**Genetic Analysis and Trait Association Studies for Yield Enhancement in Mungbean [*Vigna radiata* (L.) Wilczek]**

**ABSTRACT**

**Aims:** The aim of this study is to evaluate the genetic variability, heritability estimates, and inter-relationships among important yield and yield-contributing traits in mungbean. This information will aid in identifying promising genotypes and understanding the genetic architecture of traits, thereby facilitating the development of high-yielding, stable, and resilient mungbean varieties through effective selection strategies.

**Study design:** The experiment was laid in Randomized Complete Block Design (RCBD) comprising with three replications.

**Place and Duration of Study:** The field experiment was carried out at the experimental plot of Regional Research and Technology Transfer Station (RRTTS), Odisha University of Agriculture and Technology (OUAT), Keonjhar, situated under North Central Plateau Zone (NCPZ) of Odisha.

**Methodology:** The research materials consisted of total 14 entries which including four advanced breeding lines (F5 generation), five parental lines and five check varieties.

**Results:** The present investigation revealed substantial genetic variability among the studied mungbean genotypes for key agronomic traits, providing ample opportunities for crop improvement through selection and breeding. The elite breeding line OKGG-12 (F5) emerged as a particularly promising genotype, exhibiting superior performance in critical yield-contributing traits such as the number of pods per plant (80.33), seeds per pod (13), and the highest seed yield (1313 kg/ha), surpassing even the best-performing check LGG-460. High heritability coupled with substantial genetic advance was observed for traits such as plant height, pod length, and 100-seed weight, indicating the predominance of additive gene action and the feasibility of improving these traits through direct selection.

**Conclusion:** The strong association among branching traits, number of clusters, and pod production emphasizes the significance of plant architecture in mungbean yield improvement. Furthermore, early flowering genotypes like OKGG-12 (F5) and OKGG-9 (F5) demonstrated suitability for short-duration cropping systems, expanding their adaptability. Overall, the study underscores the potential of specific genotypes and key yield attributes in mungbean improvement programs.

***Keywords*:** *Correlation, Genetic variability, Heritability, Mungbean,*

1. **INTRODUCTION**

 Mungbean [Vigna radiata (L.) Wilczek] is an important short-duration, self-pollinated legume crop grown extensively in tropical and subtropical regions for its high-quality protein content, nitrogen-fixing ability, and role in sustainable agriculture (Nair et al., 2022; Majhi et al., 2022; Kumar et al., 2023). It serves as a significant dietary protein source, especially in vegetarian diets, and contributes to soil fertility enhancement through biological nitrogen fixation. In India, which is the largest producer and consumer of mungbean, the crop is cultivated predominantly under rainfed conditions during Kharif and summer seasons (Singh et al., 2022; Verma et al., 2023). Despite its economic and nutritional importance, mungbean productivity remains low and stagnant in many regions due to biotic and abiotic stresses, poor genetic base, and limited exploitation of available genetic resources (Singh et al., 2024). Genetic variability forms the cornerstone of any crop improvement program, providing the raw material for selection and hybridization (Kumar & Sharma, 2024). Estimation of genetic parameters such as variability, heritability, and genetic advance enables breeders to understand the extent of genetic diversity present within the population and the potential for selection-driven improvement. Heritability, when coupled with genetic advance, provides insight into the role of additive gene action and effectiveness of selection for trait improvement (Chauhan et al., 2023; Johnson et al., 2021).

 Several recent studies emphasize the importance of evaluating genetic diversity in mungbean for enhancing yield potential, stress tolerance, and quality traits (Rathore et al., 2023; Das et al., 2022). Moreover, genetic variability analysis using morphological, biochemical, and molecular markers has proven effective in identifying promising genotypes for breeding programs (Patel et al., 2023). Such studies are critical for developing high-yielding, disease-resistant, and climate-resilient mungbean varieties to meet the growing food and nutritional demands. Therefore, the present investigation was undertaken to assess the extent of genetic variability in mungbean with respect to seed quality, yield attributes, and related physiological traits, with the objective of identifying potential genotypes for future crop improvement efforts. Correlation studies further facilitate the understanding of inter-relationships among important agronomic traits, assisting breeders in formulating indirect selection strategies for complex traits like yield, which is governed by multiple physiological and morphological components (Yadav et al., 2023). Positive associations between yield and component traits such as plant height, pods per plant, and 100-seed weight indicate the possibility of simultaneous improvement for these traits (Patel et al., 2024). Given the growing demand for high-yielding, resilient mungbean varieties, it is essential to identify genotypes with desirable agronomic traits through comprehensive evaluation of genetic variability, heritability, genetic advance, and correlation among key yield and quality attributes. The present investigation was undertaken to assess the extent of genetic variability, heritability estimates, and trait interrelationships among mungbean genotypes, which would aid in developing improved varieties with enhanced productivity and adaptability.

1. **MATERIALS AND METHODS**
	1. **Experimental Site**

The field experiment was carried out at the Experimental plot of Regional Research and Technology Transfer Station (RRTTS), Odisha University of Agriculture and Technology (OUAT),Keonjhar, situated at coordinates 21.6319° N latitude and 85.5747° E longitude.The location is coming underNorth Central Plateau Zone (NCPZ) of the State.

