**Original Research Article**

**Assessment of genetic diversity in black gram [*Vigna mungo (*L) Hepper] genotypes**

**ABSTRACT**

The present investigation sought to evaluate the genetic diversity and determine well-suited genotypes for crossbreeding initiatives with the goal of augmenting the desirable traits of black gram [*Vigna mungo (*L) Hepper] commonly referred to ‘urd bean’ in India. Twenty-seven genotypes were evaluated for various quantitative and biochemical traits during late rabi season of 2020 and statistical analysis was conducted to estimate genetic parameters and determine divergence. Significant variations were observed among the genotypes for maximum traits studied, indicating wide genetic diversity. Phenotypic observation revealed the influence of both genotype and environment on the expression of traits. Traits *namely* total soluble sugars, protein content , yield per plot , yield per plant, number of pods per plant, number of pods per cluster showed high heritability coupled with high genetic advance. The result provides valuable insights for breeders to develop selection programme for genetic improvement of black gram. Additionally, clustering analysis based on D2 distance categorized the genotypes into 5 distinct clusters, highlighting their unique characteristics. The study identified traits contributing significantly to divergence, with yield per plot (31.34%) showing the highest contribution. Hybridization between the genotypes of cluster III and cluster IV may produce a wide range of variability for selection and may produce better transgressive segregants. Genotypes of cluster I could be used as source for earliness.

**Key words**: Blackgram, Diversity, Heritability, Variability, Yield

**Introduction**

“Pulses are the important source of dietary protein in vegetarian diet. Blackgram (*Vigna mungo* (L.) Hepper) commonly known as ‘urd bean ‘in India, is one of the important short durations and self-pollinated, diploid (2n=2x=22) legume crop with a small genomic size of 0.56 g/PC (574 Mbp)” (Gupta and Gopalakrishna, 2009) “belongs to the family Leguminosae and domesticated from *Vigna mungo varsilvestris”* (Lukoki *et al.*1980). “It gives vegetable protein as well as cereal based diet that contain 26% protein, which is three times more than that of cereals and other vitamins. Apart from protein, it is also a source of carbohydrates (62-65%), fibre (3.5-4.5%), oil (0.5-1.5%), amino acids (lysine), vitamins, iron (9mg/100g) and phosphoric acid (385mg/100g)” (Sohel *et al.,* 2016). “India is considered to be largest producer as well consumer of black gram” (Gnanasekaran *et al.,* 2024). During 2022–2023 more than 2.63 Mt of black gram was produced from 4 Mha in India with an average unit production of 657 kg/ha (Ministry of Agriculture 2022–2023). Despite of its importance, blackgram cultivation is ignored as minimum attention is given towards its genetic improvement. There are several reasons for the low production of crop like of genetic variability, absence of suitable ideotype, susceptibility toward biotic and abiotic stresses and planting in marginal areas of farming. “Main limits in black-gram germplasms enhancement are lack of available genetic variability, absence of appropriate ideotype for different cropping system, low harvest index, susceptibility to stresses, and non-availability of good quality seeds of improved varieties. It is mainly due to repeated usage of limited parents with high degree of similarity in crossing programmes” (Jayamani and Sathya, 2023). “The existence of genetic diversity within and between crop species helps the breeders to select superior genotypes either to directly as new varieties or to be used as parents in hybridization programs” (Nanda *et al.,* 2023). “The knowledge of genetic variability, genotypic and phenotypic coefficients of variability and heritability is helpful for identification of superior genotypes for further exploitation in breeding programs. Success of yield improvement in crops largely depends upon the magnitude and nature of genetic variability present in yield contributing traits” (Johnson *et al.,* 1955). The utility of statistics like Mahalanobis D2 helps to detect the genetic diversity between groups of genotypes and to identify the genotype which can effectively utilised in crop improvement and crossing programmes. Keeping in view of above discussed points the present study was carried out with the objective to investigate genetic variability and heritability and to identify superior black gram genotypes for further exploitation in breeding programme.

