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# Study on Genetic Diversity in Black Gram (*Vigna mungo* L. Hepper)

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***Authors' contributions***

*This work was carried out in collaboration between both authors. Both authors read and approved the final manuscript.*

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## ABSTRACT

The present study carried out with 45 black gram genotypes including one check variety were conducted at Field Experimentation Centre of the Department of Genetics and Plant Breeding, to study genetic variability, heritability, genetic advance, for 13 quantitative characters. The experiment was conducted by using Randomized Block Design with three replications during *Kharif, 2022.* Genotype SNTP- 02 (7.44 gms), PL-416 (7.35 gms), AKU-13-15 (7.26 gms), PLU - 1016 (7.22gms), KC- 153 (7.21gms) were found to be superior in seed yield per plant. High GCV and PCV were observed in Number of primary branches, Number of clusters per plant and Number of pods per plant. Moderate PCV and GCV were observed in Number of pods per plants (43.04), Biological yield (33.77), Seed Yield per plant (30.282), Harvest index (25.4), Low PCV and GCV for Days to 50% pod setting (6.24) Divergence analysis following Mahalanobis (1936) $D^2$ analysis has revealed presence of substantial amount of genetic diversity among the genotypes. These 45 genotypes were grouped into 6 clusters by following Tocher's method. Cluster I contain 19 genotypes, while the cluster II, III, IV, V, VI were Monogenotypic. The maximum inter cluster

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distance was observed between Cluster V and I (76.71) and minimum between cluster IV and II (81.02). Variance of cluster means revealed that Seed yield per plant, biological yield, harvest index had a maximum contribution towards divergence in the present material. Thus, the genotypes present in these clusters provide a wide range of segregation diversity and may be employed as parents in a future hybridization study to generate ideal genotypes for yield improvement in Black gram genotypes.

*Keywords: GCV; PCV; variability; heritability; genetic divergence.*

## 1. INTRODUCTION

Grain legumes are a great gift from nature and a significant addition to a diet that mostly consists of cereal. In Asia, they represent the main source of protein. They play a crucial role in Indian agriculture. They play a key role in food and are crucial and important source of dietary protein, especially for the Indian subcontinent's largely vegetarian population. Pulses have roughly three times the amount of high-quality protein found in cereals, making them a more affordable source of protein to combat human protein deficiency. They may be used as fodder and concentrates in cattle husbandry and are especially helpful in treating protein deficiency. Pulses have unique qualities that make them particularly useful in various cropping systems.

“Blackgram (*Vigna mungo* (L.) Hepper), also known as urd-bean, udand dal, or urad in India, is a short-lived, self-pollinating, diploid (2n=2x=22), grain legume crop belonging to the family Leguminosae with a small genome size of 574Mbp” (Gupta and Gopalakrishna *et al*., 2015). It is significant from the perspective of global food and nutritional security. It is a good pulse crop because it does better in every season. The seeds are incredibly nutrient-dense, containing 24–26% protein, 60% carbohydrates, 1.5% fat, minerals, amino acids, and vitamins. Additionally, it provides a significant amount of lysine for vegetarians and is a fair source of vitamins like thiamine, niacin, and riboflavin, as well as the essential minerals iron and phosphorus. So it is commonly referred to as "poor man's meat". “Blackgram is grown as a mixed crop, cash crop, sequential crop besides growing as sole crop under residual moisture conditions, either after the harvest of rice after the harvest of other summer crops under semi irrigated and dry land condition” [1]. It is still cultivated on marginal lands under rainfed conditions and faces terminal drought which affects its productivity to a great extent. It is mainly grown for human consumption and also used as fodder for cattle and green manure for soil fertility.

