



Genetic variability and multivariate analysis for plant architecture and yield components in blackgram (*Vigna mungo* L. Hepper) under rainfed conditions

Muhammad Jawad*, Shahid Riaz Malik, Rana Abdul Samad, Tayyaba Asif, Muhammad Arshad

Crop Sciences Institute, NARC, Islamabad, Pakistan

Key words: Blackgram, Principal component analysis, Genetic analysis, Germplasm

<http://dx.doi.org/10.12692/ijb/24.1.39-46>

Article published on January 03, 2024

Abstract

Mashbean (*Vigna mungo*) plays a vital role in Pakistan's agriculture as a prominent Kharif season pulse crop. This study investigates 18 diverse Mashbean genotypes to enhance selection efficiency and improve genetic recombination. Over two Kharif seasons, utilizing ANOVA, correlation analysis, and Principal Component Analysis (PCA), the research explores yield-contributing parameters. Significant genotypic variations between pods per plant (PP) and yield (Y) was (1.3932**), however the lowest pod length showed non-significant correlation with yield (0.0619^{NS}). The average number of pods per plant ranges from (16.67±0.74) to (29.44±1.31) pods per plant while maximum yield was exhibited by MH-16 (796.10 ± 14.11) kg/ha followed by MH-8 (791.63±14.14)g. However, minimum number of pods per plant and yield were recorded to be (16.7±0.74). Genotypic correlations highlight associations between yield and days to maturity (DM), pods per plant (PP), cluster per plant (CP), and pods per cluster (PC). PCA identifies three key components, emphasizing yield-contributing traits, plant architecture, and direct selection based on pods per plant. The study provides insights for effective Mashbean crop improvement, emphasizing Pakistan's agriculture and reducing dependency on imports.

* Corresponding Author: Muhammad Jawad ✉ jawwad2206@gmail.com

Introduction

Blackgram *Vigna mungo* (L.) Hepper, ($2n=22$) is an important Kharif season pulse crop that occupies a particular place in Pakistan's agriculture. Locally it is known as Mashbean or Mash. It is considered an important pulse because of its high seed protein (25-26%), carbohydrates (60%), fats, minerals, and essential amino acids, and ability to fix nitrogen in the soil through nodules (Asif *et al.*, 2016). In Southeast Asia, this plant is widely grown due to its numerous advantages for both soil quality and human well-being (Das *et al.*, 2021). The global production of Blackgram is more than 8.5 million tons annually. India, Myanmar, and Thailand are the major producing countries. More than half of the total world's production is produced in India (Arya *et al.*, 2017). Myanmar is the largest exporter and exports more than 65 percent of its output. Pakistan imports more than 90 percent of its consumption.

The unavailability of stable-yielding varieties in the country is the major bottleneck for such a huge import of this crop. For the improvement and breeding of crops, the selection of promising parents is very important. For an effective breeding program, estimating genetic parameters i.e., heritability, genetic advance, and correlation coefficients among developmental and productive traits are instrumental. The magnitude of the contribution of different parameters toward seed yield can only be estimated through association studies (Mathivathana *et al.*, 2015). For effective selection, the knowledge of the relationship among the traits is necessary. Correlation analysis further improves the selection phenomenon by quantifying the interrelationship among the parameters and identifies the traits that influence directly or indirectly on yield. The proper selection of diverse parents is very important to develop segregants. The principal component analysis (PCA) enables the identification of genetic diversity available in the germplasm that helps to select diverse parents to enhance genetic recombination.

The present experiment was carried out to study the correlation among yield attributing parameters and

diversity in the available germplasm to enhance selection efficiency and improvement in genetic recombination through heterotic parents.

Materials and methods

The experiment was conducted on 18 diverse Mashbean genotypes from MH 1 to MH 18. The replicated trial was conducted in a randomized complete block design for consecutive 2 years during Kharif 2018 and Kharif 2019 at the Pulses experimental area, NARC, Islamabad at under rainfed conditions. Each plot consisted of 4 rows with 4m row length and 30cm row-to-row distance with 5cm plant-to-plant distance and 3 replications. To raise a healthy crop, all the cultural practices employed under rainfed conditions were followed. Mean values for 2 years were used for the estimation of the genetic variability for the studies attributes among the population. Days to maturity (DM) were recorded when an overall plot was 90 percent matured. Plant height (PH), lowest pod height (LPH), No. of pods/plant (PP), No. of seeds/pod (SP), 100-seed weight (HSW), Pod length (PL), Cluster/Plant (CP), Pods/Cluster (PC), Plant type (PT), and seed yield (Y) were recorded from five randomly selected plants from each plot. Data were recorded according to the Blackgram descriptor published by IBPGR in 1985. PCA Correlation analysis and ANOVA were performed in R Studio (Packages: FactoMiner, factoextra, corrplot, pcor, and lm).

