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Principal Component Analysis for Yield in Black Gram Genotypes (*Vigna mungo* L. Hepper) under Rice Fallow Pulse Cropping System

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ABSTRACT: This study was conducted to analyze the yield component traits in advanced black gram lines using principal component analysis (PCA) to identify effective selection criteria for grain yield improvement and to highlight superior genotypes based on key principal components. PCA was applied to eleven quantitative traits, and among the eleven principal components (PCs), only four had eigenvalues greater than 1.00, revealing the essential features of the dataset. These four principal components explained 89.23% of the total variability. PC1, which accounted for the highest variability, was mainly associated with vegetative traits like days to 50% flowering, days to maturity, and yield-related attributes such as grains per pod and test weight. PC2 was influenced by traits such as pod length and the number of branches per plant. LBG 787, located at the negative end of PC1, was identified as a short-duration genotype, while LBG 1002 and TBG 138 were recognized as long-duration genotypes. TBG 138 was found to be superior across all traits, particularly those captured by the first two principal components, which together explained 64.75% of the variability.

Keywords: Black gram, Eigenvalues, Factor-loading, Principal component analysis, Yield.

INTRODUCTION

Black gram (Vigna mungo L. Hepper), commonly known as urdbean, is an important crop within the Asian Vigna species. While it is a dietary staple in Central and Southeast Asia, it is primarily cultivated in India and has also expanded to regions like the southern United States, the West Indies, Japan, and other tropical and subtropical areas (Malarkodi et al., 2020). India stands as the largest producer and consumer of black gram, with cultivation covering approximately 3.26 million hectares, yielding about 1.76 million tonnes annually. Black gram is a short-duration, self-pollinated diploid legume (2n = 22) with a relatively small genome size (Reddy et al., 2021). In India, pulse productivity is less than half of that in the USA and Canada, primarily due to reliance on rainfed areas with variable rainfall. In southern states like Andhra Pradesh, Tamil Nadu and Karnataka, 20% of the rice fallow pulse area is utilized for black gram cultivation (Subbarao et al., 2001). Particularly in Srikakulam district, rice fallow cultivation contributes significantly to the production of black gram and green gram. However, farmers are currently achieving lower yields of 3.75-5.00 q/ha, compared to the crop's potential yield of 15.0-20.0 q/ha.

To meet the increasing demand for pulses, India needs to enhance production while maintaining competitiveness to protect domestic output (Rana *et al.*,

2022). This requires the development and adoption of more efficient crop production technologies, supported by favourable policies and market mechanisms, to encourage the expansion of pulse cultivation (Meena et al., 2021). A key challenge to improving pulse productivity remains the lack of stable and reliable markets. Multivariate statistical methods, such as Principal Component Analysis (PCA), are useful in summarizing and describing the genetic variation among genotypes (Manojkumar et al., 2017). PCA is commonly employed to identify key plant traits that differentiate genotypes and classify populations based on trait similarities, aiding in hybridization by selecting appropriate parent plants (Duppala et al., 2018). Furthermore, principal components can serve as criteria in subsequent analyses (Barik et al., 2021). This study aims to identify superior genotypes and critical traits using PCA. The research focused on advanced breeding lines of black gram with desirable characteristics, targeting high-yield varieties suited to the needs of farmers in Andhra Pradesh and Telangana. It reports the extent of genetic variability, interrelationships, path coefficients, and principal component analysis of grain yield and yield-contributing traits in these advanced breeding lines of black gram.

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MATERIAL AND METHODS

This investigation was conducted at the Agricultural Research Station, Ragolu, located at 83.240° E longitude and 18.240° N latitude, with an altitude of 27m above mean sea level (MSL) and an annual rainfall of 1111 mm over 57 rainy days in the North-Coastal districts of Andhra Pradesh. Genetically pure seeds of 12 advanced breeding lines, developed by Acharya N.G. Ranga Agricultural University (ANGRAU), Andhra Pradesh, were used for the study. These 12 lines were sown under a rice fallow pulse cropping system within eight rows of for meters length with a spacing of 30×10 cm, in three replications, across eight rows during the Rabi season of 2022-2023 at the Agricultural Research Station, Ragolu. All recommended agronomic practices and crop protection measures were followed throughout the growth period to ensure a healthy crop.

Data on twelve traits—days to 50% flowering, days to maturity, plant height, number of branches per plant, number of clusters per plant, number of pods per cluster, pod length, number of pods per plant, number of grains per pod, test weight, and seed yield per hectare—were recorded from five randomly selected plants for each entry in three replications. The collected data was then subjected to statistical analysis. Principal Component Analysis (PCA) was performed following the procedure outlined by Banfield (1978). Statistical analysis was conducted using R software version 4.3.1 to generate association plots, while SPSS 16.0 software was employed to display frequency distributions of the traits in the form of histograms.

