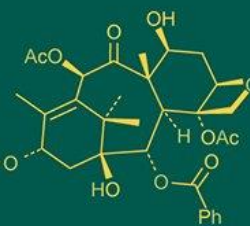
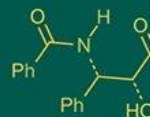


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## Assessment of genetic variability and character association in mustard (*Brassica juncea* L.)

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**Abstract**

The experiment entitled "Assessment of Genetic Variability and Character Association in Mustard (*Brassica juncea* L.)" was conducted during the Rabi season of 2024-25 at the Experimental Farm of Dev Bhoomi Uttarakhand University, India. The objective of this study was to assess the extent of genetic variability in mustard and examine the associations between seed yield and its component traits. The experiment was established using a Randomized Block Design (RBD) with three replications, incorporating fourteen genotypes and one check variety. Analysis of variance revealed highly significant differences among genotypes for most characters studied, indicating substantial genetic variability present in the experimental material. PCV values were marginally higher than corresponding GCV values for most traits, reflecting the influence of environmental factors on character expression. High heritability coupled with high genetic advance as percentage of mean was observed for several yield and yield-component traits, suggesting predominance of additive gene action and favorable prospects for improvement through direct selection. Correlation analysis revealed that important component traits including number of branches, silique per plant, biological yield, and seed-related parameters exhibited positive associations with seed yield. Path coefficient analysis demonstrated that these traits exerted positive direct and indirect effects on seed yield, confirming their importance as reliable selection criteria in mustard breeding programs. Among the evaluated genotypes, BHP1 demonstrated superior performance for several economically important traits and may be utilized in future breeding programs targeting development of high-yielding mustard varieties.

**Keywords:** Indian mustard, genetic variability, heritability, correlation analysis, path coefficient, seed yield

**1. Introduction**

Mustard (*Brassica juncea* L.) represents one of the most important oilseed crops cultivated in India and numerous other countries (Gupta, 2009) [6]. As a member of the Brassicaceae family, it is extensively cultivated for its seeds, which serve various industrial applications, condiments, edible oil extraction, and medicinal preparations (Acquaah, 2012) [1]. Given its economic importance and broad adaptability, mustard makes substantial contributions to the agricultural economies of many nations. India holds a prominent position in global oilseed production and ranks among the leading producers and consumers of rapeseed-mustard crops. Despite this importance, mustard productivity is often constrained by environmental conditions, limited availability of high-yielding genotypes, and the complex nature of seed yield and associated traits. Consequently, enhancing seed yield through direct selection alone presents considerable challenges, and effective crop improvement programs require comprehensive understanding of yield-contributing traits. Genetic variability constitutes a fundamental requirement for any successful plant breeding program, as the extent of variation within breeding material determines selection effectiveness (Allard, 1960) [2]. Adequate genotypic variability enables plant breeders to identify superior lines and develop improved varieties with desirable agronomic characteristics. Estimating genetic parameters including phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability, and genetic advance facilitates understanding of the nature and extent of variability as well as inheritance patterns of economically important traits (Burton and DeVane, 1953; Johnson *et al.*, 1955) [3, 7]. Heritability and genetic advance represent critical genetic parameters utilized in crop improvement research, as they provide insights into trait inheritance from parents to offspring and selection effectiveness.

High heritability coupled with high genetic advance typically indicates the predominance of additive gene action, suggesting that improvement through direct selection may prove highly effective. This information assists in identifying traits that can be successfully enhanced through breeding programs. Correlation analysis is commonly employed to determine the magnitude and direction of relationships between various plant characteristics and seed yield. Since yield represents a complex trait influenced by multiple component characters, correlation studies help breeders identify key traits that contribute to productivity. However, simple correlation analysis cannot establish whether a character's association with yield stems from its direct effects or indirect effects mediated through other traits.

To address this limitation, correlation coefficients are partitioned into direct and indirect effects through path coefficient analysis, which facilitates a clearer understanding of how individual traits influence seed yield. Consequently, path analysis serves as a fundamental tool in crop improvement programs and assists in identifying reliable selection criteria. Dewey and Lu (1959) [5] successfully employed correlation and path coefficient analysis in crop breeding research, demonstrating the effectiveness of these approaches in identifying key traits that contribute to yield. Analysis of Variance (ANOVA) represents a critical statistical method for assessing the extent of variability within experimental material and establishing the significance of genotypic differences. These analytical approaches provide valuable insights into the potential for genetic improvement and selection. Limited information is available regarding the performance and association of locally collected mustard genotypes under the agroclimatic conditions of Dehradun, Uttarakhand.

## 2. Materials and Methods

The present investigation, "Assessment of Genetic Variability and Character Association in Mustard (*Brassica juncea* L.)," was conducted at the Experiment Farm of Dev Bhoomi Uttarakhand University in Dehradun, Uttarakhand, India, during the Rabi season of 2024-2025. The experimental site is located at approximately 30.31° N latitude and 78.03° E longitude, at an elevation of approximately 640 meters above mean sea level. The soil pH ranged from 6.5 to 7.2, indicating slightly acidic to neutral conditions. The soil exhibited medium fertility status with adequate availability of essential nutrients required for optimal plant growth. The experimental material consisted of fifteen mustard genotypes, including fourteen test genotypes and one check variety. These genotypes were evaluated using a Randomized Block Design (RBD) with three replications to ensure accurate and reliable results. The crop was sown during the Rabi season with spacing of 10 cm between plants and 30 cm between rows. All recommended agronomic practices were followed throughout the crop growth period to ensure proper crop establishment and adequate plant development. The experimental field was thoroughly prepared through plowing, followed by harrowing and leveling to create a fine, uniform seedbed suitable for sowing. Well-decomposed farmyard manure (FYM) was incorporated into the soil during land preparation to improve soil fertility and support healthy crop growth. Fertilizers were applied at the recommended rate of 20 tonnes FYM and 60:30:30 kg

N:P<sub>2</sub>O<sub>5</sub>:K<sub>2</sub>O per hectare for mustard cultivation. Irrigation was provided during critical growth stages based on crop requirements and prevailing weather conditions. Hand weeding and regular intercultural operations were conducted to maintain effective weed management. Necessary plant protection measures were implemented to control insect pests and diseases following recommended protocols. Observations were recorded from five randomly selected plants of each genotype in each replication. Statistical analysis was conducted using mean values from the selected plants to ensure accurate interpretation of results.