* 1. **Meteorological Data**

The meteorological data for the crop growing period including temperature (oC), relative humidity (%), rainfall (in mm), rainy days and bright sunshine hours at RRTTS, Keonjhar is presented in Table 1.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Month | Year | Temperature(oC) | R.H. (%) | Rainfall (mm) | Rainy Days (days) | BSH (hrs.) |
| **Max.** | **Min.** | **Max.** | **Min.** |
|  |  |  |  |  |  |  |  |  |
| **July** | 2023 | 30.16 | 24.28 | 89.32 | 68.58 | 275.80 | 19.00 | 2.27 |
| **August** | 2023 | 29.63 | 23.94 | 89.32 | 68.74 | 323.70 | 15.00 | 1.92 |
| **September** | 2023 | 30.03 | 23.60 | 91.07 | 69.90 | 241.40 | 12.00 | 2.11 |

**Table 1. Meteorological data for the period from July 2023 to September 2023 in Keonjhar district of Odisha**

* 1. **Experimental Materials**

The research material consisted of total 14 entries which including four advanced breeding lines (F5 generation), five parental lines and five check varieties.The details of the experimental materials are mentioned in Table 2.

**Table-2. List of experimental materials used in the research programme**

|  |  |  |  |
| --- | --- | --- | --- |
| Sl. No. | Genotypes | Sl. No. | Genotypes |
|  | OKGG-9 (F5) |  | VIRAT |
|  | OKGG-10 (F5) |  | V-02-709 |
|  | OKGG-11 (F5) |  | ML-1808 |
|  | OKGG-12 (F5) |  | ML-2479 |
|  | OBGG-52 |  | IPM-410-3 |
|  | OBGG-56 |  | LGG-460 |
|  | OBGG-58 |  | OUM-11-5 |

* 1. **Experimental Design**

The field experiment was performed in Randomized Complete Block Design (RCBD) comprising three replications.

* 1. **Observations Recorded for yield and yield attributing characters**

Various observations for yield attributing traits were recorded from five plants chosen at random among the plants within each line and these included observations related to yield and yield attributing traits such as plant height (cm), number of branches per plant, number of clusters per plant, number of pods per plant, number of seeds per pod, pod length (cm), 100-seed weight (g) and seed yield per plant (g).

* 1. **Statistical Analysis**

The statistical analysis for the genetic variability, heritability and correlation were performed by using Microsoft Excel and R-Studio (Posit Team, 2022) version 4.1.2 (R Core Team, 2021)**.** Additionally, a few graphs were generated using GRAPES website (Gopinath *et al*., 2021).

1. **RESULTS AND DISCUSSION**
	1. **Analysis of variance (ANOVA) for yield related traits in mungbean**

An analysis of variance (ANOVA) test was conducted for the thirteen yield-related traits being studied. The mean genotypic sum of squares for yield-related traits is summarized in Table 3. The analysis showed that there were statistically significant variations among the genotypes for each of the characteristics examined at a 1% level of probability.

Days to first flowering recorded a mean sum of squares of 22.74 for genotypes, which was significantly higher than the error value of 0.85. The significant genetic variation observed among genotypes for flowering time highlights the potential for selecting early-maturing varieties. The genotype mean squares for days to 50% flowering and days to maturity were 42.45 and 70.35 respectively, while the corresponding error values were 1.12 and 0.92.This highlights the presence of notable differences in the reproductive phases, providing opportunities to select for early or late-maturing genotypes. Plant height exhibited a mean square of 640.16, much higher than the error value of 3.21, indicating significant variability in plant height across the genotypes. This is beneficial for selecting genotypes with desirable plant architecture, as height can be an important factor in yield potential and ease of harvest. The mean squares for the genotypes were 7.65 for number of primary branches and 13.01 for number of secondary branches, compared to smaller error values of 0.76 and 0.86. This suggests considerable genetic differences in branching patterns, which could contribute to higher pod production and yield.

The genotypic mean squares for number of clusters per plant, number of pods per cluster, and number of pods per plant were 8.21, 7.67 and 1613.69 respectively, suggesting considerable genetic variation in these pod-related traits. Pod length, number of seeds per pod and 100-seed weight also showed significant differences among genotypes with mean squares of 4.30, 3.36 and 0.59 respectively. These traits are important yield-contributing factors, and the observed variation can be exploited for improving seed size and number. Finally, seed yield showed the highest variation among genotypes with a mean square value of 33122, far surpassing the error mean square of 242. This highlights considerable genetic variability for seed yield, which is the most critical trait in mungbean breeding programs.

The analysis of variance (ANOVA) in this study revealed significant differences among genotypes for all the traits examined, indicating a broad genetic base. This is critical for breeding programs focused on enhancing specific traits. The high mean squares for yield-related traits such as the number of pods per plant, pod length as well as seed yield provide promising opportunities for selecting genotypes with higher productivity.These findings align with results published by Kumar *et al*. (2024) and Muthuswamy *et al*. (2022) who observed similar trends in mungbean with traits like seed yield and plant height displaying significant variability. The notable differences in the reproductive phases such as days to first flowering and days to 50% flowering suggest opportunities for selecting both early and late-maturing genotypes, a crucial factor in developing varieties suitable for different agro-climatic conditions.