**Materials and Methods**

The present investigation was carried out during late Rabi season 2020 at Bagusala Farm, of M.S. Swaminathan School of Agriculture, Centurion University of Technology and Management, Paralakhemundi, Odisha (23.39 0 N and 87. 42 0 E). The experimental material consists of 27 black gram genotypes collected from Regional Agricultural Research Station, Lam, Guntur Andhra Pradesh and sown in Randomized Complete Block Design in three replications. The plot size was 4m long having 4 rows and Row to row and Plant to plant spacing were maintained at 30cm and 10 cm respectively. To get healthy crops standard production techniques were followed. Data were recorded from five randomly selected plants for 14 quantitative traits *namely* plant height (cm), number of primary branches, number of secondary branches, days to maturity, days to 50% flowering, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod, pod weight (g), pod length (cm), yield per plant (g), 100 seed weight (g), and 2 biochemical traits *namely* total soluble sugars (%) and protein content (mg/g). Variability for different characters was estimated by the formula suggested by Burton (1952), while calculating the heritability, genetic advance as percent of mean the formulae given by Johnson *et al.,* (1955) was followed. Mahalanobis (1936) D2 statics was used to quantify the degree of divergence and Tocher’s method was used to group genotypes in cluster following (Rao 1952). Biochemical parameters namely total soluble sugars estimated by using anthrone as the main ingredient was proposed by Dreywood in 1946, Total protein content by using Lowry’s method was proposed by Lowry’s *et.al* in 1951.

**Results and Discussion**

Analysis of variance revealed that significant differences were existed in genotype studied and it is represented in Table 1. High significant amount of variability was recorded for traits namely yield per plot, plant height, days to 50% flowering, days to maturity, number of pods per plant, pod weight, yield per plant, carbohydrate content and protein content while 100 seed weight and number of clusters per plant showed significant differences among the genotypes. The variability on genetic parameter for 14 quantitative traits and 2 biochemical traits is presented in Table 2. The Phenotypic Coefficient of Variation was higher than the Genotypic Coefficient of Variation for all the characters under study which indicate that environmental factors influencing the characters studied. The same findings were reported by Priyanga *et al.* (2016), Hemalatha *et al.* (2017), Kumar *et al.* (2020) and Gomathi *et al.* (2021). The estimate of GCV and PCV were categorised as low (10%), moderate (10-20%) and high (more than 20%) as suggested by Burton and Devane (1953). The estimated GCV and PCV helped in getting a clear understanding of variability present among various genotypes. Higher magnitude of GCV and PCV was recorded for yield per plot (35.11%, 36.36%) followed by total soluble sugars (24.26%, 24.78%), protein content (21.88%, 22.55%) and number of pods per plant (21.54%, 23.53%) These results are in line up with Bharathi *et al.* (2019) and Gnanasekaran *et al.* (2024). and moderate GCV and PCV was recorded for number of secondary branches (16.37%, 18.51%) followed by number of pods per cluster (15.20% 17.97%), Yield per plant (14.92%, 16.11%), number of clusters per plant (12.49%, 14.96%) and 100 seed weight (11.95%, 15.50%). Similar results were observed by Tank *et al.* (2018), indicating that selection could be effective in these characters. Low magnitude of GCV and high moderate PCV was observed in pod weight per plant (9.52%, 13.46%) and number of primary branches (4.09%, 10.62%) and low magnitude of GCV and low magnitude of PCV was observed in Plant height (4.03%, 9.70%) followed by seed per pod (3.98%, 4.86%), days to maturity (3.82%, 4.57%), days to 50% flowering (2.93%, 5.02%) and pod length (1.90%, 5.26%). Indicating minimum variability exist in these traits, but slightly higher PCV than GCV which means less influenced by the environmental factors.