Blackgram is consumed in the form of 'dal' (whole or split husked and unhusked) or parched. It is the chief constituent of 'papad' and also of bark (special balls) which makes a delicious curry. Seeds are used in the preparation of many popular dishes. Blackgram differs from other pulses in its peculiarity of attaining some mucilaginous pasty character, when ground up with watt. Blackgram has been distributed mainly in tropical to subtropical countries where it is grown in Kharif and summer reason. It is utilized in various ways where seeds are consumed as source of protein, vitamins and minerals, while plant parts are used as fodder. It is cooked for consumption with roti and rice and also used in making pastes for several south Indian dishes like idly, dosa, vada etc. With a production of 2.42 million tonnes and a yield of 615 kg $ha^{-1}$, India leads the world with an area of 37.2 lakhs/ $ha^{-1}$, (Directorate of Economics and Statistics, 2019-2020). It is primarily grown in Maharashtra, Andhra Pradesh, Madhya Pradesh, Uttar Pradesh, Tamil Nadu, Rajasthan, and Karnataka, among other agro-climatic zones of the nation. Blackgram is grown on 7.01 lakh hectares in Uttar Pradesh, where it produces 2.3 lakh tonnes at a productivity of 553 kg per hectare. Blackgram originated in the Indian subcontinent, claims Vavilov. It is suitable for dry land farming and is typically grown as an intercrop with other crops because it is a drought-resistant crop. In terms of area and importance, blackgram is the second-most important pulse crop in India.

The physiological expression and genetic potential of the crop are greatly influenced by the weather conditions, which have a significant impact on crop growth. It is well known that the availability of specific optimum rainfall, solar radiation, temperature, soil moisture, heat units, etc. during different stages of crop growth determines the yield from any given crop or variety. To meet domestic demand, India imports about two lakh tons of pulses from other nations each year. “The demand for grains and legumes is growing in tandem with the increase in global population, and agriculture. Due to the low availability of pulse grains in India (36 g/day/capita versus the minimum requirement of 80 g/day/capita) and the need to maintain the protein-to-calorie ratio in the diet, pulse production is necessary. The primary limitations of blackgram Lack of genetic diversity that can be exploited, lack of ideotypes that are appropriate for various cropping systems, a poor harvest index, susceptibility to biotic and abiotic stresses, and lack of access to high-quality seeds of improved varieties are all factors that need improvement. It is primarily the result of a few parents who have a high degree of relatedness being used repeatedly in crossing programs" [2]. The degree and type of genetic variability present in traits that contribute to yield heavily influences the success of yield improvement [3].

## 2. MATERIALS AND METHODS

The experimental materials (Table 1) for the present study was procured from Department of Genetics and Plant Breeding, SHUATS during *kharif*-2022. Forty-five black gram genotypes are grown in Randomized Block Design (RBD) with three replications during *kharif*-2022. The recommended doses of fertilizers N: P: K @ 20:40:40 kg/ha were applied. The full dose of P2O5 and K2O and nitrogen were applied as basal dose at the time of sowing. The observations were recorded on plot basis for days to 50% flowering, days to physiological maturity and seed yield per plot. For the rest of the characters the data was recorded on five randomly selected plants from each genotype in each replication leaving first two border rows from all the four sides in order to avoid sampling error. The characters recorded wereDays to 50% flowering, Days to 50% pod setting ,Days to maturity, Plant height, Number of primary branches per plant, Number of clusters per plant, Number of pod per plant, Pod length, Number of seeds per pod, Biological yield per plant, Harvest index **,** Seed index**,** seed yield per plant. Data were subjected to analysis of Mahalanobis' D2-statistics [4], and intra-cluster and inter-cluster distance, cluster mean and contribution of each trait to the divergence were estimated as suggested by Singh and Chaudhary [5]. Clustering of genotypes was done by using Tocher's method [6]. The cluster distance was estimated by the formula given by Singh and Chaudhary [7].

**Table 1. List of 45 genotypes of blackgram**

| | | | | | |
|---|---|---|---|---|---|
| 1 | PLU-856 | 21 | AZAD-1 | 41 | PKGV-03 |
| 2 | TLU-328 | 22 | PLU-103 | 42 | PU-11-14 |
| 3 | LBG-648 | 23 | PDU-1 | 43 | PKRU-03 |
| 4 | BGP-21-28 | 24 | IPU-94-1 | 44 | IC-106-176 |
| 5 | KU-96-14 | 25 | PLU-570 | 45 | SEKHAR2 (check) |
| 6 | JU-2 | 26 | KU-321 | | |
| 7 | PLU-1016 | 27 | TLU-32-6 | | |
| 8 | KC-153 | 28 | UH-85-2 | | |
| 9 | ADT-3 | 29 | PLU-708 | | |
| 10 | PLU-86-C | 30 | LBG-623 | | |
| 11 | AKU-13-15 | 31 | SNTP-02 | | |
| 12 | VBN-08 | 32 | DH-85-5 | | |
| 13 | PL-416 | 33 | LBG-628 | | |
| 14 | TBG-104 | 34 | IPU-94-2 | | |
| 15 | PLU-547 | 35 | T9 | | |
| 16 | IPU-99-18 | 36 | TU-99-2 | | |
| 17 | DH-85-2 | 37 | IPU-99-16 | | |
| 18 | VBN-11-16 | 38 | AKU-14-02 | | |
| 19 | PLU-302 | 39 | BG-369 | | |
| 20 | PU-31 | 40 | IPU-99 | | |