* 1. **Genetic variability, heritability, genetic advance study in mungbean genotypes**

Genetic variation in yield attributing traits in mungbean was examined in the present investigation. The results of the genetic variability parameters for these traits are presented in Table 4. To quantify the extent of variation in the test population, various genetic parameters were estimated, including genotypic and phenotypic coefficients of variation, heritability as well as genetic advance as a percentage of the mean. The values are depicted in Fig.1. and the details of genetic variability of the yield attributes are given below:

Days to First Flowering had a mean of 35.43 days, ranging from 30 to 42 days. The GCV (7.62%) was slightly lower than the PCV (8.06%). The high heritability (89.51%) combined with moderate GAM (14.86%) suggests that selection based on this trait would be effective. Days to 50% Flowering showed a mean of 43.17 days, with a GCV of 8.60% and PCV of 8.94%. It showed high heritability (92.49%) and moderate genetic advance over mean. Days to Maturity had a GCV of 7.16% and a PCV of 7.30%. High heritability (96.16%) and moderate genetic advance over mean (14.47%). Plant height (cm) displayed significant variability, with a GCV of 19.67% and a slightly higher PCV of 19.82%. The heritability was very high (98.51%), and the genetic advance (GAM = 40.22%).

Number of Primary Branches had a GCV of 26.41% and a higher PCV of 30.47%. Heritability was high (75.13%) and the genetic advance (GAM = 47.16%).Number of Secondary Branches showed a GCV of 19.80% and a PCV of 21.80%, high heritability (82.51%) and a GAM of 37.04%.Number of Clusters per Plant had a GCV of 17.44% and a PCV of 20.54%, with heritability at 72.07% and highGAM = 30.50%. Number of Pods per Cluster exhibited a high GCV of 21.25% and a PCV of 24.12%. The heritability was high (77.65%), and the genetic advance (GAM = 38.58%) indicates the potential for moderate genetic gains through selection.

Number of Pods per Plant had one of the highest GCV (39.70%) and PCV (39.87%), indicating significant genetic variability with minimal environmental influence. With a heritability of 99.13% and a very high genetic advance (GAM = 81.43%), this trait holds the greatest potential for yield improvement through selection. Number of Seeds per Poddisplayed a lower GCV of 7.75% and PCV of 9.98%, with heritability at 60.29% and relatively low genetic advance (GAM = 12.40%). Pod Length (cm) had a moderate GCV (12.98%), high PCV (13.19%), high heritability (96.87%) and a genetic advance of 26.32%. 100-Seed Weight (g) exhibited a GCV of 13.44% and PCV of 14.17%, with high heritability (89.85%) and a GAM of 26.23%, indicating that seed weight can be effectively improved through selection. Seed Yield (kg/ha) had a GCV of 9.17% and PCV of 9.27%, with high heritability (97.84%) and a genetic advance of 213.31 kg/ha. It also has moderate genetic advance as a percentage of the mean (GAM = 18.69%) suggesting genetic influence on seed yield.

The genotypic and phenotypic coefficients of variation (GCV and PCV) obtained in this study demonstrated moderate to high variability for several traits. High values (>20%) were found for traits like number of pods per plant, number of pods per cluster, number of primary branches and number of secondary branches. The results were in consonance with the findings of Gayacharan *et al*. (2020) and Sindhu *et al*. (2023). This could be attributed to the fact that these traits are affected by a combination of genetic and environmental factors, making them complex and polygenic, and their expression is also sensitive to various environmental conditions such as nutrient availability, water supply, and plant spacing. Moderate values (10-20%) were displayed for plant height, pod length, hundred-seed weight. Similar results were noted by Ahmad *et al*. (2014); Ramakrishnan *et al*. (2018) and Desai *et al*. (2020). This may be due to the reason that these traits are typically under stronger genetic control than the highly variable traits mentioned above, but still show some environmental influence. Low values (<10%) were observed for days to first flowering, days to fifty percent flowering, days to maturity, number of seeds per pod. This may be due to the fact that low variability suggests these traits are under tight genetic control in this population, possibly due to prior selection for adaptation to a particular growing region. The number of pods per plant exhibited the highest GCV and PCV followed by number of primary branches, indicating that this trait has substantial genetic variability and minimal environmental influence. This suggests that selecting genotypes with a higher number of pods could lead to significant yield improvements. This may due to the fact that it is a complex yield component influenced by many factors, including environmental conditions and other yield-related traits. A selection program requires traits with high heritability to ensure that the desired characteristics are consistently passed on to the offspring of the selected individuals. The high heritability and genetic advance as a percentage of the mean were found for this trait further affirm its potential for improvement through selection. These findings were consistent with the findings of Kumar *et al*. (2024); Mundiyara *et al*. (2024) and Nandini (2024).

**Table 3.** Analysis of variance (ANOVA) for various characters (Mean sum of squares)

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Sources of Variation** | **df** | **DF** | **DFF** | **DM** | **PH** | **NPB** | **NSB** | **NCP** | **NPC** | **NPP** | **NSP** | **PL** | **SI** | **SY** |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **Replication** | 2 | 0.21 | 0.45 | 0.67 | 4.63 | 2.45 | 3.17 | 1.79 | 2.60 | 8.67 | 1.14 | 0.11 | 0.04 | 334.00 |
| **Genotype** | 13 | 22.74\*\* | 42.45\*\* | 70.3\*\* | 640.16\*\* | 7.65\*\* | 13.01\*\* | 8.2\*\* | 7.68\*\* | 1613.7\*\* | 3.36\*\* | 4.30\*\* | 0.59\*\* | 33122\*\* |
| **Error** | 26 | 0.86 | 1.12 | 0.92 | 3.21 | 0.76 | 0.86 | 0.94 | 0.67 | 4.69 | 0.60 | 0.05 | 0.02 | 242.00 |

\*\* Significant at 1% level of probability.