Sixteen quantitative characteristics, including days to 50% flowering, days to maturity, plant height, number of primary and secondary branches, number of siliques, length of silique, number of seeds per silique, 1000-seed weight, biological yield per plant, biological yield per plot, biological yield per hectare, seed yield per plant, seed yield per plot, seed yield per hectare, and harvest index, were recorded. The degree of genetic variability and the connection between yield and its contributing traits in Indian mustard genotypes were assessed using these observations.

In accordance with the approach recommended by Panse and Sukhatme (1985), the recorded data were statistically analyzed using Analysis of Variance (ANOVA) for Randomized Block Design (RBD). Following Singh and Narayanan (2013), statistical methods for variability and association analysis were employed. The objective of the analysis was to determine whether the genotypes under study exhibited significant differences from one another. To assess the extent of variability and inheritance of various traits, standard statistical procedures were utilized to estimate genetic parameters including Phenotypic Coefficient of Variation (PCV), Genotypic Coefficient of Variation (GCV), heritability, and genetic advance. The relationships between different traits were examined using correlation analysis, and the direct and indirect contributions of various component characters to seed yield were determined using path coefficient analysis.

**Table 1:** Experimental material of this study consists of 14 genotypes of mustard collected from different source and a local check variety.

| Sr. No. | Genotypes | Source of genotype                       |
|---------|-----------|------------------------------------------|
| 1.      | DDN1      | Local Mustard Dehradun-1 (Check variety) |
| 2.      | DDN2      | Local Mustard Dehradun-2                 |
| 3.      | DDN3      | Local Mustard Dehradun-3                 |
| 4.      | DWH1      | Doiwala Dehradun Local Farmer Variety    |
| 5.      | BHP1      | Bharatpur Dehradun Local Farmer Variety1 |
| 6.      | BHP2      | Bharatpur Dehradun Local Farmer Variety2 |
| 7.      | AJM1      | Ajmer Rajasthan variety1                 |
| 8.      | PAM1      | Patna Bihar Farmer Variety1              |
| 9.      | PAM2      | Patna Bihar Farmer Variety2              |
| 10.     | VKN1      | Vikasnagar local variety-1               |
| 11.     | VKN2      | Vikasnagar local variety-2               |
| 12.     | PNT1      | Poanta local variety-1                   |
| 13.     | DDN4      | Local Mustard Dehradun-4                 |
| 14.     | DDN5      | Local Mustard Dehradun-5                 |
| 15.     | DDN6      | Local Mustard Dehradun-6                 |

## 3. Results and Discussion

For each of the sixteen quantitative characteristics examined, the analysis of variance (ANOVA) showed highly significant differences between the fifteen mustard genotypes, suggesting that there was a significant amount of genetic variability in the experimental material. Wide

genotype variation indicated that there are enough chances for efficient selection and genetic advancement in mustard breeding initiatives. Allard (1960) <sup>[2]</sup>, Johnson *et al.* (1955) <sup>[7]</sup>, and Acquaaah (2012) <sup>[1]</sup> also reported similar results about the occurrence of significant variability in mustard, emphasizing that variability is the essential prerequisite for successful crop improvement.

For every character examined, including days to 50% flowering, plant height, number of primary and secondary branches, days to maturity, number of siliquae per plant, length of siliqua, number of seeds per siliqua, test weight, biological yield, seed yield, and harvest index, the mean sum of squares due to treatments was found to be significant. This suggested that there were notable genetic variations between these characters' genotypes. The precision and dependability of the experimental results under Randomized Block Design (RBD) were demonstrated by the comparatively lower error mean square values for the majority of traits.

The possibility of finding superior genotypes appropriate for upcoming breeding programs was suggested by the notable variations found among genotypes for yield and yield-contributing traits. Panse and Sukhatme (1985) reported similar findings, stating that significant ANOVA values show that there is exploitable variability in the experimental material.

**Table 2:** Analysis of Variance

| Trait | Replication | Treatment     | Error       |
|-------|-------------|---------------|-------------|
| D50F  | 19.374      | 39.7**        | 12.121      |
| PH    | 177.638     | 248.946**     | 89.063      |
| NPB   | 0.169       | 2.18**        | 0.138       |
| NSB   | 1.36        | 18.103**      | 0.690       |
| DM    | 53.161      | 75.769*       | 27.207      |
| NSP   | 9.209       | 5052.715**    | 253.014     |
| LS    | 0.186       | 1.303**       | 0.114       |
| NSS   | 6.53        | 16.915**      | 1.959       |
| TSW   | 0.119       | 1.481**       | 0.067       |
| BYPP  | 4.838       | 351.778**     | 10.606      |
| BYP   | 0.603       | 6.775**       | 0.269       |
| BYH   | 1343886.739 | 9353084.587** | 415,235.801 |
| SYPP  | 2.608       | 40.4**        | 1.190       |
| SYP   | 0.003       | 0.581**       | 0.014       |
| SYH   | 56657.005   | 957642.465**  | 24,692.420  |
| HI    | 3.164       | 3.875**       | 1.384       |

\*Significant at 5% level of probability, \*\*significant at 1% level of probability

For nearly every character examined, the estimates of the phenotypic coefficient of variation (PCV) were marginally greater than the corresponding genotypic coefficient of variation (GCV) values. Al-Jibouri *et al.* (1958) also reported similar findings about genotypic and environmental variance components. This suggested that these traits' expression was somewhat influenced by environmental factors. However, the relatively small differences between PCV and GCV for a number of significant characters indicated that genetic factors, with comparatively less environmental interference, were primarily responsible for the expression of these traits. Burton and DeVane (1953) <sup>[3]</sup> reported similar findings, stating that small differences between PCV and GCV indicate more genetic control over the traits and less environmental influence.

Features like the number of secondary branches per plant, the number of siliquae per plant, the biological yield per

plant, the seed yield per plant, and the harvest index all had high GCV and PCV values. These characters' high variability suggested that there was more room for selection and breeding program improvement. Plant height, number of primary branches per plant, and 1000-seed weight showed moderate variability, while days to 50% flowering and days to maturity showed low variability, indicating comparatively stable inheritance of these traits under environmental conditions.

In order to comprehend the inheritance pattern and the efficiency of selection in crop improvement programs, estimates of heritability and genetic advancement are crucial metrics. For traits like siliquae per plant, biological yield per plant, seed yield per plant, and number of secondary branches per plant, the current study found high heritability combined with high genetic advancement as a percentage of mean. Hanson *et al.* also reported similar correlations between expected genetic advancement and heritability (1956). This demonstrated that additive gene action predominated for these traits and implied that direct selection would be very successful in improving them. According to Johnson *et al.* (1955) <sup>[7]</sup>, traits with high genetic advancement and heritability are typically controlled by additive genetic effects and can be successfully enhanced by phenotypic selection.

