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# INTER CHARACTERS RELATIONSHIP IN INDIAN MUSTARD (*BRASSICA JUNCEA* L. CZERN & COSS)

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## ABSTRACT

The present investigation was conducted using a half-diallel set of cross combinations to evaluate inter-character relationships for fifteen traits in Indian mustard (*Brassica juncea* L. Czern & Coss) during the Rabi season of 2018–19 at the Oilseed Research Farm, Chandra Shekhar Azad University of Agriculture & Technology, Kanpur. Observations were recorded for traits including days to 50% flowering, days to maturity, plant height, main raceme length, leaf area index, number of primary and secondary branches per plant, number of siliquae per plant, seeds per siliqua, biological yield, 1000-seed weight, harvest index, oil content, protein content, and seed yield per plant. Analysis of variance revealed highly significant differences among genotypes for nearly all traits. Correlation analysis indicated that seed yield per plant exhibited strong positive and significant correlations with most traits, excluding protein content, which showed a non-significant positive correlation. These findings suggest that direct selection based on these yield-contributing traits could be an effective strategy for enhancing seed yield in Indian mustard.

***Keywords*****:** *Brassica juncea*, correlation analysis, genetic variability, seed yield, yield components, genotypic correlation, phenotypic correlation, oilseed crop, mustard breeding, trait association.

## Introduction

Indian mustard (*Brassica juncea* L. Czern & Coss), a key Rabi oilseed crop belonging to the family Cruciferae, is an amphidiploid species (2n = 36) derived from *Brassica rapa* (2n = 20) and *Brassica nigra* (2n = 16). Although predominantly self-pollinated, a moderate degree of cross-pollination (2–15%) occurs via insect vectors such as honeybees. Globally, mustard ranks as the second-largest source of vegetable oil and protein meal after soybean. In India, it is extensively cultivated in the northern states, with Rajasthan, Madhya Pradesh, and Uttar Pradesh being major producers.

Mustard requires relatively low water input (240–400 mm), making it well-suited for rainfed agricultural systems. The seeds typically contain 34–43% oil and contribute around 32% of the country's edible oil output. India ranks third globally in rapeseed-mustard production, following China and Canada, contributing 12% to global production as of 2016–17. Among the oleiferous *Brassica* species, *B. juncea* accounts for approximately 80% of the total production in India.

Yield in mustard is a complex trait influenced by multiple contributing characters. Thus, understanding the interrelationships among these traits is essential for devising effective selection criteria in breeding programs. Phenotypic selection is influenced by both genetic and environmental factors, necessitating studies on the correlations between yield and its components to enhance selection efficiency.

Correlation analysis helps quantify the degree and direction of association between traits and is a powerful tool for identifying components that directly or indirectly affect seed yield. Therefore, the objective of this study was to analyze the relationships among yield and quality-contributing traits in Indian mustard to identify key indicators for yield improvement.

## Materials and Methods

The experimental material comprised ten genetically diverse genotypes of Indian mustard (*Brassica juncea* L.), namely Varuna, Rohini, Vardan, PR-20, PR-21, Kranti, Narendra Ageti Rai-7, Narendra Rai-8501, KMR 17-3, and KMR 17-4. These were selected based on morphological variation across key agronomic traits. A total of 45 hybrids were generated using a half-diallel mating design and evaluated during the Rabi season of 2018–19 at the Oilseed Research Farm, Chandra Shekhar Azad University of Agriculture & Technology, Kanpur.

The experiment was laid out in a Complete Randomized Block Design (CRBD) with three replications. Each treatment was sown in a single row of 3 meters length, spaced 45 cm apart, and with 15 cm between plants maintained through thinning. Standard agronomic practices were followed throughout the crop growth period to ensure optimal performance.

Observations were recorded on fifteen quantitative traits: days to 50% flowering, days to maturity, plant height (cm), main raceme length (cm), leaf area index, number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, number of seeds per siliqua, biological yield per plant (g), 1000-seed weight (g), harvest index (%), oil content (%), protein content (%), and seed yield per plant (g). Data for days to 50% flowering and maturity were recorded on a plot basis, while the remaining traits were measured from ten randomly selected competitive plants in each replication.

Protein content was estimated using the Kjeldahl method, which involves digestion, distillation, and titration to determine total nitrogen content, converted to crude protein using a factor of 6.25. Oil content was determined using the Soxhlet extraction method with petroleum ether as a solvent, based on standard AOAC procedures.

Analysis of variance (ANOVA) was conducted to assess the significance of genotypic differences, following the methodology of Panse and Sukhatme (1967). Correlation coefficients among traits were calculated using the methods of Al-Jibouri *et al.* (1958) and Dewey and Lu (1959).