The estimates of heritability in broad sense for yield and attributing characters have been conferred in Table 2. The prediction regarding heritability in broad sense was made as suggested by Robinson (1949) for low (<50%), moderate (50-70%) and high (>70%) heritability estimates. In the present study, high heritability was observed, total soluble sugar (95%) followed by protein content (94%), yield per plot (93%), yield per plant (85%) and number of pods per plant (83%) and number of secondary branches s (78%) and number of pods per cluster (71%) similar findings were reported by Tank *et al.,* (2018) and Gowsalya *et al.* (2016). Moderate heritability was observed for days to maturity and number of clusters per plant (69%) followed by seed per pod (67%) and 100 seed weight (59 %). Low estimates of heritability were observed for pod weight per plant (48%), days to fifty percent flowering (34%), plant height (17%), number of primary branches (14%) and pod length (13%). Similar findings were reported by Gnanasekaran *et al.* (2024).As per reference Johnson *et al*. genetic advance as percentage of mean (GAM) was grouped if the value ranged from 0-10% are considered low, 10-20% are moderate and above are high. genetic advantage as percentage of mean were recorded higher value for yield per plot (69.86%), total soluble sugar (48.94%), followed by protein content (43.73%), number of pods per plant (40.64%) yield per plant (28.46%) and number of secondary branches (29.82%) and number of pod per cluster (21.47%) and moderate value for 100 seed weight 18.99%) and pod weight per plant (13.69%) whereas low for days to maturity (6.59%), days to fifty percent flowering (3.52%), plant height (3.45%), number of primary branches (3.24%) pod length (1.41%)these findings are similar with the result reported by Priya *et al.*(2018). High heritability coupled with high genetic advance were recorded for total soluble sugars (95%, 48.94%) and protein content (94%, 43.73%) yield per plot (93%, 69.86%), yield per plant (93%, 69.86%), number of pods per plant (83%, 40.64%), number of pods per cluster (71%, 26.28%). These results are in accordance with Kumawat *et al*. (2024), Panigrahi *et al.* (2014) and Gowsalya *et al.* (2016) indicating the additive gene control over these traits and could be rewarded for selection for further improvement in breeding programs. Moderate heritability coupled with high genetic advance was observed in number of clusters per pod (69%, 21.47%). moderate heritability coupled with moderate genetic advance was observed in 100 seed weight (59%, 18.99%). Present study concluded on the basis of high heritability coupled with high genetic advance as per cent of mean were recorded for yield per plot, yield per plant, number of pods per plant, number of pods per cluster and moderate heritability coupled with high genetic advance was observed in number of cluster per pod and moderate heritability coupled with moderate genetic advance was observed in 100 seed weight and selection of these traits was rewarded for selection for further improvement in breeding programs.

“Genetic divergence analysis separated the studied black gram 27 genotypes into 5 clusters by estimated D2 values as the square of distances” (Mahalanobis, 1936; Rao 1952) in Table 3. and Fig.1, among the five clusters Cluster I and cluster II were the largest clusters, each having 6 genotypes and remaining clusters, cluster III, cluster IV and cluster V were consisting of 5 genotypes. The intra and inter cluster D2 values are presented in Table 4. The intra cluster distances ranges from (53.32 to 82.77). The cluster V had the maximum D2 value (82.77) followed by the cluster III (78.30). The inter cluster distances revealed that maximum inter cluster distance was recorded between cluster III and cluster IV (199.71) and the minimum distance was recorded between cluster I and cluster III (97.06). The maximum inter cluster distance was observed in cluster III and cluster IV that means exhibiting wide divergence among genotypes. Selection of genotypes from these clusters results in achieving novel recombinants. Similar findings were earlier reported by Pangrahi *et al.* (2014). suggesting the selection in these clusters maybe used as a parent for further hybridization programme to develop desirable type which results in transgressive segregants while D2 value of cluster I and III suggested that genotypes in one cluster is close proximity with genotypes of other clusters in pair. Hence, genotypes from both clusters may not be useful in breeding programmes this is in agreement with Konda *et al*. (2007). The relative contribution of characters towards divergence in black gram is represented in table 5. The maximum percentage of genetic divergence was contributed by yield per plot (31.34%) followed by protein content (14.25%), total soluble sugars (11.11%), number of secondary branches (5.13%), yield per plant (4.84%), number of clusters per plant (4.27%), number of pods per plant (2.56%), days to maturity (1.42%), seeds per pod (0.85%) and pod weight (0.28%).Highest contribution towards genetic divergence was reported in protein content, total soluble sugars, number of secondary branches, yield per plant and number of clusters per plant were reported earlier by Chippy *et al.* (2021).