Results and discussion

The analysis of variance indicated that all the genotypes based on studied parameters, plant height (PH), lowest pod height (LPH), number of pods per plant (PP), 100-seed weight (HSW), number of cluster per plant (CP) and yield (Y) were highly significant ($P < 0.001$), however (Days to maturity (DM), Pod length (PL), number of seeds per pod (SP) and number of pods per cluster (PC) were non-significant (Table 1). It was also verified that the genotypes showed as larger amount of variation for most of the studied traits. For instance, the earliest maturity was observed in MH-5 in 80.67 days whereas MH-14 took 86.67 days to mature. Similarly,

MH-13 showed a maximum height of 62cm in contrast to MH-16 which attained the plant height of 47.37 cm (Table 1 & Fig. 1). The maximum height of the lowest pod was observed in MH-16 i.e., (22.16 ± 3.13) cm from ground level (Table 1 & Fig. 1). All the genotypes produce 6-8 seeds per pod; therefore, this parameter was non-significant. The non-significance

of black gram genotypes for seeds per pod was also reported by Ghafoor *et al.* (2001). Simple selection for this parameter in the present germplasm is of no use. MH-12 has the highest number of pods per plant i.e., (26.44 ± 4.86), and also exhibited maximum value for 100-seed weight was observed in MH-12 which was (5.47 ± 0.17) g (Table 2 & Fig 2).

Table 1. Mean, Standard deviation (S.D), Range, Sum of squares (SS), Mean squares (MS) and Probability values for different traits of 18 genotypes in Mashbean.

| Traits | Mean | S.D | Range | SS | MS | Probability |
|--------|--------|--------|----------------|-----------|----------|-------------|
| DM | 83.87 | 1.75 | 80.67 - 86.67 | 166.09 | 9.77 | 0.158 |
| PH | 53.58 | 3.97 | 47.37 - 62.26 | 851.78 | 50.10 | < 0.001 |
| LPH | 18.32 | 1.71 | 14.96 - 22.16 | 158.34 | 9.31 | 0.024 |
| PL | 3.76 | 0.56 | 2.5 - 4.9 | 17.13 | 1.00 | 0.11 |
| SP | 6.63 | 0.78 | 5.00 - 7.67 | 32.59 | 1.91 | 0.24 |
| PP | 21.06 | 3.02 | 16.7 - 26.4 | 772.81 | 45.46 | < 0.001 |
| HSW | 4.82 | 0.24 | 4.47 - 5.47 | 3.18 | 0.18 | 0.004 |
| CP | 6.07 | 1.13 | 4.00 - 8.00 | 69.70 | 4.10 | 0.001 |
| PC | 3.59 | 0.39 | 2.67 - 4.33 | 8.37 | 0.49 | 0.33 |
| Y | 650.05 | 108.01 | 438.67 - 796.1 | 629934.23 | 37055.68 | < 0.001 |

However, this genotype showed poor performance in the context of yield (763.4 ± 16.02). MH-8 showed the maximum number of clusters/plants (8.00 ± 0.49) compared to MH-5 that exhibited (4.00 ± 0.49) clusters/plants (Table 2 & Fig. 2). On the other hand, MH-7 outperformed all the genotypes in terms of

pods per cluster followed by MH-12 with 4.33 and 4.17 pods per cluster, respectively (Table 1 & Table 2) Maximum yield (796.10 ± 14.11 kg/ha) was recorded in MH-16 compared with MH-18 that showed least yield (438.67 kg/ha) among all the 18 genotypes (Table 1, 2 & Fig. 2).

Table 2. Mean values of 18 genotypes for Days to maturity (DM), Plant height (PH), Lowest pod length (LPH), Pod length (PL), Number of seeds per pod (SP), Number of pods per plant (PP), 100-seed weight (HSW), Number of clusters per plant (CP), Number of pods per cluster (PC), Yield (Y).