## Results and Discussion

The analysis of variance (Table 1) revealed highly significant differences among treatments for all studied characters, indicating the presence of substantial genetic variability within the experimental material. This is essential for effective selection and genetic improvement. Similar significant genetic variation in *Brassica juncea* has been reported by Yadava *et al.* (2012) and Awasthi *et al.* (2020), reinforcing the importance of exploring trait interrelationships for yield enhancement.

At the phenotypic level (Table 2), seed yield per plant exhibited highly significant and positive correlations with several key traits. The strongest associations were observed with leaf area index (0.887), harvest index (0.832), 1000-seed weight (0.806), oil content (0.784), and number of siliquae per plant (0.766). Moderate to strong correlations were also recorded for number of secondary branches per plant (0.687), main raceme length (0.632), biological yield per plant (0.562), days to maturity (0.500), plant height (0.447), number of primary branches (0.330), number of seeds per siliqua (0.304), and days to 50% flowering (0.248). Protein content (0.029), however, showed a non-significant but positive association with seed yield. These findings suggest that leaf area index, harvest index, and seed weight are among the most influential traits on yield under field conditions, consistent with previous reports by Singh *et al.* (2017) and Meena *et al.* (2019).

At the genotypic level (Table 3), the correlation values were generally higher than phenotypic values, suggesting that environmental influence may mask some genetic relationships at the phenotypic level. Seed yield per plant showed very strong genotypic correlations with leaf area index (0.943), number of secondary branches per plant (0.870), harvest index (0.848), 1000-seed weight (0.836), oil content (0.814), and number of siliquae per plant (0.802). Other positively correlated traits included main raceme length (0.670), biological yield (0.628), days to maturity (0.556), number of primary branches (0.510), plant height (0.469), number of seeds per siliqua (0.411), and days to 50% flowering (0.280), whereas protein content (0.025) again showed a negligible positive correlation.

These results align with earlier findings indicating that yield in mustard is significantly influenced by morphological and physiological traits such as leaf area, seed size, and raceme architecture (Thakur *et al.,* 2018; Yadava *et al.,* 2012). The stronger genotypic correlations emphasize the importance of selecting genotypes with favorable genetic makeup for these traits, which can be reliably inherited. This highlights the utility of indirect selection through associated traits to accelerate yield improvement.

## Conclusion

Based on the present investigation, it can be concluded that traits such as leaf area index, harvest index, 1000-seed weight, oil content, number of siliquae per plant, number of secondary branches per plant, main raceme length, biological yield per plant, number of primary branches, number of seeds per siliqua, days to maturity, plant height, and days to 50% flowering exhibited significant positive correlations with seed yield at both genotypic and phenotypic levels. These findings suggest that direct selection for these traits can effectively enhance seed yield in Indian mustard. The strong and consistent associations observed among multiple traits indicate the potential for simultaneous selection to develop high-yielding genotypes. Incorporating these characters into breeding strategies can accelerate genetic gains and improve the overall productivity of *Brassica juncea*.

**Table 1:** Analysis of variance for parents + $F_1$ s in 10 x 10 diallel cross of Indian mustard (*Brassica juncea* L.) for 15 metric traits: Mean sum of squares

| **Source of variance** | **DF** | **Days to 50% flowering** | **Days to maturity** | **Plant height (cm)** | **Length of main raceme** | **Leaf area index** | **No. of primary branches /plant** | **No. of second-ary ranches /plant** | **No. of siliquae / plant** | **No. of seeds / siliqua** | **Biolog-ical yield / plant (g)** | **1000-seeds weight (g)** | **Harvest index (%)** | **Oil content (%)** | **Protein (%)** | **Seed yield / plant** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Replicates | 2 | 46.570** | 62.456** | 0.095 | 4.498** | 0.002 | 0.019 | 0.403 | 28.706* | 0.377 | 0.214 | 0.000 | 0.308 | 0.000 | 0.284** | 0.126 |
| Treatments | 54 | 14.392** | 35.054** | 183.804** | 52.745** | 0.049** | 2.681** | 4.949** | 2835.603** | 2.861** | 20.175** | 1.585** | 9.699** | 2.388** | 1.374** | 5.738** |
| Parents | 9 | 19.385** | 59.252** | 395.077** | 101.274** | 0.087** | 4.076** | 6.877** | 6224.355** | 3.460** | 34.347** | 3.063** | 12.108** | 4.594** | 2.040** | 8.170** |
| $F_1$ | 44 | 9.697** | 27.379** | 144.166** | 43.521** | 0.043** | 2.323** | 4.588** | 2167.494** | 2.522** | 17.680** | 1.314** | 8.172** | 1.983** | 1.244** | 4.984** |
| Ps. Vs. $F_1$ | 1 | 176.052** | 155.004** | 26.454** | 21.842** | 0.001 | 5.873** | 3.477* | 1733.608** | 12.399** | 2.420 | 0.214** | 55.189** | 0.394** | 1.094** | 16.999** |
| Error | 108 | 1.001 | 1.856 | 1.134 | 0.735 | 0.001 | 0.844 | 0.862 | 8.999 | 0.676 | 0.993 | 0.000 | 0.615 | 0.000 | 0.020 | 0.144 |

