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MORPHOLOGICAL MARKER-BASED CHARACTERIZATION AND GENETIC DIVERGENCE ANALYSIS IN BLACKGRAM (*Vigna mungo* L. HEPPER) GENOTYPES

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ABSTRACT

Blackgram productivity remains constrained by a narrow genetic base, making the identification of genetically divergent parents essential for effective hybridization. The present study characterized nine blackgram genotypes using 21 DUS (Distinctiveness, Uniformity and Stability) descriptors prescribed by the PPV&FRA (Protection of Plant Varieties and Farmer's Rights Authority), with the objective of assessing genetic divergence and identifying suitable parental combinations for future hybridization. The experiment was laid out in a Randomized Block Design (RBD) featuring three replicates, with multivariate distances evaluated using Mahalanobis D^2 statistics. Out of the 21 assessed characteristics, eight features (hypocotyl anthocyanin colouration, plant habit, stem/leaf/pod pubescence, pod length, plant height and 100-seed weight) were monomorphic across all genotypes, while the remaining thirteen traits, namely time of flowering, growth habit, stem colour, leaflet shape, foliage colour, leaf-vein colour, petiole colour, peduncle length, intensity of green colour of premature pods, colour of mature pods, seed colour, seed lustre and seed shape, showed considerable variation. Mahalanobis D^2 analysis, based on these thirteen discriminating characters, grouped the nine genotypes into four clusters through Tocher's method. The inter-cluster distances were consistently higher than the intra-cluster distances, confirming the presence of adequate genetic diversity among the genotypes, with the maximum divergence recorded between Cluster I and Cluster IV (3.416), followed by Cluster I and Cluster II (3.360). Based on this divergence pattern, crosses such as Local Variety $\times$ PU 31, VBN 11 $\times$ VBN 9, Local Variety $\times$ LBG 904 and VBN 11 $\times$ VBN 6 were identified as the most promising combinations for maximizing heterosis and generating transgressive segregants. The study concludes that DUS descriptors, encompassing both qualitative and quantitative characters, provide a reliable and stable basis for assessing genetic divergence in blackgram and for guiding the selection of parents for future hybridization programmes aimed at broadening the genetic base of the crop.

Key words: Blackgram, DUS descriptors, Genetic divergence, Mahalanobis D^2 , Hybridization

Introduction

Blackgram [*Vigna mungo* (L.) Hepper] is an important self-pollinated pulse crop of the family Fabaceae, valued for its high-quality protein (20–25%, including lysine and tryptophan), rapid maturity, and its role in improving soil fertility through biological nitrogen fixation (Behera *et al.*, 2020; Jayamani & Sathya, 2013). India is the world's leading producer and consumer of

blackgram, cultivating the crop over 3.17 million hectares with a production of about 2.16 million tonnes and an average national productivity of 681 kg/ha (Directorate of Economics and Statistics, 2025).

Despite its agro-economic importance, blackgram productivity continues to remain low, largely on account of the narrow genetic base among cultivated genotypes (Ghafoor *et al.*, 2012; Kaewwongwal *et al.*, 2015).

Several unconventional approaches, such as induced mutagenesis (Gokulan *et al.*, 2026) and somaclonal variation (Ferreira *et al.*, 2023), have also been employed to generate genetic variability in blackgram. However, compared to these unconventional methods, conventional approaches such as hybridization remain more cost-effective and require less expertise (Anand *et al.*, 2023), and therefore continue to be one of the most effective breeding methods to widen the genetic base and generate novel variability. That said, the success of a hybridization programme depends primarily on the choice of parents; crosses involving genetically divergent parents are known to produce greater heterosis and yield desirable transgressive segregants in the subsequent generations compared to crosses between closely related genotypes (Jadhav *et al.*, 2023; Thamodharan *et al.*, 2017).