Where, **DF:**Days to First Flowering; **DFF:**Days to 50% Flowering; **DM:**Days to Maturity; **PH:**Plant height (cm); **NPB:**Number of primary branches; **NSB:**Number of secondary branches; **NCP:**Number of clusters per plant; **NPC:**Number of Pods per cluster; **NPP:**Number of Pods per plant; **NSP:**Number of Seeds per pod; **PL:**Pod length (cm); **SI:**100-seed weight (g); **SY:**Seed yield (kg/ha).

**Table 4. Evaluation of Genetic variability in yield-related traits among mungbean genotypes**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Sl. No.** | **Traits** | **Mean** | **Range** | **GCV (%)** | **PCV (%)** | **h2bs (%)** | **GA** | **GAM** |
| **Min.** | **Max.** |
|  |  |  |  |  |  |  |  |  |  |
|  | Days to First Flowering | 35 | 30 | 42 | 7.62 | 8.06 | 89.51 | 5.26 | 14.86 |
|  | Days to 50% Flowering | 43 | 38 | 53 | 8.60 | 8.94 | 92.49 | 7.35 | 17.03 |
|  | Days to Maturity | 66 | 60 | 76 | 7.16 | 7.30 | 96.16 | 9.72 | 14.47 |
|  | Plant height (cm) | 74.08 | 45 | 98.3 | 19.67 | 19.82 | 98.51 | 29.80 | 40.22 |
|  | Number of primary branches | 5.74 | 3 | 10 | 26.41 | 30.47 | 75.13 | 2.71 | 47.16 |
|  | Number of secondary branches | 10.17 | 6 | 14 | 19.80 | 21.80 | 82.51 | 3.77 | 37.04 |
|  | Number of clusters per plant | 8.93 | 5 | 12 | 17.44 | 20.54 | 72.07 | 2.72 | 30.50 |
|  | Number of pods per cluster | 7.19 | 4 | 12 | 21.25 | 24.12 | 77.65 | 2.77 | 38.58 |
|  | Number of pods per plant | 58.34 | 28 | 118 | 39.70 | 39.87 | 99.13 | 47.50 | 81.43 |
|  | Number of seeds per pod | 12.36 | 10 | 15 | 7.75 | 9.98 | 60.29 | 1.53 | 12.40 |
|  | Pod length (cm) | 9.17 | 8.1 | 12.5 | 12.98 | 13.19 | 96.87 | 2.41 | 26.32 |
|  | 100-seed weight (g) | 3.25 | 2.38 | 3.97 | 13.43 | 14.17 | 89.85 | 0.85 | 26.23 |
|  | Seed yield (kg/ha) | 1141.48 | 960 | 1331 | 9.17 | 9.27 | 97.84 | 213.31 | 18.69 |
|  |  |  |  |  |  |  |  |  |  |

Where **GCV**: Genetic Coefficient of Variability; **PCV**: phenotypic coefficient of variation; **h2bs (%):** Heritability; **GA:** Genetic advance; **GAM:** Genetic Advance as a percentage of mean

* 1. **Mean performance of different mungbean genotypes with respect to various yield attributes**

The mean performances of genotypes in relation to yield-attributing traits are shown in Table 5. The findings showed substantial variation among the genotypes, offering valuable insights for identifying promising genotypes that can be advanced for further breeding and improvement. Among the genotypes, OKGG-12 (F5) demonstrated outstanding performance in terms of number of pods per plant (80.33), number of seeds per pod (13), seed yield (1313.00 kg/ha), making it a strong candidate for breeding programs aiming at yield improvement. LGG-460 also showed excellent performance, particularly in plant height, number of pods per plant, number of primary branches, and 100-seed weight, indicating its potential for high-yield and quality traits. The differences can be attributed to varietal characteristics which are inherent to that particular genotype.

* + 1. **Days to first flowering:**

It ranged from 31.00 days (OUM-11-5) to 41.00 days (LGG-460), with a mean of 35days. Genotypes like OUM-11-5 and OKGG-12 (F5) flowered earlier. In contrast, LGG-460 and V-02-709, with later flowering, may be better suited for regions with longer growing seasons. The elite breeding lines like OKGG-9 (F5), OKGG-10 (F5), OKGG-11 (F5) and OKGG-12 (F5) showed fewer days to first flowering, ranging from 33 to 37 days, making them potentially suitable for shorter growing seasons or environments that require early maturation. These were similar to findings by Desai *et al*. (2020) and Gayacharan *et al*. (2020), who also reported high heritability for flowering time in mungbean​. Early flowering is a desirable trait in regions with short growing seasons, and genotypes exhibiting this characteristic can be selected to enhance crop adaptability to different agro-climatic conditions.