*Significant at p = 0.05;**Significant at p = 0.01

**Table 2:** Phenotypic correlation coefficients parents + crosses for 15 characters in 10 x 10 diallel cross in Indian mustard (*Brassica juncea* L.)

| **Characters** | **Days to 50% flowe-ring** | **Days to maturity** | **Plant height (cm)** | **Length of main raceme** | **Leaf area index** | **No. of primary branc-hes/ plant** | **No. of secon-dary branch-es/plant** | **No. of siliquae / plant** | **No. of seeds / siliqua** | **Biological yield / plant (g)** | **1000-seeds weight (g)** | **Har vest index (%)** | **Oil content (%)** | **Protein (%)** | **Seed yield / plant** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Days to 50% flowering | **1.000** | 0.681** | 0.435** | 0.350** | 0.428** | -0.196* | 0.307** | 0.456** | -0.126 | 0.436** | 0.399** | 0.013 | 0.235** | -0.160* | 0.248** |
| Days to maturity | | **1.000** | 0.781** | 0.538** | 0.610** | -0.032 | 0.451** | 0.601** | -0.012 | 0.673** | 0.516** | 0.158* | 0.319** | -0.129 | 0.500** |
| Plant height (cm) | | | **1.000** | 0.408** | 0.493** | -0.029 | 0.267** | 0.519** | 0.094 | 0.685** | 0.503** | 0.088 | 0.195* | -0.008 | 0.447** |
| Length of main raceme (cm) | | | | **1.000** | 0.695** | 0.145 | 0.633** | 0.667** | 0.129 | 0.570** | 0.419** | 0.382** | 0.698** | -0.302** | 0.632** |
| Leaf area index | | | | | **1.000** | 0.259** | 0.715** | 0.838** | 0.225** | 0.609** | 0.801** | 0.666** | 0.799** | -0.026 | 0.887** |
| Number of primary branches /plant | | | | | | **1.000** | 0.194* | 0.204** | 0.094 | 0.070 | 0.252** | 0.361** | 0.297** | 0.004 | 0.330** |
| Number of secondary branches /plant | | | | | | | **1.000** | 0.726** | 0.215** | 0.468** | 0.495** | 0.514** | 0.624** | -0.111 | 0.687** |
| Number of siliquae /plant | | | | | | | | **1.000** | 0.318** | 0.581** | 0.647** | 0.540** | 0.724** | -0.130 | 0.766** |
| Number of seeds /siliqua | | | | | | | | | **1.000** | 0.099 | 0.052 | 0.298** | 0.345** | 0.127 | 0.304** |

| | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Biological yield /plant (g) | | | | | | | | | | **1.000** | 0.514** | 0.010 | 0.409** | -0.058 | 0.562** |
| 1000-seed weight (g) | | | | | | | | | | | **1.000** | 0.632** | 0.657** | 0.132 | 0.806** |
| Harvest index (%) | | | | | | | | | | | | **1.000** | 0.671** | 0.071 | 0.832** |
| Oil content (%) | | | | | | | | | | | | | **1.000** | 0.046 | 0.784** |
| Protein (%) | | | | | | | | | | | | | | **1.000** | 0.029 |

*Significant at p = 0.05;**Significant at p = 0.01

**Table 3:** Genotypic correlation coefficients parents + crosses for 15 characters in 10 x 10 diallel cross in Indian mustard (*Brassica juncea* L.)

