



Research Article

ASSESSMENT OF GENETIC DIVERSITY AMONG BLACK GRAM (*Vigna mungo* (L.) Hepper) ACCESSIONS USING MORPHOLOGICAL TRAITS

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Received: October 02, 2021; Revised: October 26, 2021; Accepted: October 27, 2021; Published: October 30, 2021

Abstract: Twenty germplasm accessions were raised in randomized block design during *Kharif* 2021 and evaluated for five quantitative traits. The morphological data were subjected to correlation and principal component analysis. The correlation studies revealed that number of pods and hundred seed weight were positive and significantly associated with single plant yield. Principal component analysis based on five quantitative traits identified two principal components contributing about 72.67 per cent to the total variability among the accessions studied. The variations in PC 1 were represented by yield traits, PC 2 by plant height and flowering characters. The number of pods per plant and hundred seed weight are the important yield attributing traits and could be utilized for further improvement in black gram breeding programmes.

Keywords: Blackgram, Correlation Analysis, Principal Component Analysis

Citation: Vignesh M., et al., (2021) Assessment of Genetic Diversity Among Black Gram (*Vigna mungo* (L.) Hepper) Accessions Using Morphological Traits. International Journal of Agriculture Sciences, ISSN: 0975-3710 & E-ISSN: 0975-9107, Volume 13, Issue 10, pp.- 10906-10908.

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Introduction

Black gram (*Vigna mungo* (L.) Hepper), also known as Urd bean is an erect, fast growing annual, herbaceous legume crop belonging to the family Leguminaceae and the genus *Vigna*. It is a self-pollinating crop having a well-developed tap root system and its stems are diffusely branched from the base. It is widely cultivated in Indian subcontinent and other Asian and South Pacific countries. India is the largest producer and consumer of black gram in the world [1]. The annual production of black gram in India is 3060 thousand tonnes from 5602 thousand hectares with an average productivity of 546 kg/ha [1]. Black gram seeds comprised of protein (25- 26%), carbohydrates (60%), fat (1.5%), minerals (3.2%) and moisture (10-11%). It is also a rich source of calcium (154mg/100gm), phosphorus (385mg/100gm) and iron (9.1mg/100gm). The calorific value of black gram is 347kcal/100gm [2].

Blackgram is resistant to adverse climatic conditions and fixes atmospheric nitrogen in the soil, enhancing soil fertility. The major constraints for achieving higher yield are lack of genetic variability, absence of suitable ideotypes for different cropping system, poor harvest index and susceptibility to biotic and abiotic stresses. Consideration of genetic diversity existing in a population is the basic requirement for effective improvement programme. Morphological characterization facilitates identification and selection for desirable traits [3].

Correlation or associate analysis enables to know about association of different characters to yield. Principal component analysis (PCA) and cluster analysis serve as tools in evaluating the phenotypic diversity and selecting important traits contributing to the total variation in the genotypes. These analyses provide information that could help in better selection of parental genotypes with specific traits for yield improvement in blackgram. With this background knowledge, the present study was undertaken with the following objectives: 1) To determine the traits closely associated with yield and 2) To assess the traits contributing for maximum variation among black gram accessions

Materials and Methods

The present investigation was carried out during *kharif* season of 2021 at Imayam Institute of Agriculture and Technology, Thuraiyur. A set of 20 blackgram accessions were used for the study. The genotypes were raised in Randomized Block Design (RBD) with three replications. Each genotype was sown in a row of four-meter length in ridges and furrows with the spacing of 30 cm × 10 cm. All the recommended agronomic practices were made throughout the crop growth period. The quantitative traits were recorded based on descriptors of blackgram [4]. The traits viz., plant height, days to fifty per cent flowering, number of pods per plant, hundred seed weight and single plant yield were recorded on ten randomly selected plants in each accession. Correlation analysis was performed using the software TNAU STAT [5]. Principal Component Analysis was performed using the statistical package SPSS 16.0 version.

Results

Analysis of variance revealed that there was highly significant difference among the characters under study viz., plant height, days to fifty per cent flowering, number of pods per plant, hundred seed weight and single plant yield. The simple correlation analysis [Table-1] revealed that the traits number of pods per plant (0.686) and hundred seed weight (0.681) showed significant positive association with single plant yield. The mean data of five quantitative traits were subjected to principal component analysis to identify plant traits which contribute most towards the observed variation. PCA analysis revealed that the first two components in the PCA analysis contributed to a maximum of 72.67 per cent of the variability. These two principal components were retained based on the scree plot and threshold Eigen value greater than 1 [Table-2, Fig-1]. The Eigen values for PC 1 and PC 2 were 2.06 and 1.57 respectively.

