**Genetic Variability, Heritability, Correlation and Path Analysis of Quantitative Traits in Indian Mustard (*Brassica juncea* L.)**

**Abstract**

The present study assesses the genetic variability, correlation coefficient, heritability and path analysis for quantitative traits in Indian mustard (*Brassica juncea* L.). High heritability coupled with high genetic advance was found for seed yield per plot, seed yield per plant, number of siliqua per plant, and test weight, suggesting due importance of these traits for selection in a breeding program. The phenotypic correlation studies revealed that seed yield per plant exhibited a significant positive correlation with plant height, number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, siliqua length, seeds per siliqua and test weight. The experiment was conducted to derive information on genetic variability, heritability and genetic advance gain in twelve genotypes of mustard (*Brassica juncea* L.) during rabi season of 2023-2024 at the field experimentation centre (Pilikothi) of the department of Genetics and Plant Breeding, Tilak Dhari Post Graduate College Jaunpur Uttar Pradesh, India. All the genotypes were grown in a Randomized Block Design with 3 replications during Winter season. Plant to Plant and Row to Row distance is maintained at 15 cm. and 30 cm. respectively. The data were statistically analyzed for computation of genetic coefficient of variation using appropriate statistical analysis. ANOVA was carried out as per the procedure given. The phenotypic and genotypic coefficient of variance was estimated [2] and heritability in broad sense was estimated as per formula given. The expected genetic advance was calculated by using formula as suggested. In the experiment, analysis of variance showed significant differences among the genotypes for all the characters indicating the existence of a wide spectrum of variability among the genotypes. The phenotypic coefficient of variation (PCV) was higher than the corresponding genotypic coefficient of variation (GCV). The highest estimates (>20%) phenotypic coefficient of variability (29.89%) and genotypic coefficient of variability (29.776%) were recorded for number of secondary branches per plant followed by number of siliquae per plant. The lowest estimates (<5%) PCV (4.178%) and GCV (3.177%) were observed for days of 50% flowering. Grain yield per plant (g), length of main raceme (cm), number of primary branches per plant, number of seeds per siliquae, and 1000-seed weight showed high estimates (<20->10) of PCV and GCV. Days to maturity, plant height (cm), showed a moderate estimate (<10->5%) of phenotypic and genotypic coefficient of variability. Days to 50% flowering showed lower values of phenotypic (PCV) and genotypic coefficients of variability. The higher estimates of heritability in broad sense(>75%) were recorded for number of siliquae per plant followed by plant height (cm), number of secondary branches per plant, 1000-seed weight (g), number of primary branches per plant, length of main raceme, days to maturity, seed yield per plant and number of seed per siliquae characters (in percentage) 91.45, 99.25, 96.10, 91.57, 91.09, 98.54, 71.00 and 88.23 respectively. Comparatively low estimate of heritability (<75) observed for days to 50% flowering (57.83). Seed yield per plant showed high estimates(>20%) of genetic advance in % of mean (27.43%) followed by number of primary branches per plant (28.23%), length of main raceme (24.48%), number of siliquae per plant(47.15), number of seeds per siliquae (22.761),1000-seeds weight (30.06) and moderate estimates (<20->5%) were days to maturity (16.83%), plant height (15.55) and days to 50% (4.977%) showed low estimates (<5%) of (GA) genetic advance. The characteristics such as the number of secondary branches, number of siliquae per plant, seed yield per plant, 1000-seed weight, number of primary branches, length of main raceme, number of seeds per siliquae showed high GCV, heritability and genetic advance. Therefore, from the above obtained results it can be concluded that the characters studied are governed by additive gene effect. Hence, adoption for selection of elite genotype based on attributing characters.