| **Characters** | **Days to 50% flowering** | **Days to maturity** | **Plant height (cm)** | **Length of main raceme** | **Leaf area index** | **No. of primary branches /plant** | **No. of secondary branches /plant** | **No. of siliquae / plant** | **No. of seeds / siliqua** | **Biological yield / plant (g)** | **1000-seeds weight (g)** | **Harvest index (%)** | **Oil content (%)** | **Protein (%)** | **Seed yield / plant** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Days to 50% flowering** | **1.000** | 0.716** | 0.481** | 0.385** | 0.512** | -0.346** | 0.473** | 0.505** | -0.236** | 0.513** | 0.442** | 0.012 | 0.259** | -0.184* | 0.280** |
| **Days to maturity** | | **1.000** | 0.853** | 0.595** | 0.688** | -0.013 | 0.656** | 0.651** | -0.032 | 0.797** | 0.558** | 0.170* | 0.345** | -0.154* | 0.556** |
| **Plant height (cm)** | | | **1.000** | 0.420** | 0.509** | -0.053 | 0.351** | 0.526** | 0.154* | 0.745** | 0.508** | 0.096 | 0.196* | -0.006 | 0.469** |
| **Length of main raceme (cm)** | | | | **1.000** | 0.735** | 0.224** | 0.819** | 0.685** | 0.196* | 0.637** | 0.428** | 0.419** | 0.713** | -0.317** | 0.670** |
| **Leaf area index** | | | | | **1.000** | 0.444** | 0.964** | 0.869** | 0.348** | 0.672** | 0.824** | 0.746** | 0.823** | -0.026 | 0.943** |
| **Number of primary branches /plant** | | | | | | **1.000** | 0.381** | 0.294** | 0.283** | 0.082 | 0.388** | 0.615** | 0.459** | -0.005 | 0.510** |
| **Number of secondary branches /plant** | | | | | | | **1.000** | 0.929** | 0.346** | 0.612** | 0.633** | 0.693** | 0.798** | -0.131 | 0.870** |
| **Number of siliquae /plant** | | | | | | | | **1.000** | 0.451** | 0.626** | 0.650** | 0.600** | 0.727** | -0.136 | 0.802** |
| **Number of seeds /siliqua** | | | | | | | | | **1.000** | 0.132 | 0.072 | 0.431** | 0.480** | 0.195* | 0.411** |
| **Biological yield/plant (g)** | | | | | | | | | | **1.000** | 0.553** | 0.121 | 0.440** | -0.063 | 0.628** |
| **1000-seed weight (g)** | | | | | | | | | | | **1.000** | 0.693** | 0.657** | 0.135 | 0.836** |
| **Harvest index (%)** | | | | | | | | | | | | **1.000** | 0.736** | 0.072 | 0.848** |
| **Oil content (%)** | | | | | | | | | | | | | **1.000** | 0.048 | 0.814** |
| **Protein (%)** | | | | | | | | | | | | | | **1.000** | 0.025 |