The first principal component (PC 1) accounted for 41.23 per cent of the total variability and comprised of yield traits contributed in a positive direction.

The traits contributed to a maximum variation in first component includes, number of pods per plant (0.757) and hundred seed weight (0.731) which tends to increase the single plant yield (0.977). Plant height contributed negatively to PC 1. The second principal component (PC 2) contributed 31.44 per cent of the total variability. The traits contributed to variation in the second component include plant height (0.253) and days to fifty per cent flowering (0.914). The trait number of pods per plant contributed negatively to PC 2.

Table-1 Correlations between single plant yield and independent traits of blackgram accessions

	PH	DFPF	PPP	HSW	SPY
PH	1				
DFPF	0.064	1			
PPP	-0.034	-0.486	1		
HSW	0.094	0.437	0.015	1	
SPY	-0.050	0.078	0.686*	0.681*	1

* Significant at 5% probability, PH: Plant height, DFPF: Days to fifty per cent flowering, PPP: Number of pods per plant, HSW: Hundred seed weight, SPY: Single plant yield

Table-2 Eigen values, percent of total variation and cumulative variation among eight quantitative traits of blackgram accessions

Traits	Eigen vectors	
	PC 1	PC 2
Plant height	-0.020	0.253
Days to 50 percent flowering	0.003	0.914
No. of pods/plant	0.757	-0.567
Hundred seed weight	0.731	0.594
Single plant yield	0.977	0.002
Eigen value	2.06	1.57
Proportion of variation	41.23	31.44
Cumulative proportion	41.23	72.67

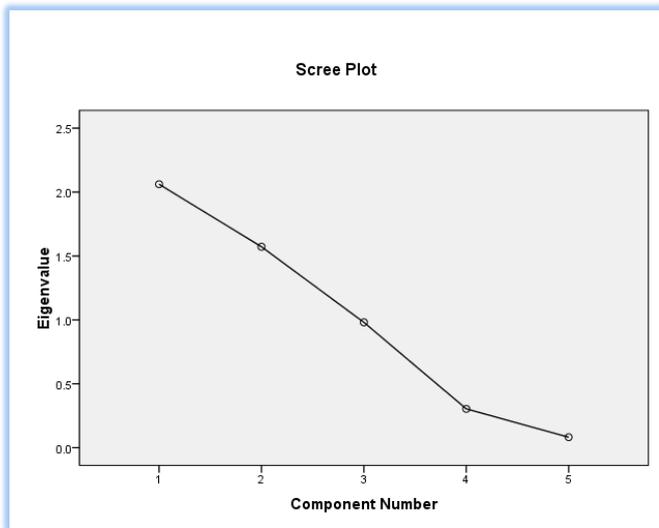


Fig-1 Scree plot

Discussion

The yield is an extremely complex quantitative character. Studying the association between yield and interrelationship among yield components enables the breeder for simultaneous improvement of these traits. Number of pods per plant and hundred seed weight showed a significant positive association with single plant yield. Mathivathana, et al., (2015); Mehra, et al., (2016); Bandi, et al., (2018); Shanthi, et al., (2019); Saran, et al., (2020) [6-10] reported similar findings for number of pods per plant, while Mathivathana, et al., (2015); Mehra, et al., (2016); Soheli, et al., (2016) [11] reported a similar finding for hundred seed weight in blackgram. Selection of parents based on these traits can help in yield improvement in blackgram.

PCA is an Eigen vector based multivariate analysis. It reduces the dimension of a large data set by transforming a number of possibly correlated variables into a smaller number of uncorrelated variables known as principal components. In the present study, PCA identified two principal components contributing to a maximum 72.67 per cent of the total variation seen among the 10 accessions.

The first principal component PC 1, explained 41.23 per cent of the total variation and was characterized by yield contributing characters viz., number of pods per plant, hundred seed weight and single plant yield. From PC 1 it was evident, that an increase in number and size of seeds led to an increased single plant yield in blackgram genotypes. The similar findings were reported by Ghafoor, et al., (2001); Ghafoor and Ahmad (2003); Mohanlal, et al., (2018) [12-14].

PC 2 accounted for 31.44 per cent of the total variation and was contributed by the trait's days to fifty per cent flowering and plant height. Here, an increase in days to flowering and height resulted in an increase in the hundred seed weight. The similar findings were reported by Nisar, et al., (2008); Rajasekhar, et al., (2020); Rajasekhar, et al., (2017) [15-17].