| Genotype | DM | PH | LPH | PL | SP | PP | HSW | CP | PC | Y |
|----------|-------------|------------|------------|-----------|---------|-----------|-----------|-------------|----------|-------------|
| MH-1 | 85.67 abc | 49.72 fg | 14.96 e | 3.5 bcd | 6.33 ab | 20.67 abc | 4.67 cde | 7.00 abcd | 3.33 abc | 747.77 abc |
| MH-2 | 81.33 de | 53.2 def | 17.13 cde | 3.57 bcd | 6.0 ab | 17.33 c | 4.57 de | 5.00 efg | 3.50 abc | 472.23 g |
| MH-3 | 81.67 cde | 51.2 efg | 17.54 bcde | 3.77 abcd | 7.67 a | 25.33 ab | 4.87 bcde | 7.33 abc | 3.83 ab | 734.37 abc |
| MH-4 | 83.67 abcde | 51.43 efg | 16.81 de | 3.67 abcd | 6.33 ab | 20.33 abc | 4.47 e | 4.67 fg | 3.83 ab | 699.47 abcd |
| MH-5 | 80.67 e | 47.9 g | 16.47 de | 4.03 ab | 6.67 ab | 16.89 c | 4.7 bcde | 4.00 g | 3.67 abc | 482.73 fg |
| MH-6 | 85.33 abcd | 53.8 cdef | 17.17 cde | 4.00 ab | 7.0 ab | 20.33 abc | 5.03 bc | 6.67 abcde | 3.5 abc | 661 abcde |
| MH-7 | 85.3abcd | 54.47 cde | 19.07 abcd | 3.13 bcd | 6.0 ab | 24.78 ab | 4.67 cde | 5.67 cdefg | 4.33 a | 745.13 abc |
| MH-8 | 84 abcde | 61.6 ab | 18.1 bcde | 2.67 cd | 5.0 b | 25.78 ab | 4.6 de | 8.0 a | 4.00 ab | 791.63 a |
| MH-9 | 84.3 abcde | 53.63 cdef | 16.79 de | 4.17 ab | 7.33 a | 22.07 abc | 5.1 ab | 7.33 abc | 3.17 bc | 680.23 abcd |
| MH-10 | 82.3 bcde | 50.77 efg | 18.64 bcd | 4.17 ab | 7.33 a | 20.67 abc | 4.53 de | 6.67 abcde | 3.17 bc | 632.9 bcde |
| MH-11 | 82 cde | 53.3 def | 17.19 cde | 4.13 ab | 7.0 ab | 20.67 abc | 4.87 bcde | 5.0 efg | 4.00 ab | 643.5 bcde |
| MH-12 | 86.33 ab | 58 abc | 18.73 bcd | 4.9 a | 7.67 a | 26.44 a | 5.47 a | 6.67 abcde | 4.17 ab | 763.4 ab |
| MH-13 | 85 abcd | 62.27 a | 19.53 abcd | 4.17 ab | 7.0 ab | 19.67 bc | 4.83 bcde | 6.33 abcdef | 3.5 abc | 616.23 cdef |
| MH-14 | 86.67 a | 52.53 ef | 20.37 abc | 3.83 abc | 7.0 ab | 19.54 bc | 4.63 cde | 5.33 defg | 3.67 abc | 566.23 defg |
| MH-15 | 82 cde | 53.9 cdef | 20.67 ab | 3.33 bcd | 6.0 ab | 17.78 c | 4.83 bcde | 4.67 fg | 3.67 abc | 539.6 efg |
| MH-16 | 85 abcd | 47.37 g | 22.17 a | 2.5 d | 5.0 b | 24.44 ab | 5.03 bc | 7.67 ab | 3.33 abc | 796.1 a |
| MH-17 | 84 abcde | 51.83 efg | 19.63 abcd | 4.03 ab | 7.33 a | 19.68 bc | 4.9 bcd | 6.0 bcdef | 3.33 abc | 689.8 abcd |
| MH-18 | 84.33 abcde | 57.5 bcd | 18.83 abcd | 4.07 ab | 6.67 ab | 16.67 c | 5.03 bc | 5.3 defg | 2.67 c | 438.67 g |

The yield is a complex trait and highly influenced by environmental fluctuations, therefore direct selection based on yield may not be effective. However, selection based on other parameters that are less influenced by the environment and positively linked to higher yield may be effective.

Thus, the knowledge of association among the parameters is important to enhance the selection efficiency for the betterment of yield. Correlation estimates are presented in Table 3. Highly Positive significant values were observed between Plant height and lowest pod height. Plant height and lowest pod height didn't show any significant relation with other

parameters. Genotypes can be selected based on these parameters for mechanized harvesting. (Sohel *et al.*, 2016), (Chauhan *et al.*, 2007) and (Umadevi and Meenakshi, 2005) reported yield is negatively correlated with plant height in the Mashbean. For better plant types with higher yields, hybridization is needed. Pods per plant showed a highly significant positive correlation with yield. (Hadimani *et al.*, 2019) they reported similar correlations between pods/plants and yield. Johnson *et al.* (1955) concluded that the estimation of heritability values along with genetic advances holds greater significance in forecasting the anticipated advancements achievable through selection processes.

