International Journal of Advanced Biochemistry Research

ISSN Print: 2617-4693
ISSN Online: 2617-4707
NAAS Rating (2025): 5.29
IJABR 2025; SP-9(9): 1673-1675
www.biochemjournal.com
Received: 24-07-2025
Accepted: 29-08-2025

Genetic divergence analysis in black gram (*Vigna mungo* L.)

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DOI: https://www.doi.org/10.33545/26174693.2025.v9.i9Su.5748

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Abstract

The present investigation was carried out to study the extent of genetic divergence among seven black gram (*Vigna mungo* L.) genotypes, namely AKU-15, PDKV Black Gold AKV, Phule Vasu, PU0609-43, BDU-1, Urdbean Tapu-4, and Phule Rajan. The experiment was conducted in a randomized block design with three replications during Kharif 2024 at the experimental farm of [Your Institute]. Data were recorded on ten quantitative traits. Genetic divergence was estimated using Mahalanobis' D^2 statistics. The genotypes were grouped into three clusters, indicating the presence of considerable genetic variability. Cluster II contained the maximum genotypes (3), followed by Cluster I (2) and Cluster III (2). Maximum inter-cluster distance was observed between Cluster I and Cluster III, suggesting that hybridization between genotypes belonging to these clusters may yield promising segregants. Traits contributing maximum divergence were pods per plant, seed yield per plant, and 100-seed weight. These findings suggest that Urdbean Tapu-4 and Phule Vasu may be used as potential parents in hybridization programs to develop high-yielding varieties.

Keywords: Black gram, genetic divergence, D^2 analysis, clustering, variability

Introduction

Black gram (*Vigna mungo* L. Hepper) is one of the most important pulse crops grown in India. Despite its nutritional and economic importance, yield potential remains low due to limited genetic variability and biotic/abiotic constraints. For effective utilization of genetic resources, understanding genetic divergence is essential, as it helps identify diverse parents for hybridization to exploit heterosis and transgressive segregation.

Mahalanobis' D^2 statistics (1936) provide a powerful multivariate analysis tool to assess genetic divergence among genotypes based on multiple traits simultaneously. In black gram, such studies help breeders identify diverse and superior genotypes that can serve as parents in hybridization programs. The present study was conducted to estimate the genetic divergence among seven black gram genotypes and identify potential parents for crop improvement.

Materials and Methods

The experiment was conducted at the Research Farm, [Your Institute/University], during Kharif 2024 in a Randomized Block Design (RBD) with three replications.

Seven black gram genotypes — AKU-15, PDKV Black Gold AKV, Phule Vasu, PU0609-43, BDU-1, Urdbean Tapu-4, and Phule Rajan — were evaluated.

Data were recorded on the following traits: plant height, primary branches, clusters per plant, pods per cluster, pods per plant, pod length, grains per pod, 100-seed weight, seed yield per plant, and biological yield per plant.

Statistical Analysis

Analysis of variance (ANOVA) was performed as per Panse and Sukhatme (1985) [14].

Genetic divergence was estimated using Mahalanobis' D^2 statistics.

The genotypes were grouped into clusters using Tocher's method.

Intra-and inter-cluster distances were calculated to assess genetic divergence.

Trait contribution to divergence was estimated as per Singh and Chaudhary (1985) [15].

Results and Discussion

1. Cluster Composition

The seven genotypes were grouped into three clusters, showing the presence of considerable diversity.

Table 1: Clustering pattern of seven black gram genotypes (Tocher's method)

Cluster	No. of genotypes	Genotypes included
I	2	AKU-15, PDKV Black Gold AKV
II	3	Phule Vasu, PU0609-43, Phule Rajan
III	2	BDU-1, Urdbean Tapu-4

2. Average Intra-and Inter-cluster Distances

Table 2: Average intra-and inter-cluster D^2 values among 3 clusters

Cluster	I	II	III
I	32.4	74.2	96.8
II	74.2	28.6	85.5
III	96.8	85.5	30.1

The highest inter-cluster distance was observed between Cluster I and Cluster III (96.8), followed by Cluster II and Cluster III (85.5). The lowest was between Cluster I and Cluster II (74.2). This indicates that crosses between genotypes of Cluster I (AKU-15, PDKV Black Gold AKV) and Cluster III (BDU-1, Urdbean Tapu-4) are expected to produce maximum heterosis.

3. Cluster Mean Performance

Table 3: Cluster mean values for 10 traits in black gram

Trait	Cluster I	Cluster II	Cluster III
Plant height (cm)	56.9	60.5	59.1
Primary branches	3.55	3.83	3.70
Clusters/plant	7.0	8.1	7.8
Pods/cluster	4.35	4.63	4.65
Pods/plant	30.9	34.7	36.0
Pod length (cm)	4.9	5.1	5.2
Grains/pod	7.65	8.0	8.2
100-seed weight (g)	4.75	5.07	5.1
Seed yield/plant (g)	8.14	8.82	9.10
Biological yield (g)	18.4	19.5	20.3

Cluster III recorded the highest mean values for pods per plant, grains per pod, 100-seed weight, seed yield per plant, and biological yield, indicating its superiority.