## 3. RESULTS AND DISCUSSION

The analysis of variance (Table 2) revealed significant differences among all the 13 characters under study at 1% level of significance. This indicates that the presence of significantly higher amount of genetic variability among the genotypes present in the investigation for all the yield related characters studied. So, there was a sample scope for selection of promising lines from the present gene pool for yield and its components. The presence of large amount of variability might be due to diverse source of materials taken as well as environmental influence affecting the phenotype. The PCV was higher than the GCV for all the characters under study which indicated that the environmental factors influencing the characters studied. The present findings are in accordance with the findings of Panigrahi et al. [8], Deepshikha et al. [9], Priyanka et al. [10] and Gowsalya et al. [11]. High estimates of heritability coupled with high genetic advance as per cent of mean was observed respectively for number of cluster per plant (98.301% and 105.841%), number of primary branches (98.01.% and 113.665%), number of pods per plant (97.423% and 86.365%), biological yield (95.837% and 66.687%), seed yield per plant (93.37% and 58.287%) and plant height (94.93%, 356.517%), This suggesting that there was preponderance of additive gene action governing the inheritance of these characters and offers the best possibility of improvement through simple selection. The findings are in agreement with the results of Aftab et al. [12], Kuralarasan et al. (2017), Gowsalya et al. [11] and Singh et al. [13]. Genetic divergence in 45 genotypes of blackgram was measured by following Mahalanobis's $D^2$ statistic. The diversity available in the crop decides the success of any crop improvement programme with manifested objectives. Assessment of divergence in the germplasm is pre- requisite to know the spectrum of diversity. Clustering of genotypes following the Tocher's method as described by Rao [6] led to formation of six clusters. Cluster I was biggest and consisted of 19 genotypes (Table 4) The cluster I, II, III and V consisted of 15,6 and 3 genotyppes, respectively. All remaining clusters *viz.* IV, and VI were solitary, with one genotype in each of both clusters [14].

### 3.1 Intra and Inter Cluster Distances

Intra and inter cluster distance values have been presented in Table 4. Intra cluster distance was ranged from zero (cluster IV and VI) to 67.46 (cluster V). The highest intra cluster distance was recorded in cluster V (67.46) followed by cluster III (63.68) and cluster II (51.99). The high intra cluster distance values revealed the presence of genetic diversity between the genotypes grouped together in those clusters. Hence, there is a lot of scope for exchange of genes among genotypes within these clusters.

From the inter cluster distance values of the six clusters, the highest divergence occurred between cluster I and V (761.71); cluster I and IV (465.11); cluster III and V (441.63); cluster I and III (392.43); cluster V and VI (307.01) Suggesting that the crosses involving genotypes from these clusters would give desirable recombination. From the closest inter cluster distance it was concluded that these genotypes were not very distant but couldn't be grouped together based on studied traits. Several authors have suggested that the crossing between the genotypes of clusters with high inter cluster would yield good segregants for selection. Panigrahi et al. [8] The intercluster distance were greater than the intra cluster distance revealing that considerable amount of genetic diversity existed among the accession. The intra cluster distance ranged from 0.00 to 67.46 and the inter cluster distance ranged from 81.02 to 761.71, indicating that the selected genotypes were highly divergent. Minimum intra cluster distance had been recorded with cluster XII (0.00) due to the presence of solitary accession