* + 1. **Days to 50% flowering:**

It varied among genotypes, ranging from 39 (OUM-11-5) to 53 days (V-02-709), with an average of 43days. Genotypes like LGG-460 and V-02-709 showed late flowering while OUM-11-5 and OKGG-12 (F5) flowered earlier, in tandem with the results of days to first flowering. The elite breeding lines like OKGG-9 (F5), OKGG-10 (F5), OKGG-11 (F5) and OKGG-12 (F5) showed lesser days to 50% flowering as compared to other genotypes, ranging from 39 to 43 days. These findings are in alignment with findings by Ramakrishnan *et al*. (2018) who reported lowest PCV and GCV for this trait. Similar high heritability values for this trait have been reported by Kumar *et al*. (2024) in mungbean​.

* + 1. **Days to Maturity:**

It ranged between 75 days (LGG-460) and 61 days (OUM-11-5) with an average of 66days. The next highest days to maturity was attributed to V-02-709 (73 days). The genotypes like OKGG-9 (F5), OKGG-10 (F5), OKGG-11 (F5) and OKGG-12 (F5) showed lesser days to maturity as compared to other genotypes, ranging from 63 to 68 days. Ahmad *et al*. (2014) observed similar high heritability values for this trait in mungbean, making this trait reliable for selection in breeding programs focused on early or late-maturing varieties.

* + 1. **Plant Height (cm):**

It varied widely among genotypes, with values ranging from 47.70 cm (ML-1808) to 97.30 cm (LGG-460) with a mean of 74.08 cm. The elite breeding lines like OKGG-9 (F5) and OKGG-12 (F5) were taller, measuring 87.37 cm and 87.77 cm respectively. Plant height showed substantial variability among the genotypes with moderate PCV and GCV indicating minimal environmental influence. Similar results were also found by Nandini (2024) and Sindhu *et al*. (2023) that showed moderate values for the trait. The heritability was very high, and the genetic advance as a percentage of the mean was also high, indicating that plant height is mainly determined by genetic factors. Moreover, additive gene action appears to predominate, thereby facilitating simple selection. The findings of Nandini (2024) and Mundiyara *et al.* (2024) corroborate the present results, with both studies reporting high heritability and significant genetic advance for plant height, highlighting its potential for improving growth and yield in mungbean​.The genotypes like OKGG-9 (F5) and OKGG-12 (F5) were taller than the mean performance of all genotypes.

* + 1. **Number of Primary and secondary Branches:**

The number of primary branches showed substantial variation, with the highest values observed in LGG-460 (9.00 branches) and V-02-709 (8.67 branches). The genotypes like OKGG-9 (F5), OKGG-10 (F5), OKGG-11 (F5) and OKGG-12 (F5) showed lesser number of primary branches in comparison to the other genotypes examined, ranging from 3.67 to 4.67 branches. In case of number of secondary branches, the variation between genotypes was comparatively lesser, with highest values seen in LGG-460 and V-02-709 (13.67 branches), while OKGG-9 (F5) (8.67 branches), OKGG-11 (F5) (8 branches) and OKGG-12 (F5) (7 branches) showed minimum values. The genotypes like OKGG-9 (F5), OKGG-10 (F5), OKGG-11 (F5) and OKGG-12 (F5) showed varied number of secondary branches in comparison to the other genotypes examined, ranging from 6.67 (OKGG-10) to 8.67 branches (OKGG-9). Similar findings were reported by Mundiyara *et al*. (2024) and Dash *et al.* (2021) which suggest that secondary branching contributes to pod production and ultimately seed yield, making it a valuable trait for breeders aiming to enhance productivity through plant architecture modifications.

* + 1. **Number of Clusters per plant:**

Here, the maximum number was seen for LGG-460 (11.67 clusters) and V-02-709 (11.67 clusters) and a mean value of 8.93 clusters per plant was observed.The elite breeding lines like OKGG-9 (F5) and OKGG-12 (F5) showed higher number of clusters per plant (8.00 and 7.67 respectively) when compared to the other genotypes examined. The results were similar to those found by Majhi *et al*. (2020a, b) and Salman *et al*. (2023) for this trait, which may be because this trait is somewhat influenced by the environment, but still holds potential for genetic improvement.

* + 1. **Number of pods per cluster:**

It also showed substantial variations with LGG-460 showing the maximum value (11.67 pods) while OUM-11-5 (6.33 pods) showed minimum values. Among the elite breeding lines, OKGG-10 (F5) and OKGG-11 (F5) showed higher than average number of pods per cluster as compared to other genotypes (7.67 and 8.00 respectively). These results are in consonance with findings of other researchers such as Salman *et al*. (2023) and Sharma *et al*. (2018) who suggested moderate variability for this trait which can enhance seed yield. Among the F5 genotypes, OKGG-10 (F5) and OKGG-11 (F5) showed higher than average number of pods per cluster as compared to other genotypes.

* + 1. **Number of Pods per Plant:**

The highest performing genotype was LGG-460, with 114.33 pods per plant, followed by OKGG-12 (F5) with 80.33 pods. The lower values were observed in IPM-410-3 (29.67 pods) and ML-1808 (32.00 pods), indicating that these genotypes may require improvement in pod production to enhance yield potential. Among the elite breeding lines studied, all the genotypes performed better than average, with OKGG-12 (F5) being the leading one with 80.33 pods per plant. The results were in consonance with almost all researches available, such as Kumar *et al*. (2024); Mundiyara *et al*. (2024) and Majhi *et al*. (2020b).