*Significant at p = 0.05;**Significant at p = 0.01

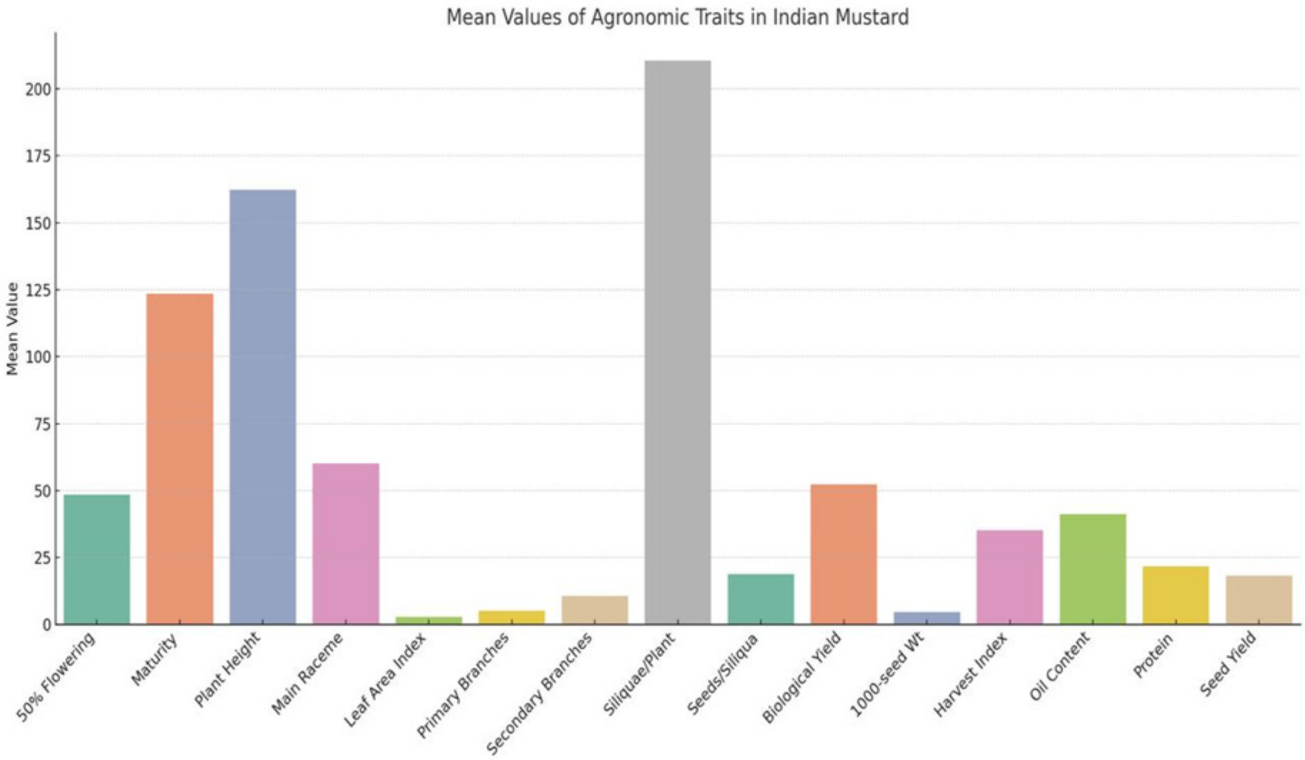