Mahalanobis' D^2 statistic (Mahalanobis, 1936) is widely employed to quantify genetic divergence among genotypes and to group them into distinct clusters through Tocher's method (Dhanraj *et al.*, 2024; Tripathi & Lal, 2025). While this analysis is conventionally restricted to quantitative traits, relying solely on such characters may not capture the complete picture of genetic divergence. In the present study, divergence was instead assessed using DUS descriptors, which encompass both qualitative and quantitative characters, thereby offering a more precise and comprehensive estimate of genetic divergence than quantitative traits alone (Katiyar *et al.*, 2010; Prathyusha *et al.*, 2017). Hence, this investigation aimed to evaluate genetic divergence across different blackgram genotypes using 21 standardized DUS traits from PPV&FRA guidelines, facilitating the selection of distinct parental lines for subsequent breeding efforts.

Materials and Methods

The present investigation was carried out in the experimental field of the Department of Plant Breeding and Genetics, Adhiparasakthi Agricultural College, Kalavai, Tamil Nadu, during kharif 2026, using nine blackgram genotypes, comprising a local variety collected from Kannamangalam village, Vellore, and remaining eight genotypes (LBG 904, T-9, PU 31, VBN 11, VBN 10, VBN 9, VBN 8 and VBN 6) obtained from Tamil Nadu Agricultural University, Coimbatore. The experiment was laid out in a RBD with three replications; the genotypes being randomly allotted within each replication. Each genotype was raised in rows of 16 plants, with a spacing of 45 × 15 cm and 16 hills per row, three seeds being dibbled per hill and later thinned to one healthy seedling. All recommended cultural practices were followed uniformly. In each replication, ten plants were randomly tagged, giving 30 sample plants per genotype across the

three replications, as described by Dhanraj *et al.*, (2024).

Observations were recorded on all 21 DUS descriptors prescribed by the PPV&FRA guidelines at their respective stages of expression: hypocotyl anthocyanin colouration at the cotyledon-unfolded stage (5–6 Days after sowing); time of flowering, recorded as days from sowing to the stage when 50% of the plants had at least one fully opened flower, along with plant growth habit, plant habit, stem colour and pubescence, terminal leaflet shape, foliage colour, leaf vein colour and leaf pubescence at the same 50% flowering stage; petiole colour, intensity of green colour of premature pods and pod pubescence at the fully developed green pod stage; peduncle length, pod length, colour of mature pod and plant height at harvest maturity; and seed colour, lustre, shape and size (100-seed weight) on mature seeds. The genetic divergence among the nine genotypes was assessed through multivariate Mahalanobis D^2 statistics computed using R software (version 3.4.1).

Results and Discussion

Morphological Characterization Based On DUS Descriptors

The nine blackgram genotypes were characterized using 21 DUS descriptors across three replications. Consensus scores derived from the replicated data and their frequency distribution across classes are presented in Table 1. Results are discussed by growth stage below.

Seedling stage traits

Hypocotyl anthocyanin colouration was present in all nine genotypes (100%; Table 1), indicating that this seedling marker is highly conserved in the tested germplasm (Fig. 1.1). This agrees with Katiyar *et al.*, (2010), reporting hypocotyl pigmentation as an invariant seedling character in urdbean, and with Gangadhar *et al.*, (2023), where seedling traits were found to carry limited discriminatory value relative to reproductive-stage characters in legumes.

Flowering stage traits

At 50% flowering, plant habit (100% determinate) (Fig.1.3), stem pubescence (100% present) (Fig.1.5) and leaf pubescence (100% present) (Fig.1.9) were uniform, while five traits differentiated the genotypes (Table 1). Genotypes were classified by time of flowering into early-flowering (<40 days; 55.55%: Local Variety, T-9, PU 31, VBN 10, VBN 8) and medium-flowering (40–50 days; 44.44%: LBG 904, VBN 11, VBN 9, VBN 6) types. Growth habit was erect (44.44%: LBG 904, T-9, VBN 11, VBN 10), semi-erect (44.44%: Local Variety, VBN 9, VBN 8, VBN 6) or spreading (11.11%: PU 31)

Table 1: Morphological Characterization of Blackgram Genotypes.

