**Assessment of Genetic Variability and Heritability in Indian Mustard (*Brassica juncea* L.) Genotypes**

**ABSTRACT**

The present study was undertaken to assess genetic variability and divergence among 42 genotypes sourced from AICRP on Rapeseed and Mustard, ZARS, Morena of Indian mustard (*Brassica juncea* L.) under field conditions at the Zonal Agricultural Research Station, Morena, Madhya Pradesh, during *Rabi* 2020–21. The experimental was laid out in a randomized block design with three replications, twelve agronomic traits were evaluated, including phenological, morphological, and yield-related characters. The results revealed that significant genotypic differences were observed for all traits, highlighting substantial variability within the studied genotypes. Notably, genotypic and phenotypic coefficients of variation were moderate to high for key traits such as secondary branches per plant (23.709 and 23.758, respectively), seed yield per plant (15.846 and 15.857, respectively), test weight (15.539 and 15.635, respectively), and siliqua length (11.198 and 15.582, respectively). High heritability (>60%) coupled with high genetic advance was recorded for several traits, including seed yield per plant (99.85%, 32.61%, respectively), indicating the predominance of additive gene action and scope for effective selection. Traits such as plant height, test weight, number of secondary branches, and siliqua length also exhibited promising genetic parameters. These findings suggest that seed yield and its contributing traits could serve as reliable selection indices in mustard breeding programs, providing valuable insights for the development of improved cultivars with higher productivity and desirable agronomic characteristics.

**Keywords:** Genetic variability, Heritability, *Brassica juncea* L., Genotypic diversity, Morphological traits, Genetic advance

**1. INTRODUCTION**

Indian mustard (*Brassica juncea* L.) is a naturally autogamous plant, outcrossing occurs frequently in this crop, ranging from 5 to 30 percent depending on climatic condition and the random diversity of pollinating insects. Indian mustard is an amphidiploid (2n=36) developed from an interspecific cross of *Brassica campestris* (2n=20) and *Brassica nigra* (2n=16), followed by natural chromosomal doubling. The seeds are used as medicine, spices, and as ingredients in salads, juices, curries, and pickles. The mustard plant is primarily cultivated for oil, and the cake produced after oil extraction is frequently utilised for cow feed. Mustard seeds contain 39 to 44 percent oil and 38 to 41 percent protein (Tomar *et al.,* 2015). Indian mustard is a major winter oil seed crop in India. India is the third largest producer of rapeseed-mustard (*Brassica* spp.) after Canada, China and contributing to around 14 % of world’s total production. Rapeseed-mustard are the important oilseed crops and also one of the second largest oilseed crops in India. Rapeseed mustard production has been expanding rapidly in a number of nations throughout the world. Of the total area and production under the nine oilseeds crops grown in India, rapeseed-mustard accounts for 30.3% of the acreage and 33.2% of the production (Anonymous, 2024). With the production of 13.2 million tons during 2023-24, rapeseed-mustard became the first largest oilseed crop in India. the average rapeseed-mustard yield is about 1443 kg/ha compared to the combined oilseeds crops average of 1314 kg/ha (2023-24). Although rapeseed-mustard is cultivated in majority of states of the country, bulk of the production comes from Rajasthan (45.40 %), Madhya Pradesh (13.28%) Uttar Pradesh (14.24 %) Haryana (10.78%),and West Bengal (6.0 %) during (Anonymous, 2024). Despite available yield-enhancing technologies, the area under cultivation remains static.

Understanding the factors responsible for high yield is challenging, as yield is a complex trait influenced by multiple interacting components. To enhance yield effectively, breeders must break down this complexity by focusing on individual yield components, even when they are negatively correlated. This requires a clear understanding of the nature and strength of relationships among these components, as well as insight into how both qualitative and quantitative traits contribute to overall yield Paroda and Joshi (1970) and Lush (1949). The research of genetic progress is also essential since it measures genetic gain based on selection in a certain character. As a result, the study of genetic variability and heritability, as well as genetic advance, is required for every crop development programme based on selection and hence, the present study was conducted with the objective to assess the Genetic Variability and Heritability in different genotypes of Indian Mustard (*Brassica juncea* L.).