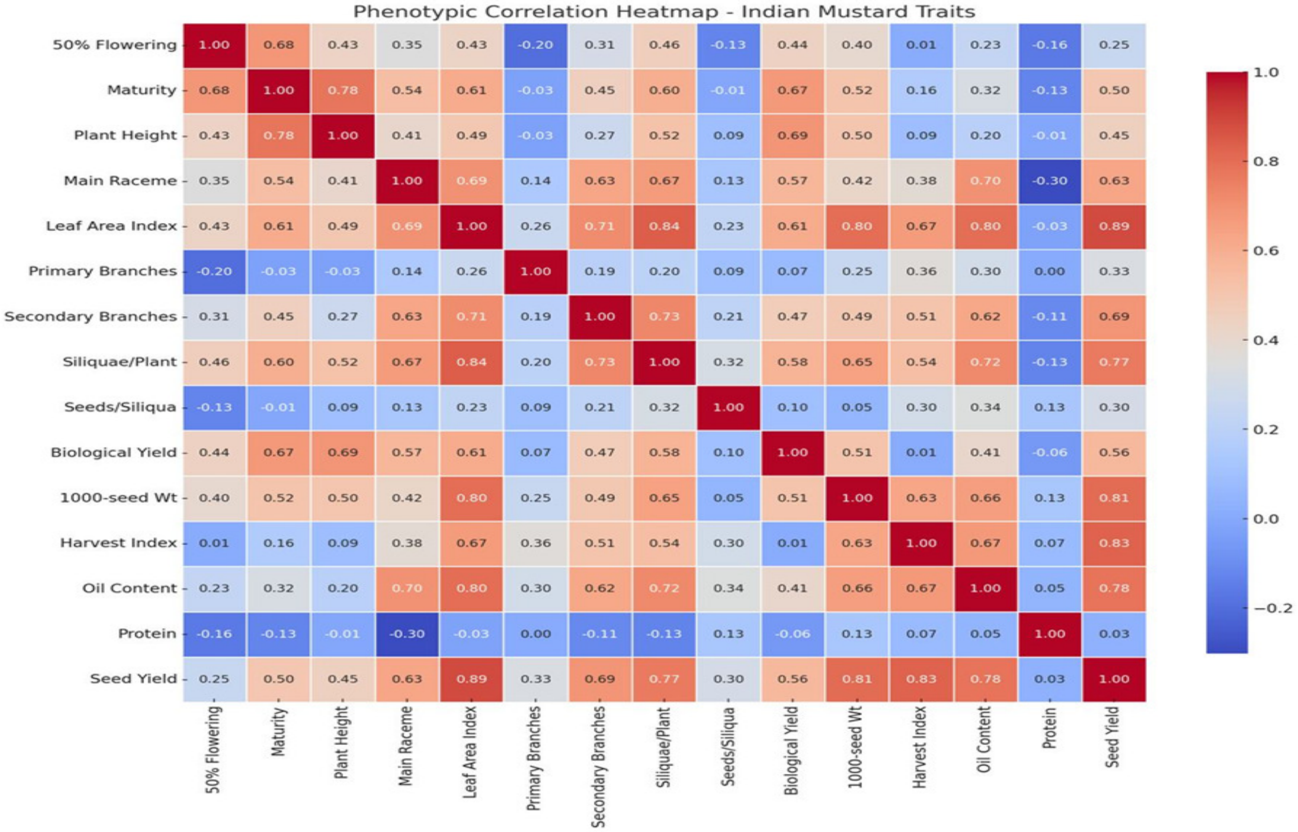
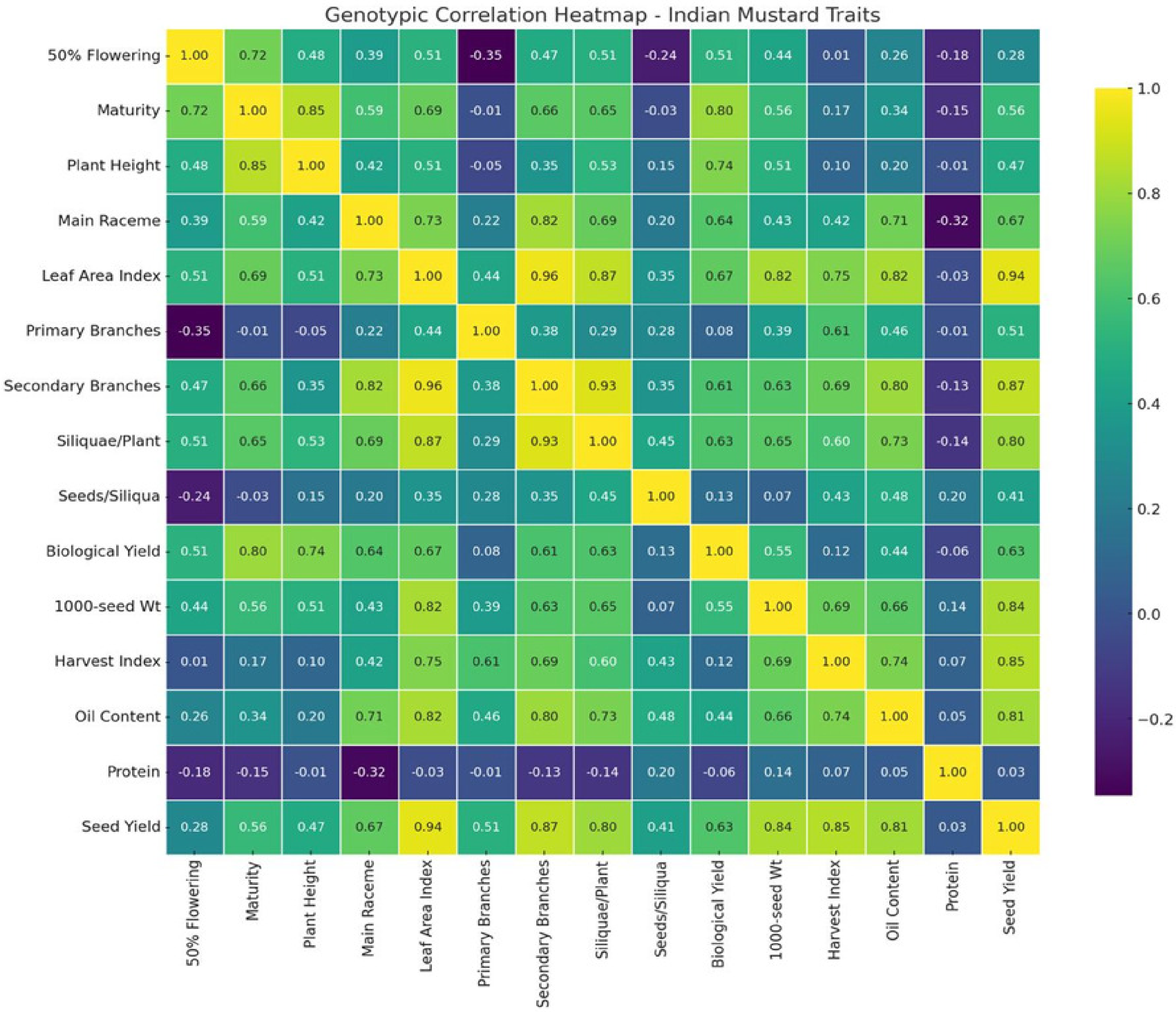


