**Genotypic and Phenotypic Correlation Analysis of Morphological and Yield-Contributing Traits in Mustard (*Brassica juncea* L.) Genotypes Under Organic Conditions**

**Abstract**

The present study was undertaken to estimate the genotypic and phenotypic correlations among eleven morphological and yield-contributing traits in twelve mustard (Brassica juncea L.) genotypes grown under organic conditions at Bundelkhand University, Jhansi, during the rabi season of 2024–2025. Understanding these relationships is essential for improving the efficiency of selection for yield and its component traits. Strong and significant genotypic and phenotypic correlations were observed among several traits. Genotypic correlations were generally stronger than phenotypic ones, indicating a stronger inherent genetic relationship among traits beyond environmental influence. Seed yield per plant (SYP) was significantly and positively correlated at the genotypic level with number of seeds per siliqua (NSS), number of siliquae per plant (NSP), and biological yield (BY), indicating their importance as selection indices. Negative associations were also observed between plant height (PH) and total branches (NTB), suggesting trade-offs in trait selection. The study provides valuable insights for mustard breeders aiming to develop high-yielding varieties suitable for organic farming systems.

**Keywords**: Mustard genotypes, Correlation analysis, Genotypic association, Phenotypic traits, Yield components, Organic farming

**Introduction**

Mustard (*Brassica juncea* L.) is an important oilseed crop, and understanding the relationship between its various traits is crucial for effective breeding programs. With about 3500 species and 350 genera, the Brassicaceae family is one of the most commercially important plant groups (Warwick et al, 2000). Mustard, referred to as 'sarson' in Hindi has been mentioned in the Ayurvedic Samhitas. Rapeseed-mustard, an oleiferous Brassica plant, is one of the most economically important agricultural commodities. The words rape and mustard are derived from the Latin word rapum, which means turnip, and the European habit of combining sweet must of old wine with crushed seeds of black mustard [B. nigra (L.) Koch] to make a heated paste. Since the fifteenth century, Europe has been growing mustard and rapeseed oilseeds.From China, the Rai was brought to India. Mustard originated in eastern Europe and Cyberia. This study focuses on analyzing the genotypic and phenotypic correlations between different morphological and yield-contributing traits in mustard genotypes. Genotypic correlation reflects the inherent genetic relationship between traits, while phenotypic correlation includes both genetic and environmental influences. By examining these correlations, breeders can identify traits that are closely associated with yield and prioritize them for selection to improve overall productivity.

Mustard, or Brassica juncea, is a significant oilseed crop, particularly in India, where it contributes substantially to oil production. Breeding efforts aimed at enhancing yield rely heavily on understanding the genetic and phenotypic relationships among various traits. Analyzing these correlations helps identify which traits, when improved, will lead to a corresponding increase in seed yield.

Genotypic correlation, specifically, reveals the extent to which traits are linked due to their shared genes. For example, if two traits exhibit a strong positive genotypic correlation, it suggests that improving one trait is likely to positively influence the other, potentially leading to a synergistic effect on yield. Phenotypic correlation, on the other hand, encompasses both genetic and environmental influences on the relationship between traits. This provides a more realistic picture of how traits interact under field conditions.

Therefore, this study aims to determine both genotypic and phenotypic correlations between various morphological and yield-related traits in mustard genotypes. By understanding these relationships, breeders can make informed decisions about which traits to target in their breeding programs to maximize seed yield and overall productivity in mustard.

**2. Materials and Methods**

**2.1 Experimental Site**

The research trial was conducted during the rabi season of 2024–2025 at the Organic Research Farm, Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Bundelkhand University, Jhansi (U.P.), India. The site lies at a latitude of 26°44′ N and longitude of 79°25′ E with an elevation of 284 meters above mean sea level. It falls under Agro-Climatic Zone VIII (Central Plateau and Hill Region) and experiences a subtropical climate with cool winters and hot summers. The soil of the experimental field was sandy loam in texture, moderately fertile with good drainage, and maintained under organic management for the last five years.