Plant height, seeds per siliqua, and 1000-seed weight all showed moderate heritability and moderate genetic advancement, suggesting that both additive and non-additive gene effects are involved in the inheritance of these traits. Under appropriate breeding techniques and repeated selection cycles, such traits may react favourably. Conversely, lower heritability estimates for some traits suggested that their expression was more influenced by the environment, which decreased the effectiveness of direct selection.

There was significant genetic diversity among the experimental material, as evidenced by the fifteen mustard genotypes' notable differences in growth, yield, and yield-contributing traits. In the agroclimatic conditions of Dehradun, the check variety DDN1 demonstrated relatively stable performance for the majority of the characters and provided a helpful benchmark for comparison.

For the majority of the significant growth and yield metrics, BHP1 outperformed all other genotypes that were assessed. The genotype showed the following characteristics: maximum number of primary branches per plant (7.267), maximum number of secondary branches per plant (18.567), maximum number of siliquae per plant (328.200), longest siliqua length (6.770 cm), maximum number of seeds per siliqua (18.733), maximum test weight (5.967 g), and minimum days to 50% flowering (37.100 days). Furthermore, BHP1 had the highest biological yield per hectare (13,570.833 q ha<sup>-1</sup>), biological yield per plant (76.100 g), biological yield per plot (10.856 kg), seed yield per plant (23.867 g), and seed yield per plot (2.863 kg). BHP1's superior performance for a number of economically significant traits demonstrated its high genetic potential and adaptability in Dehradun.

In terms of growth and yield attributes, the genotype DWH1 also did remarkably well. It outperformed many other genotypes in terms of plant height (175.533 cm), number of siliquae per plant (314.633), seed yield per plant (22.267 g), and biological yield. In a similar vein, DDN4 performed better in terms of plant height, siliquae production, and seed

yield traits, indicating its potential utility in upcoming breeding initiatives.

The genotype AJM1 demonstrated satisfactory yield performance along with relatively early flowering and maturity. When early maturity is desired, this genotype might be helpful. The local genotypes DDN2, DDN3, and DDN6 showed good adaptability to local agroclimatic conditions and moderate performance for the majority of growth and yield characteristics.

The superiority of the Vikasnagar genotype VKN2 among the local varieties was demonstrated by its comparatively higher branching pattern, siliquae production, and biological yield compared to VKN1. In a similar vein, PAM2, PNT1, and DDN5 recorded lower values for a number of yield attributes, such as test weight, biological yield, seed yield, and siliquae per plant. Under the current environmental conditions, these genotypes may perform relatively poorly due to decreased biomass accumulation and decreased reproductive efficiency.

The observed variations in growth and yield characteristics between genotypes could be explained by their varied genetic backgrounds and varying reactions to environmental factors. Allard (1960) [2], Acquaah (2012) [1], have also reported similar results regarding genotype variability and differential performance in mustard.

Because they offer useful information about the inheritance pattern of quantitative traits and the efficacy of selection in crop improvement programs, heritability and genetic advancement are regarded as significant genetic parameters in plant breeding. Robinson *et al.* (1949) also highlighted the significance of heritability estimation in crop improvement. Genetic advance calculates the anticipated improvement in a trait under selection, whereas heritability shows the percentage of total phenotypic variation attributable to genetic factors. Breeders can thus find traits that can be successfully enhanced by direct selection by combining the study of heritability and genetic advancement (Johnson *et al.*, 1955) [7].

For significant yield and yield-contributing traits like the number of siliquae per plant, the number of secondary branches per plant, the biological yield per plant, the seed yield per plant, and the harvest index, the current study found high heritability estimates combined with high genetic advance as a percentage of mean. These traits are primarily governed by transmissible genetic factors with relatively less environmental influence, as suggested by the occurrence of high heritability and high genetic advance for these characters, which indicated the predominance of additive gene action. Therefore, direct phenotypic selection for these traits would be very successful in increasing mustard productivity and seed yield. Burton and DeVane (1953) [3], Johnson *et al.* (1955) [7], and Allard (1960) [2] also reported similar findings, emphasizing that traits dominated by additive genetic effects respond well to selection and can be successfully enhanced through breeding programs.

The number of siliquae per plant and seed yield per plant showed high heritability, indicating that these characteristics are genetically stable and dependable for selection in a range of environmental circumstances. The number of secondary branches per plant and biological yield per plant both showed high genetic advancement, suggesting more room for improvement using straightforward selection techniques. Improving these traits could eventually increase mustard productivity because they directly affect the final

seed yield. The results of this study are consistent with previous reports in mustard improvement studies that identified high heritability and genetic advancement in yield-related traits as useful selection criteria (Acquaah, 2012) [1].

**Table 3:** Summary mean table for different genotypes of mustard with different parameters

| Treatment | D50F   | PH      | NPB   | NSB    | DM      | NSP     | LS    |
|-----------|--------|---------|-------|--------|---------|---------|-------|
| DDN1      | 44.367 | 162.333 | 5.267 | 12.433 | 109.967 | 245.600 | 5.230 |
| DWH1      | 38.533 | 175.533 | 6.800 | 17.267 | 101.300 | 314.633 | 6.430 |
| BHP1      | 37.100 | 180.333 | 7.267 | 18.567 | 99.597  | 328.200 | 6.770 |
| AJM1      | 39.533 | 172.633 | 6.697 | 16.800 | 104.097 | 300.400 | 6.130 |
| PAM1      | 42.667 | 165.033 | 5.933 | 14.367 | 107.633 | 268.300 | 5.630 |
| PAM2      | 47.000 | 155.467 | 4.833 | 11.333 | 113.797 | 211.633 | 4.830 |
| DDN2      | 40.837 | 168.567 | 6.133 | 15.133 | 105.067 | 285.533 | 5.930 |
| DDN3      | 43.533 | 160.567 | 5.433 | 13.267 | 107.700 | 251.100 | 5.330 |
| BHP2      | 37.800 | 170.803 | 6.697 | 16.033 | 102.997 | 296.000 | 6.030 |
| VKN1      | 45.767 | 157.967 | 5.033 | 12.167 | 111.363 | 225.933 | 5.030 |
| VKN2      | 41.533 | 167.503 | 6.033 | 14.763 | 106.200 | 270.933 | 5.730 |
| PNT1      | 48.700 | 150.467 | 4.533 | 10.600 | 116.967 | 198.867 | 4.530 |
| DDN4      | 39.963 | 173.500 | 6.567 | 16.533 | 104.300 | 305.367 | 6.230 |
| DDN5      | 47.533 | 149.170 | 4.733 | 11.033 | 114.733 | 205.933 | 4.730 |
| DDN6      | 42.763 | 163.033 | 5.833 | 14.067 | 106.933 | 262.767 | 5.530 |
| Mean      | 42.509 | 164.861 | 5.853 | 14.291 | 107.510 | 264.747 | 5.606 |
| Min       | 37.100 | 149.170 | 4.533 | 10.600 | 99.597  | 198.867 | 4.530 |
| Max       | 48.700 | 180.333 | 7.267 | 18.567 | 116.967 | 328.200 | 6.770 |
| CV (%)    | 8.190  | 5.724   | 6.353 | 5.815  | 4.852   | 6.008   | 6.010 |
| SEm       | 2.010  | 5.449   | 0.215 | 0.480  | 3.011   | 9.184   | 0.195 |
| CD @ 5%   | 5.823  | 15.784  | 0.622 | 1.390  | 8.724   | 26.604  | 0.564 |
| CD @ 1%   | 7.855  | 21.292  | 0.839 | 1.875  | 11.768  | 35.888  | 0.760 |