RESULTS AND DISCUSSION

Multivariate analysis, specifically principal component analysis (PCA) and cluster analysis, has been widely used to assess genotypes and evaluate various traits (Rajasekhar et al., 2020). While PCA helps to identify relationships between traits and classify genotypes, cluster analysis focuses on grouping previously unclassified genotypes (Reni et al., 2022). PCA simplifies complex datasets by reducing their dimensionality, uncovering underlying structures. It is particularly useful for summarizing observed variables into a smaller number of artificial variables, called principal components, which capture most of the variation in the data. The first step in PCA involves calculating eigenvalues, which represent the amount of total variation displayed on the principal component axes. The first principal component (PC1) accounts for the majority of the variability, followed by subsequent PCs, each explaining additional variability not captured by the preceding components (Kumar et al., 2022).

In this study, PCA was applied to eleven quantitative traits of black gram. Of the eleven principal components (PCs), only four exhibited eigenvalues greater than 1.00, indicating that these four PCs capture the fundamental characteristics of the dataset, as similarly observed by (Dalai *et al.*, 2021). The four principal components (PC1, PC2, PC3 and PC4) accounted for 89.23% (Table 1 and Fig. 1) of the total

variability among the traits. PC1 explained 38.45% of the variability, PC2 26.30%, PC3 14.21% and PC4 10.28%. A rotated component matrix (Table 2) showed that PC1 was negatively associated with traits such as the number of branches per plant (-0.23), number of clusters per plant (-0.42), number of pods per cluster (-0.44), pod length (-0.29), number of pods per plant (-0.38) and seed yield (-0.33), but positively related to the number of grains per pod (0.20) and vegetative traits like days to 50% flowering (0.17) and days to maturity (0.14). PC2 was more strongly related to the number of branches per plant (0.25) and pod length (0.16) and negatively associated with traits like days to 50% flowering (-0.51) and days to maturity (-0.52).

PC3 highlighted yield-related traits such as the number of pods per cluster (0.22) and number of pods per plant (0.36), though it showed a negative relationship with factors like the number of branches per plant (-0.33), pod length (-0.24) and test weight (-0.60). These results suggest that PC3 emphasizes genotypes that produce more pods per plant with fewer, lighter seeds, tending toward fewer large reproductive structures (Jeberson et al., 2019). PC4 was positively associated with traits like the number of branches per plant (0.47), number of clusters per plant (0.40) and seed yield (0.15), but negatively with pod length (-0.63) and the number of grains per pod. The rotated component matrix confirmed that the first four PCs represented most of the variability (89.23%), indicating that the traits represented by these PCs should be prioritized in breeding programs (Mohanlal et al., 2018).

Fig. 2 illustrated that all eleven variables had high loadings on different principal components after varimax rotation, grouping similar variables together on common factors. The traits were distributed based on their performance relative to the first two principal components, with most showing significant relationships to the variance, displaying either positive or negative loadings. The first principal component had high positive loadings for days to 50% flowering and days to maturity, while the second principal component had high positive loadings for pod length and the number of branches per plant (Sridhar et al., 2020). Table 3 showed that TBG 138, GBG 164, and LBG 1001 contributed significantly to PC1, while LBG 787, TBG 138, and GBG 1 were major contributors to PC2. For PC3, LBG 1003, LBG 752, and PBG 278 had the highest contributions, whereas GBG 164, GBG 137, and GBG 1 were leading contributors to PC4. Fig. 3 and 4 depict the distribution of black gram genotypes based on their performance in relation to the first two principal factors. Genotypes positioned at the positive end of PC1, such as LBG 1002, PBG 278, and TBG 138, were identified as late-maturing types with high test weights. Meanwhile, genotypes positioned at the positive end of PC2, including GBG 137, GBG 164, and TBG 138, were associated with longer pods and more branches, contributing to grain yield (Thirumalai and Murugan 2020). Based on this investigation, TBG 138 was identified as the superior genotype across all traits.

Table 1: Eigen analysis of the Correlation Matrix.

Components	Principal component analysis										
_	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11
Eigen Value (Roots)	4.23	2.89	1.56	1.13	0.47	0.39	0.19	0.09	0.03	0.02	0.00
Explained % of variance	38.45	26.30	14.21	10.28	4.25	3.54	1.72	0.79	0.26	0.21	0.00
Cumulative % of variance	38.45	64.75	78.96	89.23	93.48	97.01	98.73	99.52	99.78	100.00	100.00

Table 2: Component loading of different characters in blackgram (Vigna mungo L.).