**2.2 Plant Material and Experimental Design**

Twelve diverse genotypes of mustard (*Brassica juncea* L.) were selected for evaluation based on their morphological diversity and regional adaptability. The experiment was laid out in a Randomized Block Design (RBD) with three replications. Each plot consisted of three rows of 3 meters length with a row-to-row spacing of 30 cm and plant-to-plant spacing of 10 cm. Recommended organic cultivation practices were followed throughout the crop season. Nutrient requirements were met using farmyard manure (FYM), vermicompost, and biofertilizers such as Azotobacter and phosphate -solubilizing bacteria.

**2.3 Traits**

Eleven morphological and yield-contributing traits were recorded:

* Days to 50% flowering (DF)
* Days to maturity (DM)
* Plant height (PH, cm)
* Number of primary branches per plant (NPB)
* Number of secondary branches per plant (NSB)
* Number of total branches per plant (NTB)
* Number of seeds per siliqua (NSS)
* Number of siliquae per plant (NSP)
* Harvest index (HI, %)
* Biological yield per plant (BY, g)
* Seed yield per plant (SYP, g)

**2.4 Statistical Analysis**

Genotypic and phenotypic correlation coefficients were computed using the method described by Singh and Chaudhary (1979). The analysis was carried out using R software and Microsoft Excel. Significance of correlation coefficients was tested at both 5% and 1% probability levels. Genotypic correlation coefficients provide insights into genetic relationships, while phenotypic correlations reflect both genetic and environmental influences.

**3. Results and Discussion**

**3.1 Genotypic Correlation Coefficients**

The genotypic correlation analysis plays a vital role in plant breeding, as it reflects the inherent genetic relationships among different agronomic traits, independent of environmental influences. In the present study, genotypic correlation coefficients revealed several significant associations among the traits, providing insights into their interdependence and utility in selection strategies for mustard improvement. Seed yield per plant (SYP), a complex and economically important trait, showed highly significant and positive genotypic correlations with the number of seeds per siliqua (NSS) (r = 0.8768\*\*), number of siliquae per plant (NSP) (r = 0.6944\*), and biological yield (BY) (r = 0.6842\*). These strong positive associations indicate that NSS, NSP, and BY are key determinants of yield potential in mustard and can serve as reliable selection indices in breeding programs aimed at improving seed yield. The significant correlation between SYP and these traits suggests that increasing the number of seeds per siliqua and siliquae per plant could directly enhance seed yield.

Plant height (PH), on the other hand, showed a strong negative and significant genotypic correlation with total branches per plant (NTB) (r = -1.070\*\*). This inverse relationship suggests that as plant height increases, the number of branches may decrease, possibly due to resource allocation toward vertical growth at the expense of lateral development. This finding is consistent with earlier studies by Yadav et al. (2023) and Tripathi et al. (2022), who observed that taller mustard plants often show limited branching, which could affect canopy architecture and, ultimately, reproductive efficiency.

Moreover, days to maturity (DM) exhibited significant negative correlations with both secondary branches per plant (NSB) (r = -0.795\*\*) and total branches per plant (NTB) (r = -0.755\*\*). These results indicate that early-maturing genotypes are likely to produce more branches, which could favor the development of reproductive structures within a shorter growing period. In contrast, late-maturing genotypes may prioritize vegetative growth for an extended duration, thereby limiting branching. The negative correlation between maturity and branching traits suggests a potential trade-off that must be considered when selecting genotypes for both earliness and yield attributes.

Secondary branches per plant (NSB) exhibited a very strong and positive genotypic correlation with total branches per plant (NTB) (r = 0.991\*\*), highlighting the contribution of NSB to overall plant architecture. This relationship confirms that secondary branching is a major component of the total number of branches and can significantly influence plant morphology. Additionally, NSP also showed a positive and significant genotypic correlation with SYP, further reaffirming the role of reproductive sink traits in yield determination.

Collectively, these results suggest that traits such as NSS, NSP, BY, and branching components are closely linked to seed yield at the genetic level. Their inclusion in selection indices can lead to the development of mustard genotypes with superior productivity and efficient resource utilization.