S. No.	Characters	Classes	NG	FD	Name of genotypes
1	Hypocotyl: Anthocyanin colouration	Present	9	100	All genotypes
		Absent	0	0	Nil
2	Time of Flowering	Early (<40 DAS)	5	55.55	Local Variety, VBN 8, VBN 10, T9, PU 31
		Medium (40-50 DAS)	4	44.44	VBN9, VBN 11, LBG 904, VBN6
		Late (>50 DAS)	0	0	Nil
3	Plant: Growth Habit	Erect	4	44.44	LBG 904, T9, VBN 11, VBN 10
		Semi Erect	4	44.44	Local variety, VBN 9, VBN 8, VBN 6
		Spreading	1	11.11	PU 31
4	Plant: Habit	Determinate	9	100	All genotypes
		Indeterminate	0	0	Nil
5	Stem: Colour	Green	0	0	Nil
		Green with purple splashes	4	44.44	LBG 904, T9, VBN 10, VBN 8
		Purple with green splashes	3	33.33	Local variety, VBN 11, VBN 6
		Purple	2	22.22	PU 31, VBN 9
6	Stem: Pubescence	Absent	0	0	Nil
		Present	9	100	All genotypes
7	Leaf: Shape (Terminal)	Deltoid	3	33.33	Local variety, VBN 8, VBN 6
		Ovate	2	22.22	LBG 904, VBN 11
		Lanceolate	2	22.22	PU 31, VBN 9
		Cuneate	2	22.22	T9, VBN 10
8	Foliage: Colour	Green	4	44.44	Local variety, T9, VBN 8, VBN 6
		Dark green	5	55.55	LBG 904, PU 31, VBN 11, VBN 10, VBN 9
9	Leaf: Vein colour	Green	7	77.77	Local variety, LBG 904, T9, VBN 11, VBN 10, VBN8, VBN 6
		Purple	2	22.22	PU 31, VBN 9
10	Leaf: Pubescence	Absent	0	0	Nil
		Present	9	100	All genotypes
11	Petiole: Colour	Green	1	11.11	VBN 10
		Green with purple splashes	4	44.44	Local variety, LBG 904, T9, VBN 11
		Purple	4	44.44	PU 31, VBN 9, VBN 8, VBN 6
12	Pod: Intensity of green colour of premature pods	Yellowish green	3	0	Nil
		Green	5	100	All genotypes
		Dark green	7	0	Nil
13	Pod: Pubescence	Absent	0	0	Nil
		Present	9	100	All genotypes
14	Peduncle: Length	Short (<5cm)	0	0	Nil
		Medium (5-10cm)	7	77.78	Local variety, T-9, PU 31, VBN 11, VBN 10, VBN8, VBN 6
		Long (>10cm)	2	22.22	LBG 904, VBN 9
15	Pod: Length	Small (<5cm)	9	100	All genotypes
		Medium (7cm)	0	0	Nil
		Long (>7cm)	0	0	Nil
16	Pod: Colour of the mature pods	Buff	0	0	Nil
		Brown	3	33.33	Local variety, PU 31, VBN 10
		Black	6	66.66	LBG 904, T9, VBN 11, VBN9,VBN 8, VBN 6
17	Plant: Height	Short (<45cm)	9	100	All genotypes
		Medium (45-60cm)	0	0	Nil
		Long (>60 cm)	0	0	Nil

Continue ...1

18	Seed: Colour	Green	0	0	Nil
		Greenish brown	0	0	Nil
		Brown	1	11.11	VBN6
		Black	8	88.88	Local variety, LBG 904, T9, PU 31, VBN 11, VBN 10, VBN 9, VBN 8
		Mottled	0	0	Nil
19	Seed: Lusture	Shiny	1	11.11	LBG 904
		Dull	8	88.88	Local variety, T9, PU 31, VBN 11, VBN 10, VBN 9, VBN 8, VBN 6
20	Seed: Shape	Globose	4	44.44	LBG 904, PU 31, VBN 8, VBN 6
		Oval	4	44.44	Local variety, T9, VBN 10, VBN 9
		Drum	1	11.11	VBN 11
21	Seed: Size (weight of 100 seeds)	Small (<3g)	0	0	Nil
		Medium (3-5g)	9	100	All genotypes
NG: No. of genotypes; FD: Frequency distribution (%)					

(Fig.1.2). Stem colour ranged from green-with-purple-splashes (44.44%) through purple-with-green-splashes (33.33%) to fully purple (22.22%: PU 31, VBN 9) (Fig.1.4). Terminal leaflet shape was deltoid in 33.33% of genotypes, and evenly split among ovate, lanceolate and cuneate (22.22% each) (Fig.1.6). Foliage was predominantly dark green (55.55%) over green (44.44%) (Fig.1.7), and leaf vein colour was mostly green (77.77%) with a purple minority (22.22%: PU 31, VBN 9) (Fig.1.8).