Table 3. Genotypic (G) and phenotypic (P) correlation coefficients among different traits for 18 Mashbean genotypes.

| | | DM | PH | LPH | PL | SP | PP | HSW | CP | PC | Y |
|-----|---|----|---------------------|------------------------|----------------------|----------------------|----------------------|----------------------|----------------------|----------------------|----------------------|
| DM | G | 1 | 0.465 ^{NS} | 0.844 ^{**} | 0.435 ^{NS} | 0.597 ^{**} | 0.812 ^{**} | 1.058 ^{**} | 1.05 ^{**} | 0.40 ^{NS} | 0.9867 ^{**} |
| | P | 1 | 0.229 ^{NS} | 0.022 ^{NS} | -0.111 ^{NS} | -0.128 ^{NS} | 0.205 ^{NS} | 0.034 ^{NS} | 0.104 ^{NS} | -0.045 ^{NS} | 0.157 ^{NS} |
| PH | G | | 1 | 0.247 ^{NS} | 0.115 ^{NS} | -0.163 ^{NS} | 0.247 ^{NS} | 0.316 ^{NS} | 0.212 ^{NS} | 0.184 ^{NS} | -0.018 ^{NS} |
| | P | | 1 | 9.00e-04 ^{NS} | 0.189 ^{NS} | 0.079 ^{NS} | 0.118 ^{NS} | 0.0928 ^{NS} | 0.160 ^{NS} | 0.191 ^{NS} | 0.041 ^{NS} |
| LPH | G | | | 1 | -0.870 ^{**} | -0.935 ^{**} | -0.086 ^{NS} | 0.419 ^{NS} | 0.051 ^{NS} | -0.056 ^{NS} | 0.062 ^{NS} |
| | P | | | 1 | -0.023 ^{NS} | -0.02 ^{NS} | 0.226 ^{NS} | 0.084 ^{NS} | 0.092 ^{NS} | -0.035 ^{NS} | 0.014 ^{NS} |
| PL | G | | | | 1 | 0.858 ^{**} | -0.629 ^{**} | 1.08 ^{**} | -0.645 ^{**} | -0.280 ^{NS} | -0.667 ^{**} |
| | P | | | | 1 | 0.922 ^{**} | -0.061 ^{NS} | 0.091 ^{NS} | -0.021 ^{NS} | -0.091 ^{NS} | -0.092 ^{NS} |
| SP | G | | | | | 1 | -0.242 ^{NS} | 1.229 ^{**} | -0.353 ^{NS} | -0.134 ^{NS} | -0.515 ^{**} |
| | P | | | | | 1 | -0.026 ^{NS} | 0.057 ^{NS} | 0.043 | -0.095 ^{NS} | 0.022 ^{NS} |
| PP | G | | | | | | 1 | 0.633 ^{**} | 0.939 ^{**} | 2.655 ^{**} | 1.393 ^{**} |
| | P | | | | | | 1 | 0.101 ^{NS} | 0.593 ^{**} | 0.086 ^{NS} | 0.547 ^{**} |
| HSW | G | | | | | | | 1 | 0.453 ^{NS} | -0.466 ^{NS} | 0.245 ^{NS} |
| | P | | | | | | | 1 | 0.183 ^{NS} | 0.026 ^{NS} | 0.11 ^{NS} |
| CP | G | | | | | | | | 1 | -0.486 [*] | 0.890 ^{**} |
| | P | | | | | | | | 1 | 0.032 ^{NS} | 0.559 ^{**} |
| PC | G | | | | | | | | | 1 | 1.256 ^{**} |
| | P | | | | | | | | | 1 | 0.214 ^{NS} |
| Y | G | | | | | | | | | | 1 |
| | P | | | | | | | | | | 1 |

Genotypic and phenotypic correlation was also observed in the discussed parameters. A highly significant positive genotypic correlation was found between yield and DM (0.9867^{**}), PP (1.3932^{**}), CP (0.8904^{**}) and PC (1.2561^{**}) (Table 3). In contrast, a highly negative correlation was found between yield and pod length (-0.6665^{**}). Other parameter's

genotypic correlation was found non-significant. In the case of phenotypic correlation of yield with other parameters highly significant positive correlation was observed with PP (0.5469^{**}) and CP (0.5586^{**}) while all the other parameters were found insignificant in correlation with yield and no negative correlation was found (Table 3).