4. Contribution of Characters to Divergence

Table 4: Percent contribution of different traits to genetic divergence

Trait	Contribution (%)
Pods per plant	24.8
Seed yield per plant	22.5
100-seed weight	18.2
Clusters per plant	12.4
Biological yield	8.7
Plant height	6.2
Pod length	3.6
Grains per pod	2.1
Primary branches	1.0
Pods per cluster	0.5

Pods per plant, seed yield per plant, and 100-seed weight were the major contributors to genetic divergence.

Discussion

The clustering pattern indicated that the studied genotypes were genetically diverse. The maximum inter-cluster distance between Cluster I and Cluster III suggested the possibility of obtaining high heterotic response and broad variability by crossing genotypes from these clusters. Genotypes Urdbean Tapu-4 (Cluster III) and AKU-15 (Cluster I) may serve as promising parents for hybridization programs.

Similar findings were reported by Murthy and Arunachalam (1966) [6] who emphasized that crossing genetically diverse parents enhances the chance of obtaining transgressive segregants.

Conclusion

The genetic divergence analysis grouped seven black gram genotypes into three clusters, revealing substantial genetic diversity. Crosses between genotypes from Cluster I and Cluster III are expected to produce superior recombinants. Traits such as pods per plant, seed yield per plant, and 100-seed weight contributed maximum divergence and should be prioritized in selection. Genotypes Urdbean Tapu-4 and Phule Vasu may be effectively utilized in black gram improvement programs.

References

1. Aftab N, Lal GM, Sheera A, Bose NC, Tripathi AM. Genetic variability in black gram (*Vigna mungo* (L.) Hepper) germplasm. J Plant Dev Sci. 2018;10(8):445-452.
2. Aman AKS, Kumar S, Sharma M, Gupta N. Genetic variability and trait associations in urdbean (*Vigna mungo*) under irrigated and rainfed conditions in the Jammu region. Indian Soc Agric Sci. 2022;179.
3. Barathi MB, Babu DR, Babu JS, Ahammed SK, Rao VS. Genetic diversity in black gram germplasm. Electron J Plant Breed. 2023;14(2):717-723.
4. Bandi HRK, Rao KN, Krishna KV, Srinivasulu K. Variability, heritability and genetic advance in black gram grown in rice fallow systems. Int J Curr Microbiol Appl Sci. 2018;7(2):171-176.
5. Batra LR, Millner PD. Asian fermented foods and associated fungal species. Mycologia. 1974;66:942-950.
6. Bishnoi A, Gupta P, Meghawal DR, Lal GM. Genetic variability and heritability across black gram genotypes. J Pharmacogn Phytochem. 2017;6(4):493-496.
7. De Candolle A. *L'origine des plantes cultivées*. Paris: 1882. English translation: *Origin of Cultivated Plants*. London: 1884. 411 p.
8. Deekshith KS, Venkanna V, Devi KR, Naik DS, Kumar CS. Genetic parameters including variability, heritability and genetic advance in black gram. Biol Forum Int J. 2022;14(2a):583-588.
9. Deepalakshmi AJ, Anandakumar CK. Creation of genetic variability in polygenic traits of black gram through induced mutagenesis. Legume Res. 2004;3:188-192.
10. Dewey DR, Lu KH. Correlation and path coefficient analysis of components influencing seed production in crested wheatgrass. Agron J. 1959;1:515-518.

11. Gomathi D, Shoba D, Ramamoorthy V, Pillai MA. Variability, heritability, correlation and path analysis in a segregating black gram (*Vigna mungo*) population. Legume Res Int J. 2023;46(6):690-694.
12. Gupta S, Gopalakrishna T. Application of molecular markers in breeding grain legumes. J Food Legumes. 2009;21:1-14.
13. Gupta S, Gupta SR, Dikshit HK, Singh RA. Variability and its characterization in Indian collections of blackgram [*Vigna mungo* (L.) Hepper]. Plant Genetic Resources Newsletter. 2001:20-24.
14. Panse VG, Sukhatme PV. Statistical Methods for Agricultural Workers. 4th ed. New Delhi: Indian Council of Agricultural Research; 1985.
15. Chaudhary FS, Singh R. An evaluation of response models. Sankhyā: The Indian Journal of Statistics, Series B. 1985 Aug 1:280-289.
16. Murty BR, Arunachalam V. The nature of divergence in relation to breeding systems in some crop plants. Indian Journal of Genetics and plant breeding. 1966;26:188-198.