These patterns corroborate Panigrahi *et al.*, (2014), where stem colour and leaflet shape were used to separate landraces from mutant lines, and Kumar *et al.*, (2022), linking flowering time and growth habit to cropping duration and intercropping suitability. The uniformly determinate habit recorded across all genotypes (Table 1) likely reflects convergent selection for lodging resistance and mechanical-harvest suitability, consistent with Gangadhar *et al.*, (2023) and Prathyusha *et al.*, (2017).

Maturity stage traits

From the green-pod stage to harvest, pod pubescence (Fig.1.12), pod length (small) (Fig.1.14), plant height (short) and 100-seed weight (medium) were uniform across all genotypes (100%; Table 1), while pod-, seed- and peduncle-related traits varied. Peduncle length was medium in the majority of genotypes (77.77%) and long in the remainder (LBG 904, VBN 9) (Fig.1.13). Petiole colour split between green-with-purple-splashes and fully purple (44.44% each), with green alone in VBN 10 (11.11%) (Fig.1.10). Premature pod colour intensity was mostly green (55.55%), followed by yellowish green (33.33%) and dark green (VBN 10 only) (Fig.1.11). Mature pod colour was predominantly black (66.66%) over brown (33.33%) (Fig.1.15). Seed colour (88.88% black) and seed lustre (88.88% dull) were both strongly skewed, with VBN 6 (brown seed) and LBG 904 (shiny

seed) the sole exceptions (Fig.1.16 & 1.17). Seed shape divided evenly between globose and oval (44.44% each), with a single drum-shaped outlier (VBN 11) (Fig.1.18).

These results align with Jayamani and Sathya (2013), highlighting seed and pod characters as key taxonomic and commercial markers, and with Choudhary *et al.*, (2015), which similarly employed seed shape and pod colour as high-utility DUS descriptors. The consistency of these findings with the wider blackgram literature confirms that reproductive-stage descriptors remain among the most stable and discriminating markers for genotype identification.

Genetic Divergence Analysis (Mahalanobis D² Statistics)

Clustering pattern:

By analysing the 13 variable DUS markers, the nine genotypes were partitioned into four discrete clusters using Tocher's method (Table 2): Cluster I (Local Variety, VBN 11), Cluster II (LBG 904, VBN 8, VBN 6), Cluster III (T-9, VBN 10) and Cluster IV (PU 31, VBN 9). This grouping confirms that the germplasm harbours sufficient phenotypic variance to support targeted breeding, mirroring the trait-driven rather than geography or pedigree-driven clustering reported for *Vigna mungo* by Kumar *et al.*, (2014) and Rajalakshmi *et al.*, (2020). The Ward's-method dendrogram (Fig. 2) visually corroborated the Tocher grouping, clearly separating the four clusters

Table 2: Clustering Pattern of Blackgram Genotypes (by Tocher's Method).

Cluster	No. of genotypes	Name of genotypes (G)
I	2	Local Variety (G1), VBN 11 (G5)
II	3	LBG 904 (G2), VBN 8 (G8), VBN 6 (G9)
III	2	T-9 (G3), VBN 10 (G6)
IV	2	PU 31 (G4), VBN 9 (G7)