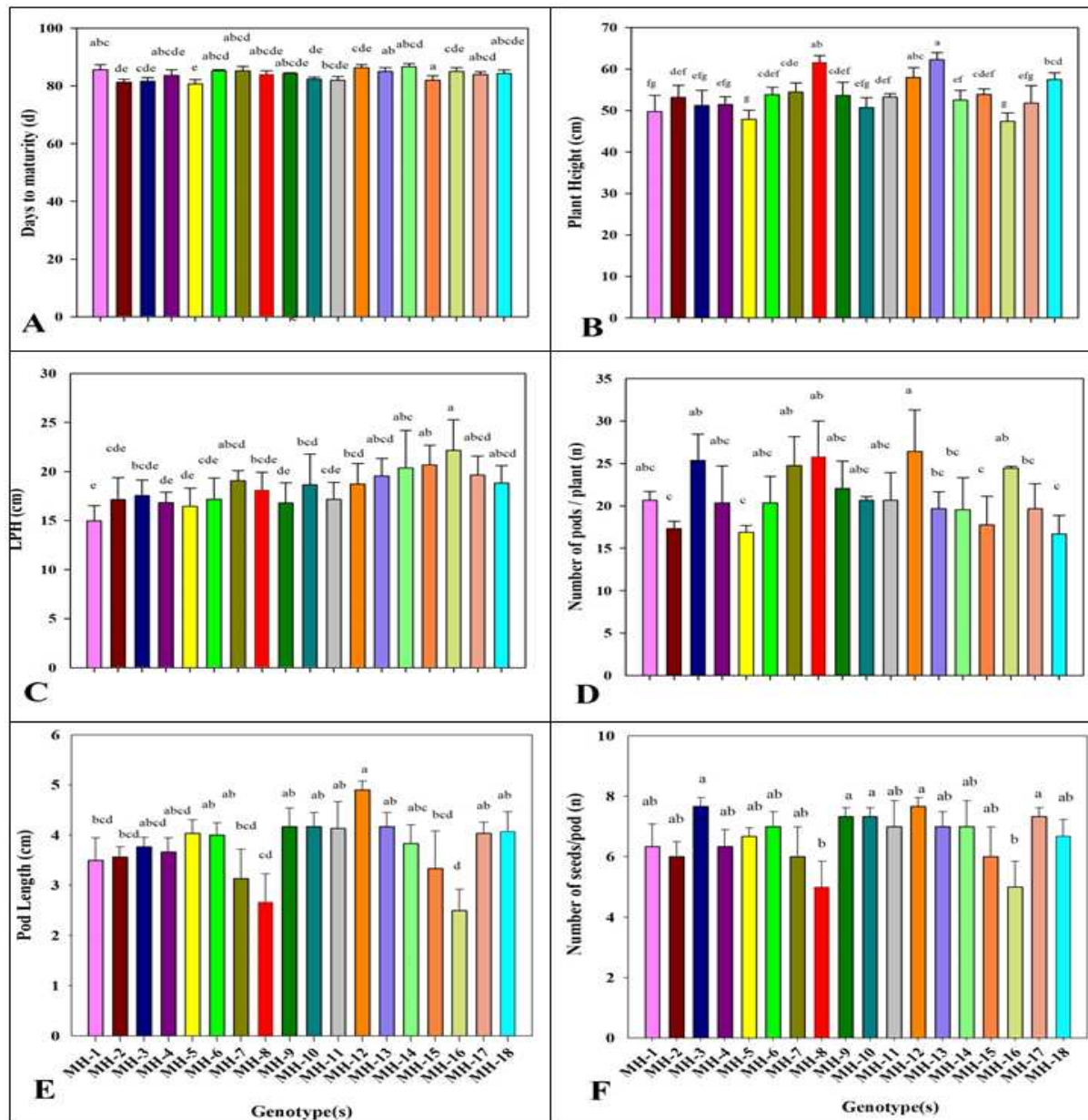


Fig. 1. Mean phenotypic performance of different Mashbean genotypes for the yield and its contributing attributes, A) Days to maturity (DM), B) Plant height (PH), C) Lowest pod length (LPH), D) Number of pods per plant (PP), E) Pod length (PL), F) Number of seeds per pod (SP).

*Values/treatments showing the same letters are statistically similar.

All genotypic and phenotypic correlations of all parameters are mentioned in the table. According to a study supporting our experiment, the count of seeds per pod exhibited a favorable genotypic direct impact on the grain yield per plant. Its indirect influences, mediated through factors like harvest index, days to 50 percent flowering, number of clusters per plant, 1000 grain weight, and plant height, played a significant role alongside its direct effect in establishing a positive correlation (Aman *et al.*,

2022). Sharma *et al.*, 2012 also supported our study by suggesting that Pods/plants exhibited a highly positive correlation with yield ($r=0.985$). Correlation coefficients between genotype, phenotype, and environment were calculated using the variances and covariances of their reseeded/productive elements, following the methodology pioneered by Singh *et al.*, in 1977. The results align closely with the findings presented in the research conducted by Kumar *et al.* (2014).

