed at further improving yield potential and productivity in Indian mustard.

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