**2. MATERIALS AND METHODS**

The present investigation was carried in the assigned experimental field of Mustard at Zonal Agriculture Research Station, Morena, Madhya Pradesh, during *Rabi* 2020-21. A total of 42 mustard genotypes sourced from AICRP on Rapeseed and Mustard, ZARS, Morena were evaluated using a Randomized Block Design (RBD) with three replications. All the genotypes were raised with good plant health by following recommended package of practices. The net plot area of the replicated plots was 0.6 m x 4.0 m maintaining the spacing of 30 cm (row to row) and 10 cm (plant to plant).

**2.1 Observations recorded:**

Evaluation of genetic variability and divergence of different traits of mustard was carried out.Observations were recorded on the ten plants of each of the plots for twelve characters *viz.,* days to 50% flowering, days to maturity, plant hight (cm), number of primary branches per plant, number of secondary branches per plant, length of main raceme (cm), number of siliquae on main raceme, number of seeds per siliquae, siliquae length (cm), test weight (g), biological yield (g/plot) and seed yield per plant (g) were worked out and the data was tabulated.

**2.2 Statistical analysis:**

The mean values of varieties in each replication were used for statistical analysis. The data were analysed for a randomized block design to test the significance of differences between the genotypes for various characters by calculating the Critical Difference (C.D.) and Standard Error of means (S.E.m) as described by Panse and Sukhatme (1967). Further, Genotypic, Phenotypic and Error variance were calculated as per the given formulae:

Genotypic variance (σ²g) = (MSt/MSe)/r

Phenotypic variance (σ²p) = σ²g + σ²e Error variance (σ²e) = MSe

Where, MSe = Mean sum square of error; MSt = Mean sum square of treatments; r = No. of replications.

For further calculations, Heritability in broad sense h² (b) was computed as a ratio of genotypic variance to phenotypic variance as described by (Allard, 1960).

h2 (b) = x 100

Where, h² (b) = Heritability in broad sense; σ²g = Genotypic variance; σ²p = Phenotypic variance

The expected Genetic Advance (G.A.) under selection for the different characters was estimated as suggested by Allard (1960).

G.A. = h² (b) × σp × k

Where, h² (b) = Heritability in broad sense; σp = Phenotypic standard deviation (); k = Intensity of selection, the value of which is 2.06 when 5 percent of the individual are selected from the population as given by Lush (1949).

Genetic advance as percent of means for each character was calculated as suggested by Johnson *et al.,* (1955).

G.A.(%) = x 100

**3. RESULTS AND DISSCUSION**

The mean performance of forty-two mustard varieties observed for twelve different characters studied along with their range and critical differences are presented in Table 1. The present investigation of 42 mustard varieties revealed significant genotypic variation across twelve agronomic traits. Days to 50% flowering varied from 42.48 (L-4) to 62.79 (Varuna), and days to maturity ranged from 120.67 (PM-25) to 141.33 (RVM-1). Plant height ranged between 158.14 cm (PM-27) and 225.89 cm (PDZM-31), while the number of primary and secondary branches per plant ranged from 3.74 (RVM-3) to 7.42 (Albeli) and 4.47 (RGN-73) to 15.37 (RH-749), respectively. The main raceme length varied from 55.59 cm (Pusa Jagannath) to 74.56 cm (L-4), and siliquae per raceme ranged from 46.56 (RVM-12-1-18) to 56.15 (L-4). Seeds per siliqua ranged from 12.91 (Maya) to 17.59 (RGN-73), with siliqua length ranging from 4.25 cm (L-4) to 6.49 cm (Albeli). Test weight ranged from 3.66 g (RMM-12-2-18) to 7.24 g (RH-749). Biological yield ranged from 62.23 g/plot (RMM-12-1-18) to 71.43 g/plot (Krishna), while seed yield per plant varied from 14.42 g/plot (PM-27) to 28.31 g/plot (Pusa Bold). These findings indicate significant genetic variation among mustard genotypes, indicating a broad genetic base that can be efficiently used in breeding operations. This diversity provides useful information for selecting superior genotypes and accelerates mustard genetic improvement for desirable features. High amount of genetic variability for many of these traits has also been reported earlier by Uddin *et al.* (1995) revealed high genotypic and phenotypic coefficients of variation for seed weight, seeds per siliquae, biological yield, oil content, secondary branches per plant and seed yield per plant. Yadav *et al.* (2011), Singh *et al.* (2013) and Shekhawat *et al.* (2014) also reported the similar results as described in the results.