**3.2 Phenotypic Correlation Coefficients**

Phenotypic correlations, unlike genotypic ones, are influenced by both genetic and environmental factors. Therefore, they provide a more realistic estimate of the trait associations under field conditions. In this study, phenotypic correlation coefficients were generally lower in magnitude compared to their genotypic counterparts, reflecting the environmental effects on trait expression. Despite environmental variability, SYP retained significant and positive phenotypic correlations with NSS (r = 0.5937\*\*) and NSP (r = 0.5147\*\*). This indicates that even under varying organic field conditions, these traits maintain their positive influence on yield and can serve as reliable indicators in indirect selection. The consistency of these traits across both genotypic and phenotypic levels makes them robust targets for yield improvement.

On the contrary, days to 50% flowering (DF50) and days to maturity (DM) exhibited weak or negative phenotypic correlations with SYP. This suggests that phenological traits such as flowering and maturity have limited direct contribution to yield under organic conditions. While these traits are essential for adapting to specific agro-ecological zones, their impact on yield may be more indirect and conditional, depending on environmental factors such as moisture availability and growing season length. A significant and negative phenotypic correlation was observed between harvest index (HI) and biological yield (BY) (r = -0.5046\*\*), suggesting a trade-off between biomass production and partitioning efficiency. This implies that genotypes with higher biomass may not necessarily convert it efficiently into economic yield, thereby highlighting the need for an optimal balance between source (biomass) and sink (seed yield) components.

The comparison between genotypic and phenotypic correlation coefficients revealed that the genotypic correlations were consistently higher for all traits studied. This trend indicates a strong inherent association among traits, with minimal interference from environmental factors. The narrow difference between genotypic and phenotypic values suggests that most of the trait associations are genetically controlled and stable across environments, thus favorable for selection.

The findings of this study are in agreement with previous research. Similar positive and significant associations between seed yield and components such as NSS, NSP, and BY were reported by Ali et al. (2002), Choudhary et al. (2003), Doddabhimappa et al. (2009), Maurya et al. (2012), and Rathod et al. (2013). These studies have consistently emphasized the utility of siliqua and seed traits as direct selection criteria for improving yield potential in mustard. Further corroboration comes from the works of Lodhi et al. (2014), Chauhan et al. (2017), and Lyngdoh et al. (2017), who highlighted the importance of biomass and branching traits in yield formation.

Additionally, the strong relationship between branching traits and yield has been supported by Rai et al. (2017), Roy et al. (2017), and Prasad & Patil (2018), who found that well-branched plants contribute significantly to reproductive success and higher seed yield. These studies affirm the current results and provide a strong basis for including branching parameters, siliqua number, and biological yield in mustard breeding programs.

From a breeding perspective, the current correlation analysis highlights several key traits that can be targeted for yield improvement. Traits with strong positive associations, such as NSS, NSP, and BY, should be prioritized in selection programs. Their consistent performance at both genotypic and phenotypic levels indicates their stability and effectiveness under varying environmental conditions.

Moreover, the significant negative correlation between PH and NTB, and between DM and branching traits, suggests that excessive vegetative growth and prolonged maturity may hinder branching and yield. Breeding efforts should therefore aim to strike a balance between plant height, maturity duration, and branching to achieve optimal plant architecture and reproductive efficiency.

The close relationship between NSB and NTB also indicates that selecting for increased secondary branching can positively influence total branches, thereby improving yield potential. The negative correlation between HI and BY calls for careful consideration of biomass partitioning while selecting for high-yielding genotypes. Breeding strategies that focus on both source and sink traits are likely to be more successful.