* + 1. **Number of Seeds per Pod:**

It also varied, with genotypes like OKGG-9 (F5), OKGG-10 (F5), OKGG-12 (F5) and V-02-709 recording the highest value of 13 seeds per pod. On the lower end, ML-1808 and OUM-11-5 had 10.33 and 11.33 seeds per pod, respectively. A higher number of seeds per pod was recorded in OKGG-9 (F5) and OKGG-10 (F5), exceeding the best check LGG-460. This meant that these genotypes directly contributed to higher seed yield. It exhibited moderate values of heritability and genetic advance which is indicative ofpresence of both additive and non-additive gene action. The lower GCV and higher PCV indicate more environmental influence on this trait. Similar results were found by studies by Nandini (2024) and Majhi *et al*. (2020b). As seed number directly impacts yield, improving this trait through selection might be challenging. To fully capitalize on yield potential, breeding programs should prioritize the development of genotypes that exhibit a higher number of seeds per pod.Among the F5 genotypes, all the genotypes performed better than average, with OKGG-9 (F5) and OKGG-10 (F5) being the leading ones.

* + 1. **Pod length (cm):**

It ranged between 12.33 cm (VIRAT) and 8.30 cm (OKGG-9 (F5) with a mean value of 9.17 cm. Among the elite breeding lines, OKGG-11 (F5) and OKGG-12 (F5) performed better than average with 9.43 and 9.70 cm respectively. It showed very high heritability and high genetic advance. Pod length affects the number of seeds per pod, and selecting for longer pods can enhance seed production, contributing to overall yield improvement. Similar kind of results was also reported by Ramakrishnan *et al*. (2018) and Sandhiya and Saravanan (2018) who regarded this as the trait with lowest values of PCV and GCV.

* + 1. **100-Seed Weight (g):**

It showed significant differences among genotypes. The highest seed weight was observed in VIRAT (3.64 g) and LGG-460 (2.47 g), while the lowest seed weight was recorded in OKGG-9 (F5) and OKGG-10 (F5) (8.30 g). Among the elite breeding lines studied, OKGG-11 (F5) and OKGG-12 (F5) performed better than average with 3.32 and 3.48 g respectively. It showed high heritability and a high genetic advance. The moderate GCV and PCV values suggest some environmental influence. However, the high heritability indicates that this trait can be improved through selection. Larger seed size is often associated with market preference and better crop quality, making it a key trait in breeding programs aimed at improving yield. The results were similar to those found by Gayacharan *et al*. (2020); Sneha *et al*. (2019) and Gadakh *et al*. (2013).

* + 1. **Seed Yield (kg/ha):**

Seed yield ranged from 977.33 kg/ha (IPM-410-3) to 1313.00 kg/ha (OKGG-12 (F5)), with a mean of 1141.48 kg/ha. OKGG-12 (F5) and OKGG-11 (F5) produced the highest seed yields emerge as promising candidates for improving mungbean productivity. Among the elite breeding lines studied, OKGG-12 (F5), with a yield of 1313 kg/ha performed better than best check LGG-460 which had 1247.33 kg/ha. The seed yield of elite breeding lines was compared with the best check available (LGG-460) and the results are displayed in Fig. 2. The yield of OKGG-11 (F5) was only slightly lower than the yield of LGG-460, signifying its potential in breeding programs in future. It is the most critical trait and showed very high heritability (97.84%) and moderate genetic advance (GAM = 18.69%). The GCV (9.17%) and PCV (9.27%) values indicate that this trait is mostly governed by genetic factors, making it an excellent candidate for selection. Improving seed yield through selection for higher pod number, seed number, and seed weight is feasible, and high heritability suggests strong potential for successful breeding interventions. The results were in consonance with almost all researches available, such as Kumar *et al*. (2024); Mundiyara *et al*. (2024) and Majhi *et al*. (2020b). Among the F5 genotypes studied, OKGG-12 (F5) had a higher yield than best check LGG-460.

* 1. **Study of correlation between yield and attributing traits**

A comprehensive correlation analysis was conducted to elucidate the complex interactions between key agronomic characteristics, including days to flowering, plant height, branching patterns, pod and seed traits and overall seed yield. The results of this analysis, presented in Fig. 3, reveal significant correlations among several traits, offering important insights into the genetic relationships underlying the yield components of mung bean, some of which are discussed in the sections below:

* + 1. **Seed Yield (kg/ha):**

There is a strong positive correlation between seed yield and the number of pods per plant (r = 0.82\*\*\*), and this relationship is highly statistically significant. Additionally, seed yield showed moderate positive correlations with plant height (r = 0.61), pod length (r = 0.56) and number of seeds per pod (r = 0.32) both of which were also highly significant (p < 0.001).