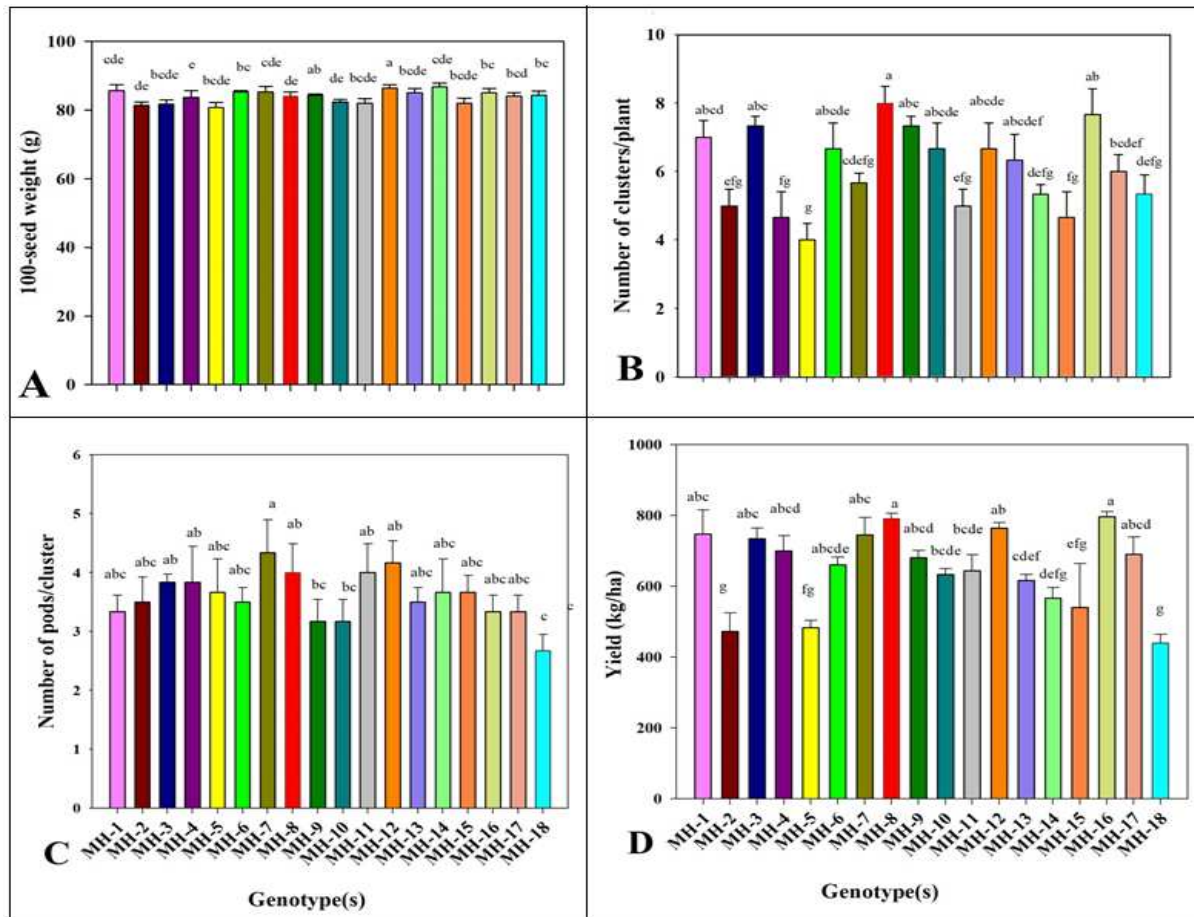


Fig. 2. Mean phenotypic performance of different Mashbean genotypes for the yield and its contributing attributes, A) 100-seed weight (HSW), B) Number of clusters per plant (CP), C) Number of pods per cluster (PC), D) Yield (Y).

*Values/treatments showing the same letters are statistically similar.

In this research, we conducted a Principal Component Analysis (PCA) to explore the underlying patterns of variability among a set of parameters. The cumulative proportion values for the first three principal components (PC1: 26.99%, PC2: 19.4%, PC3: 15.5%) collectively account for 61.89% of the total variance in the dataset (Fig. 3).