Keywords: Genetic variability, heritability, Genetic advance, mustard

**Introduction**

“The availability of genetic variation is advantageous for crop improvements. Such types of variability brought about by a group of genes which have a small individual effect, can be studied through quantitative measurement. The genetic facts are inferred from observation on phenotypes. Because phenotype is determined by the interaction of genotype and environment, non-genetic factors have a significant impact on genetic variation” (Chaudhary et al., 2023; Perween et al., 2024). Mustard and rapeseed are significant oil seed crops in India. Mustard and rapeseed belong to the Brassicaceae family. After soybeans, rapeseed mustard is India's second-most important oil seed crop in terms of both acreage and production. Crop Brassicas are a group of many different kinds of plants that are grown for their vegetables, feed, oils, and condiments (16. Akhatar et al., 2025). One of the most important agricultural commodities for the economy is the oleiferous Brassica species, commonly referred to as rapeseed-mustard. 53 countries worldwide cultivate rapeseed- mustard, which includes eight distinct species: Indian mustard, Toria, yellow sarson, brown sarson, gobhi-sarson, Karan rai, black mustard, and taramira. India, Canada, China, the European Union, Pakistan, Poland, Bangladesh, and Sweden are the countries that grow rapeseed and mustard worldwide. In 2022–23, the world's rapeseed-mustard production, productivity, and area were 36.59 million hectares (mha), 72.37 million tons (mt), and 1980 kg/ha, respectively. India remains fourth after the European Union, Canada, and China in terms of area (17.19%) and production (8.54%). India contributes 19.8% and 9.8% of global production and area, respectively. 12.25 lakh hectares, 17.10 lakh tons, and 11.85 q/ha, respectively, were the estimated area, production and productivity of rapeseed mustard in Uttar Pradesh, India. In Agra, Mathura, Aligarh, Kanpur Auraiya, Unnao and Hathras rapseed mustard is grown (Sachan et al., 2024). In terms of area, rapeseed mustard production, and productivity Mathura is the leading district.

In southern and near-east Iran, wild relatives of *Brassica juncea* have been discovered. Divergent opinions exist on *B. juncea's* origin. It was thought in the late 19th century that*B. juncea* most likely came from China and entered India through a northeastern path unrelated to any Aryan invasion. Vavilov (1949) said that the primary center of origin was Afghanistan and the Central Asian countries that bordered it, while the subsidiary centers of origin were central and western China, Eastern India, and Asia Minor, which included Iran. Others have suggested several *B. juncea* genesis sites where the probable progenitors, *B. nigra* and *B. campestris,* shared geographic sympatry. There is an evolutionary link between the six species of Brassica crops. Three fundamental diploid species—*B. rapa, B. nigra,* and *B. oleracea*—are involved. The evolution of the basic diploid level and the three amphiploid species *B. napus, B. carinata,* and *B. juncea* were caused by pairwise hybridization between these diploid species, which was followed by chromosome doubling. The F1 hybrids created as a result of artificial hybridization between these species demonstrated a high degree of similarity and frequent meiotic pairing among the comparable genomes. When *B. juncea* (AABB; 2n = 36) and *B. rapa* (AA; 2n = 20) are crossed, for example, 10 of *B. juncea's* chromosomes couple with the 10 of *B. rapa*, leaving the remaining 8 as univalent at metaphase I. Similarly, eight bivalent sare frequently seen during meiosis when *B. nigra* (CC; 2n = 18) is crossed with *B. juncea*, while the remaining ten chromosomes show their identity as univalent. This data unequivocally indicates that hybridization between these two diploid parent species is how *B. juncea* originated. The amphidiploid origin of *B. carinata* and *B. napus* has been confirmed by similar cytogenetic research. A loose secondary link between two or more bivalents is observed in addition to pairing between homologous chromosomes of similar genomes from related species. The idea that the three basic genomes descended from a single parent has been supported by the secondary connection. Initially believed to be 5, the haploid number of this ancestral genome was eventually found to be n = 6.

**Materials and Method**

The present investigation was conducted at Genetics and Plant Breeding Research Farm of agriculture (Pilikothi), Tilakdhari Post Graduate College, Jaunpur, U.P. The experimental Material consists of 12 genotypes of mustard namely viz. Bhagirathi, Kranti, RH-406, Laxmi, PusaMustard-24, Pusa-Tarak, Seeta, DRMR-IJ-31, RGN-48, Pusa-Mustard-21, BR-40 and Radhika which were obtained from Mustard Resarch Centre at Bharatpur, Rajasthan. All the genotypes were grown in a Randomized Block Design with 3 replications during Winter season. Plant to Plant and Row to Row distance is maintained at 15 cm. and 30 cm. respectively. Observations were recorded on 5 randomly selected plants from each treatment on 10 characters viz. Days to 50% flowering, Days to maturity, Plant height (cm), Number of primary branches per plant, Number of secondary branches per plant, Length of main raceme(cm), Number of siliquae per plant, Number of seed per siliquae, 1000 Seed weight(gm) and Seed Yield (gm). The data were statistically analyzed for computation of genetic coefficient of variation using appropriate statistical analysis. ANOVA was carried out as per the procedure given [1]. The phenotypic and genotypic coefficient of variance was estimated [2] and heritability in broad sense was estimated as per formula given [3]. The expected genetic advance was calculated by using the formula as suggested [4].