### 3.2 Cluster Means

The data revealed that considerable differences existed among the clusters for most of the characters. The cluster IV showed the highest mean values for five characters *viz*. Days to 50% flowering, Days to 50% pod setting Days to maturity Plant height, Number of primary branches, Number of clusters per plant, Number of pods per plant. The cluster I exhibited lowest mean for Pod Length, Number of seeds per pod, Seed index, Harvest index, Biological yield, Seed yield per plant from the results, Therefore, hybridization programme between the selected genotypes from diverse clusters is essential to combine all the targeted traits to improve phenotypic performance. The per cent contribution of thirteen characters studied towards total divergence has been presented in Table 7. Data revealed that, seed yield per plant had contributed highest (21.00%) for genetic divergence and subsequently by biological yield

**Table 2. Analysis of Variance for 13 quantitative characters of 45 black gram genotypes**

| Sr. No. | Source | Replication | Genotypes | Error |
|---|---|---|---|---|
| | **Degrees of freedom** | **2** | **44** | **88** |
| 1 | Days to 50% flowering | 3.8220 | 20.885** | 7.686 |
| 2 | Days to 50% pod setting | 7.2670 | 16.248** | 8.721 |
| 3 | Days to maturity | 4.4220 | 169.1** | 20.127 |
| 4 | Plant height (cm) | 1.2520 | 637.413** | 11.149 |
| 5 | Number of primary branches | 0.7360 | 55.615** | 0.374 |
| 6 | Number of clusters per plant | 0.6130 | 46.649** | 0.267 |
| 7 | Number of pods per plant | 0.3440 | 170.663** | 1.492 |
| 8 | Pod Length (cm) | 0.0990 | 0.178** | 0.08 |
| 9 | Number of seeds per pod | 0.0020 | 1.393** | 0.163 |
| 10 | Seed index (g) | 0.0010 | 0.956** | 0.06 |
| 11 | Harvest index (%) | 1.3790 | 165.028** | 11.747 |
| 12 | Biological yield (g) | 0.5860 | 114.962** | 1.641 |
| 13 | Seed yield per plant (g) | 0.090 | 8.099** | 0.187 |

**Table 3. Estimation of variability and genetic parameters for 13 quantitative characters in 45 black gram germplasm**

| Traits | GCV(%) | PCV (%) | $h^2$(Broad Sense) (%) | Genetic Advance | Genetic Advance as % of Mean |
|---|---|---|---|---|---|
| Days to 50% flowering | 4.722 | 7.826 | 36.404 | 2.607 | 5.869 |
| Days to 50% pod setting | 2.953 | 6.247 | 22.342 | 1.542 | 2.875 |
| Days to maturity | 10.057 | 11.923 | 71.159 | 12.245 | 17.477 |
| Plant height (cm) | 28.159 | 28.901 | 94.93 | 28.999 | 56.517 |
| Number of primary branches | 55.735 | 56.298 | 98.01 | 8.751 | 113.665 |
| Number of clusters per plant | 51.747 | 52.192 | 98.301 | 8.031 | 105.689 |
| Number of pods per plant | 42.476 | 43.034 | 97.423 | 15.269 | 86.365 |
| Pod Length (cm) | 4.521 | 8.43 | 28.76 | 0.199 | 4.994 |
| Number of seeds per pod | 11.442 | 13.523 | 71.591 | 1.116 | 19.944 |
| Seed index (g) | 12.91 | 14.155 | 83.189 | 1.027 | 24.257 |
| Harvest index (%) | 22.934 | 25.434 | 81.307 | 13.277 | 42.601 |
| Biological yield (g) | 33.068 | 33.778 | 95.837 | 12.395 | 66.687 |
| Seed yield per plant (g) | 29.282 | 30.304 | 93.37 | 3.233 | 58.287 |