Results from the present study (Table 2) in this context indicated that no genotypic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV) were high (>25%). Further GCV and PCV were moderate (10-25%) for number of secondary branches per plant (23.709 and 23.758), seed yield per plant (15.846 and 15.857), test weight (15.539 and 15.635), number of primary branches per plant (14.273 and 14.433), siliqua length (11.198 and 11.582), and low (<10%) for days to 50% flowering (8.688 and 8.738), plant height (7.723 and 7.726), number of seeds per siliqua (6.846 and 6.991), length of main raceme (6.259 and 6.266), number of siliqua on main raceme (4.531 and 4.537), biological yield (3.977 and 4.011 g/plot) and number of maturity days (3.884 and 3.910). Further, the present findings showed that estimates of PCV were generally higher than their corresponding GCV for all the character studied. Furthermore, the current data revealed that PCV estimations were significantly greater than the corresponding GCV for all of the characters tested. These findings are in agreement with the studies as reported by Kumari and Kumari (2018) who revealed that highly significant genotypic differences were found in the combined analysis of variance for number of days to flower initiation, crop plant height, number of days to 50 per cent flowering, length of the siliquae, number of days to 75% maturity, test weight and harvest index, to authenticate the probability of building up these characters through breeding program. Yadav *et al*. (2012), Yohannes and Belete (2013), Singh *et al*. (2013), Shekhawat *et al*. (2014) and Bibi *et al*. (2016) also reported the similar results as described in the results.

Most of the character under studied observed high heritability (>60%) *viz.,* for plant height (99.93%), seed yield per plant (99.85%), length of main raceme (99.78%), number of siliquae on main raceme (99.71%), number of secondary branches per plant (99.59%), days to 50% flowering (98.85%), test weight (98.77%), number of seed per siliquae (98.69%), number of maturity days (98.64%), biological yield (98.31%), number of primary branches per plant (97.79%) and siliqua length (93.48%) (Table 2). In line with the present results, Singh *et al*. (2011) also reported the relationship between heritability and GA. Goyat *et al.* (2012) and Singh *et al.* (2013) described this interaction in relation to Indian mustard. Shekhawat *et al.* (2014) also reported the similar results as described in the results. Gadi *et al*. (2020) investigated how variation, heritability in a wide sense, and anticipated genetic progress in germplasm will aid in determining the genotype's true potential. Hence, the current investigation was intended to determine the variability, heritability in broad sense and estimated genetic advance for crop output and other crop traits among the varieties. The high heritability indicates a significant share of genetic factors in the determination of these characteristics, which may be used to improve seed production. Similar supporting results were also reported in previous studies conducted at various parts by Upadhyay and Kumar (2009), Ram and Verma (2010).

Expected genetic advance expressed as percentage of mean (Table 2) was exhibited high (>20%) for number of secondary branches per plant (48.73), seed yield per plant (32.61), test weight (31.81), number of primary branches per plant (29.07) and siliquae length (22.30). Moderate GA (10-20%) was observed for days to 50% flowering (17.79), plant height (15.90), number of seed per siliquae (14.00) and length of main raceme (12.87). Low GA (<10%) was noted for number of siliquae on main raceme (9.31), biological yield (8.12) and number of maturity days (7.94). In the present investigation, high heritability coupled with high genetic advance observed for plant height, days to maturity, length of main raceme, number of siliquae on main raceme and seed yield per plant. Sarvesh *et al.* (2018) reported moderate to high level of genotypic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV). In general, phenotypic coefficient of variance was found to be higher than their genotypic coefficient of variance but the extent was quite small, indicating very less environmental influence on the expression of the characters. Genotypic coefficient of variation (GCV) was found to be higher for 1000-seed weight (24.33), biological yield per plant (22.47), secondary branches plant (22.41), seed yield per plant (19.75). Heritability and genetic advance are important selection parameters. Gadi *et al.* (2020) reported that variability in different varieties, heritability within the genotypes and estimated genetic advance in germplasm will help to investigate the actual potential of the varieties. Singh *et al.* (2012), Yohannes and Belete (2013) and Shekhawat *et al.* (2014) also reported the similar results as described in the results.