| Treatment | NSS    | TSW   | BYPP   | BYP    | BYH        | SYPP   | SYP   |
|-----------|--------|-------|--------|--------|------------|--------|-------|
| DDN1      | 13.500 | 4.300 | 52.770 | 7.903  | 9,879.163  | 15.333 | 1.840 |
| DWH1      | 17.833 | 5.600 | 71.867 | 10.420 | 13,025.000 | 22.267 | 2.667 |
| BHP1      | 18.733 | 5.967 | 76.100 | 10.856 | 13,570.833 | 23.867 | 2.863 |
| AJM1      | 16.563 | 5.300 | 68.733 | 9.770  | 12,212.500 | 20.800 | 2.493 |
| PAM1      | 14.667 | 4.800 | 60.433 | 8.877  | 11,095.830 | 18.033 | 2.163 |
| PAM2      | 11.867 | 3.900 | 45.567 | 6.750  | 8,437.500  | 13.063 | 1.570 |
| DDN2      | 15.900 | 5.000 | 63.967 | 9.147  | 11,433.333 | 19.133 | 2.293 |
| DDN3      | 13.800 | 4.400 | 54.933 | 8.043  | 10,054.166 | 16.400 | 1.960 |
| BHP2      | 16.700 | 5.200 | 67.167 | 9.377  | 11,720.833 | 19.833 | 2.380 |
| VKN1      | 12.467 | 4.100 | 48.733 | 7.183  | 8,979.167  | 14.133 | 1.693 |
| VKN2      | 15.333 | 4.900 | 61.667 | 8.983  | 11,229.167 | 18.433 | 2.213 |
| PNT1      | 11.237 | 3.600 | 41.433 | 6.313  | 7,891.667  | 11.933 | 1.430 |
| DDN4      | 17.600 | 5.400 | 70.033 | 9.820  | 12,275.000 | 21.167 | 2.537 |
| DDN5      | 11.833 | 3.800 | 44.267 | 6.580  | 8,225.000  | 12.600 | 1.510 |
| DDN6      | 14.933 | 4.700 | 59.133 | 6.580  | 10,912.500 | 17.433 | 2.093 |
| Mean      | 14.864 | 4.731 | 59.120 | 8.440  | 10,729.444 | 17.629 | 2.114 |
| Min       | 11.237 | 3.600 | 41.433 | 6.313  | 7,891.667  | 11.933 | 1.430 |
| Max       | 18.733 | 5.967 | 76.100 | 10.856 | 13,570.833 | 23.867 | 2.863 |
| CV (%)    | 9.415  | 5.451 | 5.509  | 6.140  | 6.006      | 6.187  | 5.647 |
| SEm       | 0.808  | 0.149 | 1.880  | 0.299  | 372.038    | 0.630  | 0.069 |
| CD @ 5%   | 2.341  | 0.431 | 5.447  | 0.867  | 1,077.750  | 1.824  | 0.200 |
| CD @ 1%   | 3.158  | 0.582 | 7.348  | 1.169  | 1,453.864  | 2.461  | 0.269 |

For characteristics like plant height, number of seeds per siliqua, and 1000-seed weight, moderate heritability and moderate genetic advancement were noted, suggesting that both additive and non-additive gene effects are involved in the inheritance of these traits. Under appropriate breeding techniques involving hybridization and selection, such traits may react well to repeated cycles of selection. The moderate estimates also imply that these characters' expression is partially influenced by their surroundings.

However, days to 50% flowering and days to maturity showed comparatively lower heritability estimates, suggesting that these traits are more influenced by the environment. Because environmental factors play a significant role in phenotypic variation, lower heritability generally reduces the effectiveness of direct phenotypic selection. Therefore, in order to achieve stable performance, improvement of such traits may necessitate careful selection over several environments and generations.

Overall, the study's findings made it abundantly evident that characteristics with high heritability and high genetic advancement could be used as trustworthy selection criteria to create superior, high-yielding mustard genotypes. Breeders will be able to improve seed yield and related agronomic traits in mustard under a variety of agroclimatic conditions by using the data produced by these genetic parameters.

An essential statistical method for figuring out the strength and direction of relationships between various plant traits and how they affect yield is correlation analysis. Singh and Narayanan (2013) described similar biometrical methods for character association research in crop plants. Significant positive correlations between seed yield and a number of mustard yield-contributing characteristics were found in the current study's correlation analysis.

The biological yield per plant, the number of siliques per plant, the number of secondary branches per plant, the number of primary branches per plant, the number of seeds per silique, and the harvest index all showed a strong positive and significant correlation with seed yield per plant. These positive correlations suggested that improving these

component traits might tangentially increase mustard seed yield.

Biological yield per plant had the strongest positive correlation with seed yield among the traits examined, indicating that plants with higher biomass accumulation typically yield more economically. Dewey and Lu (1959) [5] also reported similar results, noting that crop plant productivity is significantly influenced by biological yield.

Additionally, there was a strong positive correlation between the number of siliques per plant and seed yield, suggesting that plants with more siliques directly contribute to higher seed production. Increased branching boosts siliques production, which raises overall productivity, according to the positive correlation between secondary branches and yield. Similar findings have been documented in a number of mustard improvement studies, where siliques and branches were found to be significant yield-contributing characteristics (Acquaah, 2012) [1].

Taller plants with better vegetative growth may contribute to higher biomass production and better seed formation, as evidenced by the moderately positive correlation between plant height and seed yield. The number of seeds per silique and the weight of 1000 seeds were two seed-related characteristics that showed a positive correlation with seed yield, indicating their importance in seed development and ultimate productivity.