***GCV*** *genotypic coefficient variance ,* ***PCV*** *phenotypic coefficient of variance*

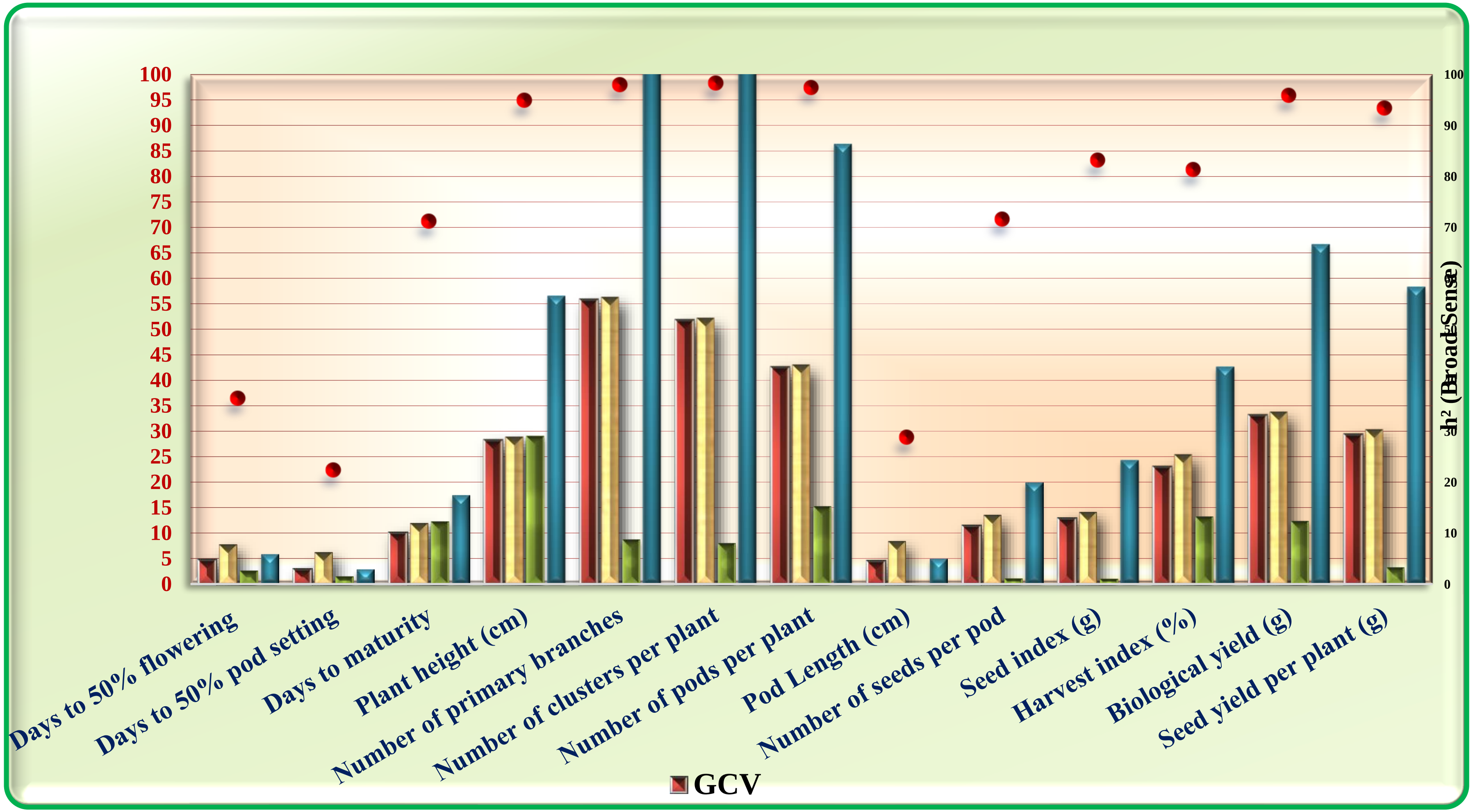

**Fig. 1. Histogram depicting GCV, PCV, Genetic advance and h2 for quantitativecharacters of black gram genotype**

**Table 4. Grouping of 45 blackgram genotypes based on D2 values**

| Cluster Group | No. of genotype | List of genotypes |
|---|---|---|
| Cluster I | 19 | TBG - 104, IPU - 99, PKRU - 03, IC - 106 - 176, VBN -08, VBN - 11- 16, PKGV - 03, LBG - 623, KU - 321, IPU - 94 - 1, AKU - 14 - 02, IPU - 94 - 2, PU - 11 - 14, IPU - 99 - 18, SEKHAR - 2 (CHECK), TU - 99 - 2, UH - 85 - 2, PU - 31 &PLU - 103 |
| Cluster II | 15 | PL - 416, PDU - 1, BGP - 21- 28, PLU - 856, AKU - 13- 15, IPU - 99 - 16, PLU - 86 -C, JU - 2, BG - 369, DH - 85 - 2, LBG - 628, T9, PLU- 547, TLU-328 & PLU- 708 |
| Cluster III | 6 | PLU- 302, AZAD - 1, PLU - 570, LBG - 648, TLU - 32 - 6 & DH - 85 - 5 |
| Cluster IV | 1 | PLU- 1016 |
| Cluster V | 3 | KC - 153, ADT - 3 & KU - 96- 14 |
| Cluster VI | 1 | SNTP - 02 |