**4. CONCLUSION**

Genetic variability of the forty-two varieties among the twelve different characters suggests that all characters *viz.,* days to 50% flowering, number of maturity days, height of plant, primary branches plant-1, secondary branches plant-1, main raceme length, siliquae on major raceme, seeds siliquae-1, length of siliquae, test weight, biological yield per plant and seed yield per plant can be relied upon direct selection for further improvement. High heritability coupled with high genetic advance were observed for the characters under study revealed that the characters undergo the influence of additive gene action. Seed yield per plant exhibiting significant stable and positive correlation with the characters. Biological yield per plant displayed high order of direct effect on seed yield per plant. All these results indicate that they can be considered as guidelines for further selection programmes.

Disclaimer (Artificial intelligence)

Option 1: Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, manuscript.

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**Table 1: Mean performance of forty-two mustard genotypes for twelve characters.**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **S. No.** | **Genotypes** | **Days to 50% Flowering** | **Days to maturity** | **Plant height (cm)** | **Number of primary branches/ plant** | **Number of secondary branches/ plant** | **Length of main raceme (cm)** | **Number of siliquae on main raceme** | **Number of seed per siliquae** | **Siliquae length (cm)** | **Test weight (g)** | **Biological yield**  **(g/ plot)** | **Seed yield per plant (g)** |
| 1 | **Pusa Bold** | 54.820 | 123.333 | 186.130 | 5.920 | 13.350 | 59.230 | 51.120 | 14.340 | 4.340 | 4.530 | 68.520 | 28.360 |
| 2 | **Varuna** | 62.787 | 125.000 | 208.610 | 5.640 | 8.540 | 63.560 | 53.230 | 15.420 | 5.700 | 5.030 | 64.530 | 25.060 |
| 3 | **Rohini** | 51.050 | 121.333 | 204.970 | 4.780 | 7.230 | 55.850 | 51.430 | 14.520 | 6.480 | 4.650 | 63.450 | 17.900 |
| 4 | **Kranti** | 47.350 | 125.333 | 215.390 | 5.690 | 13.350 | 58.740 | 50.240 | 15.440 | 5.270 | 4.220 | 64.230 | 15.450 |
| 5 | **Krishna** | 53.550 | 135.000 | 213.770 | 6.710 | 14.650 | 63.530 | 52.330 | 15.630 | 4.860 | 4.020 | 71.430 | 23.700 |
| 6 | **Maya** | 48.907 | 132.667 | 210.387 | 6.267 | 9.910 | 64.580 | 52.920 | 12.907 | 4.340 | 6.163 | 66.580 | 24.260 |
| 7 | **Vardan** | 47.653 | 130.000 | 208.640 | 6.463 | 11.687 | 72.433 | 55.300 | 15.557 | 5.273 | 5.430 | 65.247 | 26.303 |
| 8 | **Vasundhara** | 47.467 | 134.333 | 216.187 | 5.420 | 10.613 | 68.263 | 52.303 | 14.440 | 4.417 | 4.340 | 68.593 | 21.427 |
| 9 | **Swarnjyoti** | 45.500 | 130.667 | 194.077 | 4.883 | 8.770 | 63.477 | 50.693 | 17.270 | 4.597 | 6.230 | 65.010 | 19.310 |
| 10 | **Pusa Jagannath** | 53.533 | 132.000 | 209.540 | 5.410 | 7.650 | 55.587 | 47.687 | 16.383 | 5.633 | 6.233 | 64.857 | 18.743 |
| 11 | **Pusa Mahak** | 52.517 | 130.000 | 212.773 | 5.587 | 11.480 | 60.617 | 52.370 | 14.127 | 5.540 | 4.820 | 63.627 | 20.287 |
| 12 | **Pusa Jaikisan** | 50.630 | 126.000 | 217.960 | 5.680 | 14.767 | 62.117 | 51.440 | 15.400 | 4.433 | 6.250 | 64.560 | 21.640 |
| 13 | **Albeli** | 49.860 | 123.333 | 191.870 | 7.417 | 11.797 | 59.823 | 51.553 | 15.280 | 6.493 | 4.313 | 68.267 | 21.440 |
| 14 | **Sej 2** | 49.837 | 130.667 | 217.880 | 5.303 | 11.567 | 63.767 | 51.113 | 15.323 | 5.617 | 4.693 | 71.070 | 21.350 |
| 15 | **Shraddha** | 54.227 | 135.667 | 192.280 | 6.543 | 14.610 | 69.797 | 53.330 | 16.297 | 4.490 | 5.460 | 68.420 | 26.607 |
| 16 | **L-4** | 42.483 | 140.000 | 217.470 | 5.787 | 14.877 | 74.557 | 56.153 | 16.273 | 4.250 | 7.050 | 64.023 | 27.507 |
| 17 | **L-6** | 49.597 | 125.000 | 207.677 | 5.620 | 14.670 | 68.653 | 53.127 | 14.617 | 4.727 | 6.233 | 68.953 | 24.310 |