Variables studied	Principal components / Factors/ Eigenvectors										
variables studieu	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11
Days to 50 per cent flowering (DFF)		-0.51	0.06	0.07	0.22	-0.47	0.07	-0.03	0.27	0.45	0.40
Days to maturity (DM)	0.14	-0.52	0.06	0.04	0.44	0.22	-0.36	-0.18	-0.43	-0.03	-0.35
Plant height (PH)	-0.19	-0.48	-0.09	0.00	-0.29	0.56	0.16	0.38	-0.12	0.01	0.38
Number of branches per plant (NBPP)	-0.23	0.25	-0.33	0.47	0.52	0.25	-0.14	0.28	0.25	0.24	0.00
Number of clusters per plant (NCPP)	-0.42	-0.02	0.09	0.40	-0.15	0.07	0.40	-0.57	-0.19	0.31	-0.11
Number of pods per cluster (NPPC)	-0.44	-0.05	0.22	-0.09	-0.08	0.10	-0.62	-0.35	0.35	-0.13	0.28
Pod length (PL)	-0.29	0.16	-0.24	-0.63	0.06	-0.04	-0.11	0.03	-0.31	0.56	0.01
Number of pods per plant (NPPP)	-0.38	-0.15	0.36	0.18	-0.24	-0.34	-0.18	0.52	-0.03	0.13	-0.43
Number of grains per pod (NGPP)	0.34	-0.29	-0.13	-0.38	0.27	0.01	0.41	-0.03	0.45	-0.27	-0.36
Test weight (TW)	0.20	-0.20	-0.60	0.09	-0.49	0.01	-0.25	-0.14	0.27	0.18	-0.34
Seed yield per ha (SY)	-0.33	-0.10	-0.50	0.15	0.03	-0.47	-0.05	0.00	-0.37	-0.44	0.23

Table 3: PCA scores of divergences in black gram (Vigna mungo L.) genotypes.

Genotypes	Dim.1	Dim.2	Dim.3	Dim.4	Dim.5	Dim.6	Dim.7	Dim.8	Dim.9	Dim.10	Dim.11
GBG 190	7.20	1.56	0.04	1.27	31.53	5.07	31.50	1.00	0.18	1.96	2.73
TBG 104	0.37	0.25	0.65	5.26	1.46	34.18	1.86	5.44	6.93	14.95	12.67
LBG 1001	12.62	3.41	5.27	5.38	0.01	15.95	0.00	0.24	0.59	4.32	36.23
GBG 164	17.39	2.08	2.83	39.89	4.41	0.01	2.66	4.96	9.66	0.05	0.08
PBG 278	0.34	4.60	13.29	0.45	16.83	5.95	0.46	5.33	20.17	16.57	0.03
LBG 1002	6.68	12.26	2.23	0.50	11.14	6.66	5.37	11.23	19.37	1.69	6.90
TBG 138	19.61	13.04	1.59	1.86	0.98	3.64	19.18	17.08	3.81	1.10	2.14
LBG 752	4.47	0.68	13.73	0.43	14.32	14.07	10.24	11.14	3.11	8.35	3.47
LBG 1003	7.31	0.05	36.41	1.36	2.57	2.13	15.07	0.04	0.64	13.73	4.72
LBG 787	1.81	40.75	4.70	9.12	3.78	1.55	0.00	12.37	1.96	1.42	6.58
GBG 137	5.69	0.03	8.48	17.44	4.41	0.39	3.70	18.16	2.80	21.09	1.84
GBG 1	8.18	12.94	2.43	8.72	0.22	2.06	1.62	4.69	22.46	6.42	14.28



Fig. 1. Estimation of variance in black gram (Vigna mungo L.) genotypes.





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Fig. 3. Distribution of genotypes on the major principal components.



Fig. 4. Distribution of genotypes and variables on the major principal components.

CONCLUSIONS

The traits identified as key contributors to divergence include days to 50% flowering, days to maturity, number of grains per pod, test weight, pod length, and number of branches per plant. Among these, the number of grains per pod emerged as the primary selection trait based on principal component analysis. LBG 787, positioned at the negative end of PC1, was identified as a short-duration genotype, while LBG 1002 and TBG 138 were categorized as long-duration genotypes. TBG 138 stood out as superior across all traits, as reflected in the first two principal components, which together accounted for 64.75% of the variability.

FUTURE SCOPE

The promising genotypes identified in the present study, need to be evaluated across seasons and locations prior to their potential commercial exploitation as high yielding genotype with early duration. Grains per pod is the effective attribute for yield promotion and selection factor identified for direct selection. TBG 138 was identified as potential yielder in rice fallow pulse situations in north coastal zone of Andhra Pradesh.

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REFERENCES

Banfield, C. F. (1978). Multivariate analysis in genstat. Journal of Statistical Computation and Simulation., 6(4), 211-222.