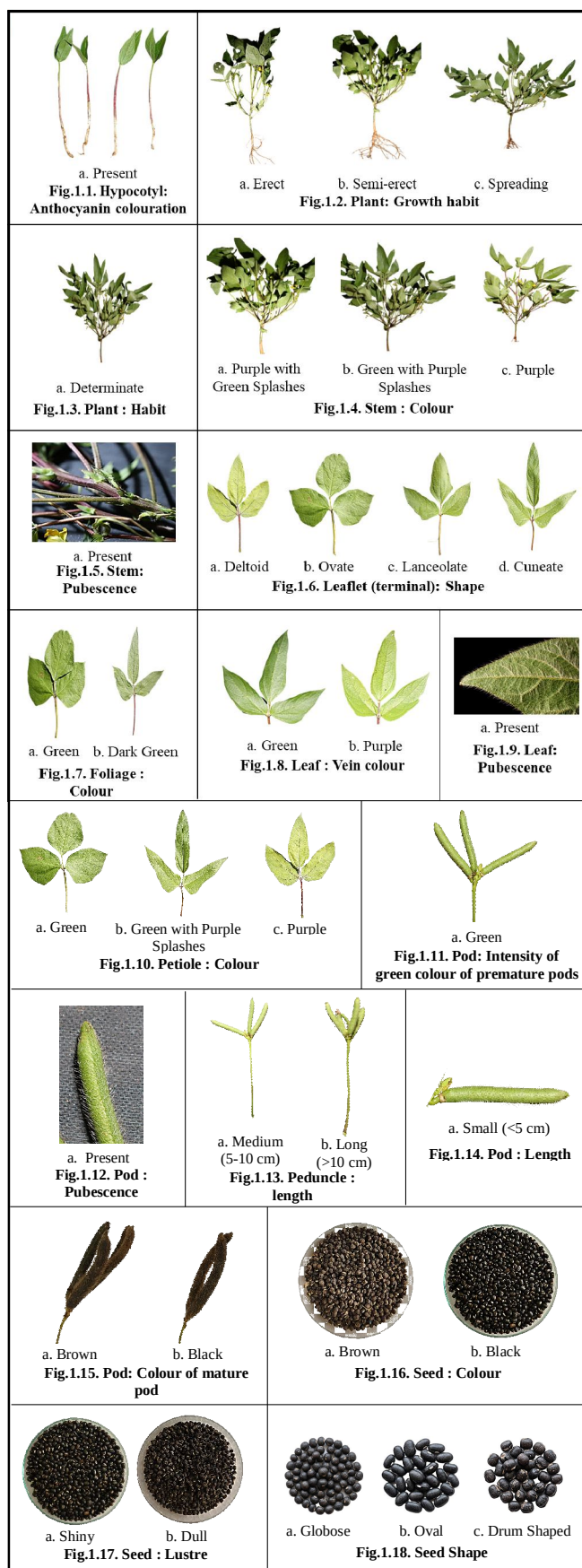


Fig. 1: DUS characters observed among nine blackgram genotypes.

along the divergence axis -an agreement similarly reported by Dhanraj *et al.*, (2024) and Ayesha *et al.*, (2021) in other pulse crops.

Intra- and inter-cluster divergence:

Intra-cluster distances (Table 3) ranged from 1.237 (Cluster III) to 2.924 (Cluster II), with Clusters I and IV both recording an identical intermediate value of 2.717. The low intra-cluster distance in Cluster III indicates close morphological similarity between T-9 and VBN 10, while the higher value in Cluster II reflects greater internal variation among LBG 904, VBN 8 and VBN 6, consistent with Sridhar *et al.*, (2020) on the diversity stability trade-off within clusters.

Among inter-cluster distances (Table 3), Cluster I–IV was highest (3.416), followed by Cluster I–II (3.360) and Cluster II–IV (3.354), marking these as the most divergent and therefore most promising parental combinations. This is consistent with the breeding rationale of Tripathi and Lal (2025) and Rukminidevi *et al.*, (2025) for broadening the genetic base of polygenic traits, and with the heterosis-maximizing strategy of Kumar *et al.*, (2021).

Cluster mean performance:

Cluster means for the 13 DUS characters (Table 4) show that no single cluster dominates every trait, indicating genuinely independent axes of divergence. Cluster IV recorded the highest means for growth habit (6.000), leaf vein colour (2.000), stem colour (4.000), petiole colour (3.000) and peduncle length (6.000). Cluster III recorded the highest pod-intensity mean (6.000) and leaflet-shape mean (4.000), alongside the earliest flowering and lowest growth-habit scores (3.000 each). Cluster II showed the highest time-of-flowering (4.333) and pod-colour (3.000) means, together with a perfectly uniform seed-shape mean (1.000), reflecting the shared globose seed shape of all three member genotypes (LBG 904, VBN 8, VBN 6). Cluster I remained comparatively intermediate across most traits but recorded the highest seed-shape mean (2.500).