The cluster mean of all characters studied in black gram is tabulated in Table 6. It revealed that cluster I with 6 genotypes (LBG-979, TAU-1, LBG-975, BIVT-RU-18-24, PU-1530, LBG-974) showed lowest mean value for days to 50% flowering, days to maturity and maximum mean value for yield per plant hence, these genotypes could be used as source as earliness. The highest mean value was recorded by cluster II for seeds per pod and yield per plot (248.94g); Cluster III for number of pods per plant (22.04), number of pods per cluster (3.80), pod length (4.38), clusters per plant (5.81). Cluster IV recorded maximum mean value for plant height (15.80cm) days to maturity (69.13), total soluble sugars (54.98%), seeds per pod (5.97), pod weight per plant (10.44g) and days to 50% flowering (37.20); cluster V recorded maximum mean value for number of primary branches (5.24), number of secondary branches (3.65) and protein content (7.71mg/g).

**Conclusion**

It is well known that crosses between divergent parents normally produce greater erotic effects than between closely related ones. Considering the importance of genetic parameters, genetic distance and relative contribution of characters towards total divergence it may be concluded from the present investigation, that the traits *namely* total soluble sugars, protein content , yield per plot , yield per plant, number of pods per plant, number of pods per cluster showed high heritability coupled with high genetic advance, indicating the control of additive gene action over these traits and could be rewarded for selection for further improvement in breeding programs and further study. The hybridization between the genotypes of cluster III (RU-17-28, BIVT-RU-29, BIVT-RU-18-21, BIVT-RU-18-23, IPU-2-43) and cluster IV (BIVT-RU-18-20, BIVT-RU-18-26, BIVT-RU-18-B4, BIVT-RU-18-32, TBG-104) may produce a wide range of variability for selection and may produce better transgressive segregants. Six genotypes (LBG-979, TAU-1, LBG-975, BIVT-RU-18-24, PU-1530, LBG-974) of cluster I could be used as source for earliness.

**Disclaimer (Artificial intelligence)**

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text to image generators have been used during the writing or editing of this manuscript.

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**Table 1:** Analysis of variance of quantitative and biochemical traits of blackgram genotypes

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **S.NO** | **Characters** | **Mean sum of squares** | | |
| **Source of variation** | **Replication** | **Genotype** | **Error** |
| **Degrees of freedom** | **2** | **26** | **52** |
| 1 | Plant height(cm) | 1.19 | 3.04\*\* | 1.87 |
| 2 | No. of primary branches | 2.82 | 0.36 | 0.23 |
| 3 | No of secondary branches | 0.61 | 0.84 | 0.07 |
| 4 | Days to 50% flowering | 10.08 | 5.64\*\* | 2.21 |
| 5 | Days to maturity | 33.92 | 22.62\*\* | 2.83 |
| 6 | No. of clusters per plant | 2.34 | 1.54\* | 0.19 |
| 7 | No. of pods per cluster | 0.59 | 0.99 | 0.11 |
| 8 | No. of pods per plant | 32.27 | 55.36\*\* | 3.34 |
| 9 | Pod length (cm) | 0.02 | 0.06 | 0.04 |
| 10 | Pod weight per plant (g) | 1.72 | 3.21\*\* | 0.83 |
| 11 | No. of Seeds per pod | 0.008 | 0.18 | 0.02 |
| 12 | 100 seed weight(g) | 0.03 | 1.23\* | 0.22 |
| 13 | Yield per plant (g) | 0.14 | 4.15\*\* | 0.21 |
| 14 | Carbohydrate content (%) | 6.40 | 307.69\*\* | 4.35 |
| 15 | Protein content(mg/g) | 0.32 | 6.91\*\* | 0.14 |
| 16 | Yield per plot | 346.90 | 10123.26\*\* | 237.76 |