**Table 1: Genotypic correlation coefficient among different traits in mustard genotypes**

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Chr** | **DF50** | **DM** | **PH** | **NPB** | **NSB** | **NTB** | **NSS** | **NSP** | **HI** | **BY** | **SYP** |
| **DF50** | 1 \*\* | 0.882 \*\* | 0.5679 | -0.1038 | -0.5346 | -0.4826 | -0.2772 | -0.3791 | -0.0708 | 0.1583 | 0.0484 |
| **DM** |  | 1 \*\* | 0.7569 \*\* | -0.3581 | -0.795 \*\* | -0.755 \*\* | -0.0507 | -0.2949 | -0.0029 | 0.1763 | 0.083 |
| **PH** |  |  | 1 \*\* | -0.957 \*\* | -1.033 \*\* | -1.070 \*\* | -0.0148 | -0.3913 | 0.3535 | 0.117 | 0.2734 |
| **NPB** |  |  |  | 1 \*\* | 0.6785 \* | 0.7706 \*\* | 0.1504 | 0.5877 \* | 0.2845 | -0.1887 | 0.1104 |
| **NSB** |  |  |  |  | 1 \*\* | 0.991 \*\* | 0.102 | 0.2834 | -0.1301 | -0.1923 | -0.1866 |
| **NTB** |  |  |  |  |  | 1 \*\* | 0.1159 | 0.3529 | -0.061 | -0.2012 | -0.1418 |
| **NSS** |  |  |  |  |  |  | 1 \*\* | 0.5064 | 0.1975 | 0.7824 \*\* | 0.8768 \*\* |
| **NSP** |  |  |  |  |  |  |  | 1 \*\* | 0.3075 | 0.4072 | 0.6944 \* |
| **HI** |  |  |  |  |  |  |  |  | 1 \*\* | -0.2928 | 0.4941 |
| **BY** |  |  |  |  |  |  |  |  |  | 1 \*\* | 0.6842 \* |
| **SYP** |  |  |  |  |  |  |  |  |  |  | 1 \*\* |

**Table 2: Phenotypic correlation coefficient among different traits in mustard genotype**

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Chr** | **DF50** | **DM** | **PH** | **NPB** | **NSB** | **NTB** | **NSS** | **NSP** | **HI** | **BY** | **SYP** |
| **DF50** | 1 \*\* | 0.707 \*\* | 0.1856 | -0.139 | -0.4787 \*\* | -0.445 \*\* | -0.1661 | -0.3197 | 0.0686 | 0.0399 | 0.0662 |
| **DM** |  | 1 \*\* | 0.4833 \*\* | -0.2467 | -0.6827 \*\* | -0.6443 \*\* | -0.0981 | -0.2258 | -0.1119 | 0.2888 | 0.1831 |
| **PH** |  |  | 1 \*\* | -0.3682 \* | -0.5745 \*\* | -0.5738 \*\* | -0.1416 | -0.1456 | -0.0214 | 0.0332 | 0.0132 |
| **NPB** |  |  |  | 1 \*\* | 0.5822 \*\* | 0.7047 \*\* | 0.0217 | 0.4838 \*\* | 0.0595 | 0.0122 | 0.1226 |
| **NSB** |  |  |  |  | 1 \*\* | 0.9871 \*\* | 0.1049 | 0.2996 | -0.0539 | -0.0813 | -0.0881 |
| **NTB** |  |  |  |  |  | 1 \*\* | 0.0958 | 0.3567 \* | -0.0354 | -0.0686 | -0.0528 |
| **NSS** |  |  |  |  |  |  | 1 \*\* | 0.4324 \*\* | 0.3186 | 0.3008 | 0.5937 \*\* |
| **NSP** |  |  |  |  |  |  |  | 1 \*\* | 0.2585 | 0.211 | 0.5147 \*\* |
| **HI** |  |  |  |  |  |  |  |  | 1 \*\* | -0.5046 \*\* | 0.2378 |
| **BY** |  |  |  |  |  |  |  |  |  | 1 \*\* | 0.7107 \*\* |
| SYP |  |  |  |  |  |  |  |  |  |  | 1 \*\* |

**4. Conclusion**

The findings of the study underline the presence of significant genotypic and phenotypic correlations among key yield-contributing traits in mustard genotypes. Seed yield per plant showed strong positive associations with number of seeds per siliqua, siliquae per plant, and biological yield, establishing them as potential selection criteria. The negative associations observed between plant height and branching traits, as well as between harvest index and biological yield, indicate the need for a balanced selection approach. Overall, the results provide a valuable foundation for formulating breeding strategies aimed at enhancing mustard yield under organic farming systems. Future studies should consider multi-location and multi-season trials to validate these trait relationships and improve selection accuracy.

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