- Barik, B. R., Lenka, D., Agarwal, A. K., Mishra, A., Nayak, G. and Tripathy, S. K. (2021). Genetic Variation and Extent of Genetic Diversity in Urdbean [Vigna mungo (L.) Hepper]. Biological Forum– An International Journal, 13(3a), 556-561.
- Dalai, S. K., Bishnoi, R. and Lal, G. M. (2021). Multivariate Analysis in Blackgram (Vigna mungo (L.) Hepper). International Journal of Agricultural Science and Research, 11(2), 141-148.
- Duppala, M. K., Beena, N., Gowtham, K. S. and Rathod, A. (2018). Evaluation of Advanced Breeding Lines of Indian Mustard using Principal Component Analysis. *Journal of Oilseed Brassica*, 9(1), 45-48.
- Jeberson, M. S., Shashidhar, K. S. and Singh, A. K. (2019). Genetic variability, principal component and cluster analyses in black gram under Foot-hills conditions of Manipur. Legume Research-An International Journal, 42(4), 454-460.
- Kumar, B. V., Lal, G. M., Reddy, Y. V. S., Kumar, E. S. and Bhupal, G. (2022). Prinicipal Component Analysis and Traits Association in Blackgram (*Vigna mungo* (L.) Hepper). *International Journal of Plant & Soil Science*, 34(23), 37-48.
- Malarkodi, A., Murugan, S., Anandan, R., Thirumalai, R. and Padmanaban, J. (2020). Assessment of genetic diversity for yellow mosaic virus resistance in black gram cultivars based on molecular and morphological studies. *Plant Archives*, 20(1), 1153-1163.
- Manojkumar, D., Beena, N and Gowtham, K. S. (2017). Evaluation of Advanced Lines of Mustard Spp. Using Hierarchical Cluster Analysis. *The Bioscan.* 10 (1), 299-307.
- Meena, S., Sharma, N. K., Sharma, A. K., Kumar, R. and Gour, G. (2021). Study of Genetic Variability Parameters for Seed Yield and Component Traits in Mothbean [Vigna aconitifolia (Jacq) Marechal] under Arid Environment. Biological Forum– An International Journal, 13(3a), 180-182.

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- Mohanlal, V. A., Saravanan, K. and Sabesan, T. (2018). Multivariate analysis in blackgram (*Vigna mungo* (L) hepper) genotypes. *Journal of Pharmacognosy and Phytochemistry*, 7(6), 860-863.
- R Core Team (2022) R: A Language and Environment for Statistical Computing. R Foundation for Statistical Computing, Vienna, Austria. <u>http://www.Rproject.org/</u>
- Rajasekhar, D., Yadav, B. N. P., Hemalatha, K., Ranjithkumar, G., & Lal, G. M. (2020). Multivariate Analysis in Blackgram (*Vigna mungo* (L.) Hepper). *The Bioscan*, 15(2), 257-260.
- Rana, V. B., Makati, J. P., Chaudhary, Rutvik J. Joshi, Shivangi Vanapariya, Zarna, S. Shah, A. V. Malaviya and Sanyam Patel (2022). Evaluation of Genetic Variability Parameters in 185 F₃ Progenies of Black Gram [*Vigna mungo* (L.) Hepper] for Seed Yield and Related Components. *Biological Forum– An International Journal*, 14(4), 1056-1060.
- Reddy, A. K., Priya, M. S., Reddy, D. M. and Reddy, B. R. (2021). Principal Component Analysis for Yield in

Blackgram (*Vigna mungo* L. Hepper) under Organic and Inorganic Fertilizer Managements. *International Journal of Plant & Soil Science*, *33*(9), 26-34.

- Reni, Y. P., Ramana, M. V., Rajesh, A. P., Madhavi, G. B. and Prakash, K. K. (2022). Principal component analysis for yield and quality traits of black gram (*Vigna mungo* (L.) Hepper). *International Journal of Plant & Soil Science*, 34(7), 38-47.
- Subbarao, G. V., Kumar Rao, J. V. D. K., Kumar, J., Johansen, C., Deb, U. K., Ahmed, I. and Harris, D. (2001). Spatial distribution and quantification of ricefallows in South Asia: potential for legumes, 9(1), 114.
- Sridhar, V., Prasad, B. V., Shivani, D. and Rao, S. S. (2020). Evaluation of genetic divergence in black gram (*Vigna mungo* L.) genotypes by D2 statistic. *International Journal of Chemical Studies.*, 8(1), 1236-1239.
- Thirumalai, R., & Murugan, S. (2020). Multivariate analysis in blackgram (*Vigna mungo* (L.) Hepper) genotypes for Mungbean Yellow Mosaic Virus (MYMV) resistance. *Plant Archives*, 20(1), 2473-2480.

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