Our analysis revealed distinct clusters of parameters based on their positions in the principal component analysis biplot. Notably, three groups were identified. In cluster 1 parameters, namely seeds/pod and Plant height, exhibit similar patterns of variation. This implies a shared influence on the major sources of variability captured by PC1. In cluster 2 parameters pods/cluster, plant height, and lower plant height form a cohesive cluster, indicating common patterns of variation along both PC1 and PC2. These

parameters collectively contribute to the observed structure in the data. In cluster 3 parameters pods/plant, Cluster/plant, and yield form another distinct cluster, suggesting shared patterns of variation along PC1, PC2, and potentially PC3.

The arrangement of these parameters in the biplot indicates their joint influence on the observed variability (Fig. 3).

The biplot visually represents the relationships between variables and the distribution of samples in the seeds/pods defined by the principal components. Arrows in the biplot represent the direction and magnitude of the contribution of each variable to the corresponding principal component. Longer arrows indicate a stronger influence on that component (Fig. 3).

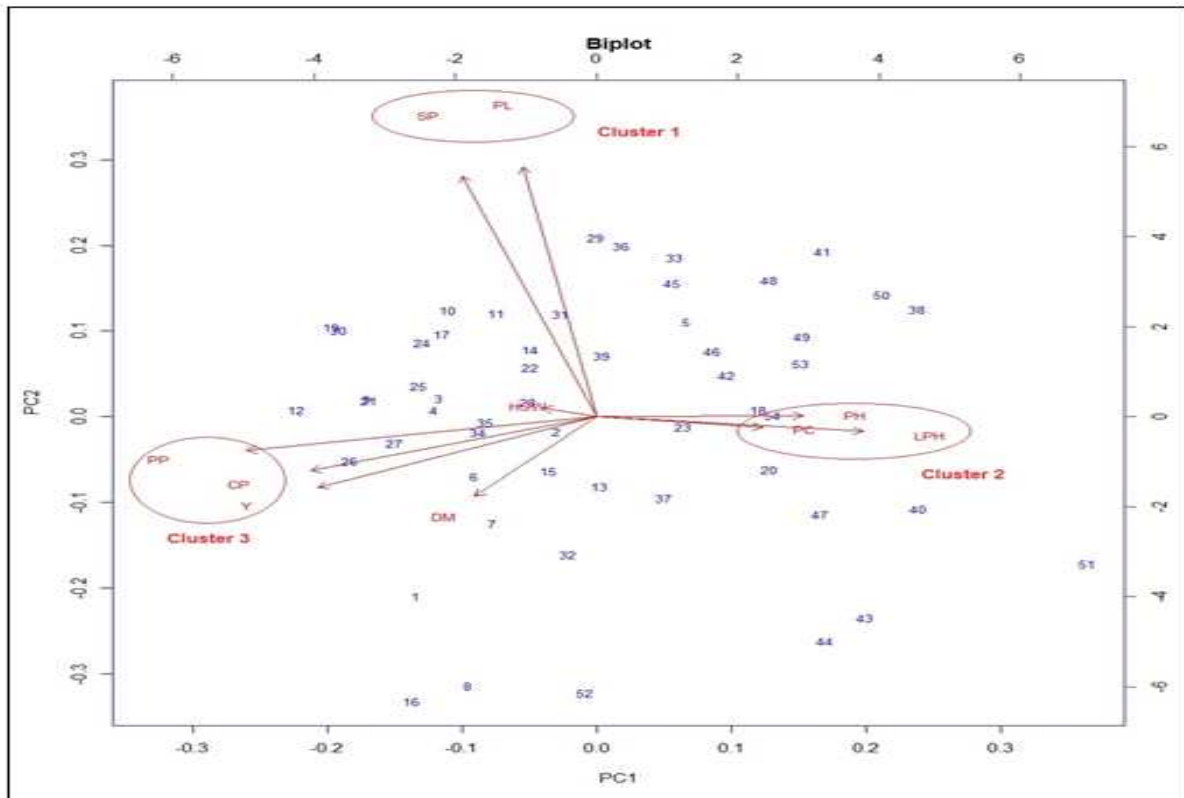


Fig. 3. Biplot diagram for clustering 18 genotypes of mashbean based on 10 yield related attributes.

The cumulative proportion values, while not exhaustive, provide a meaningful representation of the overall dataset variance captured by the top three principal components. Depending on the research objectives, consideration may be given to additional components if a more comprehensive explanation of variability is required.

Our principal component analysis analysis elucidates the inherent structure within the dataset, revealing distinct clusters of parameters with shared patterns of variation.