Because selection can simultaneously improve related traits, the positive correlations found among yield-contributing traits are very helpful in breeding programs. Therefore, in mustard breeding programs, the traits that exhibit a strong positive correlation with yield ought to be regarded as crucial selection criteria.

**Table 4:** Estimation of phenotypic correlation matrix for different characters in mustard genotypes  
Phenotypic Correlation Matrix

| Trait | D50F  | PH       | NPB      | NSB      | DM       | NSP      | LS       | NSS      | TSW      | BYPP     | BYP      | BYH      | SYP      | SYH      | HI       | SYPP     |
|-------|-------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|
| D50F  | 1.000 | -0.609** | -0.682** | -0.714** | 0.769**  | -0.735** | -0.680** | -0.720** | -0.712** | -0.735** | -0.675** | -0.709** | -0.760** | -0.705** | -0.409** | -0.737** |
| PH    |       | 1.000    | 0.674**  | 0.747**  | -0.341*  | 0.754**  | 0.716**  | 0.719**  | 0.728**  | 0.741**  | 0.711**  | 0.736**  | 0.773**  | 0.713**  | 0.573**  | 0.752**  |
| NPB   |       |          | 1.000    | 0.968**  | -0.668** | 0.968**  | 0.963**  | 0.822**  | 0.972**  | 0.973**  | 0.915**  | 0.966**  | 0.959**  | 0.927**  | 0.699**  | 0.966**  |
| NSB   |       |          |          | 1.000    | -0.690** | 0.984**  | 0.984**  | 0.818**  | 0.994**  | 0.993**  | 0.941**  | 0.988**  | 0.983**  | 0.954**  | 0.697**  | 0.994**  |
| DM    |       |          |          |          | 1.000    | -0.689** | -0.663** | -0.635** | -0.698** | -0.716** | -0.648** | -0.695** | -0.723** | -0.685** | -0.430** | -0.716** |
| NSP   |       |          |          |          |          | 1.000    | 0.983**  | 0.841**  | 0.987**  | 0.991**  | 0.938**  | 0.988**  | 0.986**  | 0.954**  | 0.657**  | 0.991**  |
| LS    |       |          |          |          |          |          | 1.000    | 0.791**  | 0.993**  | 0.984**  | 0.942**  | 0.987**  | 0.970**  | 0.944**  | 0.687**  | 0.984**  |
| NSS   |       |          |          |          |          |          |          | 1.000    | 0.820**  | 0.845**  | 0.781**  | 0.828**  | 0.890**  | 0.820**  | 0.724**  | 0.853**  |
| TSW   |       |          |          |          |          |          |          |          | 1.000    | 0.995**  | 0.942**  | 0.993**  | 0.983**  | 0.951**  | 0.703**  | 0.995**  |
| BYPP  |       |          |          |          |          |          |          |          |          | 1.000    | 0.939**  | 0.994**  | 0.990**  | 0.953**  | 0.713**  | 0.997**  |
| BYP   |       |          |          |          |          |          |          |          |          |          | 1.000    | 0.935**  | 0.936**  | 0.892**  | 0.673**  | 0.944**  |
| BYH   |       |          |          |          |          |          |          |          |          |          |          | 1.000    | 0.986**  | 0.948**  | 0.692**  | 0.995**  |
| SYP   |       |          |          |          |          |          |          |          |          |          |          |          | 1.000    | 0.953**  | 0.700**  | 0.994**  |
| SYH   |       |          |          |          |          |          |          |          |          |          |          |          |          | 1.000    | 0.665**  | 0.958**  |
| HI    |       |          |          |          |          |          |          |          |          |          |          |          |          |          | 1.000    | 0.699**  |

**Table 5:** Estimation of genotypic correlation matrix for different characters in mustard genotypes  
Genotypic Correlation Matrix

| Trait | D50F  | PH       | NPB      | NSB      | DM       | NSP      | LS       | NSS      | TSW      | BYPP     | BYP      | BYH      | SYP      | SYH      | HI       | SYPP     |
|-------|-------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|
| D50F  | 1.000 | -0.545** | -0.646** | -0.679** | 0.745**  | -0.718** | -0.637** | -0.659** | -0.676** | -0.710** | -0.639** | -0.665** | -0.739** | -0.672** | -0.353*  | -0.703** |
| PH    |       | 1.000    | 0.659**  | 0.728**  | -0.349*  | 0.736**  | 0.698**  | 0.685**  | 0.707**  | 0.724**  | 0.691**  | 0.714**  | 0.755**  | 0.693**  | 0.598**  | 0.732**  |
| NPB   |       |          | 1.000    | 0.968**  | -0.631** | 0.963**  | 0.963**  | 0.820**  | 0.972**  | 0.971**  | 0.916**  | 0.966**  | 0.957**  | 0.928**  | 0.679**  | 0.966**  |
| NSB   |       |          |          | 1.000    | -0.650** | 0.979**  | 0.983**  | 0.816**  | 0.994**  | 0.991**  | 0.942**  | 0.987**  | 0.980**  | 0.954**  | 0.675**  | 0.994**  |
| DM    |       |          |          |          | 1.000    | -0.672** | -0.617** | -0.562** | -0.656** | -0.690** | -0.606** | -0.644** | -0.700** | -0.646** | -0.436** | -0.676** |
| NSP   |       |          |          |          |          | 1.000    | 0.974**  | 0.822**  | 0.981**  | 0.990**  | 0.932**  | 0.979**  | 0.986**  | 0.950**  | 0.640**  | 0.986**  |
| LS    |       |          |          |          |          |          | 1.000    | 0.793**  | 0.993**  | 0.980**  | 0.943**  | 0.987**  | 0.965**  | 0.944**  | 0.666**  | 0.983**  |
| NSS   |       |          |          |          |          |          |          | 1.000    | 0.819**  | 0.833**  | 0.782**  | 0.831**  | 0.875**  | 0.817**  | 0.684**  | 0.850**  |
| TSW   |       |          |          |          |          |          |          |          | 1.000    | 0.993**  | 0.943**  | 0.993**  | 0.980**  | 0.951**  | 0.679**  | 0.995**  |
| BYPP  |       |          |          |          |          |          |          |          |          | 1.000    | 0.937**  | 0.990**  | 0.989**  | 0.952**  | 0.694**  | 0.995**  |
| BYP   |       |          |          |          |          |          |          |          |          |          | 1.000    | 0.935**  | 0.932**  | 0.893**  | 0.650**  | 0.945**  |
| BYH   |       |          |          |          |          |          |          |          |          |          |          | 1.000    | 0.979**  | 0.947**  | 0.667**  | 0.994**  |
| SYP   |       |          |          |          |          |          |          |          |          |          |          |          | 1.000    | 0.950**  | 0.681**  | 0.992**  |
| SYH   |       |          |          |          |          |          |          |          |          |          |          |          |          | 1.000    | 0.643**  | 0.958**  |
| HI    |       |          |          |          |          |          |          |          |          |          |          |          |          |          | 1.000    | 0.676**  |

While correlation analysis offers valuable insights into character relationships, it is unable to discern between the direct and indirect effects of various traits on seed yield. Consequently, as recommended by Wright (1921), path coefficient analysis was used to divide the correlation coefficients into direct and indirect effects. Singh and Narayanan (2013) also addressed the value of path analysis in plant breeding.