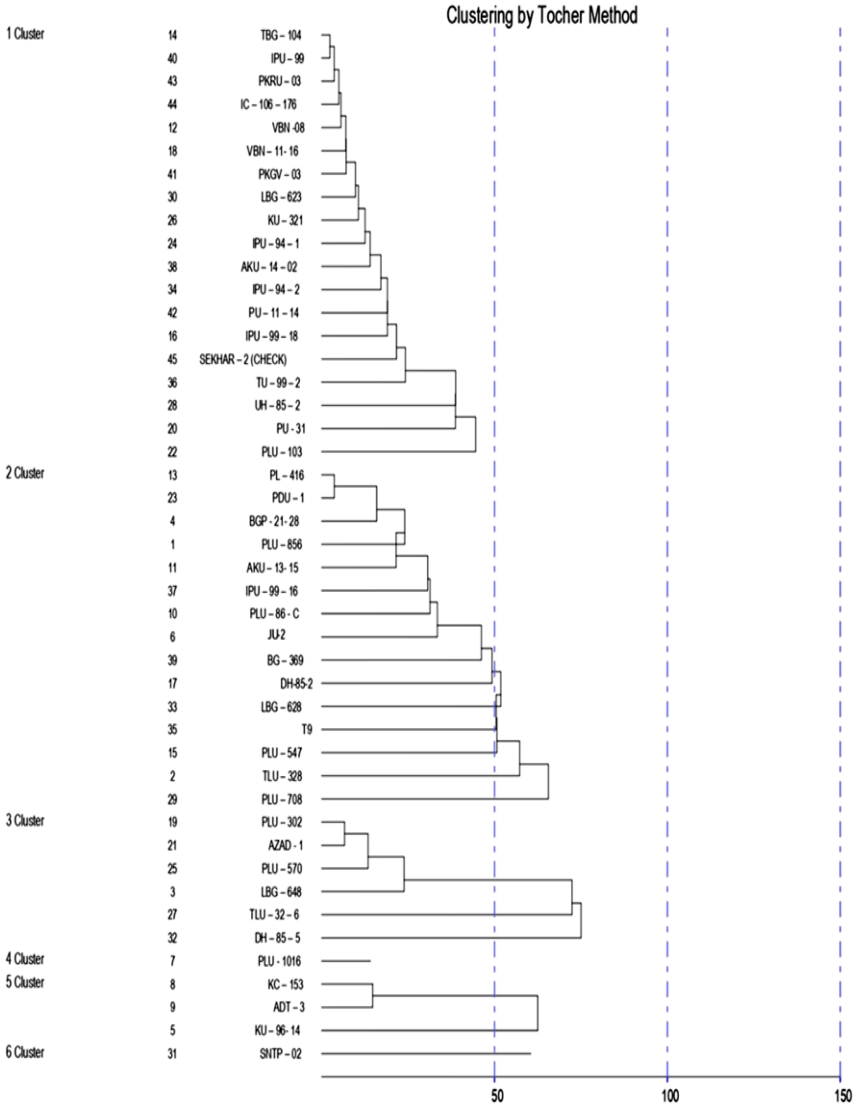

Fig. 2. **Dendrogram depicting clustering of blackgram genotypes into 6 cluster**

**Table 5. Average intra and inter cluster distance (D2) values for six clusters in 45 black gram genotypes**

| | **Cluster Distances** | | | | | |
|---|---|---|---|---|---|---|
| | **Cluster 1** | **Cluster 2** | **Cluster 3** | **Cluster 4** | **Cluster 5** | **Cluster 6** |
| Cluster I | 24.83 | 392.43 | 135.97 | 465.11 | 761.71 | 221.34 |
| Cluster II | | 51.99 | 164.36 | 81.02 | 137.12 | 140.76 |
| Cluster III | | | 63.68 | 177.82 | 441.63 | 120.26 |
| Cluster IV | | | | 0.00 | 207.00 | 222.20 |
| Cluster V | | | | | 67.46 | 307.01 |
| Cluster VI | | | | | | 0.00 |