**Fig. 1:** Here's a bar graph showing the mean values of key agronomic traits in Indian mustard (simulated for illustration). This helps visualize which traits have the highest contributions or ranges.



| | 50% Flowering | Maturity | Plant Height | Main Raceme | Leaf Area Index | Primary Branches | Secondary Branches | Siliquae/Plant | Seeds/Siliqua | Biological Yield | 1000-seed Wt | Harvest Index | Oil Content | Protein | Seed Yield |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 50% Flowering | 1.00 | 0.68 | 0.43 | 0.35 | 0.43 | -0.20 | 0.31 | 0.46 | -0.13 | 0.44 | 0.40 | 0.01 | 0.23 | -0.16 | 0.25 |
| Maturity | 0.68 | 1.00 | 0.78 | 0.54 | 0.61 | -0.03 | 0.45 | 0.60 | -0.01 | 0.67 | 0.52 | 0.16 | 0.32 | -0.13 | 0.50 |
| Plant Height | 0.43 | 0.78 | 1.00 | 0.41 | 0.49 | -0.03 | 0.27 | 0.52 | 0.09 | 0.69 | 0.50 | 0.09 | 0.20 | -0.01 | 0.45 |
| Main Raceme | 0.35 | 0.54 | 0.41 | 1.00 | 0.69 | 0.14 | 0.63 | 0.67 | 0.13 | 0.57 | 0.42 | 0.38 | 0.70 | -0.30 | 0.63 |
| Leaf Area Index | 0.43 | 0.61 | 0.49 | 0.69 | 1.00 | 0.26 | 0.71 | 0.84 | 0.23 | 0.61 | 0.80 | 0.67 | 0.80 | -0.03 | 0.89 |
| Primary Branches | -0.20 | -0.03 | -0.03 | 0.14 | 0.26 | 1.00 | 0.19 | 0.20 | 0.09 | 0.07 | 0.25 | 0.36 | 0.30 | 0.00 | 0.33 |
| Secondary Branches | 0.31 | 0.45 | 0.27 | 0.63 | 0.71 | 0.19 | 1.00 | 0.73 | 0.21 | 0.47 | 0.49 | 0.51 | 0.62 | -0.11 | 0.69 |
| Siliquae/Plant | 0.46 | 0.60 | 0.52 | 0.67 | 0.84 | 0.20 | 0.73 | 1.00 | 0.32 | 0.58 | 0.65 | 0.54 | 0.72 | -0.13 | 0.77 |
| Seeds/Siliqua | -0.13 | -0.01 | 0.09 | 0.13 | 0.23 | 0.09 | 0.21 | 0.32 | 1.00 | 0.10 | 0.05 | 0.30 | 0.34 | 0.13 | 0.30 |
| Biological Yield | 0.44 | 0.67 | 0.69 | 0.57 | 0.61 | 0.07 | 0.47 | 0.58 | 0.10 | 1.00 | 0.51 | 0.01 | 0.41 | -0.06 | 0.56 |
| 1000-seed Wt | 0.40 | 0.52 | 0.50 | 0.42 | 0.80 | 0.25 | 0.49 | 0.65 | 0.05 | 0.51 | 1.00 | 0.63 | 0.66 | 0.13 | 0.81 |
| Harvest Index | 0.01 | 0.16 | 0.09 | 0.38 | 0.67 | 0.36 | 0.51 | 0.54 | 0.30 | 0.01 | 0.63 | 1.00 | 0.67 | 0.07 | 0.83 |
| Oil Content | 0.23 | 0.32 | 0.20 | 0.70 | 0.80 | 0.30 | 0.62 | 0.72 | 0.34 | 0.41 | 0.66 | 0.67 | 1.00 | 0.05 | 0.78 |
| Protein | -0.16 | -0.13 | -0.01 | -0.30 | -0.03 | 0.00 | -0.11 | -0.13 | 0.13 | -0.06 | 0.13 | 0.07 | 0.05 | 1.00 | 0.03 |
| Seed Yield | 0.25 | 0.50 | 0.45 | 0.63 | 0.89 | 0.33 | 0.69 | 0.77 | 0.30 | 0.56 | 0.81 | 0.83 | 0.78 | 0.03 | 1.00 |

**Fig. 2:** Here's the heatmap of phenotypic correlations among the 15 traits in Indian mustard. This visual representation helps quickly identify which traits are strongly associated with seed yield and each other.