Conclusion

A set of 20 blackgram genotypes was characterized at morphological level to study the extent of genetic diversity present in the genotypes. In correlation studies, two traits number of pods per plant and hundred seed weight were positively and significantly correlated with single plant yield. Principal component analysis revealed that, the first two principal components contributed to a maximum of 72.67 per cent of variability present among the genotypes. All the traits studied had greater contribution in the divergence of the germplasm.

Application of research: The selection strategy in blackgram improvement programme can be formulated based on understanding the correlation and variation exhibited by the quantitative traits of mungbean.

Research Category: Plant Breeding and Genetics

Abbreviations: PCA-Principal Component Analysis

PC-Principal Component

RBD-Randomized Block Design

Acknowledgement / Funding: Authors are thankful to Department of Plant Breeding and Genetics, Imayam Institute of Agriculture and Technology, Thuraiyur, 621 206, Tamil Nadu Agricultural University, Coimbatore, 641003, Tamil Nadu, India.

****Research Guide or Chairperson of research:** Dr S. M. Samyuktha

University: Tamil Nadu Agricultural University, Coimbatore, 641003, India

Research project name or number: Research station study

Author Contributions: All authors equally contributed

Author statement: All authors read, reviewed, agreed and approved the final manuscript. Note-All authors agreed that- Written informed consent was obtained from all participants prior to publish / enrolment

Study area / Sample Collection: Imayam Institute of Agriculture and Technology, Thuraiyur

Cultivar / Variety / Breed name: Black Gram (*Vigna mungo* (L.) Hepper)

Conflict of Interest: None declared

Ethical approval: This article does not contain any studies with human participants or animals performed by any of the authors.

Ethical Committee Approval Number: Nil

References

- [1] Ministry of Agriculture and Farmers Welfare, Department of Agriculture, Cooperation and Farmers Welfare, Government of India, (2018)18.
- [2] Mishra A. and Lavanya R. (2021) *International Journal of Current Microbiology and Applied Sciences*, 10(1), 372-381.

- [3] Ghafoor A. and Arshad M. (2008) *Pakistan Journal of Botany*, 40(6), 2307-2313.
- [4] IBPGR. Descriptors for *Vigna mungo* and *Vigna radiata* (Revised). (1985) *International Board for Plant Genetic Resources, Rome*.
- [5] Manivannan N. (2014) *TNAU STAT-Statistical package*. Retrieved from <https://sites.google.com/site/tnaustat>.
- [6] Mathivathana M.K., Shanmugavalli N., Muthuswamy A. and Harris C.V. (2015) *Agricultural Research Communication Centre*, 35(2), 158-160.
- [7] Mehra R., Tikle A.N., Saxena A., Munjal A., Rekhakhandia and Singh M. (2016) *International Research Journal of Plant Science*, 7(1), 1-11.
- [8] Bandi H.R.K., Rao K.N. Krishna K.V. and Srinivasalu K. (2018) *International Journal of Current Microbiology and Applied sciences*, 7(3), 3304-3309.
- [9] Shanthy P., Ganesan K.N., Manivannan N. and Natarajan C. (2019) *Electronic Journal of Plant breeding*, 10(3), 1218-1222.
- [10] Saran R., Sharma P.P. and Tan H.K. (2020) *International Journal of Current Microbiology and Applied Sciences*, 9(4), 2029-2033.
- [11] Sohail M.H., Miah M.R., Mohinddin S.J., Islam A.K.M.S., Rahman M.M. and Haque M.A. (2016) *Journal of Bioscience and Agriculture Research*, 7(2), 621-629
- [12] Ghafoor A., Sharif A., Ahmad Z., Zahid M.A. and Rabbani M.A. (2001) *Field Crops Research*, 69, 183-190.
- [13] Ghafoor A. and Z.Ahmad. (2003) *Pakistan Journal of Botany*, 35(2), 187-196.
- [14] Mohanlal V.A., Saravanan K. and Sabesan T. (2018) *Journal of Pharmacognosy and Phytochemistry*, 7(6), 860-863.
- [15] Nisar M., Ghafoor A., Ahmad H., Khan M.R., Qureshi A.S., Ali H. and Islam M. (2008) *Pakistan Journal of Botany*, 40(5), 2081-2086.
- [16] Rajasekhar D., Yadav B.N.P., Hemalatha K., Ranjithkumar G. and Lal G.M. (2020) *The Bioscan- An International Quarterly Journal of Life Science*, 15(2), 257-259.
- [17] Rajasekhar D., Lal S.S. and Gabriel M.L. (2017) *Plant Archives*, 17(1), 467-471.