**Table 6. Mean values of the Six clusters for 13 characters in black gram genotypes**

| | **Cluster Means: Tocher Method** | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | **Days to 50% flowering** | **Days to 50% pod setting** | **Days to maturity** | **Plant height** | **Number of primary branches** | **Number of clusters per plant** | **Number of pods per plant** | **Pod Length** | **Number of seeds per pod** | **Seed index** | **Harvest index** | **Biological yield** | **Seed yield per plant** |
| Cluster I | 43.14 | 55.16 | 78.00 | 37.38 | 3.43 | 3.96 | 12.35 | 3.83 | 4.97 | 3.85 | 33.30 | 12.19 | 3.82 |
| Cluster II | 44.87 | 51.87 | 64.24 | 63.61 | 11.63 | 10.84 | 23.04 | 4.08 | 6.15 | 4.31 | 29.13 | 23.92 | 6.92 |
| Cluster III | 47.11 | 53.94 | 65.72 | 54.51 | 7.45 | 6.20 | 14.31 | 4.15 | 5.90 | 4.42 | 29.74 | 21.61 | 6.30 |
| Cluster IV | 46.33 | 54.00 | 59.67 | 81.33 | 12.53 | 11.40 | 12.93 | 3.69 | 5.73 | 5.40 | 26.82 | 26.92 | 7.22 |
| Cluster V | 45.78 | 53.44 | 63.78 | 61.82 | 14.91 | 15.13 | 30.38 | 4.20 | 5.98 | 4.83 | 30.15 | 23.15 | 6.95 |
| Cluster VI | 40.00 | 50.00 | 62.00 | 50.86 | 4.73 | 10.13 | 25.20 | 4.03 | 6.20 | 6.10 | 37.31 | 19.94 | 7.44 |

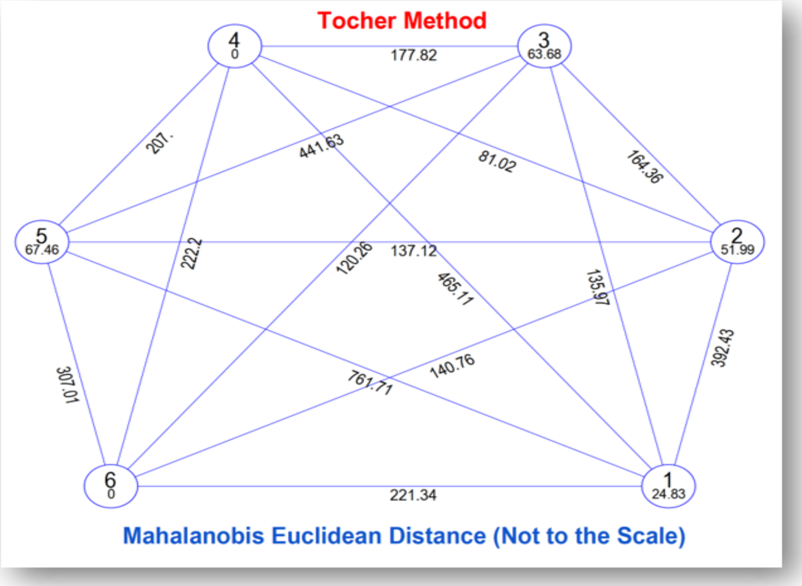

**Fig. 3. Cluster diagram depicting intra and inter-cluster distances. (The figure is not exactly to the scale)**

**Table 7. Per cent contribution towards divergence of 13 different characters of blackgram genotypes**

| Sl.No. | Source | Contribution % | Times ranked 1st |
|---|---|---|---|
| 1 | Days to 50% flowering | 0.30 | 3 |
| 2 | Days to 50% pod setting | 4.92 | 49 |
| 3 | Days to maturity | 4.00 | 40 |
| 4 | Plant height | 6.53 | 65 |
| 5 | Number of primary branches | 5.76 | 57 |
| 6 | Number of clusters per plant | 8.45 | 84 |
| 7 | Number of pods per plant | 9.81 | 97 |
| 8 | Pod length | 2.30 | 23 |
| 9 | Number of seeds per pod | 6.54 | 65 |
| 10 | Seed index | 5.64 | 56 |
| 11 | Harvest index | 10.21 | 101 |
| 12 | Biological yield | 14.54 | 144 |
| 13 | Seed yield per plant | 21.00 | 208 |

(14.54%), harvest index (10.21%), number of pods per plant (9.81%), number of clusters (8.46%), plant height (6.53%).