* + 1. **Number of Pods per Plant:**

The number of pods per plant was strongly positively correlated with seed yield (r = 0.82), plant height (r = 0.77), and pod length (r = 0.54), with all these relationships being highly significant. In contrast, it showed a weak but highly significant negative correlation with 100-seed weight (r = -0.44). These results are in consonance with findings of other researchers such as Sabatina *et al*. (2021) and Ramakrishnan *et al*. (2018)

* + 1. **Plant Height (cm):**

Plant height had a positive correlation with seed yield and number of pods per plant, with correlation coefficients of 0.61 and 0.77, respectively, and both were highly significant. Additionally, plant height was moderately positively correlated with pod length, with a correlation coefficient of 0.34, which was also highly significant. These results are in consonance with findings of other researchers such as Kumar *et al*. (2024) and Khatik *et al*. (2022).

* + 1. **Flowering and Maturity Traits:**

A robust positive correlation was observed between days to first flowering and days to 50% flowering, with a correlation coefficient of 0.70, denoting a highly significant association. Furthermore, both of these variables exhibited moderate to strong positive correlations with days to maturity, with correlation coefficients of 0.79 and 0.83, respectively, indicating a highly significant relationship in both instances.

* + 1. **100-Seed Weight (g):**

The 100-seed weight displayed a pattern of weak to moderate negative correlations with certain traits. Notably, significant negative correlations were observed with the number of pods per plant and days to first flowering, both with a correlation coefficient of -0.44. A weak negative correlation was also found with the number of pods per cluster, with a correlation coefficient of -0.36. In contrast, all other correlations involving 100-seed weight were non-significant. These results are in consonance with findings of other researchers such as Ramakrishnan *et al*. (2018) and Gadakh *et al*. (2013).

* + 1. **Branching Traits:**

A strong correlation was observed between the number of primary branches and secondary branches, as evidenced by a correlation coefficient of 0.96, thereby underscoring a statistically significant relationship. Furthermore, a robust correlation was discerned between number of primary branches and the number of clusters per plant, with a correlation coefficient of 0.91. Similarly, a strong positive correlation was observed between number of secondary branches and the number of clusters per plant, yielding a correlation coefficient of 0.95. These results are in consonance with findings of other researchers such as Desai *et al*. (2020); Majhi and Mogali (2020); Majhi *et al*. (2020b).

This correlation analysis provides valuable insights for mungbean breeding strategies. The strong relationship between number of pods per plant and seed yield offers a clear primary target for selection. Plant height and pod length also emerge as important secondary traits. The challenge lies in balancing these traits with seed size, given the negative correlations of 100-seed weight with other yield components. Future breeding efforts should focus on optimizing the balance between these traits to maximize yield potential while maintaining desirable seed characteristics. Additionally, consideration of flowering time and maturity could help in developing varieties adapted to specific agricultural systems or environments.

**Table 5. Mean Performance of different mungbean genotypes with respect to various yield attributing traits**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Sl. No.** | **Genotype** | **DF** | **DFF** | **DM** | **PH** | **NPB** | **NSB** | **NCP** | **NPC** | **NPP** | **NSP** | **PL** | **SI** | **SY** |
| **1.** | **OKGG-9 (F5)** | 37 | 43 | 68 | 87.37 | 4.67 | 8.67 | 8.00 | 6.33 | 64.33 | 13.00 | 8.30 | 2.60 | 1115.67 |
| **2.** | **OKGG-10 (F5)** | 36 | 42 | 67 | 77.50 | 3.67 | 6.67 | 6.00 | 7.67 | 67.67 | 13.00 | 8.30 | 2.58 | 1152.67 |
| **3.** | **OKGG-11 (F5)** | 34 | 40 | 63 | 72.60 | 3.67 | 7.00 | 6.33 | 8.00 | 72.67 | 12.67 | 9.43 | 3.32 | 1275.33 |
| **4.** | **OKGG-12 (F5)** | 33 | 39 | 63 | 87.77 | 4.00 | 8.00 | 7.67 | 7.00 | 80.33 | 12.33 | 9.70 | 3.48 | 1313.00 |
| **5.** | **OBGG-52** | 35 | 42 | 68 | 70.14 | 6.33 | 11.33 | 9.67 | 7.00 | 41.00 | 11.33 | 8.50 | 3.38 | 1120.33 |
| **6.** | **OBGG-56** | 34 | 42 | 70 | 66.17 | 5.67 | 10.33 | 9.67 | 6.00 | 47.00 | 14.67 | 8.73 | 3.02 | 1143.33 |
| **7.** | **OBGG-58** | 32 | 41 | 63 | 71.57 | 5.67 | 10.33 | 8.67 | 7.00 | 55.33 | 12.67 | 8.23 | 3.28 | 1119.00 |
| **8.** | **VIRAT** | 34 | 42 | 61 | 76.80 | 6.00 | 10.67 | 9.67 | 8.00 | 63.33 | 13.00 | 12.33 | 3.64 | 1231.00 |
| **9.** | **V-02-709** | 36 | 53 | 73 | 85.37 | 8.67 | 13.67 | 11.67 | 8.33 | 73.33 | 13.00 | 9.03 | 3.68 | 1215.33 |
| **10.** | **ML-1808** | 33 | 43 | 65 | 47.70 | 6.33 | 11.00 | 9.33 | 5.67 | 32.00 | 10.33 | 8.87 | 3.01 | 1046.67 |
| **11.** | **ML-2479** | 32 | 42 | 64 | 56.13 | 5.33 | 10.00 | 8.33 | 5.00 | 37.33 | 11.33 | 8.70 | 3.81 | 1001.33 |
| **12.** | **LGG-460** | 41 | 49 | 75 | 97.30 | 9.00 | 13.67 | 11.67 | 11.67 | 114.33 | 12.00 | 11.20 | 2.47 | 1247.33 |
| **13.** | **OUM-11-5** | 31 | 39 | 61 | 87.53 | 6.00 | 10.67 | 9.67 | 6.67 | 38.33 | 11.33 | 8.67 | 3.61 | 1022.33 |
| **14.** | **IPM-410-3** | 35 | 42 | 64 | 53.13 | 5.33 | 10.33 | 8.67 | 6.33 | 29.67 | 12.33 | 8.43 | 3.59 | 977.33 |
| **Grand mean** | 35 | 43 | 66 | 74.08 | 5.74 | 10.17 | 8.93 | 7.19 | 58.33 | 12.36 | 9.17 | 3.25 | 1141.48 |
| **Standard Error (±)** | 0.53 | 0.61 | 0.55 | 1.03 | 0.50 | 0.54 | 0.56 | 0.47 | 1.25 | 0.45 | 0.12 | 0.08 | 8.99 |
| **C.D. (5%)** | 1.55 | 1.78 | 1.61 | 3.01 | 1.46 | 1.56 | 1.63 | 1.38 | 3.64 | 1.30 | 0.36 | 0.25 | 26.13 |
| **C.D. (1%)** | 2.10 | 2.40 | 2.18 | 4.06 | 1.98 | 2.10 | 2.20 | 1.86 | 4.91 | 1.76 | 0.49 | 0.33 | 35.32 |