**Table 2:** Genetic components of variance various quantitative and biochemical traits of blackgram genotypes

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Parameters** | **σ2 G** | **σ2 P** | **GCV (%)** | **PCV (%)** | **h² (broad sense) %** | **GA as % of Mean** |
|
| Plant height (cm) | 0.39 | 2.26 | 4.03 | 9.70 | 17 | 3.45 |
| Number of primary branches | 0.04 | 0.28 | 4.09 | 10.62 | 14 | 3.24 |
| Number of secondary branches | 0.25 | 0.33 | 16.37 | 18.51 | 78 | 29.82 |
| Days to 50% flowering | 1.14 | 3.35 | 2.93 | 5.02 | 34 | 3.52 |
| Days to maturity | 6.59 | 9.43 | 3.82 | 4.57 | 69 | 6.59 |
| Number of clusters per plant | 0.45 | 0.64 | 12.49 | 14.96 | 69 | 21.47 |
| Number of pods per cluster | 0.29 | 0.40 | 15.20 | 17.97 | 71 | 26.48 |
| Number of pods per plant | 17.33 | 20.68 | 21.54 | 23.53 | 83 | 40.64 |
| Pod length (cm) | 0.006 | 0.005 | 1.90 | 5.26 | 13 | 1.41 |
| Pod weight per plant (g) | 0.79 | 1.62 | 9.52 | 13.64 | 48 | 13.69 |
| Seeds per pod | 0.05 | 0.08 | 3.98 | 4.86 | 67 | 6.71 |
| 100 seed weight (g) | 0.33 | 0.56 | 11.95 | 15.50 | 59 | 18.99 |
| Yield per plant (g) | 1.31 | 1.52 | 14.92 | 16.11 | 85 | 28.46 |
| Total soluble sugars (%) | 101.11 | 105.46 | 24.26 | 24.78 | 95 | 48.94 |
| Protein content (mg/g) | 2.25 | 2.40 | 21.88 | 22.55 | 94 | 43.73 |
| Yield per plot (g) | 3295.16 | 3532.92 | 35.11 | 36.36 | 93 | 69.86 |

**Table 3**: Clustering pattern of studied genotypes in black gram

|  |  |  |
| --- | --- | --- |
| Cluster | Number of genotypes | Genotypes |
| I | 6 | LBG-979, TAU-1, LBG-975, BIVT-RU-18-24, PU-1530, LBG-974 |
| II | 6 | BIVT-RU-18-30, BIVT-RU-18-33, BIVT-RU-18-22, PU-31, BIVT-RU-18-28, BIVT-RU-18-25 |
| III | 5 | RU-17-28, BIVT-RU-29, BIVT-RU-18-21, BIVT-RU-18-23, IPU-2-43 |
| IV | 5 | BIVT-RU-18-20, BIVT-RU-18-26, BIVT-RU-18-B4, BIVT-RU-18-32, TBG-104 |
| V | 5 | LBG-956, BIVT-RU-18-31, LBG-978, BIVT-RU-18-27, LBG-968 |

**Table: 4** Average intra (diagonal) and inter-cluster (between) distance of blackgram genotypes

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Cluster** | **I** | **II** | **III** | **IV** | **V** |
| **I** | **53.32** | 142.13 | 97.06 | 101.94 | 121.13 |
| **II** |  | **61.63** | 143.08 | 140.52 | 104.91 |
| **III** |  |  | **78.30** | 199.71 | 122.05 |
| **IV** |  |  |  | **72.89** | 171.36 |
| **V** |  |  |  |  | **82.77** |