| | 50% Flowering | Maturity | Plant Height | Main Raceme | Leaf Area Index | Primary Branches | Secondary Branches | Siliquae/Plant | Seeds/Siliqua | Biological Yield | 1000-seed Wt | Harvest Index | Oil Content | Protein | Seed Yield |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 50% Flowering | 1.00 | 0.72 | 0.48 | 0.39 | 0.51 | -0.35 | 0.47 | 0.51 | -0.24 | 0.51 | 0.44 | 0.01 | 0.26 | -0.18 | 0.28 |
| Maturity | 0.72 | 1.00 | 0.85 | 0.59 | 0.69 | -0.01 | 0.66 | 0.65 | -0.03 | 0.80 | 0.56 | 0.17 | 0.34 | -0.15 | 0.56 |
| Plant Height | 0.48 | 0.85 | 1.00 | 0.42 | 0.51 | -0.05 | 0.35 | 0.53 | 0.15 | 0.74 | 0.51 | 0.10 | 0.20 | -0.01 | 0.47 |
| Main Raceme | 0.39 | 0.59 | 0.42 | 1.00 | 0.73 | 0.22 | 0.82 | 0.69 | 0.20 | 0.64 | 0.43 | 0.42 | 0.71 | -0.32 | 0.67 |
| Leaf Area Index | 0.51 | 0.69 | 0.51 | 0.73 | 1.00 | 0.44 | 0.96 | 0.87 | 0.35 | 0.67 | 0.82 | 0.75 | 0.82 | -0.03 | 0.94 |
| Primary Branches | -0.35 | -0.01 | -0.05 | 0.22 | 0.44 | 1.00 | 0.38 | 0.29 | 0.28 | 0.08 | 0.39 | 0.61 | 0.46 | -0.01 | 0.51 |
| Secondary Branches | 0.47 | 0.66 | 0.35 | 0.82 | 0.96 | 0.38 | 1.00 | 0.93 | 0.35 | 0.61 | 0.63 | 0.69 | 0.80 | -0.13 | 0.87 |
| Siliquae/Plant | 0.51 | 0.65 | 0.53 | 0.69 | 0.87 | 0.29 | 0.93 | 1.00 | 0.45 | 0.63 | 0.65 | 0.60 | 0.73 | -0.14 | 0.80 |
| Seeds/Siliqua | -0.24 | -0.03 | 0.15 | 0.20 | 0.35 | 0.28 | 0.35 | 0.45 | 1.00 | 0.13 | 0.07 | 0.43 | 0.48 | 0.20 | 0.41 |
| Biological Yield | 0.51 | 0.80 | 0.74 | 0.64 | 0.67 | 0.08 | 0.61 | 0.63 | 0.13 | 1.00 | 0.55 | 0.12 | 0.44 | -0.06 | 0.63 |
| 1000-seed Wt | 0.44 | 0.56 | 0.51 | 0.43 | 0.82 | 0.39 | 0.63 | 0.65 | 0.07 | 0.55 | 1.00 | 0.69 | 0.66 | 0.14 | 0.84 |
| Harvest Index | 0.01 | 0.17 | 0.10 | 0.42 | 0.75 | 0.61 | 0.69 | 0.60 | 0.43 | 0.12 | 0.69 | 1.00 | 0.74 | 0.07 | 0.85 |
| Oil Content | 0.26 | 0.34 | 0.20 | 0.71 | 0.82 | 0.46 | 0.80 | 0.73 | 0.48 | 0.44 | 0.66 | 0.74 | 1.00 | 0.05 | 0.81 |
| Protein | -0.18 | -0.15 | -0.01 | -0.32 | -0.03 | -0.01 | -0.13 | -0.14 | 0.20 | -0.06 | 0.14 | 0.07 | 0.05 | 1.00 | 0.03 |
| Seed Yield | 0.28 | 0.56 | 0.47 | 0.67 | 0.94 | 0.51 | 0.87 | 0.80 | 0.41 | 0.63 | 0.84 | 0.85 | 0.81 | 0.03 | 1.00 |

**Fig. 3:** Here's the genotypic correlation heatmap among the 15 traits in Indian mustard. This visual confirms even stronger correlations than the phenotypic ones, indicating dominant genetic influence.

## References

Al-Jibouri, H.A., Miller, P.A. & Robinson, H.F. (1958). Genotypic and environmental variances and covariances in an upland cotton cross of interspecific origin. *Agronomy Journal*, **50**, 633–637.

Anonymous (2016–17). Area, production, productivity of mustard in India and Karnataka. Retrieved from: www.indiastat.com

Anonymous (2017–18). Canola history. Retrieved from: www.canolacouncil.org

Awasthi, A., Singh, A. and Srivastava, R. (2020). Genetic variability, correlation and path analysis for yield and its components in Indian mustard (*Brassica juncea* L.). *Journal of Oilseed Brassica*, **11**(1), 33–37.

Dewey, D.I. and Lu, K.H. (1959). A correlation and path-coefficient analysis of components of crested wheatgrass seed production. *Agronomy Journal*, **51**, 515–518.

Meena, M.L., Kumar, A. and Verma, S. (2019). Character association and path coefficient analysis in Indian mustard (*Brassica juncea* L.). *International Journal of Current Microbiology and Applied Sciences*, **8**(5), 1332–1339.

Panse, V.G. and Sukhatme, P.V. (1967). *Statistical Methods for Agricultural Workers* (2nd Ed.). Indian Council of Agricultural Research, New Delhi.

Singh, D., Yadava, D.K. and Singh, N. (2017). Genetic variability and correlation analysis for yield and its components in Indian mustard (*Brassica juncea* L.). *Indian Journal of Agricultural Sciences*, **87**(4), 507–511.

Thakur, D.S., Chand, P. and Kumar, V. (2018). Correlation and path coefficient analysis for yield and its components in mustard. *Research on Crops*, **19**(1), 134–137.

Yadava, D.K., Kumar, P.R. and Singh, N. (2012). Genetic variability and trait association analysis in Indian mustard. *Indian Journal of Genetics and Plant Breeding*, **72**(2), 175–177.