Where, **DF:**Days to First Flowering; **DFF:**Days to 50% Flowering; **DM:**Days to Maturity; **PH:**Plant height (cm); **NPB:**Number of primary branches; **NSB:**Number of secondary branches; **NCP:**Number of clusters per plant; **NPC:**Number of Pods per cluster; **NPP:**Number of Pods per plant; **NSP:**Number of Seeds per pod; **PL:**Pod length (cm); **SI:**100-seed weight (g); **SY:**Seed yield (kg/ha)



**Fig. 1. GCV, PCV, Heritability and Genetic Advance as percent of mean of yield attributes in mungbean**

Where, **DF:** Days to First Flowering; **DFF:** Days to 50% Flowering; **DM:** Days to Maturity; **PH:** Plant height (cm); **NPB:** Number of primary branches; **NSB:** Number of secondary branches; **NCP:** Number of clusters per plant; **NPC:** Number of Pods per cluster; **NPP:** Number of Pods per plant; **NSP:** Number of Seeds per pod; **PL:** Pod length (cm); **SI:** 100-seed weight (g); **SY:** Seed yield (kg/ha)

**Fig. 2. Comparison of seed yield between elite breeding lines and best check**



Where, **DF:** Days to First Flowering; **DFF:** Days to 50% Flowering; **DM:** Days to Maturity; **PH:** Plant height (cm); **NPB:** Number of primary branches; **NSB:** Number of secondary branches; **NCP:** Number of clusters per plant; **NPC:** Number of Pods per cluster; **NPP:** Number of Pods per plant; **NSP:** Number of Seeds per pod; **PL:** Pod length (cm); **SI:** 100-seed weight (g); **SY:** Seed yield (kg/ha).

**Fig. 3. Pearson’s Correlation matrix for yield attributing traits in mungbean**

1. **CONCLUSION**

The present investigation revealed substantial genetic variability among the studied mungbean genotypes for key agronomic traits, providing ample opportunities for crop improvement through selection and breeding. The elite breeding line OKGG-12 (F5) emerged as a particularly promising genotype, exhibiting superior performance in critical yield-contributing traits such as the number of pods per plant (80.33), seeds per pod (13), and the highest seed yield (1313 kg/ha), surpassing even the best-performing check LGG-460. High heritability coupled with substantial genetic advance was observed for traits such as plant height, pod length, and 100-seed weight, indicating the predominance of additive gene action and the feasibility of improving these traits through direct selection. Traits like days to flowering and maturity also showed high heritability, suggesting their reliability for selection in breeding programs, especially for environments with specific growing season requirements. The correlation analysis provided valuable insights into trait interrelationships that can guide effective selection strategies. Seed yield exhibited a strong positive correlation with the number of pods per plant, plant height, pod length, and the number of seeds per pod, highlighting these as critical targets for selection to enhance overall productivity. However, a notable negative correlation was observed between 100-seed weight and pod-related traits, indicating the need to balance seed size with pod production to achieve optimal yield gains. The strong association among branching traits, number of clusters, and pod production emphasizes the significance of plant architecture in mungbean yield improvement. Furthermore, early flowering genotypes like OKGG-12 (F5) and OKGG-9 (F5) demonstrated suitability for short-duration cropping systems, expanding their adaptability. Overall, the study underscores the potential of specific genotypes and key yield attributes in mungbean improvement programs. Future breeding efforts should focus on exploiting the identified genetic variability, maintaining a balance between seed size, pod production, and plant architecture to develop high-yielding, adaptable mungbean varieties suited to diverse agro-ecological conditions.

COMPETING INTERESTS DISCLAIMER:

Authors have declared that they have no known competing financial interests OR non-financial interests OR personal relationships that could have appeared to influence the work reported in this paper.

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