Conclusion

In conclusion, our study on 18 diverse Mashbean genotypes has shed light on significant genotype variations and positive correlations, particularly between pods per plant and yield. The analysis, employing ANOVA and Principal Component Analysis (PCA), underscores the critical role of selecting diverse parents for effective crop improvement. Notably, the negative correlation observed between yield-contributing parameters and plant architecture emphasizes the necessity of

hybridization for developing genotypes with higher yields and suitability for mechanized harvesting. Furthermore, we recommend prioritizing diverse parental lines in Mash bean breeding programs and focusing on hybridization to enhance plant types and overall crop efficiency. Long-term monitoring of selected genotypes under varying conditions is vital for understanding genotype-environment interactions and ensuring the stability of improved traits. Additionally, the integration of molecular techniques in future studies can expedite the breeding process by identifying specific genes associated with desirable traits. Collaboration among research institutions, agricultural experts, and policymakers is essential to address challenges and streamline the adoption of improved Mashbean varieties in Pakistan's agriculture. In summary, this research serves as a foundational step towards enhancing Mashbean crop productivity in Pakistan, contributing to national food security and reducing dependency on imports. The identified correlations and principal components provide a strategic way for targeted breeding strategies aligned with the dynamic needs of the agricultural landscape.

Author's contribution

M. Jawad and T. Asif conducted the experiment, gathered data, and authored the article. SR Malik conceptualized the idea and reviewed the manuscript. RA Samad analyzed the data, while M. Arshad provided technical insights at every stage and assisted in the experiment's execution.

References

Singh AK, Kumar S, Sharma M, Gupta N. 2022. Genetic variability and character association studies in Urdbean (*Vigna mungo* L.) under irrigated and rainfed conditions of Jammu region. *Annals of Agricultural Research* **43(2)**, 179-188.

Parveen SI, Sekhar MR, Reddy DM, Sudhakar P. 2011. Correlation and path coefficient analysis for yield and yield components in blackgram (*Vigna mungo* (L.) Hepper). *International Journal of Applied Biology and Pharmaceutical Technology* **2(3)**, 619-625.

Asif H, Konda CR, Nidagundi JM, Rajendragouda P. 2016. Genetic Variability analysis in black gram (*Vigna mungo* (L.) Hepper) based on quantitative traits. *Green Farming* **7(3)**, 598-601.

Chauhan MP, Mishra AC, Singh AK. 2007. Correlation and path analysis in urd bean. *Legume Research-An International Journal* **30(3)**, 205-208.

Das D, Baruah IK, Panda D, Paswan RR, Acharjee S, Sarmah BK. 2021. Bruchid beetle ovipositioning mediated defense responses in black gram pods. *BMC Plant Biology* **21**, 1-22.
<https://doi.org/10.1186/s12870-020-02796-4>.

Ghafoor A, Sharif A, Ahmad Z, Zahid MA, Rabbani MA. 2001. Genetic diversity in blackgram (*Vigna mungo* L. Hepper). *Field Crops Research* **69(2)**, 183-190.
[https://doi.org/10.1016/S0378-4290\(00\)00141-6](https://doi.org/10.1016/S0378-4290(00)00141-6).

Hadimani A, Konda CR, Kulkarni V. 2019. Correlation and path coefficient analysis for yield and yield components in Blackgram (*Vigna mungo* (L.) Hepper). *International Journal of Chemical Studies* **7(1)**, 2240-2243.

Johnson HW, Robinson HF, Comstock RE. 1955. Estimates of genetic and environmental variability in soybeans¹. *Agronomy journal* **47(7)**, 314-318.

Mathivathana MK, Shunmugavalli N, Muthuswamy A, Vijulan HC. 2015. Correlation and path analysis in black gram. *Agriculture Science Digest* **35(2)**, 158-160.

Sohel MH, Miah MR, Mohiuddin SJ, Islam AK, Rahman MM, Haque MA. 2016. Correlation and path coefficient analysis of Blackgram (*Vigna mungo* L.). *Journal of Bioscience and Agriculture Research* **7(02)**, 621-629.
<https://doi.org/10.18801/jbar.070216.74>

Sharma P, Sekhon HS, Bains TS. 2012. Performance and growth analysis in mash bean genotypes. *World Journal of Agricultural Sciences* **8(3)**, 303-308.

Singh RK, Chaudhary BD. 1977. Variance and covariance analysis. *Biometrical Methods in Quantitative Genetics Analysis*, Kalyani publishers, New Delhi, 39-68 p.

Umadevi M, Ganesan NM. 2005. Correlation and path analysis for yield and yield components in blackgram (*Vigna mungo* (L.) Hepper.). *Madras Agricultural Journal* **92(10-12)**, 731-734.