## 4. CONCLUSION

It is concluded that analysis of variance showed significant variation to all the characters. Among 45 genotypes, SNTP-02(7.44) and PL -416 (7.353), genotypes were found to be superior for seed yield per plant over the check (SEKHAR – 2). High to moderate estimates of GCV, PCV, high heritability coupled with high genetic advance as percent mean were recorded for Number of cluster per plant, number of pod per plant, number of primary branches indicating predominance of additive gene effects and possibilities of effective selection for genetic improvement of the characters. Cluster V and I (761.71), cluster IV and I (465.1) had high inter cluster distances, were most diverse from each other and hybridization between genotypes in these clusters provide a broad spectrum of variability in segregation. As a result, these genotypes could be employed as parents in a future hybridization experiment to create attractive genotypes for seed yield improvement in black gram.

## COMPETING INTERESTS

Authors have declared that no competing interests exist.

## REFERENCES

1. Parveen S, Sekhar MR, Reddy DM, Sudhakar P. Correlation and path coefficient analysis for yield and yield Components in blackgram (*Vigna mungo* (L.) Hepper). International Journal of Applied Biology and Pharmaceutical Technology. 2011;2:616-623.
2. Jayamani P, Sathya M. Genetic diversity in pod characters in blackgram. Legume Research. 2013;36(3):220-223.
3. Johnson HW, Bernard RL. Soybean genetics and breeding. Advances in Agronomy. 1955;14: 149-221.
4. Mahalanobis PC. On the Generalized distance in statistics. In: Proceedings of National Academy of Science, India. 1936;49-55.
5. Singh RK, Chaudhary BD. Biometrical methods in quantitative genetic analysis. Kalyani Publisher, New Delhi. 1985;57-78.
6. Rao CR. Advanced Satistical method in Biometric Research. Ednl. John Wiley and Sons, NewYork. 1952;36-38.
7. Singh RK, Chaudhary BD. Biometrical methods in quantitative genetic analysis. New Delhi. Kalyani Publication. 1977; 318.
8. Panigrahi KK, Mohanty A, Baisakh B. Genetic divergence, variability and character association in landraces of blackgram (*Vigna mungo* [L.] Hepper) from Odisha. Journal of Crop and Weed. 2014;10(2):155-165.
9. Deepshikha Lavanya GR, Kumar S. Assessment of genetic variability for yield and its contributing traits in black gram. Trends in Biosciences. 2014;7: 2835-2838.
10. Priyanka S, Rangaiah S, Showkath Babu BM. Genetic variability estimates of quantitative and qualitative traits in blackgram. International Journal of Agriculture Sciences. 2016;40: 1821-1824.
11. Gowsalya P, Kumaresan D, Packiaraj D, Kannan JR, Bapu JR. Genetic variability and character association for biometrical traits in blackgram (*Vigna mungo* (L.) Hepper). Electronic Journal of Plant Breeding. 2016;7(2):317-324.
12. Nashra Aftab, Lal GM, Ashish Sheera, Chandra Bose N , Avneesh M. Tripathi. Evaluation of Genetic Variability in Blackgram (*Vigna mungo* L. Hepper) Germplasm Journal of Plant Development Sciences. 2018;10(8):445-452.
13. Singh KA, Gautam RK, Singh PK, Kumar K, Kumar N, Swain S, Dam RS. Estimation of genetic variability and association analysis in the indigenous landraces of Urdbean (*Vigna mungo* (L.) Hepper) of Andaman Islands. Vegetos. 2014;27(1): 113-122.
14. Kuralarasan V, Vanniarajan C, Kanchana S, Veni K, Anandhi Lavanya S. Genetic divergence, heritability and genetic advance in mutant lines of urdbean [*Vigna mungo* (L.) Hepper]. Legume Res. 2018 ;41:833-836.

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