**Results and Discussion**

All ten characters underwent the analysis of variance (ANOVA) for the randomized block design utilized for twelve genotypes, which is shown in Table 1. According to the variance analysis, there was sufficient variability. For each of the ten characters, there were notable differences between the genotypes.

**Table: 1 Analysisofvariancefor10charactersinIndianMustard:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Sourceof variation** | **Degree of**  **freedom** | **Days to50%**  **flowering** | **Daysto maturity** | **Plant**  **Height**  **(cm)** | **Length of main**  **raceme (cm)** | **Primary branches/ plant** |
| **Replication** | **2** | **4.861** | **2.694** | **23.111** | **4.166** | **0.049** |
| **Treatment** | **11** | **13.081\*\*** | **357.240\*\*** | **596.57\*\*** | **153.32\*\*** | **2.065\*\*** |
| **Error** | **22** | **2.558** | **1.755** | **18.020** | **4.843** | **0.061** |

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Source of variation** | **Degree of**  **freedom** | **Secondary branches/ plant** | **Siliquae/ plant** | **Seeds/ siliquae** | **1000seeds weight(g)** | **Seed yield/plant (g)** |
| **Replication** | **2** | **0.250** | **1.129** | **0.861** | **0.041** | **3.921** |
| **Treatment** | **11** | **21.853\*\*** | **11004.4\*\*** | **8.838\*\*** | **1.515\*\*** | **44.547\*\*** |
| **Error** | **22** | **0.055** | **2.673** | **0.376** | **0.020** | **5.338** |

**\*\*,significant at1%probability level**

Further, the mean performance (table-2) also showed highly significant differences between the characters among the genotypes which show sufficient variability for all the characters.

The results are as follows, Genotype KRANTI take a minimum time to 50 % flowering (55.00)days whereas genotype DRME-IJ-31 takes maximum time (62.33)days. With respect to days to maturity minimum and maximum days taken by BR-40 (110.00)days and RADHIKA (141.667)days respectively. The genotype PUSA-TARAK obtained a minimum plant height (150.00 cm) and maximum was observed for DRMR-IJ-31 (196.333 cm). Similarly, the data obtained from Number of siliquae per plant genotype DRMR-IJ-31 (181.243) minimum siliquae per plant whereas KRANTI (373.967) maximum. Genotype RADHIKA (4.580) have a minimum Number of primary branches per plant where as the maximum for SEETA (7.640). In case of number of seeds per siliquae, the highest and lowest number of seeds per siliquae were obtained by the genotype DRMR-IJ-31 (17.333) and PUSAMUSTARD-21, LAXMI & SEETA (12.00) respectively. The maximum 1000-seed weight was obtained from PUSA-TARAK (5.90 gm) where as, minimum in BR-40 (4.00 gm). In addition, genotype KRANTI was recorded with a maximum number of secondary branches (14.580) where as, minimum in DRMR-IJ-31 (4.770). Similarly, maximum seed yield was reported in genotype SEETA (27.267 gm), while minimum in RH-406 (16.60 gm) and maximum length of main raceme was found in DRMR-IJ-31 (68.733 cm) whereas, minimum in KRANTI (46.600 cm). Similar, findings were reported, which indicate the variability among the genotype for most of the characters under study.

“All the variability among the genotype of mustard for all the characters under investigation were analyzed for genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (broad sense) and genetic advance as per cent of mean given (table 2). In the present investigation, magnitude of GCV for all the characters was less than the corresponding PCV which indicates the influence of environmental components on the characters expression” [5-7]. However, the difference between GCV and PCV was relatively small specifying the expression of the characters was highly controlled by genetic factors rather than environmental causes. Thus, the selection could be based on the basis of phenotypic performance offering scope for crop improvement. The phenotypic coefficient of variation (PCV) ranges from 4.178 % to 29.889 %. The high amount of PCV was recorded for number of secondary branches (29.889 %) followed by number of siliquae per plant (22.906 %), seed yield (18.754 %), 1000-seed weight (15.184 %), number of primary branches (14.967 %), length of main raceme (13.048 %) and number of seed per siliquae (12.523 %). And the low amount of PCV was recorded for days to maturity (8.288 %), plant height (8.252 %) and days to 50% flowering (4.178 %).