Flowering time, pod intensity and growth habit thus emerge as the principal contributors to divergence, consistent with the yield-attributing traits identified by Jayamani and Sathya (2013) and Panigrahi *et al.*, (2014). Because DUS descriptors are standardized for distinctness, uniformity and stability (Choudhary *et al.*, 2015), the groupings obtained here reflect stable morphological differences rather than transient environmental effects - a conclusion also supported by the morphological and molecular work of Kumawat *et al.*, (2025).

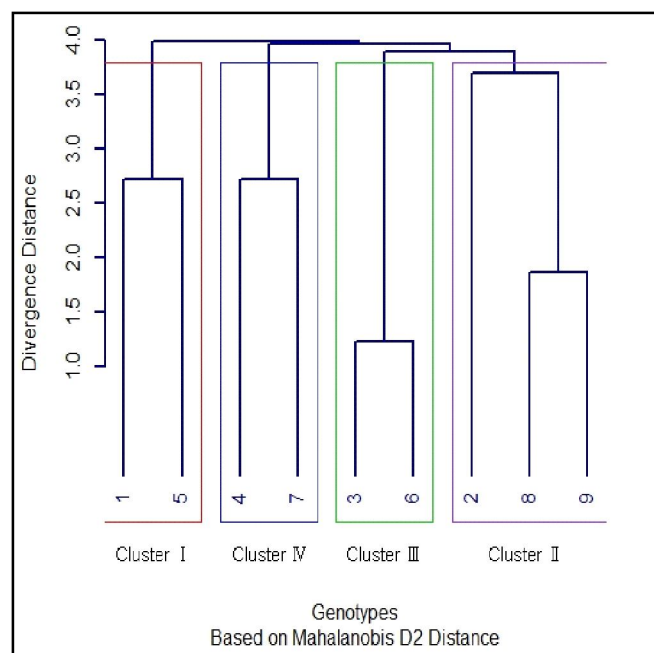
Table 3: Matrix of Inter- and Intra-Cluster Divergence Distances among the four clusters.

	Cluster I	Cluster II	Cluster III	Cluster IV
Cluster I	2.717	3.360	3.146	3.416
Cluster II		2.924	3.084	3.354
Cluster III			1.237	3.142
Cluster IV				2.717

Recommended Crosses for Future Hybridization

The most divergent cluster pairs identified in Table 4 point to two priority cross combinations: Cluster I $\times$ Cluster IV (Local Variety $\times$ PU 31; VBN 11 $\times$ VBN 9) and Cluster I $\times$ Cluster II (Local Variety $\times$ LBG 904; VBN 11 $\times$ VBN 6). Both combinations are expected to maximize heterosis and yield transgressive segregants, consistent with the divergent-parent selection strategy of Rajalakshmi *et al.*, (2020) and Rukminidevi *et al.*, (2025).

Beyond statistical distance, these crosses also offer trait complementarity (Sridhar *et al.*, 2020): Local Variety $\times$ PU 31 combines the semi-erect, early-flowering habit of Local Variety with the spreading habit and brown pod colour of PU 31 (Table 1), while VBN 11 $\times$ LBG 904 unites a shared erect growth habit with contrasting seed lustre - dull in VBN 11, shiny in LBG 904 (Table 1). Such complementary combinations are expected to break unfavourable genetic linkages and generate transgressive segregants, an approach supported by Ayesha *et al.*, (2021), Kumawat *et al.*, (2025) and Kumar *et al.*, (2021), each emphasizing rigorous progeny-level validation of D²-based parental selection.

**Fig. 2:** Mahalanobis D² Cluster Dendrogram of Blackgram Genotypes.**Table 4:** Mean trait expressions of 13 DUS markers across clusters.