| 18 | **JMWR-908-1** | 43.743 | 130.333 | 212.837 | 5.697 | 14.647 | 60.427 | 52.417 | 15.643 | 5.613 | 6.227 | 68.423 | 23.097 |
| 19 | **RGN-73** | 43.993 | 129.333 | 210.970 | 5.723 | 4.473 | 62.510 | 53.497 | 17.593 | 4.830 | 5.457 | 68.550 | 23.373 |
| 20 | **NRCHB-101** | 47.477 | 125.000 | 225.390 | 5.450 | 10.633 | 58.483 | 51.377 | 14.293 | 4.297 | 5.650 | 62.960 | 21.493 |
| 21 | **RVM-3** | 48.790 | 129.333 | 205.750 | 3.740 | 7.163 | 61.457 | 51.307 | 15.230 | 4.530 | 5.243 | 63.440 | 20.683 |
| 22 | **RH-406** | 43.977 | 132.000 | 168.397 | 4.387 | 6.640 | 62.667 | 53.423 | 16.337 | 5.690 | 5.693 | 62.413 | 23.483 |
| 23 | **RH-749** | 48.007 | 133.667 | 202.813 | 5.440 | 15.367 | 60.717 | 50.407 | 16.410 | 5.293 | 7.237 | 63.217 | 20.403 |
| 24 | **Giriraj** | 49.033 | 131.333 | 218.663 | 5.563 | 11.450 | 60.297 | 50.537 | 16.303 | 4.517 | 5.170 | 64.700 | 19.517 |
| 25 | **JM-1** | 45.290 | 131.000 | 202.517 | 5.373 | 9.620 | 63.733 | 53.337 | 14.423 | 5.150 | 4.657 | 68.653 | 24.503 |
| 26 | **JM-2** | 44.727 | 134.000 | 185.947 | 7.330 | 13.250 | 62.403 | 52.247 | 15.423 | 5.503 | 5.347 | 69.687 | 22.490 |
| 27 | **JM-3** | 44.907 | 125.333 | 199.713 | 5.313 | 11.433 | 64.280 | 53.177 | 14.323 | 5.123 | 5.967 | 62.693 | 23.613 |
| 28 | **RVM-1** | 48.160 | 141.333 | 205.530 | 5.293 | 9.593 | 62.417 | 50.230 | 15.393 | 5.417 | 6.250 | 69.997 | 20.580 |
| 29 | **RVM-2** | 44.207 | 140.667 | 166.357 | 5.427 | 14.940 | 63.570 | 54.407 | 13.707 | 5.333 | 5.323 | 65.233 | 25.577 |
| 30 | **PM-25** | 45.833 | 120.667 | 208.797 | 6.393 | 9.567 | 64.020 | 54.367 | 15.437 | 5.670 | 5.430 | 67.730 | 24.530 |
| 31 | **PM-26** | 49.017 | 132.000 | 196.570 | 5.590 | 14.747 | 61.690 | 52.313 | 17.260 | 5.383 | 5.340 | 69.497 | 22.427 |
| 32 | **PM-27** | 43.700 | 131.333 | 158.143 | 4.353 | 9.517 | 59.313 | 46.993 | 16.367 | 4.490 | 5.003 | 68.500 | 14.417 |
| 33 | **PM-28** | 48.317 | 137.333 | 186.113 | 4.597 | 8.437 | 60.263 | 52.777 | 16.183 | 4.510 | 5.177 | 69.710 | 18.330 |
| 34 | **PM-30** | 45.237 | 131.000 | 209.280 | 6.583 | 10.743 | 58.680 | 48.353 | 16.327 | 4.637 | 5.243 | 65.683 | 17.350 |
| 35 | **Pusa Vijay** | 46.523 | 129.000 | 210.500 | 5.720 | 10.530 | 58.660 | 47.187 | 14.433 | 5.683 | 5.120 | 65.643 | 14.493 |
| 36 | **PDZM-31** | 48.543 | 133.000 | 225.893 | 5.660 | 12.700 | 59.447 | 48.337 | 14.337 | 5.313 | 4.357 | 62.983 | 16.333 |
| 37 | **JMM-927** | 43.770 | 132.000 | 205.203 | 5.560 | 13.883 | 65.290 | 55.290 | 14.220 | 4.643 | 5.817 | 67.317 | 24.303 |
| 38 | **JMM-991** | 56.760 | 135.000 | 220.130 | 5.230 | 12.750 | 64.360 | 50.270 | 15.360 | 5.427 | 4.030 | 68.560 | 20.520 |
| 39 | **RMM-10-1-1** | 55.720 | 134.333 | 203.190 | 4.430 | 14.030 | 59.630 | 48.330 | 16.220 | 5.480 | 4.520 | 65.330 | 26.650 |
| 40 | **RMM-12-1-18** | 52.010 | 122.333 | 173.810 | 4.260 | 11.530 | 62.940 | 46.560 | 14.720 | 4.590 | 4.240 | 62.230 | 24.760 |
| 41 | **RMM-12-2-18** | 50.280 | 126.333 | 217.650 | 4.520 | 10.550 | 64.960 | 53.480 | 15.240 | 4.280 | 3.660 | 64.230 | 18.460 |
| 42 | **RMM-12-3-18** | 53.140 | 125.000 | 197.550 | 5.450 | 9.560 | 65.760 | 54.670 | 17.560 | 4.840 | 5.160 | 63.180 | 21.330 |
| **Mean** | | **48.879** | **130.310** | **203.412** | **5.529** | **11.364** | **62.680** | **51.705** | **15.428** | **5.064** | **5.262** | **66.236** | **21.818** |
| **Range** | | **42.483-62.787** | **120.66-141.333** | **158.143- 225.893** | **3.740-7.417** | **4.473-15.367** | **55.587-74.557** | **46.560-56.153** | **12.907- 17.593** | **4.250-6.493** | **3.660- 7.237** | **62.230- 71.430** | **14.417- 28.360** |
| **SEm ±** | | **0.456** | **0.595** | **0.415** | **0.118** | **0.173** | **0.181** | **0.123** | **0.122** | **0.150** | **0.091** | **0.345** | **0.132** |
| **C.D. at 5%** | | **1.286** | **1.673** | **1.188** | **0.332** | **0.487** | **0.514** | **0.354** | **0.342** | **0.421** | **0.256** | **0.972** | **0.371** |