According to the path coefficient analysis, the number of siliquae per plant, the number of secondary branches per plant, and the harvest index had the next greatest positive direct effects on seed yield, after biological yield per plant. These traits should be given more weight during selection in breeding programs since their high positive direct effects suggest that they have a significant impact on seed yield.

The greatest direct contribution to seed yield was shown by biological yield per plant, indicating that greater dry matter production and biomass accumulation are necessary for increased mustard productivity. Dewey and Lu (1959) [5] also reported similar results, emphasizing that traits with high positive direct effects are trustworthy selection criteria

for crop improvement.

Additionally, the number of siliquae per plant demonstrated a strong positive direct effect on seed yield, suggesting that this trait makes a significant contribution to overall productivity. The importance of secondary branches in determining yield was demonstrated by their positive direct and indirect effects on biological yield and siliquae production per plant.

Due to their correlation with other characteristics, certain traits showed indirect effects on seed yield. For instance, yield was indirectly impacted by primary branches through the production of siliquae and secondary branches. Similarly, through increased reproductive growth and biomass accumulation, plant height indirectly influenced seed yield.

The main characteristics that contribute to mustard yield are biological yield, siliquae per plant, secondary branches, and harvest index, according to the combined results of correlation and path coefficient analyses. As a result, these traits might be useful selection criteria for creating mustard genotypes with high yields.

**Table 5:** Estimation of genotypic path matrix for different characters in mustard genotypes

| Trait | D50F    | PH      | NPB     | NSB     | DM      | NSP     | LS      | NSS     | TSW     | BYPP    | BYP     | BYH     | SYP     | SYH     | HI      | SYPP      |
|-------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|-----------|
| D50F  | 0.0044  | -0.0024 | -0.0029 | -0.0030 | 0.0033  | -0.0032 | -0.0028 | -0.0029 | -0.0030 | -0.0032 | -0.0028 | -0.0030 | -0.0033 | -0.0030 | -0.0016 | -0.7026** |
| PH    | 0.0011  | -0.0020 | -0.0013 | -0.0014 | 0.0007  | -0.0014 | -0.0014 | -0.0013 | -0.0014 | -0.0014 | -0.0014 | -0.0014 | -0.0015 | -0.0014 | -0.0012 | 0.7315**  |
| NPB   | 0.0421  | -0.0429 | -0.0651 | -0.0631 | 0.0411  | -0.0627 | -0.0627 | -0.0534 | -0.0633 | -0.0633 | -0.0596 | -0.0629 | -0.0623 | -0.0604 | -0.0442 | 0.9663**  |
| NSB   | -0.1648 | 0.1766  | 0.2351  | 0.2427  | -0.1577 | 0.2375  | 0.2386  | 0.1981  | 0.2413  | 0.2405  | 0.2286  | 0.2396  | 0.2379  | 0.2315  | 0.1640  | 0.9938**  |
| DM    | -0.0130 | 0.0061  | 0.0110  | 0.0114  | -0.0175 | 0.0117  | 0.0108  | 0.0098  | 0.0115  | 0.0121  | 0.0106  | 0.0113  | 0.0122  | 0.0113  | 0.0076  | -0.6759** |
| NSP   | -0.0534 | 0.0547  | 0.0716  | 0.0728  | -0.0500 | 0.0744  | 0.0725  | 0.0611  | 0.0729  | 0.0736  | 0.0693  | 0.0728  | 0.0733  | 0.0706  | 0.0476  | 0.9860**  |
| LS    | 0.0671  | -0.0735 | -0.1014 | -0.1036 | 0.0650  | -0.1027 | -0.1053 | -0.0836 | -0.1046 | -0.1032 | -0.0993 | -0.1039 | -0.1016 | -0.0994 | -0.0702 | 0.9833**  |
| NSS   | -0.0259 | 0.0269  | 0.0323  | 0.0321  | -0.0221 | 0.0323  | 0.0312  | 0.0393  | 0.0322  | 0.0328  | 0.0308  | 0.0327  | 0.0344  | 0.0321  | 0.0269  | 0.8496**  |
| TSW   | -0.2265 | 0.2368  | 0.3253  | 0.3327  | -0.2198 | 0.3284  | 0.3322  | 0.2743  | 0.3347  | 0.3325  | 0.3156  | 0.3324  | 0.3281  | 0.3185  | 0.2274  | 0.9949**  |
| BYPP  | 0.0505  | -0.0514 | -0.0690 | -0.0704 | 0.0490  | -0.0703 | -0.0696 | -0.0592 | -0.0706 | -0.0711 | -0.0666 | -0.0703 | -0.0703 | -0.0677 | -0.0493 | 0.9951**  |
| BYP   | -0.0251 | 0.0272  | 0.0360  | 0.0371  | -0.0239 | 0.0367  | 0.0371  | 0.0308  | 0.0371  | 0.0369  | 0.0393  | 0.0368  | 0.0367  | 0.0351  | 0.0256  | 0.9447**  |
| BYH   | -0.1836 | 0.1973  | 0.2669  | 0.2728  | -0.1780 | 0.2704  | 0.2726  | 0.2295  | 0.2743  | 0.2734  | 0.2584  | 0.2763  | 0.2706  | 0.2617  | 0.1843  | 0.9936**  |
| SYP   | -0.1562 | 0.1596  | 0.2023  | 0.2072  | -0.1480 | 0.2084  | 0.2040  | 0.1850  | 0.2072  | 0.2092  | 0.1972  | 0.2071  | 0.2114  | 0.2010  | 0.1439  | 0.9919**  |
| SYH   | -0.0209 | 0.0215  | 0.0288  | 0.0296  | -0.0201 | 0.0295  | 0.0293  | 0.0254  | 0.0296  | 0.0296  | 0.0277  | 0.0294  | 0.0295  | 0.0311  | 0.0200  | 0.9580**  |
| HI    | 0.0017  | -0.0029 | -0.0032 | -0.0032 | 0.0021  | -0.0031 | -0.0032 | -0.0033 | -0.0032 | -0.0033 | -0.0031 | -0.0032 | -0.0032 | -0.0031 | -0.0048 | 0.6759**  |