Trait	CI	CII	CIII	CIV
Time of flowering	4.000	4.333	3.000	4.000
Plant Growth habit	4.000	4.333	3.000	6.000
Stem Colour	3.000	2.333	2.000	4.000
Leaflet Shape	1.500	2.000	4.000	3.000
Foliage Colour	1.500	1.000	2.000	2.000
Leaf Vein colour	1.000	1.000	1.000	2.000
Petiole Colour	2.000	2.667	1.500	3.000
Pod Intensity	3.000	4.333	6.000	5.000
Peduncle Length	5.000	5.667	5.000	6.000
Pod Colour	2.500	3.000	2.500	2.500
Seed Colour	4.000	3.667	4.000	4.000
Seed Lustre	2.000	1.667	2.000	2.000
Seed Shape	2.500	1.000	2.000	1.500

C: Cluster

Conclusion

The present study demonstrates that DUS descriptors, incorporating phenotypic variance across both qualitative and quantitative traits, provide a robust and reliable framework for characterizing genetic divergence in blackgram beyond what conventional quantitative-trait-based approaches alone can offer. Of the 21 descriptors evaluated across seedling, flowering and maturity stages, thirteen showed clear phenotypic variation among the nine genotypes, while eight remained conserved, underscoring the discriminatory value of reproductive- and pod-stage traits in particular. Mahalanobis D² analysis partitioned the genotypes into four genetically distinct clusters, a pattern further validated by hierarchical dendrogram analysis, with Cluster I and Cluster IV showing the maximum inter-cluster divergence, followed closely by Cluster I and Cluster II. Based on this divergence pattern, crosses such as Local Variety $\times$ PU 31, VBN 11 $\times$ VBN 9, Local Variety $\times$ LBG 904 and VBN 11 $\times$ VBN 6 represent potential parental pairs expected to express high hybrid vigour and yield superior transgressive offspring. These findings offer breeders a practical, morphology-based framework for parental selection and provide a foundation for future hybridization programmes aimed at expanding the restricted genetic variability of cultivated Blackgram.