The amount of genetic coefficient of variation (GCV) ranged from 3.177 % to 29.776 %. Higher magnitude of GCV was recorded for number of secondary branches (29.776 %), followed by number of siliquae per plant (22.897%), seed yield (15.802 %), 1000-seed weight (14.885 %), number of primary branches (14.323 %), length of main raceme (12.453 %) and number of seed per siliquae (11.763 %). And the low amount of GCV was recorded for days to maturity (8.228 %), plant height (7.892 %) and days to 50% flowering (3.177 %).

“Heritability estimate provides a guide for the selection procedure to be followed by the breeder for the improvement of these characters under a given environment. The estimates of heritability per cent in broad sense for all the characters range from 57.872% (days to 50% flowering) to 99.927% (number of siliquae per plant). Generally higher estimates of heritability in broad sense(>75%) were recorded for number of siliquae per plant followed by plant height(cm), number of secondary branches per plant, 1000-seed weight (g), number of primary branches per plant, length of main raceme, days to maturity, seed yield per plant and number of seed per siliquae characters 91.454, 99.248, 96.098, 91.573, 91.087, 98.540, 71.001 and 88.231(in percentage) respectively. Comparatively low estimate of heritability (<75) observed for days to 50% flowering (57.827). The characters such as number of secondary branches, number of siliquae per plant and days to maturity shows high heritability and these similar results are also reported” [8-10].

**Table 2: Mean, range, genotypic and phenotypic coefficient of variation, heritability (%) in broad sense for different characters in Indian mustard:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Variables** | **Mean** | **Range** | **GCV (%)** | **PCV(%)** | **Heritabiliy in broad**  **Sense(%)** | **GA in % of mean** |
| **Days to50% flowering** | **58.944** | **55.00-62.33** | **3.177** | **4.178** | **57.827** | **4.977** |
| **Days to maturity** | **132.306** | **110-141.66** | **8.228** | **8.288** | **98.540** | **16.825** |
| **Plant height**  **(cm)** | **174.972** | **150-196.33** | **7.892** | **8.252** | **91.454** | **15.547** |
| **Length of main raceme** | **56.492** | **46.60-68.7** | **12.453** | **13.048** | **91.087** | **24.484** |
| **No. of**  **primary**  **branches** | **5.706** | **4.58-7.640** | **14.323** | **14.967** | **91.573** | **28.234** |
| **No. of secondary branches** | **9.053** | **4.77-14.58** | **29.776** | **29.889** | **99.248** | **61.107** |
| **No. of siliquae/plant** | **264.476** | **181.243-**  **373.967** | **22.897** | **22.906** | **99.927** | **47.151** |
| **No. of seed/siliquae.** | **14.278** | **12.0-17.33** | **11.763** | **12.523** | **88.231** | **22.761** |
| **1000-seed weight (gm)** | **4.742** | **4.00-5.900** | **14.885** | **15.184** | **96.098** | **30.058** |
| **Seed- yield/plant** | **22.878** | **16.6-27.267** | **15.802** | **18.754** | **71.001** | **27.430** |

“The genetic advance (GA) gives a thought of expected advancement through selection in the next generation. The higher estimate of GA coupled with higher heritability without a doubt indicates the possibility of improvement through selection. Genetic advance (GA) in % of mean shows significant variations for different traits. The GA in percentage of mean ranged from 4.977% (days to 50% flowering) to 61.107% (number of secondary branches per plant). Seed yield per plant showed high estimates(>20%) of genetic advance in % of mean (27.430%) followed by number of primary branches per plant (28.234%), length of main raceme (24.484%), number of siliquae per plant(47.151), number of seeds per siliquae (22.761),1000-seeds weight (30.058) and moderate estimates (<20->5%) were days to maturity (16.825%), plant height (15.547) and days to 50% (4.977%) showed low estimates (<5%) of (GA) genetic advance. The characteristics such as number of secondary branches, number of siliquae per plant and seed yield coupled with a high amount of GCV, heritability and Genetic advance as percent of mean. It also shows a higher response for the selection of high yielding genotypes as these characters are governed by additive gene action. The similar finding also reported in” [11-13].

**Conclusion:**

High heritability coupled with high GCV and genetic advance as percent of mean was observed number of secondary branches, number of siliquae per plant, seed yield per plant, 1000-seed weight, number of primary branches, length of a main raceme, number of seed per siliquae and these characters are governed by additive gene effects. Thus the selection for these characters would be quiet effective in enhancing grain yield per plant and also simultaneously its relative attributes. Therefore, emphasis should be paid on the above-mentioned traits for improving productivity during selection.

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