**Note:** Diagonal value are direct effect values and the remaining values are indirect effect values

#### Significance Key

\* Correlation is significant at the 0.05 level ( $r \geq 0.2939$ )

\*\* Correlation is significant at the 0.01 level ( $r \geq 0.3801$ )

**Table 6:** Estimation of phenotypic path matrix for different characters in mustard genotypes

| Trait | D50F    | PH      | NPB     | NSB     | DM      | NSP     | LS      | NSS     | TSW     | BYPP    | BYP     | BYH     | SYP     | SYH     | HI      | SYPP      |
|-------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|-----------|
| D50F  | 0.0064  | -0.0039 | -0.0044 | -0.0046 | 0.0049  | -0.0047 | -0.0043 | -0.0046 | -0.0045 | -0.0047 | -0.0043 | -0.0045 | -0.0049 | -0.0045 | -0.0026 | -0.7367** |
| PH    | 0.0042  | -0.0068 | -0.0046 | -0.0051 | 0.0023  | -0.0052 | -0.0049 | -0.0049 | -0.0050 | -0.0051 | -0.0049 | -0.0050 | -0.0053 | -0.0049 | -0.0039 | 0.7524**  |
| NPB   | 0.0481  | -0.0476 | -0.0706 | -0.0683 | 0.0472  | -0.0683 | -0.0679 | -0.0580 | -0.0686 | -0.0686 | -0.0646 | -0.0682 | -0.0677 | -0.0654 | -0.0493 | 0.9661**  |
| NSB   | -0.1446 | 0.1513  | 0.1959  | 0.2024  | -0.1396 | 0.1991  | 0.1990  | 0.1655  | 0.2012  | 0.2009  | 0.1905  | 0.1999  | 0.1989  | 0.1930  | 0.1411  | 0.9937**  |
| DM    | -0.0113 | 0.0050  | 0.0098  | 0.0101  | -0.0147 | 0.0101  | 0.0097  | 0.0093  | 0.0103  | 0.0105  | 0.0095  | 0.0102  | 0.0106  | 0.0100  | 0.0063  | -0.7160** |
| NSP   | -0.0963 | 0.0987  | 0.1267  | 0.1288  | -0.0902 | 0.1309  | 0.1287  | 0.1101  | 0.1292  | 0.1297  | 0.1228  | 0.1294  | 0.1291  | 0.1249  | 0.0861  | 0.9906**  |
| LS    | 0.1002  | -0.1055 | -0.1419 | -0.1450 | 0.0977  | -0.1449 | -0.1474 | -0.1166 | -0.1464 | -0.1451 | -0.1389 | -0.1454 | -0.1430 | -0.1392 | -0.1013 | 0.9839**  |
| NSS   | -0.0061 | 0.0060  | 0.0069  | 0.0069  | -0.0053 | 0.0071  | 0.0066  | 0.0084  | 0.0069  | 0.0071  | 0.0066  | 0.0070  | 0.0075  | 0.0069  | 0.0061  | 0.8526**  |
| TSW   | -0.2682 | 0.2741  | 0.3660  | 0.3744  | -0.2631 | 0.3716  | 0.3740  | 0.3090  | 0.3767  | 0.3749  | 0.3548  | 0.3742  | 0.3704  | 0.3582  | 0.2647  | 0.9949**  |
| BYPP  | 0.0595  | -0.0600 | -0.0789 | -0.0804 | 0.0580  | -0.0803 | -0.0797 | -0.0684 | -0.0807 | -0.0810 | -0.0761 | -0.0806 | -0.0802 | -0.0773 | -0.0578 | 0.9966**  |
| BYP   | -0.0222 | 0.0234  | 0.0301  | 0.0309  | -0.0213 | 0.0308  | 0.0310  | 0.0257  | 0.0310  | 0.0309  | 0.0329  | 0.0307  | 0.0308  | 0.0293  | 0.0221  | 0.9442**  |
| BYH   | -0.1551 | 0.1611  | 0.2116  | 0.2162  | -0.1521 | 0.2163  | 0.2159  | 0.1813  | 0.2174  | 0.2176  | 0.2046  | 0.2189  | 0.2157  | 0.2074  | 0.1514  | 0.9945**  |
| SYP   | -0.2304 | 0.2343  | 0.2908  | 0.2980  | -0.2191 | 0.2989  | 0.2941  | 0.2698  | 0.2981  | 0.3000  | 0.2837  | 0.2988  | 0.3032  | 0.2887  | 0.2120  | 0.9944**  |
| SYH   | -0.0184 | 0.0186  | 0.0242  | 0.0249  | -0.0179 | 0.0249  | 0.0246  | 0.0214  | 0.0248  | 0.0249  | 0.0233  | 0.0247  | 0.0249  | 0.0261  | 0.0174  | 0.9577**  |
| HI    | -0.0026 | 0.0037  | 0.0045  | 0.0045  | -0.0028 | 0.0042  | 0.0044  | 0.0047  | 0.0045  | 0.0046  | 0.0043  | 0.0045  | 0.0045  | 0.0043  | 0.0064  | 0.6987**  |

**Note:** Diagonal value are direct effect values and the remaining values are indirect effect values

Under the agro-climatic conditions of Dehradun during the Rabi season of 2024-2025, the current study found significant variation among the fifteen mustard genotypes

for growth, yield, and yield-attributing characters. Significant genetic diversity among the genotypes was revealed by the analysis of variance, indicating plenty of

room for efficient selection and crop improvement. Recent studies by Meena *et al.* (2019)<sup>[9]</sup>, Kumar *et al.* (2020)<sup>[8]</sup>, Patel *et al.* (2021)<sup>[11]</sup>, and Rathore *et al.* (2022)<sup>[12]</sup> have also reported similar findings about the existence of significant variability in Indian mustard. Wide genetic variability is thought to be necessary for successful plant breeding because it makes it possible to find superior genotypes with desired agronomic traits.

The check variety DDN1 demonstrated comparatively stable performance for the majority of the traits among the assessed genotypes, making it a helpful benchmark for comparison. Under local environmental conditions, the Dehradun genotypes DDN2, DDN3, DDN4, DDN5, and DDN6 demonstrated moderate to good adaptability. In contrast, DDN4 and DDN5 showed favourable genetic potential for yield improvement in terms of vegetative growth, branching pattern, siliquae production, and seed yield. Additionally, the Doiwala region's genotype DWH1 demonstrated robust plant growth and adequate siliquae production, indicating good biomass accumulation and adaptability.