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References

Anand, A., Subramanian M. and Kar D. (2023). Breeding

- techniques to dispense higher genetic gains. *Frontiers in Plant Science*, **13**, 1076094.
- Ayesha, M., Babu D.R., Rajesh A.P., Md L.A. and Kumar V.M. (2021). Estimation of genetic distances among various genotypes of blackgram [*Vigna mungo* (L.) Hepper] using D² statistics. *Electronic Journal of Plant Breeding*, **12(4)**, 1268–1273.
- Behera, L., Samal K.C., Pavithra B.S., Swain D., Prusti A.M. and Rout G.R. (2020). Genetic assessment of Indigenous landraces of *Vigna mungo* L. and its evaluation for YMV resistance. *Plant Biology and Crop Research*, **1**, 1020–1028.
- Choudhary, B.R., Pandey S., Rao E.S. and Sharma S.K. (2015). DUS characterization of muskmelon (*Cucumis melo*) varieties. *Indian Journal of Agricultural Sciences*, **85(12)**, 1597–1601.
- Directorate of Economics and Statistics (2025). “Ministry of agriculture and farmers welfare department of agriculture, cooperation and farmers welfare,” in *Third Advance Estimates of Production of Food grains for 2025-26* (Government of India).
- Dhanraj, D., Sruthi S.R. and Anbuselvam Y. (2024). DUS Characterization of Blackgram [*Vigna mungo* (L.) Hepper] Genotypes using Morphological Characters and clustering them using Mahalanobis D² Analysis. *Indian Journal of Natural Sciences*, **15(86)**, 80036–80048.
- Ferreira, M.D.S., Rocha A.D.J., Nascimento F.D.S., Oliveira W. D.D.S., Soares J.M.D.S., Reboucas T.A. *et al.* (2023). The role of somaclonal variation in plant genetic improvement: A systematic review. *Agronomy*, **13(3)**, 730.
- Gangadhar, L., Nikhil A., Rathore M., Shanmugavadivel P.S., Lal G.M. and Gayathri G. (2023). Morphological Variability and Molecular Diversity in Blackgram [*Vigna mungo* (L.) Hepper] Genotypes Using SSR Markers. *International Journal of Plant and Soil Science*, **35(19)**, 2050–2062.
- Ghafoor, A., Sultana T. and Rizvi Z.F. (2012). Genetic diversity in blackgram [*Vigna mungo* (L.) Hepper] for randomly amplified polymorphic DNA (RAPD) markers. *Pakistan Journal of Botany*. **44(2)**, 473–478.
- Gokulan, D., Arjun P., Subalesh K., Pradeepkumar B., Chidambaramoorthy K., Arunkumar S. *et al.* (2026). Elucidating mutagenic sensitivity and Lethal Dose 50 (LD50) of Black gram variety Vamban 11 under laboratory condition. *International Journal of Research in Agronomy*; **9(4)**, 695–699.
- Jadhav, R.A., Mehtre S.P., Patil D.K. and Gite V.K. (2023). Multivariate analysis using D² and principal component analysis in Mung bean [*Vigna radiata* (L.) Wilczek] for study of genetic diversity. *Legume Research*, **46(1)**, 10–17.
- Jayamani, P. and Sathya M. (2013). Genetic diversity in pod characters of blackgram [*Vigna mungo* (L.) Hepper]. *Legume Research*, **36(3)**, 220–223.
- Kaewwongwal, A., Kongjaimun A., Somta P., Chankaew S., Yimram T. and Srinives P. (2015). Genetic diversity of the black gram [*Vigna mungo* (L.) Hepper] gene pool as revealed by SSR markers. *Breeding Science*, **65(2)**, 127–137.
- Katiyar, P.K., Dixit G.P. and Singh B.B. (2010). Varietal characterization of urdbean for distinctiveness, uniformity and stability. *Journal of Food Legumes*, **23(2)**, 106–109.
- Kumawat, R., Kumar S., Sharma S., Raina S. and Singh A. (2025). Morphological and molecular (SSRs) characterization of different diverse genotypes of blackgram (*Vigna mungo* L.). *Genetic Resources and Crop Evolution*, **72(4)**, 4305–4319.
- Kumar, P., Singh S.K., Shukla R.S., Elahi T., Prajapati S.S. and Rahangdale S. (2022). Morphological characterization for important breeding traits in blackgram [*Vigna mungo* (L.) Hepper] genotypes. *Biological Forum – An International Journal*, **14(2)**, 1323–1330.
- Kumar, V., Thakur J., Salam J.L., Pujari P. and Karishma (2021). Study of genetic divergences using mahalanobis D² analysis in black gram [*Vigna mungo* L. Hepper] germplasm. *The Pharma Innovation Journal*, **10(8)**, 315–319.
- Kumar, Y.L., Anuradha C.H., Reddy S.S. and Subbaiah K.V. (2014). Genetic divergence and variability studies in blackgram [*Vigna mungo* L. Hepper]. *Research Journal of Agricultural Sciences*, **5(6)**, 1299–1303.
- Mahalanobis, P.C. (1936). On the generalized distance in statistics. *Proceedings of National Institute of science of India*, **2**, 49–55.
- Rajalakshmi, K., Manivannan N., Anand G., Vanniarajan C. and Harish S. (2020). Genetic divergence among blackgram [*Vigna mungo* (L.) Hepper] genotypes using Mahalanobis D² statistic. *Electronic Journal of Plant Breeding*, **11(01)**, 116–119.
- Panigrahi, K.K., Baisakh B., Kar M. and Mohanty A. (2014). Genetic divergence in mutants and land races of blackgram [*Vigna mungo* (L.) Hepper] from Odisha. *Electronic Journal of Plant Breeding*, **5(3)**, 578–583.
- Prathyusha, V.B., Rao Y.K., Rao G.P., Prasanthi L., Hari Y., Mallikarjuna G. *et al.* (2017). SSR polymorphism and distinctiveness, uniformity and stability (DUS) features in selected genotypes of blackgram [*Vigna mungo* (L.) Hepper]. *Journal of Food Legumes*, **30(2)**, 1–8.
- Rukminidevi, K., Supriya B., Nagaswathi K. and Venugopal G. (2025). Genetic diversity studies in blackgram [*Vigna mungo* (L.) Hepper] genotypes using D² statistics. *Plant Archives* (09725210), **25(2)**, 428–433.
- Thamodharan, G., Ramalingam A. and Geetha S. (2017). Estimation of genetic parameters and combining ability analysis in blackgram [*Vigna mungo* (L.) Hepper]. *Legume Research*, **40(1)**, 19–23.
- Tripathi, A.M. and Lal G.M. (2025). Genetic Divergence Analysis Using Mahalanobis D² Statistics in Black Gram [*Vigna mungo* (L.) Hepper]. *Plant Cell Biotechnology and Molecular Biology*, **26(9–10)**, 61–72.