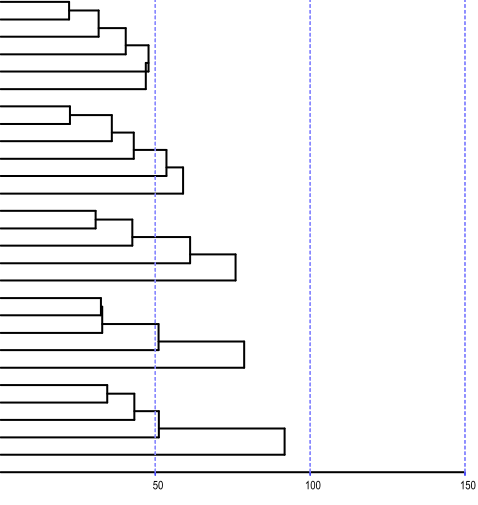
**Table: 5** contributions of characters towards genetic divergence in blackgram genotypes

|  |  |  |  |
| --- | --- | --- | --- |
| **S.No** | **Characters** | **Times ranked 1st** | **Percent contribution** |
| 1 | Plant height (cm) | 0 | 0.001% |
| 2 | Number of primary branches | 0 | 0.001% |
| 3 | Number of secondary branches | 18 | 5.13% |
| 4 | Days to 50% flowering | 0 | 0.001% |
| 5 | Days to maturity | 5 | 1.42% |
| 6 | Number of clusters per plant | 15 | 4.27% |
| 7 | Number of pods per cluster | 0 | 0.001% |
| 8 | Number of pods per plant | 9 | 2.56% |
| 9 | Pod length (cm) | 0 | 0.001% |
| 10 | Pod weight per plant (g) | 1 | 0.28% |
| 11 | Seeds per pod | 3 | 0.85% |
| 12 | 100 seed weight (g) | 0 | 0.001% |
| 13 | Yield per plant (g) | 17 | 4.84% |
| 14 | Total soluble sugars (%) | 39 | 11.11% |
| 15 | Protein content (mg/g) | 50 | 14.25% |
| 16 | Yield per plot (g) | 110 | 31.34% |

**Table: 6** cluster wise Mean performance various quantitative and biochemical traits of blackgram genotypes

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Parameters | Cluster I | Cluster II | Cluster III | Cluster IV | Cluster V |
| Plant height (cm) | 15.45 | 15.43 | 15.79 | 15.80 | 15.03 |
| Number of primary branches | 4.91 | 5.06 | 4.88 | 4.85 | 5.24 |
| Number of secondary branches | 3.26 | 2.88 | 2.87 | 2.88 | 3.65 |
| Days to 50% flowering | 35.72 | 37.17 | 35.93 | 37.20 | 36.33 |
| Days to maturity | 64.94 | 68.11 | 67.87 | 69.13 | 65.53 |
| Number of clusters per plant | 5.31 | 5.48 | 5.81 | 5.37 | 4.89 |
| Number of pods per cluster | 3.79 | 3.44 | 3.80 | 3.75 | 2.97 |
| Number of pods per plant | 19.97 | 19.16 | 22.04 | 20.08 | 15.26 |
| Pod length (cm) | 4.35 | 4.29 | 4.38 | 4.31 | 4.29 |
| Pod weight per plant (g) | 9.09 | 9.11 | 9.43 | 10.44 | 8.76 |
| Seeds per pod | 5.94 | 5.85 | 5.79 | 5.97 | 5.62 |
| 100 seed weight (g) | 4.83 | 5.33 | 4.93 | 4.67 | 4.40 |
| Yield per plant (g) | 8.24 | 7.61 | 7.76 | 8.21 | 6.44 |
| Total soluble sugars (%) | 42.94 | 43.48 | 30.96 | 54.98 | 34.13 |
| Protein content (mg/g) | 5.84 | 7.67 | 5.49 | 7.68 | 7.71 |
| Yield per plot (g) | 117.00 | 248.94 | 157.40 | 138.20 | 147.93 |

Clustering by torcher’s method

1Cluster 4

18

2

14

7

1

2Cluster 22

23

17

27

20

21

3Cluster 11

26

15

24

9

4Cluster 13

16

10

12

8

5Cluster 6

25

3

19

5

**Fig 1:** Clustering pattern of the studied genotypes in black gram by Tocher’s method.