BHP1 and BHP2, which were collected from Bharatpur, outperformed all other genotypes examined in a number of economically significant traits, including the number of secondary branches, siliquae per plant, biological yield, harvest index, and seed yield. Due to its improved overall yield performance and reproductive efficiency, BHP1 in particular emerged as the top-performing genotype, suggesting its suitability for upcoming breeding initiatives. Yadava *et al.* (2020)<sup>[16]</sup> and Chandra *et al.* (2020)<sup>[4]</sup> reported similar results regarding superior genotype performance and adaptability in mustard. Although its yield performance remained moderate, the Ajmer genotype AJM1 showed early flowering and maturity, making it useful for breeding programs aimed at developing short-duration varieties. Under Dehradun conditions, the Patna-origin genotypes PAM1 and PAM2 also showed satisfactory adaptability, with PAM2 exhibiting relatively better siliquae formation and seed development. Similarly, VKN2 from Vikasnagar demonstrated superior siliquae production and secondary branching, suggesting its value as a donor parent for branching-related traits.

For the majority of characters, the estimates of the phenotypic coefficient of variation (PCV) were marginally higher than the corresponding genotypic coefficient of variation (GCV), suggesting that the influence of the environment on trait expression was minimal. The number of siliquae per plant, biological yield, harvest index, and seed yield, on the other hand, showed relatively small differences between PCV and GCV, indicating that these traits were primarily controlled by genetic factors. Verma *et al.* (2018)<sup>[15]</sup> and Meena *et al.* (2022)<sup>[10]</sup>, who noted significant yield traits in mustard with high genetic variability and relatively little environmental influence, also reported similar findings.

The number of secondary branches, siliquae per plant, biological yield, harvest index, and seed yield per plant all showed high heritability and high genetic advancement as a percentage of mean. These results suggested that direct phenotypic selection for these traits would be successful in increasing yield potential and demonstrated the predominance of additive gene action. Kumar *et al.* (2020)<sup>[8]</sup>, Patel *et al.* (2021)<sup>[11]</sup>, and Saini *et al.* (2021)<sup>[13]</sup> reported similar findings, emphasizing that traits with high

heritability and genetic advancement offer greater chances for successful selection in mustard breeding programs.

According to correlation analysis, biological yield, the number of siliquae per plant, the number of primary and secondary branches, the number of seeds per silique, and the harvest index were all strongly positively correlated with seed yield per plant. The strongest positive correlation between biological yield and seed yield among these characteristics highlights the significance of biomass accumulation in raising productivity. Meena *et al.* (2019)<sup>[9]</sup>, Saini *et al.* (2021)<sup>[13]</sup>, and Rathore *et al.* (2022)<sup>[12]</sup> have also reported similar positive associations between yield and yield-contributing traits.

The number of siliquae per plant, the number of secondary branches per plant, and the harvest index all had strong positive direct effects on seed yield, according to path coefficient analysis. This suggests that these characteristics are the main factors that determine productivity and should be given more weight during selection. Through their effects on biomass accumulation and siliquae production, primary and secondary branches also indirectly contributed to seed yield. Chandra *et al.* (2020)<sup>[4]</sup> and Rathore *et al.* (2022)<sup>[12]</sup> reported similar results emphasizing the significance of siliquae number and branching traits as trustworthy selection criteria.

Overall, the current study showed that there is significant genetic variation among mustard genotypes for crucial growth and yield characteristics. The superior performance of genotypes like BHP1, BHP2, DDN4, DDN5, DWH1, and VKN2 suggested their potential utility in upcoming mustard improvement initiatives targeted at creating high-yielding and adaptable varieties for a range of agroclimatic conditions. In mustard breeding programs, traits with high heritability, high genetic advancement, strong positive correlation, and high direct effects on seed yield may be used as dependable selection criteria.

#### 4. Conclusion

The current study, "Assessment of Genetic Variability and Character Association in Mustard (*Brassica juncea* L.)," found significant genetic variation among the fifteen mustard genotypes examined in Dehradun's agroclimatic conditions during the Rabi season of 2024-2025. For each of the sixteen quantitative characters, the analysis of variance revealed significant genotype differences, indicating that there is enough variability to be effectively used in future mustard improvement initiatives. Plant breeders have more opportunities to find superior genotypes and create high-yielding varieties through selection and hybridization programs because of the genotype's wide genetic variation. For the majority of the characters, the estimates of the phenotypic coefficient of variation (PCV) were marginally higher than the corresponding genotypic coefficient of variation (GCV), suggesting some degree of environmental influence on trait expression. Nonetheless, the relatively small differences between PCV and GCV for a number of significant characteristics indicated that genetic factors were primarily responsible for these traits. For significant yield-contributing traits like the number of siliquae per plant, the number of secondary branches per plant, the biological yield per plant, the seed yield per plant, and the harvest index, high heritability and high genetic advancement as a percentage of mean were noted. This suggested that direct phenotypic selection for these traits would be very

successful in increasing mustard productivity and demonstrated the predominance of additive gene action. Significant variations in growth and yield characteristics among the tested materials were found in the mean performance analysis of various genotypes. The majority of the economically significant characteristics, such as plant height, number of branches, siliquae production, biological yield, seed yield, and test weight, showed superior performance for BHP1 among the genotypes assessed, suggesting its high yield potential and adaptability under Dehradun conditions. Genotypes like DWH1, DDN4, and BHP2 may be useful genetic resources for upcoming breeding initiatives because they also showed encouraging performance for a number of yield-related traits. Important yield-contributing characteristics, including biological yield per plant, number of siliquae per plant, number of secondary branches, seeds per silique, and harvest index, showed a strong positive correlation with seed yield, according to correlation analysis. These correlations implied that enhancing these constituent traits might indirectly lead to an increase in seed yield. Additionally, path coefficient analysis revealed that secondary branches, biological yield, and the number of siliquae per plant all had significant positive direct effects on seed yield, underscoring their significance as trustworthy selection criteria in mustard breeding programs. Overall, the results of this study indicated that there is enough genetic variation among the mustard genotypes under study for efficient crop improvement and selection. In order to create superior high-yielding mustard varieties, traits with high heritability, high genetic advance, positive correlation, and strong direct effects on seed yield may be used as selection criteria. Breeding Oilseed Crops for Sustainable Production has also highlighted the significance of improving oilseed crops (Gupta, 2009) [6]. These results are consistent with the biometrical research described by Hanson *et al.* (1956). Future breeding programs aiming at enhancing productivity, adaptability, and yield stability in mustard under various agroclimatic conditions can further utilize the superior genotypes found during the study, especially BHP1 and other promising lines.

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