**Table 2: Estimates of variability parameters for twelve characters in mustard (*Brassica juncea*) varieties.**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Sr. No.** | **Characters** | **GCV (%)** | **PCV (%)** | **Heritability (%) (Broad sense)** | **Genetic Advance** | **Genetic Advance**  **(% of Mean)** |
| **1** | Days to 50% Flowering | 8.688 | 8.738 | 98.85 | 8.697 | 17.79 |
| **2** | Days to maturity | 3.884 | 3.910 | 98.64 | 10.353 | 7.94 |
| **3** | Plant height (cm) | 7.723 | 7.726 | 99.93 | 32.350 | 15.90 |
| **4** | Number of primary branches/ plants | 14.273 | 14.433 | 97.79 | 1.600 | 29.07 |
| **5** | Number of secondary branches/ plants | 23.709 | 23.758 | 99.59 | 5.538 | 48.73 |
| **6** | Length of main raceme (cm) | 6.259 | 6.266 | 99.78 | 8.072 | 12.87 |
| **7** | Number of siliquae on main raceme | 4.531 | 4.537 | 99.71 | 4.818 | 9.31 |
| **8** | Number of seed per siliquae | 6.846 | 6.891 | 98.69 | 2.161 | 14.00 |
| **9** | Siliquae length (cm) | 11.198 | 11.582 | 93.48 | 1.129 | 22.30 |
| **10** | Test weight (g) | 15.539 | 15.635 | 98.77 | 1.673 | 31.81 |
| **11** | Biological yield | 3.977 | 4.011 | 98.31 | 5.380 | 8.12 |
| **12** | Seed yield per plant (g) | 15.846 | 15.857 | 99.85 | 7.116 | 32.61 |

GCV: Genotypic Coefficients of Variation; PCV: Phenotypic Coefficients of Variation